
Preface

WHAT THIS BOOK IS ABOUT

A PHILOSOPHY OF BIOLOGY

Our aim in this book is to develop some general principles to help describe the patterns to be found in the seemingly disparate facts about the diversity of life on Earth. It is an effort to assemble and digest observations made by naturalists and biologists from Aristotle to scientists publishing today—of organisms that live at temperatures above the boiling point of water and others that live in ice, organisms that fly and others that swim, those that inhale oxygen and those that expel it; how they are different and what they share. How can evolution, the single phenomenon that we invoke to explain how this endless diversity arose from one beginning, have produced it all?

Modern biological theory is thoroughly gene-centered, and this book is no exception. Genes are considered the essential storehouses of biological information and the mechanism through which evolution works. Thus, our specific interest in this book is in explaining the role of nucleic acids—DNA and RNA—in the evolution of complex organisms. At the same time, there is a danger in attributing too much to one cause, genetic or otherwise, or to one evolutionary process, or in considering the issues in such a detailed and itemized way that the broader picture gets lost. In this book we explore the ways in which an overly gene-based approach to biology can constrain our understanding of evolution.

Much of what we write about necessarily assumes evolution as its basic framework, that is, that organisms today have descended from ancestral organisms. But much of what we present considers alternative or supplemental general principles that we think are about as fundamental and ubiquitous in life as the core principles originally articulated by Darwin and Wallace. The theory of evolution was formalized as population genetics almost a century ago, but population genetics has little to say about the actual traits in organisms, how they are made, and how they evolve.

Natural selection is at the heart of the classical theory, but there is more going on than that, and we try to show what it is and where it might apply. Biology is forced to guess at the particulars of the evolution of traits and organisms because of millions of years of unobserved history that lies behind them. Natural selection is a rather generic explanation, which does not provide a very satisfying account of the particulars of the high degree of complexity found in organisms or even in cells themselves. To look at these, we consider aspects of life such as development, sensory systems, reproduction, and even perception. They illustrate some general

principles that provide a remarkably consistent picture of processes involved in very disparate traits across the spectrum of life.

Organisms confront their world in a multitude of successful ways involving a comparable diversity of pathways to, or consequences of, complexity. Complexity requires that an organism have, for example, extensive mechanisms for communicating internally among its cells, and many such mechanisms have evolved in all branches of life, which we will discuss. Externally, organisms are surrounded by a wide diversity of information with possible relevance to their safety, reproduction, and food acquisition, and organisms have evolved many ways to use (or dismiss or get along without) that information, and we will discuss these. Indeed, the external environment contains “information” only when or if it is needed or used. Most of our attention in this book is on complex multicellular species, but we consider simpler organisms as well.

For reasons that probably go back to the way life first began, an elegant few strategies have been employed to confront the challenges of life (we do not imply conscious intent here). The word “logic” in our title refers to the way that the diversity of complex organisms has come about through a few general mechanisms that, along with shared history, enable a trait or developmental pathway or gene, once it has arisen, to be used, reused, and modified. Very similar characteristics and relationships are found among entirely different and/or unrelated genes across the living world. These facts make it much easier to understand complex nature than did earlier and simpler views of genes as each individually coding for a specific protein with a unitary function. Many of these attributes of life have been long known, though not always to all persons working in diverse areas of biology, or well integrated into their work.

We discuss specific genes throughout, but it is the relationship or process, not the detail, that counts. We also cover aspects of life not yet explained very well in genetic terms, but a major point is that one can predict the *nature* of those genes and processes, based on generalizations derived from what we already know. Such predictions are possible because the logic of life can be reduced to a small number of basic, ubiquitous principles. Nevertheless, a main point will be that this is not a prespecified system that follows necessary rules, or “laws of nature,” the way formal mathematical logic does. Only in the broadest terms can there be a single theory of the contingent, largely chance-driven process that is the evolution of life. We can’t prove that some mechanism other than the one we try to reconstruct might not have yielded the same diversity of life we see on Earth; that is the nature of retrospective analysis that we are stuck with in trying to understand the unobserved past.

We try to develop a broad and unifying sense of life and the ways that organisms live it. Our attempt is intended for any reader wishing to understand some of the most important generalizations to emerge from recent biological research. This is not only edifying—it is to us—but can also provide a guide for future work.

We hope especially to stimulate students learning about biology and evolution to see that there are broad principles at work in life that go beyond the one darwinian view so often taught. A theory helps us construct a consistent worldview but is always at risk of becoming a constraining ideology. Although we are involved in molecular biology ourselves, we seek to understand the unity of life in broader terms, compatible with the effort to reduce an understanding of biology to an understanding of genes and their action, but that always keeps its eye on the organism as

a whole or on the phenomena that essentially rest on the interactions of molecules, cells, or even organisms.

