

Preface

Over the past 30 years, one of the most rapidly expanding areas in ecology has been the development of structured population models, where individuals have attributes such as size, age, spatial location, sex, or disease status that affect their interactions and fate. These models can be roughly divided into conceptual models where the effects of biological structure are explored in the simplest possible setting to expose general principles and data-driven models in which the parameters and functions are estimated from observations of actual individuals, allowing inferences about population behavior. By far the most popular data-driven models are matrix projection models, which assume that the population can be divided into discrete classes. Much of the success of matrix models is a consequence of Hal Caswell writing a detailed “how to” book (Caswell 2001, 1st edition 1989) in which he described, with appropriate MATLAB code, how to build and use matrix models.

The Integral Projection Model (IPM), introduced by Easterling et al. (2000), is a generalization of matrix models to cover populations where individuals are classified by continuous traits. An IPM makes full use of hard-won data on the precise state of individuals, without an increase in the number of parameters to estimate; in fact it often needs fewer parameters, especially when the model includes environmental variability. The aim of this book is to do for IPMs what Caswell did for matrix models. We want this book to be useful and accessible to ecologists and evolutionary biologists interested in developing data-driven models for animal and plant populations. IPMs can seem hard as they involve integrals, and the link between data and model, although straightforward, can seem abstract. We hope to demystify IPMs so that they can become the model of choice for populations structured by continuously varying attributes. To do this, we structure the book around real examples of increasing complexity and show how the life cycle of the study organism naturally leads to the appropriate statistical analysis, which in turn leads to the IPM itself. We also provide complete, self-contained R code (R Core Team 2015) to replicate all of the figures and calculations in the book at <https://github.com/ipmbook/first-edition>.

We set out to summarize the state of the art, taking advantage of book format to start from the beginning, and to provide more details, more examples, more practical advice, and (we hope) clearer explanations. But we could not always resist the impulse to go beyond the current literature. Much of Chapters 3 and 9 is new. Chapter 4 takes a new approach to eigenvalue sensitivity analysis. Chapter 10 introduces a general way of putting demographic stochasticity into an IPM and some ideas about fitting IPMs to mark-recapture data that we hope might spur more applications to animal populations (or better yet, spur some statisticians to bemoan our naiveté and come up with something better). And while we were writing, the current literature often went beyond us, so we apologize to everyone whose new papers we ignored in the push to finish this book.

We also apologize to beginning IPM users and to advanced users. Advanced users will find that we start at the beginning, with things they already know. But we take a new approach to some of the first steps, so we hope that you will read the whole book. Beginners will find that we don't stop until we hit the limits of what we know, so we urge you to *not* read the whole book until you've gotten some hands-on experience with IPMs. And we hope that you won't give up completely when you hit something confusing. The start of the next section or chapter will probably be written for you, unless it starts with a warning to the contrary.

It has been just over three years since we started preparing this book. We have been fortunate to receive guidance and support from many friends and colleagues during this time. We have also been very fortunate to work with and learn from many students, postdocs, and other collaborators. The list starts with Philip Dixon (who got this started nearly 20 years ago by posing the question, `histogram:kernel density estimate = matrix projection model:what?`, and helping to answer it) – and it continues to expand. Those who have shaped our thinking over the years include Peter Adler, Ottar Bjørnstad, Ben Bolker, Yvonne Buckley, Hal Caswell, Peter Chesson, Margaret Cochran, Evan Cooch, David Coomes, Tim Coulson, Mick Crawley, Johan Dahlgren, Michael Easterling, Roberto Salguero-Gómez, Edgar González, Peter Grubb, Nelson Hairston Jr., Elze Hesse, Giles Hooker, Eelke Jongejans, Dave Kelly, Patrick Kuss, Jonathan Levine, Svata Louda, Marc Mangel, Jess Metcalf, Sean McMahon, Cory Merow, Heinz Müller-Schärer, Arpat Ozgul, Satu Ramula, Richard Rebarber, Karen Rose, Sebastian Schreiber, Kat Shea, Andy Sheppard, Robin Snyder, Britta Teller, Shripad Tuljapurkar, Lindsay Turnbull, Larry Venable, and really each and every one of our students and postdocs.

Two anonymous reviewers of some early chapter drafts provided advice and much needed encouragement to carry on developing the text. A further three reviewers of the nearly complete manuscript offered yet more encouragement, as well as some valuable and constructive suggestions. Achi Dosanjh, our editor at Springer, has shown great patience throughout the process of taking the book from inception to publication. Parts of the book are based on our published papers, and we thank the reviewers and editors who read our manuscripts and helped us improve them.

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