



Capturing conservation in the post-genomics era: a book review of “Conservation and the Genomics of Populations.”

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Abstract

Conservation genetics is a relatively new discipline, and yet has rapidly evolved in the last decade with massive advances in sequencing technologies. Here, we review the newest edition of an influential textbook in the field, “Conservation and the Genomics of Populations”, which seeks to bridge the transition from population genetics to genomics and its application to conservation management. This textbook—complete with 24 chapters (one completely new), 25 guest boxes, and two new authors over the previous edition—navigates the rich and sometimes complex history of conservation and population genetics, while also providing a comprehensive catalog of how genomics broadens our understanding of diversity in a changing world. Despite some sections requiring an advanced understanding of population genetic theory, we foresee this text being used as a reference for conservation geneticists and for teaching upper level undergraduate or graduate students. While we anticipate the field of conservation genetics will continue to rapidly advance with new technologies, this textbook provides a strong foundation of population genetics, while also celebrating the new horizon of genomics for conservation management.

Keywords Conservation biology · Conservation genetics · Conservation genomics · Wildlife · Forestry · Fisheries · Management

Introduction

Conservation genetics—a discipline focused on using molecular tools to inform the conservation and management of threatened species and ecosystems—has a recent history. This interdisciplinary field emerged in the 1970s, beginning

with articles on the merits of preserving genetic diversity (Frankel 1970, 1974) followed by empirical studies (e.g., Bonnell and Selander 1974; Gartside et al. 1977). Discipline-focused journals, like *Molecular Ecology* (est. 1992) and *Conservation Genetics* (est. 2000) emerged at the turn of the twenty-first century. Comprehensive textbooks written by foundational figures in the field were developed, including “An Introduction to Conservation Genetics” (Frankham et al., 2002, 2010) and “Conservation and the Genetics of Populations” (Allendorf and Luikart 2006; Allendorf et al. 2013).

Conservation genetics is experiencing rapid change due to unprecedented advances in high-throughput sequencing technologies (Hohenlohe et al. 2021). What began as a discipline that uses a handful of genetic markers has advanced towards using many thousands of genome-wide variants, transcriptomes, and epigenomes. This year, a new edition of an established textbook has emerged to capture this transition from genetics to genomics: “*Conservation and the Genomics of Populations*” (Allendorf et al. 2022). Here, we provide a review of this textbook, a comparison to other textbooks in the field, and the merits of its use in teaching, research, and conservation management.

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Conservation and the Genomics of Populations

Book overview

“[Conservation and the Genomics of Populations](#)” is the third edition of the influential textbook, with a slight name change (‘genetics’ to ‘genomics’) to signal recent advancements in the field. While the original textbook leveraged the expertise of two prominent researchers in the field (Allendorf and Luikart), subsequent editions expanded the authorship, including Funk, Aitken, and Byrne in the current edition. The book is divided into four sections: *Introduction*, *Mechanisms of Evolutionary Change*, *Evolutionary Responses to Anthropogenic Change*, and *Conservation and Management*. The *Introduction* gives a broad overview of the history of the field and the molecular tools used, from earlier methods such as allozymes, to newer methods leveraging next-generation sequencing. *Mechanisms of Evolutionary Change* provides a comprehensive treatment of the theory and mathematics underlying population genetics, with some application to new genomic technologies. *Evolutionary Responses to Anthropogenic Change* explores how molecular tools have been used to understand hybridization, invasive species, exploitation, and climate change. Finally, *Conservation and Management* examines clear examples of genetic and genomic application to management (e.g., inbreeding, taxonomic units, and connectivity). This textbook is longer than previous editions, adding new text to chapters, new guest boxes, and two additional chapters compared to the last book. An important addition is a final, new chapter that outlines the gap between genetic research and its implementation to conservation management—coined the ‘conservation genomics gap’ by Shafer et al. (2015)—and offers practical next steps towards closing the gap for academics.

Targeted review

“[Conservation and the Genomics of Populations](#)” benefits from the authors’ extensive backgrounds in population genetics applied to real-world conservation problems. This textbook delivers a comprehensive take on population genetics theory, conservation application, and how these concepts bridge into new genomic technologies. A strength of the text are the plentiful boxes highlighting recent research and guest boxes in each chapter that provide real-world examples of genetics and genomics in conservation biology. We found these boxes to be engaging, representative of diverse taxa (e.g., plants, invertebrates, and vertebrates),

and demonstrative of chapter concepts for enhanced comprehension.

