Preface

I wrote this textbook for a course that I developed for first-year college students intending to study biology at the University of Chicago as a part of curriculum reform initiated by the Master of Biological Sciences Collegiate Division José Quintáns. Biology is changing at a break-neck pace and is becoming ever more reliant on complex computational tools and quantitative models, while the curriculum for biology majors has been largely stuck in the pre-genomics era. This is especially true of the quantitative component, which is traditionally limited to (at most) a year of calculus and a statistics course. This is not enough to even begin to follow the ideas and methods of current research, which heavily relies on stochastic models, differential equations, and computational algorithms.

In the last few years, these challenges have been recognized by the biology community and have resulted in a boom in bio-calculus textbooks and materials. While combining the concepts of calculus (derivatives, integrals, series) with biological applications sounds good, in my view it still doesn't supply the critical missing components mentioned above. In fact, I started out teaching this course using a bio-calculus approach but realized that this severely restricts the range of biological applications that could be discussed. I also found that the traditional mathematics pedagogy of working out problems on paper is not sufficient for addressing many questions of interest. Instead, I realized that computation is the most useful, as well as the most challenging, skill needed for a quantitative understanding of modern biology.

These hard-won empirical observations led me to develop the course and the textbook as a chimeric beast made up of elements

of statistics, probability, Markov models, and differential equations. The thread that holds these pieces together is programming, which enables students to see and experience fairly complex mathematical ideas. Therefore, each chapter in the textbook contains a modeling section, a mathematics section, and computational section, which all reinforce each other and provide different viewpoints on the same concept. Based on my experience, students with no prior programming experience find the first steps to be tough going, but by the end of course they often achieve a level of comfort with basic coding that they find very valuable in their research and education.

As mentioned above, the person who is most responsible for the existence of this book is José Quintáns. He had a vision of a biology curriculum that served the needs of students and firmly believed in the necessity of greater quantitative literacy in this field. He allowed me to develop my courses the way I saw fit, while providing support and guidance when needed, and encouraged me to start writing up my notes as a book. I am greatly indebted to him, so I thank him and wish him a happy and active retirement.

I also want to thank my colleagues in Biological Sciences Collegiate Division for providing an excellent work environment, and in particular Esmael Haddadian and Elizabeth Kovar, who helped me teach this course in earlier iterations. Donald Frederick, a former student who later worked as a TA and then served as computer lab director for the course, helped me greatly with finding the right approach for the computational assignments. I also thank all of the TAs over the years, whose contributions and feedback have helped shape the course: Colin Pesyna, Chris Bun, Lamont Samuels, Pooya Hatami, Denis Pankratov, Sandra Fernandez, Negar Mirsattari, Mladen Rasic, Kristen Voorhies, Tim Armstrong, Erik Bodzsar, Alexander Ostapenko, Tasneem Amina, Jason McCreery, Andrea Garofalo, Davis Bennet, Aleks Penev, Kirstie Wade, Sven Auhagen, Sneha Popley, Sobha Naderi, Matthew Battifarano, Brad Cohn, Adam Filipowicz, Hunter Chase, Erika Dunn-Weiss, Charles Frye, and Lynda Lin-Shiu.

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This book was written and typeset using a number of open-source tools, so I would like to thank the developers and the communities that maintain and improve these phenomenal resources and keep them available to all. I use the R language `https://www.r-project.org/` for programming and generating many of the figures in the text and R Studio `https://www.rstudio.com/` as the user-friendly interface for working with R. The manuscript was typeset using LaTeX `https://www.latex-project.org/` with the MacTeX distribution `https://tug.org/mactex/` and the TeXShop front end `http://pages.uoregon.edu/koch/texshop/obtaining.html`. The combination of R and LaTeX was done using the knitr package `http://yihui.name/knitr/` and many of the figures were generated using the TikZ graphics package `http://www.texample.net/tikz/`. I also thank the biomathematics community and specifically acknowledge the new QUBES hub `https://qubeshub.org/` for providing a repository for teaching resources and for connecting colleagues teaching at the interface of mathematics, computation, and biology.

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