context of the research most enjoyable and recommend it to anyone interested in how scientific theories evolve and revolve.

In a short but grand finale, Steriade addresses the question of consciousness. In light of comments such as Francis Crick's claim that "consciousness depends crucially on thalamocortical connections with the cortex" [*The Astonishing Hypothesis* (Scribner, New York, 1994)], someone who has spent a career searching for treasures in this terrain is unlikely to remain neutral on the issue. Steriade does not. He candidly recommends that those interested in the subject read Dostoyevsky, Proust, or Joyce and devote their limited research time to topics that can be defined and successfully attacked. With this delightfully entertaining conclusion, the author has voluntarily distanced himself from the competition in the consciousness battlefield. If the leading expert of the thalamocortical systems advises us to avoid this topic of *ignoramus et ignorabimus*, perhaps we should listen.

BOOKS: EVOLUTION

Growing Trees from Molecular Data

Axel Meyer

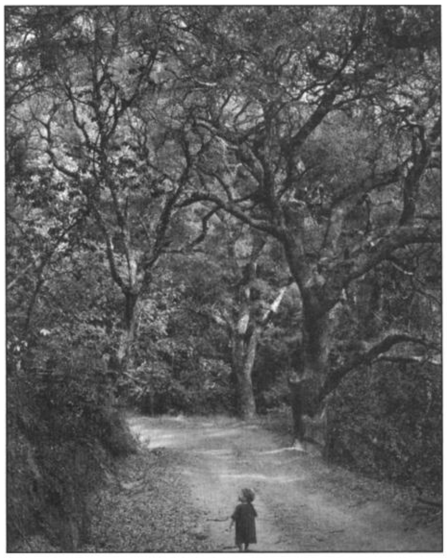
Phylogenetic Trees Made Easy
A How-To Manual for Molecular Biologists
by Barry G. Hall
Sinauer Associates, Sunderland, MA, 2001. 191 pp. Paper, $24.95, £18.99. ISBN 0-87893-311-5.

Former president Ronald Reagan claimed that if you have seen one redwood tree, you have seen them all. But one doesn't have to wander through an awe-inspiring old-growth redwood forest to know that Reagan was wrong. Every redwood tree is unique, and the same can be said for each phylogenetic tree—a graphical depiction of evolutionary relationships (among organisms or their traits, including DNA and protein sequences). The latter have the great advantage that they do not take hundreds of years to create, but building them well isn't easy and interpreting them isn't straightforward, either. Students and researchers wanting to learn more about the practical aspects of constructing reliable phylogenetic trees from molecular data will find Barry Hall's *Phylogenetic Trees Made Easy* tremendously helpful.

In these days of genomics, phylogenetic trees based on biochemical data abound in specialists' journals in molecular evolution and molecular systematics. They are also found in the journals representing widely diverse fields, from developmental biology to physiology and morphology. Although trees and "tree-thinking" are now all around us, many published phylogenies based on molecular data, especially those in the nonspecialist literature, are quite possibly wrong. Errors commonly arise because one cannot simply assume that a gene is a gene is a gene, and the default settings of computer programs often do not do justice to the intricacies of molecular evolution. The pitfalls of tree construction are manifold: the complexity of tree-building methods can bewilder even experts and the choice among alternative analyses is often confusing.

The author, a geneticist at the University of Rochester, offers an excellent, long overdue, and inexpensive "how-to" manual for those wishing to create phylogenetic trees from protein or nucleic acid sequences. His clear explanations of the computer software packages that have become the tools of the trade will allow novices to go beyond the default settings. A series of "learn more about" boxes introduces some of the background theory and includes references to literature that will help users to better understand the assumptions underlying the various analyses and to choose appropriately from among the wide range of parameter settings. In addition, the publisher hosts a Web page (www.sinauer.com/hall) that provides sample files and other utilities to alleviate a beginner's frustrations with correctly formatting files for the different software packages.

