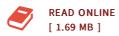




# High-performance Metagenome Gene Identification

By Savran, Ibrahim

Condition: New. Publisher/Verlag: LAP Lambert Academic Publishing | Processing Big Data in Bioinformatics with Super Computers | Computational Genomics, or Computational Genetics, refers to the use of computational and statistical analysis for understanding the structure, and the function, of genetic material in organisms. The primary focus of research in computational genomics in the past three decades has been the understanding of genomes and their functional elements by analyzing biological sequence data. The high demand for low-cost sequencing has driven the development of high-throughput sequencing technologies, next-generation sequencing (NGS), that parallelize the sequencing process, producing thousands or millions of sequences concurrently. Moore's Law, is the observation that the number of transistors on integrated circuits doubles approximately every two years, correspondingly, the cost per transistor halves. The cost of DNA sequencing is declining much faster, which implies more new DNA data we will be obtained. This large-scale sequence data, produced with high throughput sequencing technologies, needs to be processed in a time-effective and cost-effective manner. In this book, you will find fundamental techniques to process big metagenome data on super computers. | Format: Paperback | Language/Sprache: english | 80 pp.



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