uate or high school students, covering nearly all of the first-order facets of complexity within dynamics, information, computation, evolution, and networks. But even researchers familiar with the traditional stomping grounds may enjoy many of Mitchell's metadiscussions on where the field of complexity stands today, and whether it is progressing or dying. This volume may itself exemplify a very good reason for maintaining "complexity" as a moniker for the suite of disciplines it unites: books such as this may be pedagogically useful for the growth of young scientists. First, the topics discussed are exciting to newcomers, tapping into the romance of science many of us researchers once had (and now struggle to recall). Second, the issues in complexity require interdisciplinary training, which may serve to motivate students to *get* interdisciplinary training, something they will never regret wherever they end up in science (and odds are they will not end up in "complexity" proper). Third, an introduction to the problems under the heading of complexity helps put students in a nonreductionist mindset, so that when such complexity-fed students land in traditional scientific disciplines, they push their fields toward the development and testing of large-scale, unifying theories. If Mitchell's book were required reading for undergraduate freshmen, I would anticipate a large surge in the number of students interested not only in complexity, but interested in science more generally. And not just more students, but students more exercised about what may lie ahead as they attempt come to grips with nature.

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BIOLOGICAL MODELING AND SIMULATION: A SURVEY OF PRACTICAL MODELS, ALGORITHMS, AND NUMERICAL METHODS. *Computational Molecular Biology.*

By Russell Schwartz. *Cambridge (Massachusetts): MIT Press.* $45.00. xii + 389 p.; ill.; index. ISBN: 978-0-262-19584-3. 2008.

In this amazingly comprehensive book, the author guides readers through a myriad of different approaches to solving computational biology problems. Two major strengths of the work are its breadth and logical organization: readers are provided with clear strategies (including useful pseudocode) for constructing computational algorithms. Although the book is heavy on methods, it does provide case studies that demonstrate how these methods can be used to solve problems in sequence assembly, molecular evolution, and inferring gene regulatory networks. Although all of the problems that Schwartz tackles are at the mo-

lecular level, modelers who want to become familiar with a powerful list of computational techniques will also find algorithms that can be exported to problems at other biological scales.

This volume contains numerous diagrams that are generally effective at illustrating key concepts, although quite a few of these diagrams contain minor errors with the potential to cause confusion. The book also utilizes a consistent sequence of presentation that will probably be more intuitive to computer scientists than biologists: abstract concepts and programming approaches come first, with applied problems that ground the rationale for the prescribed approaches bringing up the rear. I suspect that this will cause the more biologically oriented to double back in the text in order to understand the abstract concepts after being presented with the example of how those concepts might be applied.

So who might utilize this volume, and how should it be used? I imagine many biological modelers, including those with significant experience in the field, will find this a helpful desk reference. Undoubtedly, this will be a valuable resource for any instructor charged with empowering students to computationally investigate a variety of phenomena at the molecular end of the biological spectrum. This is not a book for readers without a fairly strong background in mathematics and computer science, but a competent instructor who is prepared to support students with specific workable examples can use the superstructure provided by this volume to great effect.

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BIOINFORMATICS, VOLUME I: DATA, SEQUENCE ANALYSIS AND EVOLUTION. *Methods in Molecular Biology, Volume 452.*

Edited by Jonathan M. Keith. *Totowa (New Jersey): Humana Press.* $119.00. xii + 562 p.; ill.; general index and evolution index. ISBN: 978-1-58829-707-5. 2008.

BIOINFORMATICS, VOLUME II: STRUCTURE, FUNCTION AND APPLICATIONS. *Methods in Molecular Biology, Volume 453.*

Edited by Jonathan M. Keith. *Totowa (New Jersey): Humana Press.* $119.00. xiv + 502 p.; ill.; index. ISBN: 978-1-60327-428-9. 2008.

Bioinformatics is a discipline that spans computational techniques, data analysis and visualization, machine learning, and efficient data management in the context of research questions that seek to answer biological questions. These two volumes provide an in-depth and problem-driven exploration of topics in computational biology and bioinformatics.