Before phylogenetic trees can be built, one must align the molecular sequences (whether those are determined by the user or downloaded from genetic databases). The importance of a correct alignment cannot be overstated—all of the tree-building algorithms depend on it and wrong alignments guarantee incorrect results. ClustalX (*1*) has become the industry standard for alignments, but one must understand the alignment parameters, such as "gap penalties," to evaluate whether the resulting alignment makes sense. Users must know their genes and proteins better than ClustalX does, because they will have to spend time with the computer generated alignment to "refine it by eye"—to ensure, for example, that functional domains are not interrupted by gaps and that the ends are truncated.



Searching for the best tree. Some phylogenetic data sets may leave researchers feeling like the subject of Wynn Bullock's *Child on a Forest Road.*

Once one trusts the sequence alignment, one can begin to create phylogenetic trees. Of the several sophisticated software packages now available for such analyses, David Swofford's powerful and influential PAUP* (*2*) is the most often used, and Hall discusses it in some detail. The menu-driven Macintosh version of PAUP* is tremendously popular, and rightly so, because it is easy to use; Windows and Unix versions are also available, but these require a higher degree of familiarity with the software and methods because control of the programs relies on manipulation of command lines. (Throughout the book, Hall presents examples using the Macintosh versions of the software he discusses. Although users of Windows and Unix platforms may find this a drawback, the book will still provide them with considerable guidance.) During the last 15 years, the technology available to researchers in the field of molecular evolution has progressed from cumbersome DNA sequencing using radioactively labeled nucleotides to automatic capillary sequencers that permit genome centers to sequence the entire genome of a bacterium in a day. (The increased efficiency has helped expand the field of molecular evolution from studies of the evolution of particular gene families to comparative or phylogenetic genomics.) Similarly, PAUP* has grown from a rather crude DOS program to a slick, deceptively easy-to-use software package that includes a sophisticated graphics interface for presentation of the results. The package allows tree-building by any one of several methods and thus encourages comparisons of the results from different methods. It not only includes neighbor-joining and parsimony, methods which have been widely used for many years, but also sports the more complex maximum likelihood approach.

I think it is fair to say that likelihood methods currently enjoy the greatest popularity among experienced builders of molecular trees, and that the resulting phylogenies are often deemed the most reliable. Unfortunately, these methods are also the most difficult to understand. Therefore users, especially beginners, will appreciate Hall's guid-

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ance on the implementation of the often complex models of DNA evolution in a maximum likelihood setting. For readers facing tasks that even PAUP* can't handle, such as maximum likelihood analyses of amino acid sequences, the author briefly discusses Puzzle (*3*) and mentions (but does not discuss) the PHYLIP package (*4*) for other eventualities. Hall also discusses MrBayes (*5*), which uses Bayesian methodology to evaluate trees and to reconstruct ancestral DNA sequences. The program, which is quite fast and can handle very large phylogenies, also provides a means of estimating how much confidence one can have in different branches of the tree.

Many of the tree calculations discussed in the book are very computer-intensive and can take over one's computer for days. Before hitting the "execute" button, a researcher must recognize the magnitude of the task at hand and warn labmates accordingly.

Typically, one picks up a how-to manual to fix something, perhaps in a car, a house, or a computer program. One often turns directly to the section covering a particular task, such as how to adjust a carburetor. Although Hall's book can be used like this, its easy-to-follow structure and numerous diagrams invite the reader to simply peruse it from start to finish. *Phylogenetic Trees Made Easy* will become an invaluable source for students and researchers in a wide range of biological disciplines.

References and Notes

1. J. D. Thompson *et al., Nucleic Acids Res.* **25**, 4876 (1997). ClustalX is available from http://inn-prot.weizmann.ac.il/software/ClustalX.html.
2. D. L. Swofford, *PAUP*: Phylogenetic Analysis Using Parsimony and Other Methods* (Sinauer Associates, Sunderland, MA, 2000).
3. Puzzle is available at www.tree-puzzle.de.
4. The source code, some executable files, and documentation for the PHYLogeny Inference Package are available at http://evolution.genetics.washington.edu/phylip.html.
5. Developed by J. P. Hulsenbeck and Fredrik Ronquist, MrBayes: Bayesian Inference of Phylogeny is available at http://morphbank.ebc.uu.se/mrbayes.

NOTA BENE: OCEANS

Why Did the Penguins Gasp?

