

# Genome Analysis

## Current Procedures and Applications



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In recent years there have been tremendous achievements made in DNA sequencing technologies and corresponding innovations in data analysis and bioinformatics that have revolutionized the field of genome analysis.

In this book, an impressive array of expert authors highlight and review current advances in genome analysis. This volume provides an invaluable, up-to-date and comprehensive overview of the methods currently employed for next-generation sequencing (NGS) data analysis, highlights their problems and limitations, demonstrates the applications and indicates the developing trends in various fields of genome research. The first part of the book is devoted to the methods and applications that arose from, or were significantly advanced by, NGS technologies: the identification of structural variation from DNA-seq data; whole-transcriptome analysis and discovery of small interfering RNAs (siRNAs) from RNA-seq data; motif finding in promoter regions, enhancer prediction and nucleosome sequence code discovery from ChIP-Seq data; identification of methylation patterns in cancer from MeDIP-seq data; transposon identification in NGS data; metagenomics and metatranscriptomics; NGS of viral communities; and causes and consequences of genome instabilities. The second part is devoted to the field of RNA biology with the last three chapters devoted to computational methods of RNA structure prediction including context-free grammar applications.

An essential book for everyone involved in sequence data analysis, next-generation sequencing, high-throughput sequencing, RNA structure prediction, bioinformatics and genome analysis.

**Chapter 1.** Identification of Structural Variation. *Suzanne S. Sindi and Benjamin J. Raphael*

**Chapter 2.** Methods for RNA Isolation, Characterization, and Sequencing. *Paul Zumbo and Christopher E. Mason*

**Chapter 3.** Transcriptome Reconstruction and Quantification from RNA Sequencing Data. *Sahar Al Seesi, Serghei Mangul, Adrian Caciula, Alex Zelikovsky and Ion M&#259;ndoiu*

**Chapter 4.** Identification of Small Interfering RNA from Next-generation Sequencing Data. *Thomas J. Hardcastle*

**Chapter 5.** Motif Discovery and Motif Finding in ChIP-Seq Data. *Ivan V. Kulakovskiy and Vsevolod J. Makeev*

**Chapter 6.** Mammalian Enhancer Prediction. *Dongwon Lee and Michael A. Beer*

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**Chapter 8.** Hypermethylation in Cancer. *Marta Sánchez-Carbayo*

**Chapter 9.** Identification and Analysis of Transposable Elements in Genomic Sequences. *Laurent Modolo and Emmanuelle Lerat*

**Chapter 10.** The Current State of Metagenomic Analysis. *Pieter De Maayer, Angel Valverde and Don A. Cowan*

**Chapter 11.** Metatranscriptomics. *Atsushi Ogura*

**Chapter 12.** Inferring Viral Quasispecies Spectra from Shotgun and Amplicon Next-generation Sequencing Reads. *Irina Astrovskaya, Nicholas Mancuso, Bassam Tork, Serghei Mangul, Alex Artyomenko, Pavel Skums, Lilia Ganova-Raeva, Ion M&#259;ndoiu and Alex Zelikovsky*

**Chapter 13.** DNA Instability in Bacterial Genomes: Causes and Consequences. *Pedro H. Oliveira, Duarte M. F. Prazeres and Gabriel A. Monteiro*

**Chapter 14.** Comparative Methods For RNA Structure Prediction. *Eckart Bindewald and Bruce A. Shapiro*

**Chapter 15.** Context-free Grammars and RNA Secondary Structure Prediction. *Markus E. Nebel and Anika Schulz*

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