Ruth Nussinov wrote an improved version of her chapter on protein docking in a recent review article), the overall collection of topics in this book is impressive.

This book is fairly up-to-date and includes many references as recent as 2000; even the upcoming field of systems biology is represented by a chapter on the Kyoto Encyclopaedia of Genes and Genomes (KEGG) database of biochemical pathways. However, it is particularly difficult to write a book about a field as multidisciplinary as bioinformatics. A specific topic can be addressed from a variety of perspectives, such as computer science, statistics, and biology, and the field is moving so quickly that often techniques are outdated almost as soon as they are published. To date, there is no text that can please everyone, and this text is no exception.

The text is written from a computational viewpoint, rather than a biological one. Thus, various algorithms are covered in detail, but any discussion of the biological implications of using one algorithm rather than another is given little attention. This book is not an introductory text for students of human biology and medicine. In addition to an update on the human genome sequencing project, it deals briefly, but clearly, with numerous medically relevant topics, for example, how transcriptional processes may be used to distinguish subtypes of lymphomas and to direct the use of tailored therapies. The text effectively explains DNA microarrays, a technology increasingly used to recognize patterns of gene expression that correlate with specific disease states. However, the section on single-nucleotide polymorphisms barely covers an aspect of the human genome that underlies an important realm of molecular diagnostics.

Each chapter begins by listing the learning objectives a reader should achieve by studying it. Although aimed at undergraduate students of molecular biology, the learning objectives are appropriate for anyone non-specialist wishing to read the book in lieu of enrolling in an organized course of instruction. Particularly helpful are the boxes scattered throughout the text that summarize significant features of a topic, extend discussion of an interesting topic, or engage in speculation about unresolved issues. The book also contains an extensive glossary (40 pages) to assist the nonspecialist in interpreting the increasingly arcane language of genomics.

Appropriate for a textbook devoted to such a rapidly advancing field, Brown’s book includes an appendix that informs the reader of where to find the latest developments, either in selected journals or at Internet sites devoted to genome science. Finally, an adequate index makes the book a practical tool for the typical user who will occasionally want to acquire a specific fact rather than read the book from cover to cover.

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This is an extremely informative and timely text that summarizes the current research in the rapidly expanding area of copper metabolism and toxicology. The preface gives a concise overview in addition to introducing the importance of copper in biological systems and the disorders arising from the mishandling of copper. It is therefore extremely useful to those with only a cursory knowledge of copper metabolism. The book is divided into six sections: “Copper in Mammals”, “Copper Proteins”, “Copper Transport”, “Molecular Pathogenesis of Diseases of Copper Metabolism”, “Copper Toxicity and Therapeutics”, and “Copper Metabolism and Homeostasis”, followed by an extensive index. Each section includes contributions from recognized leaders in the field of copper metabolism and homeostasis.

The first section provides an excellent overview of the flow of copper ions in mammalian cells from uptake to excretion and introduces all the major copper-containing and transporting proteins currently identified. This chapter also introduces the major genetic disorders of copper metabolism: Menkes and Wilson diseases and aceruloplasminemia. The figures in this section are sufficient to