



# Next-Generation DNA Sequencing Informatics, Second Edition

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## Next-Generation DNA Sequencing Informatics, Second Edition

Next-generation DNA sequencing (NGS) technology has revolutionized biomedical research, making genome and RNA sequencing an affordable and frequently used tool for a wide variety of research applications including variant (mutation) discovery, gene expression, transcription factor analysis, metagenomics, and epigenetics. Bioinformatics methods to support DNA sequencing have become and remain a critical bottleneck for many researchers and organizations wishing to make use of NGS technology. This new edition provides a thorough, plain-language introduction to the necessary informatics methods and tools for analyzing NGS data and provides detailed descriptions of algorithms, strengths and weaknesses of specific tools, pitfalls, and alternative methods. Four new chapters cover experimental design, sample preparation, and quality assessment of NGS data; public databases for DNA sequencing data; de novo transcript assembly; proteogenomics; and emerging sequencing technologies. The remaining chapters from the first edition have been updated with the latest information. This book also provides extensive reference to best-practice bioinformatics methods for NGS applications and tutorials for common workflows. This edition addresses the informatics needs of students, laboratory scientists, and computing specialists who wish to take advantage of the explosion of research opportunities offered by new DNA sequencing technologies.

## Authors

Alexander Alekseyenko  
Silvia Argimón  
Brian D. Athey  
Miroslav Blumenberg  
Stuart M. Brown  
Lisa Cohen  
Efstratios Efstathiadis  
David Fenyő  
Jeremy Goecks  
Gerald A. Higgins  
D. Frank Hsu  
Kranti Konganti  
Konstantinos Krampis  
Guillermo I. Perez-Perez  
Kelly V. Ruggles  
Christina Schweikert  
Steven Shen  
Phillip Ross Smith  
Zuojian Tang  
Jinhua Wang

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