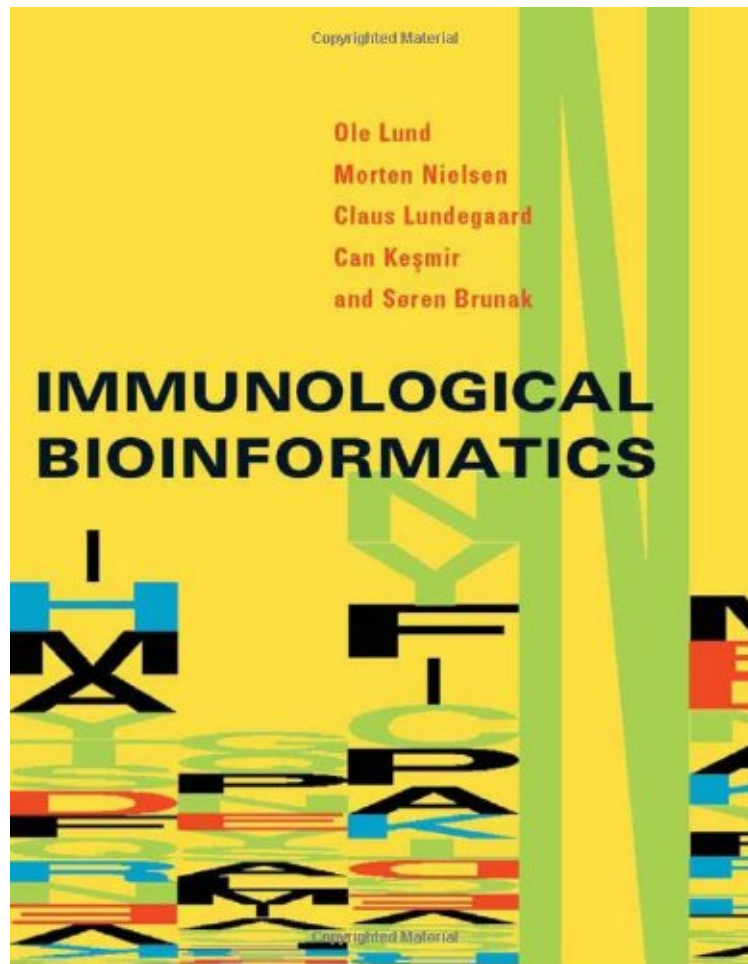


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Immunological Bioinformatics (Computational Molecular Biology)

Ole Lund, Morten Nielsen, Claus Lundegaard, Can Kesmir, Sren Brunak
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Ole Lund, Morten Nielsen, Claus Lundegaard, Can Kesmir, Sren Brunak : Immunological Bioinformatics (Computational Molecular Biology) before purchasing it in order to gage whether or not it would be worth my time, and all praised Immunological Bioinformatics (Computational Molecular Biology):

8 of 9 people found the following review helpful. Bioinformatics at workBy wiredweirdThe huge majority of bioinformatics (BI) books seem to treat the topic as an end in itself. I have to admit, there is a lot to enjoy in the algorithms people have developed and in clever implementations. Often, though, the calculations appear to be fine art, to enjoy in abstract, or for creating point solutions to isolated problems. This book breaks the mold. It addresses every aspect of immunology, using BI as the tool and as the unifying language for discussing immunology's many aspects. The content gets off to a slow start, starting with two chapters describing the topic and its importance. The next three chapters summarize a few of the basic algorithms: alignment and multiple alignment, motif-finding, Gibbs sampling, clustering, and neural networks. The discussion is competent, and the authors' handling of neural nets stands out from

the crowd of BI books. Still, the pace is too brisk and the range of topics is too narrow to recommend this book as a general BI text. It's not one, and never meant to be. That section just reminds the knowledgeable reader of the mathematical tools and BI terms to be used in the remaining nine chapters. Here's where an immunology background will help a lot. I know, because I lack one. Still, the discussion holds to a level that a determined reader with a general bio and BI background can follow. Even at my barely-following level, it's exciting stuff. At this writing, the 2005 H5N1 bird flu is all over the front pages, so medical response to emerging viruses is on people's minds. This book explores the whole range of issues in immunological response to the threat: identifying specific viral features that stand out as vaccine targets, understanding the immunological mechanisms that need to be engaged, evolution of the pathogens to emerging human resistance, and the ways that human variation affects the decisions in medicine and public policy. That last surprised me, but makes perfect sense. Different human populations have slightly different sets of alleles for immunological response. It's one of the reasons that humanity does so well in a world of ever-changing antigenic threats. As a species, we have so many possible responses to any challenge that someone somewhere is bound to be able to survive almost any pathogen around. The range of immune-response alleles, their different sensitivities and combinations, and their distributions in different gene pools helps decide how a vaccine must be crafted. If the vaccine antigen generally triggers a good response in African Americans but not East Asians, it answers only part of the question. This is the first text I know that really shows BI at work in clinically important ways. It's a guided tour of the world of immunological attacks and responses, measured using BI tools - not just pathogens, but allergens, autoimmune triggers, and even possible cancer treatment. Beginners will have a rough time following the discussion, but this is a book for people deep in their specialty. It gave me a good idea of what questions are asked, and why, and how BI answers them. I look forward to seeing an immunological researcher's review of this text - from the pure BI stand point, it's narrow, but shows the versatility of the tools it chooses. //wiredweird

Using bioinformatics methods to generate a systems-level view of the immune system; description of the main biological concepts and the new data-driven algorithms. Despite the fact that advanced bioinformatics methodologies have not been used as extensively in immunology as in other subdisciplines within biology, research in immunological bioinformatics has already developed models of components of the immune system that can be combined and that may help develop therapies, vaccines, and diagnostic tools for such diseases as AIDS, malaria, and cancer. In a broader perspective, specialized bioinformatics methods in immunology make possible for the first time a systems-level understanding of the immune system. The traditional approaches to immunology are reductionist, avoiding complexity but providing detailed knowledge of a single event, cell, or molecular entity. Today, a variety of experimental bioinformatics techniques connected to the sequencing of the human genome provides a sound scientific basis for a comprehensive description of the complex immunological processes. This book offers a description of bioinformatics techniques as they are applied to immunology, including a succinct account of the main biological concepts for students and researchers with backgrounds in mathematics, statistics, and computer science as well as explanations of the new data-driven algorithms in the context of biological data that will be useful for immunologists, biologists, and biochemists working on vaccine design. In each chapter the authors show interesting biological insights gained from the bioinformatics approach. The book concludes by explaining how all the methods presented in the book can be integrated to identify immunogenic regions in microorganisms and host genomes.

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