

The Ten Most Wanted Solutions in Protein Bioinformatics (Chapman & Hall/CRC Mathematical and Computational Biology)

By Anna Tramontano

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Utilizing high speed computational methods to extrapolate to the rest of the protein universe, the knowledge accumulated on a subset of examples, protein bioinformatics seeks to accomplish what was impossible before its invention, namely the assignment of functions or functional hypotheses for all known proteins.

The Ten Most Wanted Solutions in Protein Bioinformatics considers the ten most significant problems occupying those looking to identify the biological properties and functional roles of proteins.

- Problem One considers the challenge involved with detecting the existence of an evolutionary relationship between proteins.
- Two and Three studies the detection of local similarities between protein sequences and analysis in order to determine functional assignment.
- Four, Five, and Six look at how the knowledge of the three-dimensional structures of proteins can be experimentally determined or inferred, and then exploited to understand the role of a protein.
- Seven and Eight explore how proteins interact with each other and with ligands, both physically and logically.
- Nine moves us out of the realm of observation to discuss the possibility of designing completely new proteins tailored to specific tasks.
- And lastly, Problem Ten considers ways to modify the functional properties of proteins.

After summarizing each problem, the author looks at and evaluates the current approaches being utilized, before going on to consider some potential approaches.

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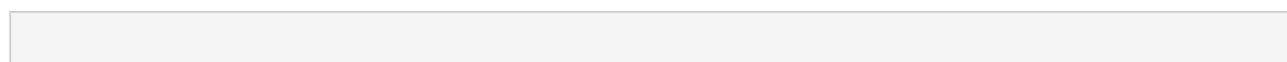
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Editorial Review

Review

The book is comprehensive and succinct; people on busy schedules can read it in a short period of time. ...I believe that it is a great book. I will definitely include it as a recommended text for one of my Bioinformatics Graduate courses. I highly recommend this text to anyone interested in protein bioinformatics.

-Kay C Wiese, Biomedical Engineering OnLine

It succeeds in providing an introduction ... [for] someone with little or no knowledge of protein bioinformatics. For such a reader it would provide a fairly comprehensive, but necessarily brief overview of the research challenges the field faces. ... I would recommend this book to a new prospective researcher...

-D.R. Westhead, UK Nonlinear News

...Clarity and conciseness is apparent throughout the text, and at no point does it get weighted down by excessive detail. The text is equally adroit in its description of biological processes and structures. These are detailed in such a manner as to be easily understood by those with only a limited understanding of protein biology, without oversimplification ... [This book] has something to offer both biologists and informaticians alike, treating computation techniques and biological processes in balanced amounts. If a general high-level and broad ranging discussion of the state of research in protein bioinformatics is sought, then this book comes recommended.

-Dr. Matthew J. Sullivan, Proteomics

To introduce newcomers to this area is not an easy task and this book is a serious attempt to help many of them.

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