# Computational methods in population biology

ECL/PBG 233, Winter 2017

Lecture: Tuesdays 2:10-4:00pm, Wickson 2124

Optional Lab: Thursday 2:10-3:00pm, Wickson 2124

#### Instructors

<u>Email</u> <u>Office</u> <u>Office hours</u>

Marissa Baskett (ESP) mlbaskett@ucdavis.edu Wickson 2112 Wednesdays 2:10pm Sebastian Schreiber (EVE) sschreiber@ucdavis.edu Storer 5348 Mondays 9:30am

### Course description

Numerical methods for simulating population dynamics using the computational software package R. An emphasis will be placed on model formulation and development, theoretical concepts and philosophical principles to guide simulation efforts, and implementing simulations with R. Topics covered include simulation of difference & differential equations, discrete & continuously structured models, stochastic difference equations, discrete & continuous-time Markov processes, and model selection methods. Applications covered include structured population dynamics, spread of diseases, spatial spread of invasive species, population viability analysis, time series analysis of species interactions, and metapopulation and metacommunity dynamics.

**Pre-requisites**: a course in theoretical ecology (e.g., ECL 231 or an equivalent to ESP 121 from your undergraduate institution) or consent of instructor; no programming experience required.

# Course expectations

Readings: There will typically be one required reading per week, intended to provide either background on or an illustration of the models that we will explore numerically in each lecture. Please read each paper before the lecture indicated. The readings will be posted on Canvas (Readings folder under the Files tab). For most weeks, we list one or two chapters from the Encyclopedia of  $Theoretical Ecology^{\dagger}$  that provide a more in depth background on the topic of the week. We encourage you to read these chapters. In addition, we will post optional supplemental readings to provide additional examples or perspectives on the topics covered in lecture.

Weekly assignments: Each week we will designate a plot or set of plots for you to produce with R code in order for you to practice and apply the topics discussed in lecture (learning by doing is the fastest way to pick up programming). We will make time to start the code and plot(s) during class time and they can be completed during the optional Lab time on Fridays or at home. We expect you to turn in the code and designated plot(s), with captions/explanations, to Canvas before the **start** of the next class.

**Term project:** You will do one project outside class assignments that use the methods we cover. This might be re-creating a figure from a paper, extending an existing analysis, or doing a preliminary analysis related to your research. You will need to turn in your project idea on **Feb. 7th** (uploaded to Canvas **before** class time), and you will present your results to the class during the final exam period, Friday, **March 24th at 3:30-5:30pm**.

**Grade distribution:** To receive a pass in the class, we require that you receive a satisfactory in at least eight of the ten weekly assignments as well as a satisfactory in the term project.

**Optional lab:** The optional lab is intended to be a free time for you to work on our assignments in a structured setting where you can both work together and solicit help from the instructors. We will also briefly review the models covered in the following week's lecture at the start of the optional lab.

**Additional logistics:** All course materials will be available on Canvas. You will need to bring a laptop to class.

## Course outline

| Date                         | Topic   | Readings  |
|------------------------------|---|---|
| Part I: Deterministic models |   |   |
| 1/10                         | Introduction: Philosophy of numerical methodology; basics of programming in R (MB)  | Required: May (2004)  |
| 1/17                         | Discrete-time models I: scalar difference equations; Lyapunov exponents; bifurcation diagrams (MB)  | Required: May (1974) TE $^{\dagger}$ : Single-Species Population Models       |
| 1/24                         | Discrete-time models II: matrix models;<br>multi-species difference equations; sensitivity<br>analysis (MB & SJS)                             | Required: de Kroon et al. (1986)<br>TE: Matrix Models                         |
| 1/31                         | Discrete-time models III: generalized linear models, integral projection models, integrodifference equations (SJS)                            | Required: Merow et al. (2014)<br>TE: Integrodifference Equations              |
| 2/7                          | Continuous-time models: simulating ordinary differential equations; model selection methods (MB)  | Required: Leslie (1957) TE: Ordinary Differential Equations                   |
| Part II: Stochastic models   |   |   |
| 2/14                         | Probabilistic preliminaries: distributions; random variables; maximum likelihood; branching processes (SJS)                                   | Required: Lloyd-Smith et al. (2005)<br>TE: Model Fitting, Branching Processes |
| 2/21                         | Environmental stochasticity I: scalar stochastic difference equations; stationary distributions; quasi-extinction (SJS)                       | Required: McLaughlin et al. (2002)<br>TE: Stochasticity, Environmental        |
| 2/28                         | Environmental stochasticity II: random matrix products; Lyapunov exponents; nonlinear multivariate stochastic difference equations (SJS)      | Required: Boyce et al. (2006)   |
| 3/7                          | Demographic stochasticity I: discrete-time Markov chains; transition matrices; stationarity versus quasi-stationarity; extinction times (SJS) | Required: Melborne and Hastings (2008)<br>TE: Stochasticity, Demographic      |
| 3/14                         | Demographic stochasticity II: continuous  | Required: Alonso et al.   |

 $<sup>^\</sup>dagger Encyclopedia$  of Theoretical Ecology, Editors: Alan Hastings & Louis Gross, University of California Press

TE: SIR Models

time Markov chains; Gillespie's algorithm (MB)