The analysis and interpretation of genomic data relies on the theory and practice of population genetics. As such, the authors were explicit about the need to cover population genetics theory, and they dedicated much of the text to doing so. Part II of this text (*Mechanisms of Evolutionary Change*) included a comprehensive treatment of population genetic theory that may be challenging for readers without an advanced understanding of mathematics and genetics. Further, we suggest Part II could have been better connected with the following chapters on conservation genomic application. For instance, many researchers face decisions about the filtering (e.g., minor allele frequency cut-offs, pruning for gametic disequilibrium, etc.) and analysis of next generation sequencing data that can have significant impacts on downstream conclusions. A significant gap in the field of conservation genetics is the lack of standard practices for these bioinformatic decisions. Because Parts III and IV of this book tackle different conservation questions (e.g., hybridization, inbreeding, local adaptation), there is an opportunity to highlight how population genetics theory can be appropriately applied to genomic data, and the different questions that are now tractable with these data. This would provide more cohesion between different sections of the book, and ensure the audience receives the ‘genomics’ promise of the book title.

This textbook generated good discussion amongst us regarding the nuanced differences between genetics and genomics, and how non-genetics experts might interpret these differences. Given the advancements in the field over the last two decades and the substantial overhaul of new literature in this edition, we appreciate why the authors incorporated genomics into the title for this new book and anticipate they did so after careful discussion. Still, apart from the glossary, the terms “conservation genetics,” “conservation genomics,” and the nuances between the two are not explicitly defined in the text. We believe there is an opportunity to continue this discussion on standardizing genetic vs. genomic terminology in the literature for improved understanding amongst geneticist and non-geneticist collaborators alike. This would make a great guest box in the next edition of the textbook.

What distinguishes conservation genetics from population genetics is its application to management. We were delighted to see an entire chapter dedicated to conservation science and practice and applaud guest author Helen Taylor for providing a thorough summary of the literature available to better bridge the gap between conservation genetic research and policy. The conversation regarding conservation genetic application is ever-evolving, and we anticipate this final chapter might be expanded in future editions to discuss the fair and equitable sharing of data

(Marden et al. 2021; Roche et al. 2022) and new organizations geared towards research and practice integration (e.g., The Coalition for Conservation Genetics; Kershaw et al. 2022). Given the interwoven nature of conservation genetics, we would have liked to have seen a more thorough consideration of work led by social scientists throughout the text, including this final chapter (Bennett et al. 2017; Moon et al. 2019). While there was a brief discussion on incorporating knowledge from Indigenous Peoples and local communities (IPLC) into conservation genetic research, there is an opportunity to expand this section to acknowledge the important advancements in co-developed genetic research with varied stakeholders, including IPLC (e.g., Henson et al. 2021; Rayne et al. 2022), and the ethical and equitable use of DNA from culturally significant species (Collier-Robinson et al. 2019).

This book now acknowledges the complex and discriminatory origins of population genetics, with Box 1.1 exploring the ties between early founders of population genetics (e.g., R.A. Fisher) and the eugenics movement. We are glad to see this recognized in a textbook and feel there is room for even more discussion on diversity, equity, and inclusion in this text. Many guest boxes are authored primarily from continents where conservation genetic research is being conducted the most (e.g., North America, Europe, Australasia), although there were more authors from Africa and Asia than the previous editions (Fig. 1). This bias is pervasive in the entire field of conservation genetics, and science, more generally. Given growth in conservation genetics in Asia, Africa (Anthony et al. 2012), and South America (Torrez-Florez et al. 2018), and the benefit from learning from diverse world views, we expect future textbooks to highlight additional researchers from around the globe.

Comparison to other textbooks

Several textbooks have been dedicated towards the field of conservation genetics (Table 1), with even more available in the field of population genetics. In terms of citation count, the most influential textbooks have been “Conservation and the Genetics/Genomics of Populations” (Allendorf and Lusk 2006; Allendorf et al. 2013, 2022) and “Introduction to Conservation Genetics” (Frankham et al. 2002, 2010). In our view, we see these as comparable textbooks, as they both cover the essentials of population genetics and application to conservation biology; although we would argue that the Frankham textbooks lean more towards application, while the Allendorf textbooks dwell more heavily on population genetic theory. With the current “Conservation and the Genomics of Populations” edition, Allendorf et al. (2022) is one of the few textbooks discussing the incorporation of new genomic technologies for population management.

Target audience

This textbook is foremost a great reference for upper level undergraduate or graduate courses, as well as a good go-to reference for conservation genetic professionals. As mentioned previously, this textbook requires a moderate, and sometimes advanced, understanding of population genetic principles and molecular biology. Fortunately for those with little to no genetic background, chapters in sections II and IV stand alone, and there are references to previous chapters and the glossary if the reader wants to learn more about the underlying theory. As a teaching resource, the plentiful boxes and guest boxes that present recent literature and contextual examples provide great platforms for student discussion and improved comprehension. This textbook provides thorough coverage of older genetic methods, such as allozymes and microsatellites. Although these methods

