

exchange) and determinants of body temperature (heat exchange). This extensive coverage of such a diversity of topics highlights one huge advantage of having someone of Koehl's caliber write a book such as this: Koehl is as intimately familiar with the physics as she is the intertidal zone, and she explains complex engineering principles in simple terms without obfuscation or inaccuracy. My one (very minor) complaint is that I do wish she had thrown some mathematics into the mix—while a bit scary to some audiences, math too can be beautiful in its own way, and in showing how counterintuitive nature can be. Nevertheless, this book will serve to draw in a host of new

initiates who will delve deeper into intertidal ecology and biophysical ecology, and may even cause several old salts to view intertidal ecology through a new lens.

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RENEWING THE DIALECTIC OF FOOD-WEB RESEARCH

Pascual, Mercedes, and Jennifer A. Dunne, editors. 2006. **Ecological networks: linking structure and dynamics in food webs.** Santa Fe Institute Studies in the Sciences of Complexity. Oxford University Press, New York. xviii+ 386 p. \$64.50, ISBN: 0-19-518816-0.

Key words: complexity; food webs; graph theory; networks; trophic structure.

The ongoing dialectic of science—initial theories giving way in the face of better data, which inspire more sophisticated analysis, which in turn is confronted with still more detailed data—is displayed clearly in the study of food webs. For more than a century, approaches to studying food webs have oscillated between compilations of detailed natural history observations into illustrations of trophic relationships and the search for, and statistical analysis of, general patterns of food-web structure. The search by food-web theorists in the 1970s for general metrics of food webs, such as linkage density and connectance (summarized in the proceedings of the first international food-web symposium: DeAngelis, D. L., W. M. Post, and G. Sugihara, editors. 1983. *Current trends in food web theory*. Oak Ridge National Laboratory ORNL-5983, Oak Ridge, Tennessee, USA), was scorned by the empiricists of the 1980s who emphasized natural history detail and environmental variability (summarized in the proceedings of the second international food-web symposium: Polis, G. A., and K. O. Winemiller, editors. 1996. *Food webs: integration of patterns and dynamics*. Chapman and Hall, New York, New York, USA). In true dialectic fashion, the third international symposium (de Ruiter, P., V. Wolters, and J. C. Moore, editors. 2005. *Dynamic food webs: multispecies assemblages, ecosystem development and environmental change*. Elsevier, Burlington, Massachusetts, USA) synthesized these two approaches and provided myriad directions for novel theoretical work and simultaneously pointed out key empirical lacunae.

Ecological networks opens the next dialectical cycle. The product of an international workshop held at the Santa Fe Institute in February, 2004 (just three months after the third international food-web symposium), the focus of this volume is on new general models and metrics of food-web structure. New insights are gained from cross-fertilization of ecological models with models of other complex networks that include the internet and World Wide Web, social and financial networks, and protein interaction networks. All of these approaches, including

the models of food-web structure presented in the book's 15 chapters, use language and methods of graph theory. Many of the illustrations are done using the FoodWeb3D software (<http://www.foodwebs.org>).

As the subtitle suggests, the contributors address both the structure and dynamics of complex networks, of which food webs are a special case. The four chapters in the first section (following the introduction), accounting for nearly half the book, present different ways of quantifying food-web structure. Jennifer Dunne provides a lengthy review of the history of food-web studies; her attention to historical gems unknown to many contemporary ecologists is most welcome. Cecile Cartozo et al. introduce the language of graph theory and its application to quantifying food-web structure. Andy Dobson et al. illustrate the added complexity that parasites add to food webs, while Jordi Bascompte and Pedro Jordano expand the discussion to include networks of coevolutionary mutualists. The remaining three sections of the book attempt to illustrate how these new metrics food-web structure change as food webs change through time. Of these nine chapters, two are real stand-outs.

James Gillooly et al. show how the evolving metabolic theory of ecology (a.k.a. Jim Brown's "theory of everything"; Brown, J. H., J. F. Gillooly, A. P. Allen, V. M. Savage, and G. B. West. 2004. Toward a metabolic theory of ecology. *Ecology* 85:1771–1789) might be used to link food-web models based on abundances and trophic dynamics to those based on energy fluxes. Their nascent model may lead to a rapprochement between classical "community" and "ecosystem" approaches to ecological dynamics. Or it may not. But either way, interesting data will be collected along the way. Jane Memmott et al. discuss the relationship between the structure of complex ecological networks and the loss of biodiversity. They focus on the role of habitat structure, species interactions, and minimum viable areas for maintaining resilient, functioning food webs. Each section of their chapter includes a clear discussion of what is known (not much) and what needs to be known (a lot) in order to apply food-web theory to the conservation and restoration of ecosystems and their biological diversity. There are literally dozens of dissertation topics waiting for enthusiastic graduate students in this chapter alone.

