
Phylogenomics as a separate field was named 15 years ago (Eisen 1998) and appears to be growing exponentially, judging from the number of publication titles containing the term: 27 between 2000 and 2005, 89 between 2006 and 2010, and 76 from 2010 to the middle of 2013 (Web of Science search on 5 July 2013). Phylogenomics covers the intersection of molecular biology and evolution, or perhaps more precisely, phylogenetics and genomics (Eisen and Fraser 2003). We are aware of only one other attempt at a textbook prior to Phylogenomics: A Primer, namely the collection of protocols and resources compiled by Murphy (2008). The primer now offered by Rob DeSalle and Jeffrey Rosenfield is timely and probably eagerly awaited by many professors under pressure to offer courses in phylogenomics. This, at least, was our case.

The book is, according to the authors, intended for “advanced undergraduate students and graduate students in molecular biology, comparative biology, evolution, genomics, biodiversity, and informatics.” These students may enjoy the easy writing style, and with guidance they will benefit from parts of this primer. However, this is not the introduction to the research questions, approaches, and tools of phylogenomics we were hoping for. There is too much phylogenetics and too little genomics.

The first chapter of Phylogenomics starts with a description of the increasing role of bioinformatics in the analysis of DNA data, a half page on microarrays (followed by a long table on microarray data that has no apparent connection to anything), a paragraph on the human genome project, and sections on non-parametric statistical analyses, maximum-likelihood analyses, and Bayesian analyses. All of this is without citations or references to later sections of the book, where these topics are taken up in more depth. Here and throughout, there is frequent name-dropping without any indication about why a person’s work is brought up, when it was done, or how it relates to phylogenomics. Typical examples are: “This is the basis of science; as Immanuel Kant stated, ‘Science is organized knowledge’” (p. 11; this appears to be a confusion with the philosopher Ernst Cassirer); “Recently the entire genomes of Dr Craig Venter and Dr James Watson have been sequenced by using only a fraction of the time and cost expended in the initial human genome projects” (p. 24; there is nothing before or after this sentence about these doctors); and “Interestingly, Charles Darwin and Gregor Mendel lived around the same time, and if communication at the time had been more extensive, then each would have known about the other’s theories and a quicker synthesis of genetics and evolution might have occurred” (p. 36). Actually, communication in Old Europe was not what held things back. Mendel studied The Origin of Species in a German translation of 1863, and in his personal copy he made many notes in the margin. Conversely, Darwin had several opportunities to read Mendel’s results, but seems to have shied away from the mathematical annotations (Galton 2009). We doubt that students will benefit from such haphazard stressing in of the history of biology, especially without mention of years or even relevant centuries.

Chapter 2 covers the structure of DNA, the codon code, protein folding, next-generation sequencing, and microarrays, all in a cursory manner. Chapter 3 covers microevolution, macroevolution, species concepts, and...
have developed a program called SplitsTree” (p. 198).

Chapter 12 is about “adapting population genetics to genomics” (p. 201), and introduces SNPs, Tajima’s D, Fst values, and the Structure software (without any indicated further reading). Chapters 13 and 14 explain codon bias and how to test for selection, using $d_{N}/d_{S}$ ratios; and Chapter 15 introduces the coalescent, and soft and hard selective sweeps.

The final group of chapters (16–18) returns to the focus on genes that characterizes the entire book, although the topic stays reduced to simple presence/absence matrices of genes, while the organization of genes in a genome and gene synteny are not covered (synteny is not in the index). Chapter 17 presents a few large phylogenies, and describes barcoding on six pages, which is hardly a core concern of phylogenomists. The final chapter returns to the topic of microarrays (already discussed in two previous chapters), and devotes three more pages (pp. 314–316) to the calculation of Bremer support, but without referring back to page 158 where Bremer’s decay index was first introduced.

In summary, DeSalle and Rosenfeld have identified an important empty niche and are among the first to occupy it; therein lies their main achievement with *Phylogenomics*. Nevertheless, we were disappointed with the balance of the book, which spends too much time on approaches that are not especially relevant to phylogenomics, while omitting areas at the very core of the new field, such as research on synteny and the filtering-out or use of repetitive DNA. An ideal primer would also provide more information about the online tools used daily by phylogeneticists, have more student exercises that could be used in courses, and provide clearer information about further reading.

REFERENCES


Susanne S. Renner and Mathieu Piednoel, Systematic Botany and Mycology, Department of Biology, Munich University, Münchnerstr. 67, Munich 80338, Germany. E-mails: renner@lmu.de, piednoel@clis.univ-lyon1.fr

Eldredge and Gould’s punctuated equilibrium from 1977, which is one of 23 papers listed in a Further Reading list at the end of this chapter. Since the topics discussed in each chapter are not linked to the Further Reading list by citation or a numbering system, students have no way to find specific papers that introduce or develop a particular topic. The reading lists are therefore of limited use.

Chapter 4 introduces databases relevant for phylogenomics, but never mentions Repbase, the Gypsy database (GyDB), any microsatellite database (e.g., UgMicroSatdb), or the Sequence Read Archive (SLA), which is important for today’s whole genome sequencing, the first step of which requires dealing with millions of reads of repetitive DNA. The Further Reading section for this chapter consists of a mere four papers, published between 1992 and 2009.

Next follow chapters on homology, alignment, and BLAST searches, which are among the best in the book, and also have suggestions for practical exercises using the different BLAST options. Most examples here and throughout come from animals, but human genome, which would be okay if de novo sequencing of non-model organisms were also discussed somewhere, but it is not. Instead, the focus is squarely on model organisms and their genes. The world of repetitive DNA and transposons, which comprises a large part of phylogenomics, and which has as-yet untapped potential for revealing species histories (Piednoel et al. 2013), is reduced to satellites addressed in a short section, while transposable elements are nowhere mentioned. (The terms repetitive DNA, repeats, RepeatMasker, and transposable elements, accordingly, are not in the index.)

Chapter 8 covers tree-building algorithms in some detail, but has no exercises for students, only four discussion questions, and five references (to Farris, Felsenstein, and work by Nei and colleagues). Exploration of tree space by branch swapping is the next topic; and there is also a lengthy discussion of Bremer’s decay index ("named after Kåre Bremer, a Swedish botanist”; p. 158). We do not know of a paper (pp. 314–316) to the calculation of Bremer support, but without referring back to page 158 where Bremer’s decay index was first introduced.

In summary, DeSalle and Rosenfeld have identified an important empty niche and are among the first to occupy it; therein lies their main achievement with *Phylogenomics*. Nevertheless, we were disappointed with the balance of the book, which spends too much time on approaches that are not especially relevant to phylogenomics, while omitting areas at the very core of the new field, such as research on synteny and the filtering-out or use of repetitive DNA. An ideal primer would also provide more information about the online tools used daily by phylogeneticists, have more student exercises that could be used in courses, and provide clearer information about further reading.