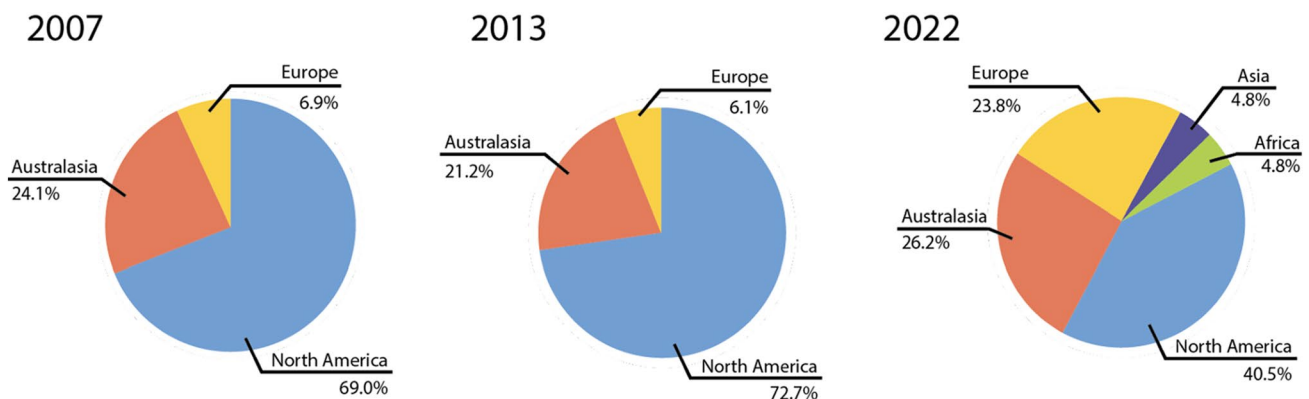


Fig. 1 Distribution of primary and guest box author host institutions across continents for the three editions of this book. Note, North America is defined here as the United States of America and Canada,

as Mexico was not represented. Australasia includes only Australia and New Zealand, as no other countries in Melanesia were represented

Table 1 List of conservation genetics textbooks released over the last four decades

Authors/Editors	Title	Print year(s)
Allendorf, Funk, Aitken, Byrne, Luikart	“Conservation and the Genetics/Genomics of Populations”	2006, 2013, 2022
Kumar, Choudhury, Dayanandan, Khan (Editors)	“Molecular Genetics and Genomics Tools in Biodiversity Conservation”	2022
Hohenlohe, Rajora (Editors)	“Population Genomics: Wildlife”	2021
Frankham, Ballou, Ralls, Eldridge, Dudash, Fenster, Lacy, Sunnucks	“Genetic management of fragmented animal and plant populations”	2017
Hedrick	“Genetics of Populations”	1983, 2000, 2005, 2011
Frankham, Ballou, Briscoe	“Introduction to Conservation Genetics”	2002, 2010
DeWoody, Bickham, Michler, Nichols, Rhodes, and Woeste (Editors)	“Molecular Approaches in Natural Resource Conservation and Management”	2010
Amato, DeSalle, Ryder, Rosenbaum (Editors)	“Conservation Genetics in the Age of Genomics”	2009
Höglund	“Evolutionary Conservation Genetics”	2009
Lowe, Harris, Ashton	“Ecological Genetics: Design, Analysis, and Application”	2004
Conner and Hartl	“A Primer of Ecological Genetics”	2004
Frankham, Ballou, Briscoe	“A Primer of Conservation Genetics”	2004
Smith & Wayne	“Molecular Genetic Approaches in Conservation”	1996
Avise & Hamrick (Editors)	“Conservation Genetics: Case Histories from Nature”	1996
Schondewald-Cox, Chambers, MacBryde, Thomas (Editors)	“Genetics and Conservation”	1983

Although population and ecological genetics is a discipline of its own right, we included the foundational textbook by Hedrick (2011), and Lowe et al. (2004), and as they cover many conservation principles as well. Note, the specification of (Editors) denotes books that are a collection of literature, with different authors writing each chapter

are becoming less popular as next-generation sequencing becomes more accessible, these technologies are still useful (Hauser et al. 2021) and play a vital role in conservation planning worldwide. Thus, this textbook could serve as a reference for managers interested in the comparative strengths and biases of these types of genetic data.

On the horizon

Creating a textbook that encapsulates the conservation genetics in the post-genomics era is no easy task, given the rapidly evolving technologies available to better understand and manage genome-wide diversity. There will certainly be the need for another textbook covering new advancements and even bigger and more complex datasets to come. In the next edition of the textbook, we envision the incorporation of emerging topics in conservation genetics and genomics that are gaining momentum—including the conservation implications of within-species structural variants (Wold et al. 2021), epigenetics (O’Ray et al. 2020), biobanking (Howell et al. 2021, 2022), and the contribution of multi-species interactions to observed phenotypes (i.e., the ‘holobiont’; Carthey et al. 2020, Akoijam and Joshi 2022) Until then, the textbook by Allendorf et al. (2022) successfully captures the long

history of population genetics and the exciting applications of genomics to understand and manage the biodiversity on this planet.

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Declarations

Competing interests The authors declare no competing interests for this work.

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