Breathtaking. Take a lungful of air and plunge in. *The Blue Planet* comprises a series of eight television films produced by the British Broadcasting Company's Natural History Unit. Each episode is paired with a short *Making Waves* epilogue that looks at the making of the films. The films are also accompanied by a large format, extensively illustrated book, which could grace coffee tables and perhaps classroom shelves. The films and book alike are stuffed with fantastic, mind-boggling images, and the technical virtuosity of the filmmaking is obvious.

The Blue Planet
A Natural History of the Oceans
by Andrew Byatt, Alastair Fothergill, and Martha Holmes

BBC One, Fall, 2001. Discovery Channel, January, 2002. Eight 50-minute episodes.

BBC Worldwide, London, 2001. 384 pp. £24.99. ISBN 0-563-38498-0. DK, New York, 2002. $40. ISBN 0-7894-8265-7.

Each program is devoted to a different sector of Earth's oceans: the open waters, the abyssal depths, coasts, seasonal seas, frozen seas, tropical seas, and tidal zones. The information that can be absorbed from an ambitious survey of this kind is limited, but we can still marvel. Nevertheless, the limitations of trying to comprehensibly sample each zone do become obvious. For several minutes of the open ocean episode, the mountains of Baja California are visible on the horizon, and each film includes a similar sequence of a shoal of small fry being gobbled up by ravenous predators of various magnitude and ferocity. The sound track is always tasteful and unobtrusive, but sometimes confusing. Ctenophores and jellyfish cannot possibly make audible noises, yet we seem to hear them. But unless you know that parrot fish really are noisy eaters, you might be deluded into thinking sounds accompanying footage of them scraping algae off a coral reef are simply more amusing "radiophonics."

Yet there are plenty of revelations. Despite knowing that life can thrive in the most extreme environments, it is still a shock to see some of them. For instance, the remarkable cold seeps in the Gulf of Mexico are so saline that submersibles bounce on their surfaces. Their shorelines hum with bizarre life, but tantalizingly, we learn nothing about what is within the seeps. We do learn, however, in graphic, gruesome detail what happens to a gray whale calf assaulted by orcas. Their attack is apparently just for fun, and the corpse sinks unconsumed until discovered by large numbers of revolting hagfish. We are also shown amazing views of emperor penguins rocketing underwater, generating trails of bubbles, and shooting out of the deep to break through the surface and bounce onto the ice. If they were lucky, they escaped the leopard seal and were only captured on film. Spectator penguins stand close-packed on the ice floe: watching their companions leap ashore, gasping in unison when the leopard seal attacks, swaying together like a football crowd.

One shortcoming of the films is the limited attention paid to small organisms. Although we see something of copepods and ctenophores and we learn about the chemical and light trails formed in the water by planktonic organisms, there is little about bacteria and algae. When they are featured, the small fry tend to be a foil for bigger, celebrity animals: sailfish after sardines; sharks after anchovies; yellowfin tuna, dolphins, and fin whales cavorting and streaking around the shoals of herring and mackerel attracted to plankton blooms. And even the majestic sunfish presenting its flanks to passing gulls so they could peck off the parasites.

Listening in the dark. Hairy anglers are covered with long antennae that are senstive to minute movements in the water.

CREDIT: DAVID SHALE/BBC *THE BLUE PLANET*

Although plenty of facts are presented, our understanding of many aspects of these largely unknown and unexplored environments is based on little more than wild guesses. There are many more questions to ask than the established facts can answer. By the end of the series, we have marveled a lot but not actually learned much.

It is easy to criticize television natural history as superficial. Doing so is a little unfair because such programs are supposed to be entertainment and making such films requires courage and patience. Nevertheless, there is a deeper problem. Although we armchair naturalists may have become intimate with certain aspects of the sex lives of lions and the home economics of mole rats, few of us will ever see these animals in the flesh. Wildlife and pristine environments are becoming increasingly dispensable to humankind—not least because wild animals and places will be forever extant in virtual environments, so why should we care about their continued real existence? What is worse, by concentrating on a very few large and glamorous species, armchair naturalists fail to gain a sense of the real diversity and interdependence of life on Earth. —CAROLINE ASH AND SAMUEL ASH CROFT