OUR APOLOGIES

In this connection, it is certain that what follows will contain errors. Biology is a rapidly changing field, and facts are continually being amended or their importance reinterpreted, sometimes because of error and sometimes because of increasing knowledge. We are just two people confronting an enormous literature, and our own understanding will sometimes be flawed or we will have missed important papers; we will post errors and issues that we learn of on the <http://www.wiley.com> worldwide web page for this book. However, we think our general picture will be of some durability, and we hope that our attempt to go beyond the usually accepted principles of evolution, and to call some of those into question, will be useful and, if nothing else, thought-provoking.

We present some detail and technical material here but have tried to provide self-contained explanations; our intent is invariably conceptual rather than technical. Readers should be able to “read around” technical aspects that, because so much of the relevant genetics is of very recent vintage, are likely to be incomplete at best at this stage. We try to give a sense of what is known, with leads into the literature, without providing extensive lists of genes or pathways (we cite many excellent books, reviews, and scientific papers that do that). A reader interested in following up any particular points can easily find more about them through the literature and the internet—which would also help limit the damage that might be done by errors that we have made. If only because of the necessary lag time between writing and publication, no book can safely be regarded as definitive in detail, in a rapidly changing world.

A major risk in an era of exploding research and the sense of major discovery that now pervades genetics is that the firmness or importance of new results is probably overstated. However, we have tried to cite what seem to be reasonable interpretations of recent work that illustrate the generalities. We hope we have not been too restricted or parochial in doing so.

We have been unable even to approximate a thorough bibliography. As in the Technical Notes (below), internet web sources are so extensive and accessible that we think exhaustive citation is not as important for knowledge as it has been. We have cited primary literature to document our interpretation of various specific points, but as a rule we have preferentially cited recent reviews, texts, or convenient summary sources where we felt they would be useful, and/or that provide bibliographic entrée to the broader literature. Unfortunately, this nearly unavoidable way to handle information overload does undermine the proper assignment of credit for work and ideas because the authors of reviews are not always the sources of the material itself. We offer sincere apologies to many, many authors whose work we are aware of, staring us in the face from big piles on our floor, but that for practical reasons could not be cited.

Writing this book was a joint, interactive, and often grueling effort over several years as we tried to develop a credible understanding of fields entirely new to us, and to find the common threads among them. Although the illustrations new to the book were primarily done by one of us (AB), the writing itself was a joint, integrated effort in every respect regarding the ideas and the content.

If the ideas we present are interesting or stimulating to those who read this book, we will have succeeded, no matter how well our own particular views on life stand the test of time.

TECHNICAL NOTES

GENE NOMENCLATURE

Genes are being discovered by the hundreds, often by automated means. The nomenclature system is somewhat undisciplined and not entirely consistent. In this book we have discussed results from work in most areas of biology, many of which have their own conventions for gene nomenclature, not always even internally consistent. Designation conventions change and seem likely to do so even more as an ever-larger set of species and their genes are identified, and genes are grouped ever more accurately and into more extensive phylogenies. Thus we have tried at least to be clear and consistent within the bounds of this book, to minimize distracting readers with confusing gene designations. We generally use italics for gene names (*Bmp4*), and corresponding standard font for their respective coded protein (Bmp4). This may be the single most consistent general aspect of nomenclature in the field. Our own consistency with these guidelines varies from strict to yielding to well-established conventions in various fields where a strict adherence would strike the informed reader as strange.

We have hopefully been clear about whether we are referring to a gene or to its product, although the distinction can usually be inferred in context. We try to identify relevant homologous genes among species, when they have very different names. Above all, while we undoubtedly have missed things and not been perfectly consistent, nomenclature should provide only a minimal distraction.

BIBLIOGRAPHIC SUPPORT

Internet resources

We have not cited many internet URLs (worldwide web sites) in this book although the internet is a valuable resource for genetics. Readers who want to know more can usually use keywords to go right to major and minor resources for anything in the book and can follow up various issues by finding diagrams, DNA sequences, protein structures, technical descriptions, and even animations of many kinds and all levels. Unfortunately, the internet is a moving target, so that many URLs we would list here would be gone by the time a user wished to find them. The URLs we have cited seem to us to be likely to be relatively stable.

Reference citations

For the same reason, we have been especially sparing in our use of generic references. We usually give one or a few for broad topics. Similarly, it is utterly impossible to include all relevant technical references. The US National Center for Biotechnology Information (www.ncbi.nlm.nih.gov) provides many references and links, including PubMed (Medline) in which keyword searching can easily lead to the most recent literature. Readers should not rely on the accuracy of a conceptual survey such as ours, especially in an age in which so much is being learned so rapidly, and can be checked so easily.