Integrating Omics Data

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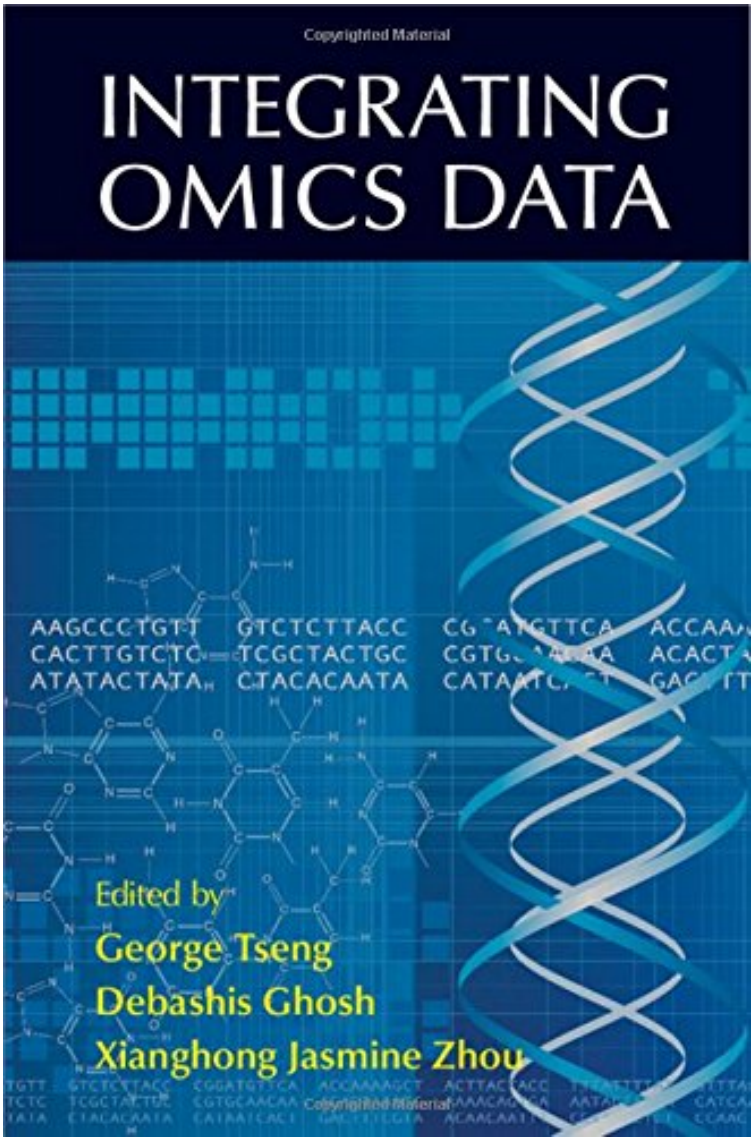

#3356842 in Books Xianghong Jasmine Zhou George Tseng Debashis Ghosh 2015-09-23Original language:EnglishPDF # 1 8.98 x 1.18 x 5.98l, 1.82 #File Name: 1107069114476 pagesIntegrating Omics Data | File size: 38.Mb

George Tseng, Debashis Ghosh, Xianghong Jasmine Zhou : Integrating Omics Data before purchasing it in order to gage whether or not it would be worth my time, and all praised Integrating Omics Data:

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 and next-generation sequencing such as CHiP and RNA-Seq. 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.

About the AuthorGeorge Tseng completed his Sc.D. 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.Debashis Ghosh completed his Ph.D. in biostatistics from the University of Washington. After serving on the faculty in the Department of Biostatistics at the University of Michigan and in the Department of Statistics at Pennsylvania State University, he is currently Chair and Professor in the Department of Biostatistics and Informatics at the Colorado School of Public Health. His interests in statistical genomics have primarily focused on the development of novel methods for integration of high-throughput data from different platforms. These motivating problems have also led to lines of methodologic research in the areas of multiple comparisons procedures, machine learning techniques and Empirical Bayes procedures. Ghosh is a recipient of several awards including Fellow of the American Statistical Association and the 2013 recipient of the Mortimer Spiegelman Award, for early career contributions of statistics in applied public health problems.Jasmine Zhou completed her Ph.D. at the Swiss Federal Institute of Technology (ETH Zurich), and conducted her post-doc training at Harvard University. She is currently a professor of biological sciences and computer science 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. Dr Zhou heads the laboratory of computational integrative genomics at the University of Southern California, 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.