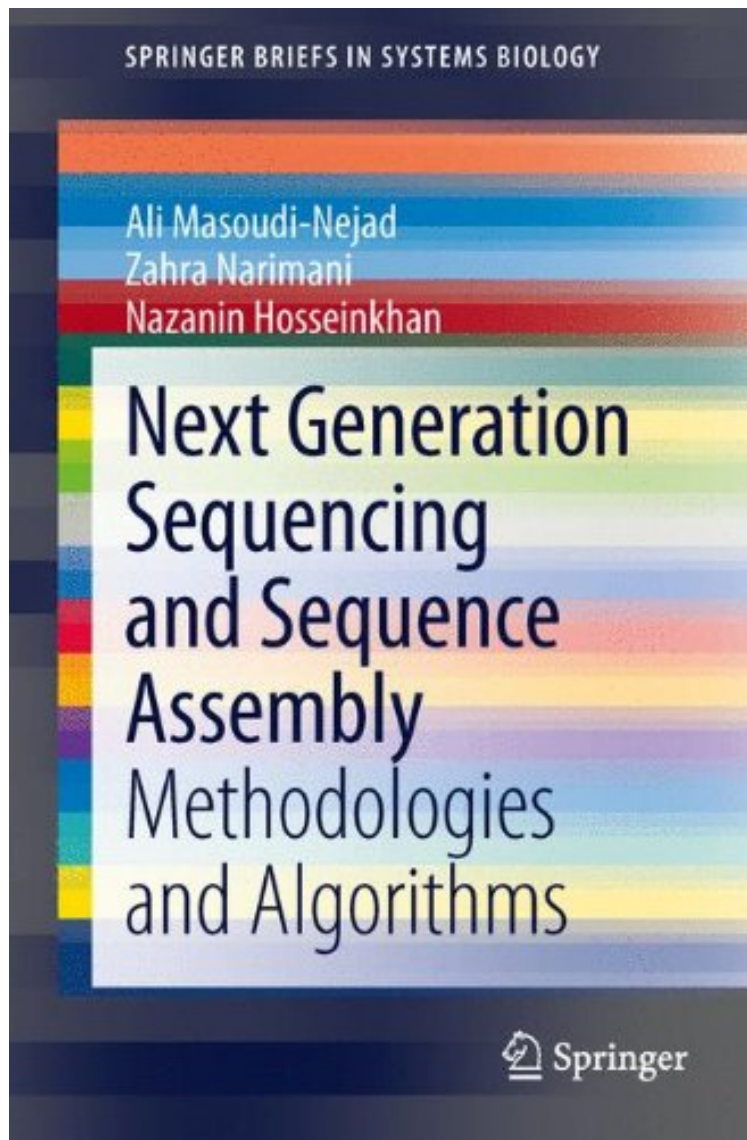


[E-BOOK] Next Generation Sequencing and Sequence Assembly: Methodologies and Algorithms
(SpringerBriefs in Systems Biology)

Next Generation Sequencing and Sequence Assembly: Methodologies and Algorithms (SpringerBriefs in Systems Biology)

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Ali Masoudi-Nejad, Zahra Narimani, Nazanin Hosseinkhan : Next Generation Sequencing and Sequence Assembly: Methodologies and Algorithms (SpringerBriefs in Systems Biology) before purchasing it in order to gage whether or not it would be worth my time, and all praised Next Generation Sequencing and Sequence Assembly: Methodologies and Algorithms (SpringerBriefs in Systems Biology):

0 of 0 people found the following review helpful. A Short Introduction to Sequencing By Dr. Terrence McGarty The test by Nejad et al is one of the Springer texts called Briefs in Systems Biology. This book is brief, less than 80 pages. Simply stated it covers four areas: 1. Classic Sanger approaches to reading DNA 2. Next Gen approaches including the Illumina and other now current systems 3. Collection of segments and purging them 4. Assembling the segments into ordered sequences Overall the book is brief, it mentions most areas, the presentation is reasonable. If one has been exposed to the material and understands most of the key factors the book presents an outline of the issues you should be concerned with. It is in no way something to learn from. Nor was it touted to be such. Its descriptions are quite brief. For example the Illumina technique is explained in one page of text and one graphic. If you know the answer then the presentation presents another view. If, however, you are new to this, you most likely will not gain a great deal. Again the title expresses the fact that this is a Brief. This book can be used to layout for many the areas that they should be focused on and then one is left to seek out other materials. For example Chapter 4 discusses many of the algorithms used to assemble a genome. This is an exceptionally high level presentation and if you understand the issues then it can provide an interesting context. If you do not understand the issue one may quickly get lost. The graph theory approach really requires that one understands graph theory and that is a level of depth well beyond the text. Also there are many probabilistic approaches that the authors do not get into. The authors do discuss some of the pros and cons of the techniques but all too often there are strong schools of thought in each area. Overall the book has value and for those working around the edges and understanding of the issue it may help provide additional directions to explore. As a stand-alone text, it is what it is, a Brief. The book would strongly benefit from a list of terms defined. For the inexperienced reader there are many terms the authors assume are well known but that the target audience may need help with. The graphics are dense and again if you have seen versions of them before they are fine but if it is your first time seeing the descriptions then more space and detail may be needed.

0 of 0 people found the following review helpful. Five Stars By Ruben Agrelo Best book to understand NGS basics. It's a short one and very clear 2 of 3 people found the following review helpful. Poorly edited mixed bag By Andrew Veale Don't bother buying this book. I am beginning a postdoc in molecular ecology involving some next-gen work, and I thought that it would be nice to have a light overview of next-gen techniques. I have a good understanding of genetics, but wanted a concise update on next-gen techniques covering the basics to make sure I have a good general understanding. This is obviously what the book is meant to be, however it fails at the task. A great deal of it is at the extremely basic level which wikipedia deals with as well (better). When it does focus on more technical aspects it doesn't explain them clearly, and you must then go and look up terms that are never defined in the text. I would recommend a browse through wikipedia above this book. Also, throughout there are grammatical errors - which generally are interpretable, however it does detract from the understanding and flow. There are a few sentences that make no sense and I have no idea what the authors meant. This field is moving very rapidly, and while it would be nice to have a concise overview of the topics, this probably doesn't exist yet.

The goal of this book is to introduce the biological and technical aspects of next generation sequencing methods, as well as algorithms to assemble these sequences into whole genomes. The book is organized into two parts; part 1 introduces NGS methods and part 2 reviews assembly algorithms and gives a good insight to these methods for readers new to the field. Gathering information, about sequencing and assembly methods together, helps both biologists and computer scientists to get a clear idea about the field. Chapters will include information about new sequencing technologies such as ChIP-seq, ChIP-chip, and De Novo sequence assembly.