

Preface

Evolutionary biology has changed dramatically during the 15 years we have worked on *Evolutionary Analysis*. As one measure of this change, consider that when the first edition went to press, the genomes of just five cellular organisms had been sequenced: three bacteria, one archaean, and one eukaryote. As the fifth edition goes to press, Erica Bree Rosenblum and colleagues reported in the *Proceedings of the National Academy of Sciences* (110: 9385–9390) that they had sequenced the genomes of 29 strains of a single species, the chytrid fungus *Batrachochytrium dendrobatidis*. This work was part of an effort to unravel the evolutionary history of an emerging pathogen that has decimated amphibian populations around the world and driven some species to extinction. The avalanche of sequence data has allowed evolutionary biologists to answer long-standing questions with greatly increased depth and clarity. In Chapter 20, *Human Evolution*, for example, we discuss a recent analysis of differences among genomic regions in the evolutionary relationships among humans, chimpanzees, and gorillas. For some questions, the answers have changed completely. In the fourth edition we noted that available sequence data provided no support for the hypothesis that modern humans and Neandertals interbred. But in the fifth edition we describe genomic analyses suggesting that the two lineages interbred after all.

Evolutionary Analysis provides an entry to this dynamic field of study for undergraduates majoring in the life sciences. We assume that readers have completed much or all of their introductory coursework and are beginning to explore in more detail areas of biology relevant to their personal and professional lives. Therefore, throughout the book we attempt to show the relevance of evolution to all of biology and to real-world problems.

Since the first edition, our primary goal has been to encourage readers to think like scientists. We present evolutionary biology not as a collection of facts but as an ongoing research effort. When exploring an issue, we begin with questions. Why are untreated HIV infections typically fatal? Why do purebred Florida panthers show such poor health, and what can be done to save their dwindling population? Why do mutation rates decrease with genome size among some kinds of organisms, but increase with genome size among others? We use such questions to engage students' curiosity and to motivate discussions of background information and theory. These discussions enable us to frame alternative hypotheses, consider how they can be tested, and make predictions. We then present and analyze data, consider its implications, and highlight new questions for future research. The analytical and technical skills readers learn from this approach are broadly applicable, and will stay with them long after the details of particular examples have faded.

New to This Edition

Many of the research areas we cover are advancing at a rate we would not have dreamed possible just a few years ago. We have looked closely at every chapter to both improve how we are teaching today's students and to thoroughly update our coverage.

- We have enhanced our traditional emphasis on scientific reasoning by including a data graph, evolutionary tree, or other piece of evidence to accompany the photo on the first page of every chapter. These one-page case studies engage students as active readers and help them become skilled at working with and interpreting data.
- We have enhanced our strong coverage of tree thinking by thoroughly revising Chapter 4. Consistent with the ever-growing use of phylogenetic analysis by scientists, we incorporate more phylogenies throughout the book. Among the new examples are a tree-based discussion of evolution of vertebrate eyes (Chapter 3); a new case study reconstructing the history of a patient's cancer (Chapter 14); and phylogeny-based reconstructions of the fish-tetrapod transition, the dinosaur-bird transition, and the origin of mammals (Chapter 18). Frequent practice at tree thinking helps students develop this essential skill.

Every chapter contains something new. Most of the new material is from the recent literature.

- Chapter 1 includes updated statistics on the status of the HIV pandemic, newer thinking on how HIV causes AIDS, new data on the origin of HIV, and new ideas and evidence on why HIV is lethal.
- Chapter 2 has a new organization featuring sections on evidence for microevolution, speciation, macroevolution, and common ancestry; discussions of why evolution at each level is relevant to humans outside of textbooks and classrooms; evidence of macroevolution presented using evolutionary trees showing the order in which derived traits are inferred to have evolved; and several new examples, including a terrestrial fish that does not like to swim.
- Chapter 3 brings new evidence on the evolution of development in the beaks of Darwin's finches, a new example of exaptation featuring carnivorous plants, and new coverage of the evolution of complex organs featuring a phylogeny-based discussion of the evolution of vertebrate eyes.
- Chapter 4 has been completely rewritten to offer an improved introduction to tree thinking; more detailed explanations of parsimony, maximum likelihood, and Bayesian phylogeny inference; and new examples of phylogenies used to answer interesting questions—such as identifying the surprising infectious agent responsible for a sexually transmitted tumor in dogs.
- Chapter 5 includes a new section on kinds of variation, featuring new and detailed examples of genetic variation and environmental variation; genotype-by-environment interaction; improved discussion of the mechanisms and consequences of mutation; new examples of gene duplication; and covers rates and fitness effects of mutation in a dedicated section with new examples and data.
- Chapter 6 is bookended with a powerful new example in which genetic engineers made a new gene, accurately predicted its effects on individuals carrying it, introduced it into a population, and used population genetics theory to accurately predict how its frequency would change over a span of 20 generations.
- Chapter 7 is bookended with a new example of conservation genetics involving the Florida panther. The chapter also includes a new example illustrating the founder effect in Polynesian field crickets; improved coverage of the inter-

action of drift and selection, the neutral theory, and the nearly neutral theory; and a new introduction to coalescence.

