**DESCRIPTION**

*Structural Bioinformatics* was the first major effort to show the application of the principles and basic knowledge of the larger field of bioinformatics to questions focusing on macromolecular structure, such as the prediction of protein structure and how proteins carry out cellular functions, and how the application of bioinformatics to these life science issues can improve healthcare by accelerating drug discovery and development. Designed primarily as a reference, the first edition nevertheless saw widespread use as a textbook in graduate and undergraduate university courses dealing with the theories and associated algorithms, resources, and tools used in the analysis, prediction, and theoretical underpinnings of DNA, RNA, and proteins.

This new edition contains not only thorough updates of the advances in structural bioinformatics since publication of the first edition, but also features eleven new chapters dealing with frontier areas of high scientific impact, including: sampling and search techniques; use of mass spectrometry; genome functional annotation; and much more.

Offering detailed coverage for practitioners while remaining accessible to the novice, *Structural Bioinformatics, Second Edition* is a valuable resource and an excellent textbook for a range of readers in the bioinformatics and advanced biology fields.

**Praise for the previous edition:**

"This book is a gold mine of fundamental and practical information in an area not previously well represented in book form."

—*Biochemistry and Molecular Education*
"... destined to become a classic reference work for workers at all levels in structural bioinformatics... recommended with great enthusiasm for educators, researchers, and graduate students."

—BAMBED

"...a useful and timely summary of a rapidly expanding field."

—Nature Structural Biology

"...a terrific job in this timely creation of a compilation of articles that appropriately addresses this issue."

—Briefings in Bioinformatics

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ABOUT THE AUTHOR

Jenny Gu, PhD, is Assistant Professor at the Skaggs School of Pharmacy and Pharmaceutical Sciences University of California, San Diego. This is her first book.

Philip E. Bourne, PhD, is professor in the Department of Pharmacology at the University of California, San Diego, and Director of Integrated Biosciences at the San Diego Supercomputer Center. He is past president of the International Society for Computational Biology (ISCB). He is author of over 125 peer-reviewed scientific papers and four previous books.

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FEATURES

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A compilation of chapters contributed from leading experts in the field. There are no other books that directly and so comprehensively address the field in this way.

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Updates include new frontiers for the field of Structural Bioinformatics, such as understanding membrane proteins, protein motion, dynamics, and evolution, not well covered by other texts.

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A powerful textbook from which advanced undergraduate or graduate courses in structural bioinformatics can be constructed. See for example http://www.sdsc.edu/pb/edu/pharm201/

• Useful for both those new to the field as well as seasoned professionals.

• Comprehensive reference list on each topic for those who wish to dig deeper.

• Where structural bioinformatics has had significant impact on other fields such as immunology and drug discovery are highlighted.

• A logical organisation which takes the reader from the fundamentals of protein, DNA and RNA structure, through the methods of data collection to inherent errors in the data. This is followed by how the data are classified, stored and subsequently used in a myriad of scientific studies.

• Expanded section on the application of structural bioinformatics to facilitate drug discovery and new therapeutics.

• Expanded section on nucleic acid structures, in particular protein-DNA interactions and RNA structures, which recent findings significantly highlights the complexity of biological processes.

• Unique discussion on leveraging protein structures to understand properties encoded in protein sequence for structure prediction, protein design, and understanding molecular dynamics.

• A unique view into the future of the field defined by today’s experts.

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