

Phylogenomics intersects and unites many areas in evolutionary biology including molecular and genomic evolution, systems biology, molecular systematics, phylogeography, conservation genetics, DNA barcoding, and others. Although these disciplines differ from each other in their study questions and methods of data analysis, they all use DNA sequence datasets. Phylogenomics is moving forward at a dizzying pace owing to advances in biotechnology, bioinformatics, and computers. This is reminiscent of what occurred two decades ago when the field of molecular systematics was coming of age. Another major factor that undoubtedly helped spur the growth of molecular systematics was the arrival of *Molecular Systematics*, 2nd edition (Hillis et al. 1996), a book that allowed me (along with countless others) to jump into this exciting field. As phylogenomics has grown substantially since the dawn of the genomics era—in large part due to the advent of next generation sequencing—the time is right for a book that presents the principles and practice of obtaining phylogenomic data.

This book enables beginners to quickly learn the essential concepts and methods of phylogenomic data acquisition so they can confidently and efficiently collect their own datasets. Directed at upper level undergraduate and graduate students, this book also benefits experienced researchers. The inference of gene trees from DNA sequence data represents one of the fundamental aspects of phylogenomic analysis. Accordingly, because

robust gene tree inferences are generally made using longer DNA sequences (e.g., ~200–2,000 base pairs long), this book focuses on methods for obtaining sequences in this length range.

This book is organized as follows. Chapter 1 introduces phylogenomics within a historical context, points out connections between DNA sequence data and gene trees, discusses gene trees versus species trees, and provides an overview of the methods used today to acquire phylogenomic datasets. Chapter 2 describes the landscapes of eukaryotic genomes followed by discussion of molecular processes that govern the evolution of DNA sequences. Chapter 3 continues the discussion about properties of DNA sequence loci by reviewing six common assumptions that pertain to data characteristics before describing the different types of DNA sequence loci used in phylogenomic studies. Chapter 4 covers DNA extraction methods including high-throughput methods. Chapter 5 reviews PCR theory, discusses applications in phylogenomics, and considers high-throughput workflow. Chapter 6 describes Sanger sequencing including high-throughput sequencing. Chapter 7 explains Illumina sequencing technology and how it is used to obtain phylogenomic datasets. Chapter 8 reviews theory and methods for designing novel DNA sequence loci. Finally, Chapter 9 offers a vision of the future in phylogenomic data acquisition.

Most of the information contained in this book can be found elsewhere, but it is worthwhile to

PREFACE

bring it together. This synthesis provides detail including reference to the foundational papers. I hope these discussions will stimulate and direct the reader—especially students—to study these classic papers. Not only will these extra readings provide additional details about the subject at hand, but should also evoke feelings of admiration for those works and thereby generate inspiration and excitement about phylogenomics research. This book is biased toward eukaryotic organisms because of my research experience and interests in vertebrates. Therefore, an apology is in order to my colleagues who study microorganisms though they may still find at least some parts of this book useful.

I am grateful to a number of colleagues who reviewed earlier versions of chapters and provided helpful comments. For their help and encouragement I thank David Blackburn, Steve Donnellan, Andrew Gottscho, Fábio Raposo, Sean Reilly, Todd Schlenke, and especially Ryan Kerney who read four of the chapters. Any remaining errors are my own. I thank my editor Chuck Crumly at Taylor & Francis for suggesting that I undertake this project and for his constant encouragement and patience. I would also like to thank Cynthia Klivecka of Taylor & Francis as well as Mohamed Hameed and Karthick Parthasarathy of Novatechset for their tremendous help to produce the final book. Special thanks go to my doctoral advisor Eric Pianka who first encouraged me to apply molecular data to study evolutionary questions. I am indebted to all my mentors—Samuel Sweet, Jonathan Campbell, Eric Pianka, and Scott Edwards—who have helped me with my career and provided inspiration.

I would also like to thank some colleagues from my graduate school days: Mark and Kris Holder, Tom Wilcox, Marty Badgett, and Todd Schlenke taught me many things in the laboratory and provided much assistance while David Hillis and James Bull generously allowed me to work in their laboratory. One of the pleasures of being a professor is having excellent graduate students who help to inspire me. I thus want to thank my students Andrew Gottscho, Sean Reilly, Igor Rodrigues da Costa, Carla Quijada, and Piero Ruschi. I would like to thank my Humboldt colleagues especially Jacob Varkey, Sharyn Marks, Brian Arbogast, Jeffrey White, John Reiss, Anthony Baker, Julie Davy, Leslie Vandermolen, and Christopher Callahan for their support of my teaching and research. I am also very grateful to my colleagues at the Federal University of Rio de Janeiro for their support and wonderful collaborations. In particular I wish to thank Ronaldo Fernandes, Paulo Buckup, Marcelo Weksler, Jose Pombal Jr, Paulo Passos, Ulisses Caramaschi, Marcos Raposo, Marcelo Britto, and Francisco Prosdocimi. This work was made possible through support from HHMI, Humboldt State University, Dean of Graduate Studies and Research (PR-2) at the Federal University of Rio de Janeiro, and the Brazilian funding agencies CAPES, CNPq, and FAPERJ. My wife Vivian Menezes Leandro provided me with constant support and encouragement, which enabled me complete this book. I dedicate this book to her.

W. BRYAN JENNINGS
Rio de Janeiro, Brazil
December 2016