- Chapter 8 carries a new example—on Crohn's disease in humans—showing how linkage disequilibrium due to genetic hitchhiking can lead to spurious associations between genotype and phenotype and a revised and updated section on the adaptive significance of sex, featuring recent experiments using *C. elegans* as a model organism.
- Chapter 9 has improved narrative coherence due to the inclusion throughout the chapter of examples on the quantitative genetics of performance and prize winnings in thoroughbred racehorses.
- Chapter 10 includes an improved primer on statistical hypothesis testing, using research on the evolution of wild barley populations in response to a warming climate, and a new example of comparative research involving color in feather lice.
- Chapter 11 improves our coverage of the evolution of female choice by presenting the Fisher-Kirkpatrick-Lande model as the null hypothesis. New examples and data consider Bateman's principle in a hermaphrodite; female preferences in genetically modified zebrafish; correlated displays and preferences in Hawaiian crickets; and sexual selection in humans.
- Chapter 12 features enhanced coverage, with examples, of the four basic kinds of social behavior; improved coverage of kin selection and spite; a new section on multilevel selection and the evolution of cooperation; and several data sets on human social behavior.
- Chapter 13 has new examples on telomeres and aging; the evolution of menopause; life history traits and biological invasion; and life history traits and vulnerability to extinction.
- Chapter 14 discusses new evidence, from genome architecture, on the origin of influenza A; a new example using phylogenetic analysis to reconstruct the history of a cancer; and updated coverage of diseases of civilization, including a dramatic example from Iceland and new material on obesity.
- Chapter 15 has been completely rewritten, bringing new sections on the evolution of genome architecture; the evolution of mutation rates and gene families; and updated treatment of mobile genetic elements and the molecular basis of adaptation.
- Chapter 16 features new sections on mechanisms of divergence; hybridization and gene flow; and drivers of diversification. The chapter includes new examples illustrating the application of species concepts; updated coverage of vicariance in snapping shrimp; and new examples on mechanisms of isolation—including temporal isolation in a moth and single-gene speciation in snails.
- Chapter 17 incorporates updated coverage of the effort to create self-replicating RNAs and of the prebiotic synthesis of activated nucleotides.
- Chapter 18 has greatly expanded coverage of evolutionary transitions, featuring phylogeny-based reconstructions of the fish-tetrapod transition, the dinosaur-bird transition, and the origin of mammals; a new section on taxonomic and morphological diversity over time; updated treatment of mass extinctions, including the Permian-Triassic extinction; and a new section on fossil and molecular divergence timing.

- Chapter 19 has been completely rewritten. It includes revised coverage of Hox genes and detailed discussions of deep homology, developmental constraints and trade-offs, and the evolution of novel traits.
- Chapter 20 discusses new evidence from complete genomes on incomplete lineage sorting among humans, chimps, and gorillas, and on genetic differences between these species; new evidence, also from complete genomes, on hybridization between modern humans and Neandertals and between modern humans and Denisovans; and updated coverage of the human fossil record and the evolution of spoken language.

Hallmark Features

While fully updating this edition, we also maintained core strengths for which this book is recognized.

- We continue to strive for clarity of presentation, ensuring each chapter contains a coherent, accessible narrative that students can follow.
- We remain committed to strong information design and a tight integration between the text and illustration program. Nearly all phylogenies are presented horizontally, with time running from left to right, because research has shown this makes it easier for students to interpret them correctly.
- Boxes contain detailed explorations of quantitative issues discussed in the main text. These are called *Computing Consequences*, after physicist Richard Feynman's concise description of the scientific method: "First, we guess . . . No! Don't laugh—it's really true. Then we compute the consequences of the guess to see if this law that we guessed is right—what it would imply. Then we compare those computation results to nature—or, we say, to experiment, or experience—we compare it directly with observation to see if it works. If it disagrees with experiment, it's wrong."

All chapters end with a set of questions that encourage readers to review the material, apply concepts to new issues, and explore the primary literature.

Additional Resources for Instructors and Students

At the Pearson Instructor Resource Center, you can download JPEG and PowerPoint files containing all of the line art, tables, and photos from the book. You can access versions with and without labels to best suit your needs.

A thorough test bank and TestGen software is available to help you generate tests. Each chapter has dozens of multiple choice, short answer, and essay questions.

The updated Companion Website has been revised and updated to reflect the new edition. The website can be found at: www.pearsonhighered.com/herron

Activities such as case studies and simulations challenge students to pose questions, formulate hypotheses, design experiments, analyze data, and draw conclusions. Many of these activities accompany downloadable software programs that allow students to conduct their own virtual investigations. Students will also find chapter study quizzes that allow them to check their understanding of key ideas in each chapter.