In most new theses, much is left out, and *Ecological networks* is no exception. Stable isotopes, a now common part of the empirically minded food-web ecologist's tool-kit, are nowhere evident. The role of body size and the abundance of individuals at each node in the food web, a large focus of the 2003 international food web symposium, are similarly absent.

Analysis of food-web dynamics remains fundamentally a question of small departures from equilibrium; non-equilibrium dynamics are mentioned only once, in passing. High-quality data remain scant—it is hard work to assemble food webs with high levels of taxonomic resolution, and few such webs are presented in *Ecological networks* or exist elsewhere in the ecological literature. It remains unclear how the analysis of only a handful of exemplary webs can lead to general principles of either the structure or the dynamics of food webs.

Like most edited volumes, the individual chapters of *Ecological networks* are of uneven quality and completeness, and are not well integrated with each other. Several short chapters (on niche models by Martinez and Cushing; a reply to Martinez and Cushing by Bersier et al.; and a discussion of the impact of sea lampreys on Great Lakes' food webs by Cobey) masquerade as independent text boxes without obvious linkages to the rest of the text. The editors are to be applauded for moving this volume rapidly into print following the February 2004 conference. However, the production of the volume is unsatisfying: the paper is thin and figures and text bleed through pages; many figures are so poorly scanned at such low resolution that they are virtually illegible; there are numerous typographical and grammatical

errors and missing (or inaccurate) citations that a careful copy editor ought to have caught; and the insertion of text-boxes is inconsistent—sometimes they follow immediately (within a page or two) upon first reference in the text, other times they don't appear until 20 pages later. Nonetheless, most food-web ecologists will want to have *Ecological networks* on their shelf, for the many thought-provoking ideas that it contains as well as for a record of the topics that are missing. We can be certain that *Ecological networks* will provoke the next generation of ecologists to collect the data needed to fit the models and address the hypotheses presented by the chapters' authors, and that one or two decades hence, another synthesis will emerge.

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COMPUTATIONAL STATISTICS FOR BIOLOGICAL DATA

Roff, Derek A. **Introduction to computer-intensive methods of data analysis in biology**. 2006. Cambridge University Press, New York. vii + 368 p. \$125.00 (cloth), ISBN:0-521-84628-5; \$65.00 (paper), ISBN: 0-521-60865-1.

Key words: Bayesian analysis; bootstrap; classification and regression tree; confidence interval; cross-validation; general additive model; hypothesis test; jackknife; likelihood; Monte-Carlo; randomization methods; regression; statistical analysis.

When I was a graduate student, longer ago than I like to admit, I was visiting my parents in Tennessee, bringing with me a three-inch stack of computer output recently produced by our laboratory's VAX mainframe. After looking over the lines of ANOVA results, my father, then a professor of psychology at George Peabody College, went to his study and returned with a leather date book. He showed me an entry from 1939, the year he was finishing his Ph.D. A bold line of ink blocked out three days. Below the line read the entry: "Calculate standard deviation." Note singular for standard deviation and plural for days.

One of the most important revolutions in science is the emergence of fast, cheap computers. This is more than a matter of efficiency—yes it is possible to calculate thousands of standard deviations in seconds rather than days, but more importantly, we are able to gain insights that were infeasible as recently as decades ago. In his book, *Introduction to computer-intensive methods of data analysis in biology*, Derek Roff offers an overview of methods of statistical analysis based on computationally intensive, iterative processes made feasible by this revolution in computing power. The book targets graduate students and biological researchers with nominal training in mathematics and statistics. It is organized around six general

topics—maximum likelihood, the jackknife, bootstrapping, randomization methods, regressions, and Bayesian analysis. Each chapter contains a description of the approaches and algorithms needed for parameter estimation and hypothesis testing. There are many worked examples. Each example is accompanied by detailed code in S-Plus.

The strength of the work is its coverage of contemporary, computer-intensive methods and the detailed templates provided for implementing each one. Many people learn most quickly by working through an example that resembles a problem of their own, and so I think this aspect of the book will be widely appreciated. S-Plus is a good choice for implementing examples because of its relationship to the free software, R, both of which are widely used. With the notable exception of likelihood and Bayesian methods, the book offers a valuable treatment of how to go about performing the general types of analyses it presents. If you know *when* it is appropriate to use the techniques described in this book, there is useful information on how to implement them.

The book has weaknesses, however. It fails to explain well *why* a method would be used. In my experience, students are often frustrated by traditional statistics courses, which present a collection of different methods for analyzing data without much foundation in the theory supporting those analyses. After taking three or four of these courses, students leave bewildered by a seemingly disconnected array of methods, confused about how they relate one to another. Roff offers a modernized version of this traditional shortcoming. He catalogs contemporary methods with scarce attention paid to any unifying, statistical framework—there is no treatment urging the reader to think about models and their relationship to data or what this relationship has to do with the choice of methods for analysis. As a result, it is often unclear why someone would use one computational method over another (e.g., likelihood vs. the jackknife vs. bootstrapping) or why a computationally intensive