Next-Generation Sequencing Data Analysis

Xinkun Wang
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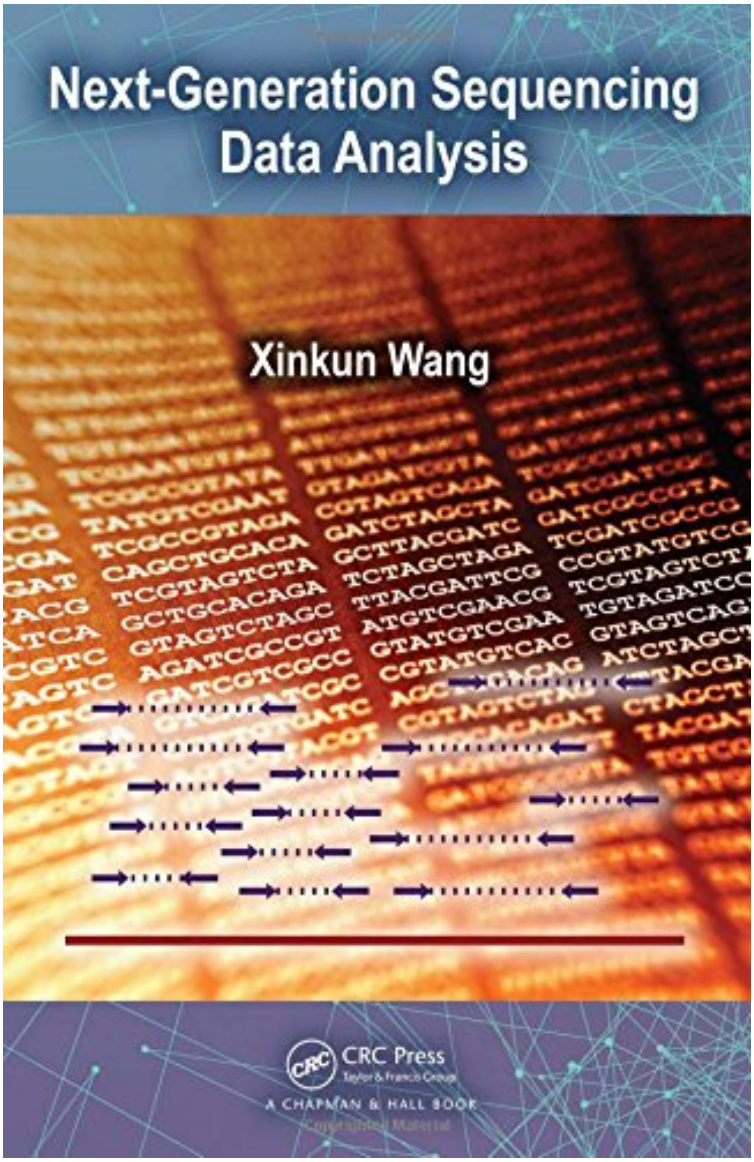

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Xinkun Wang : Next-Generation Sequencing Data Analysis before purchasing it in order to gage whether or not it would be worth my time, and all praised Next-Generation Sequencing Data Analysis:

1 of 1 people found the following review helpful. READER REVIEW.By Tianhao XuI bought this book right around Christmas, it is a very good overview of today's technology in High through-put sequencing field. Although the price of the book is higher than other books, it is relatively useful for people who want to know about the sequencing. ~50 pages of introduction. No programming detail, which makes sense because there are so many ways you can analyze

your data. If you have the money, not bad to own one, the book is systematic. By the way, there are also a lot of materials that you can find online.0 of 0 people found the following review helpful. 3) of this book provides a very good introduction to molecular biology for non-biologists (in particular Statisticians/ComputeBy Kwame OkrahThe first section (Chapter 1, 2, 3) of this book provides a very good introduction to molecular biology for non-biologists (in particular Statisticians/Computer Scientists interested in high-throughput genomics analysis).

A Practical Guide to the Highly Dynamic Area of Massively Parallel Sequencing The development of genome and transcriptome sequencing technologies has led to a paradigm shift in life science research and disease diagnosis and prevention. Scientists are now able to see how human diseases and phenotypic changes are connected to DNA mutation, polymorphism, genome structure, and epigenomic abnormality. Next-Generation Sequencing Data Analysis shows how next-generation sequencing (NGS) technologies are applied to transform nearly all aspects of biological research. The book walks readers through the multiple stages of NGS data generation and analysis in an easy-to-follow fashion. It covers every step in each stage, from the planning stage of experimental design, sample processing, sequencing strategy formulation, the early stage of base calling, reads quality check and data preprocessing to the intermediate stage of mapping reads to a reference genome and normalization to more advanced stages specific to each application. All major applications of NGS are covered, including: RNA-seq: mRNA-seq and small RNA-seq Genotyping and variant discovery through genome re-sequencing De novo genome assembly ChIP-seq to study DNAprotein interaction Methylated DNA sequencing on epigenetic regulation Metagenome analysis through community genome shotgun sequencing Before detailing the analytic steps for each of these applications, the book presents the ins and outs of the most widely used NGS platforms, with side-by-side comparisons of key technical aspects. This helps practitioners decide which platform to use for a particular project. The book also offers a perspective on the development of DNA sequencing technologies, from Sanger to future-generation sequencing technologies. The book discusses concepts and principles that underlie each analytic step, along with software tools for implementation. It highlights key features of the tools while omitting tedious details to provide an easy-to-follow guide for practitioners in life sciences, bioinformatics, and biostatistics. In addition, references to detailed descriptions of the tools are given for further reading if needed. The accompanying website for the book provides step-by-step, real-world examples of how to apply the tools covered in the text to research projects. All the tools are freely available to academic users.

About the AuthorDr. Xinkun "Sequen" Wang is the director of the NUSeq Core Facility and research associate professor in the Department of Biochemistry and Molecular Genetics at Northwestern University. He was previously an associate research professor of neurogenomics in the Higuchi Biosciences Center and Department of Pharmacology and Toxicology at the University of Kansas, where he was also the director of the Genomics Facility and Genome Sequencing Core. Dr. Wangs research focuses on unraveling genomic changes that underlie neurodegeneration in brain aging and neurodegenerative diseases, such as Alzheimers disease.