

In most modern biomedical research projects, application of high-throughput genomic, proteomic, and transcriptomic experiments has gradually become an inevitable component. Popular technologies include microarray, next generation sequencing, mass spectrometry, and proteomics assays. As the technologies have become mature and the price affordable, omics data are rapidly generated, and the problem of information integration and modeling of multi-lab and/or multi-omics data is becoming a growing one in the bioinformatics field.

This book provides comprehensive coverage of these topics and will have a long-lasting impact on this evolving subject. Each chapter, written by a leader in the field, introduces state-of-the-art methods to handle information integration, experimental data, and database problems of omics data.

George Tseng completed his ScD in biostatistics with a concentration in genomics from the Harvard School of Public Health. He is currently a professor of biostatistics, human genetics, and computational and systems biology at the University of Pittsburgh. His research interests focus on statistical and computational method development for analyzing high-throughput omics data.

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Xianghong Jasmine Zhou completed her PhD at the Swiss Federal Institute of Technology (ETH Zurich) and conducted her post-doc training at Harvard University. She is currently Director and Professor of the Computational Biology and Bioinformatics program at the University of Southern California. Dr. Zhou is the PI of the NIH center for knowledge base on disease connections within the MAPGen consortium. She heads the laboratory of computational integrative genomics, addressing the "Big Data" challenges brought by the enormous amount of extremely diverse genomic data in public repositories. She was a recipient of several awards, including an Alfred Sloan fellowship and a NSF Career award.

Cover image: Abstract illustration of DNA double helix © scotspencer

Cover design by James F. Brisson

CAMBRIDGE
UNIVERSITY PRESS
www.cambridge.org

ISBN 978-1-107-06911-4

