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Providing genome-informed personalized treatment is a goal of modern medicine. Identifying new translational targets in nucleic acid characterizations is an important step toward that goal. The information tsunami produced by such genome-scale investigations is stimulating parallel developments in statistical methodology and inference, analytical frameworks, and computational tools. Within the context of genomic medicine and with a strong focus on cancer research, this book describes the integration of high-throughput bioinformatics data from multiple platforms to inform our understanding of the functional consequences of genomic alterations. This includes rigorous and scalable methods for simultaneously handling diverse data types such as gene expression array, miRNA, copy number, methylation, and next-generation sequencing data. This material is written for statisticians who are interested in modeling and analyzing high-throughput data. Chapters by experts in the field offer a thorough introduction to the biological and technical principles behind multiplatform high-throughput experimentation.

"Chapter 1 An introduction to next-generation biological platforms Virginia Mohlere, Wenting Wang, and Ganiraju Manyam The University of Texas. MD Anderson Cancer Center 1.1 Introduction When Sanger and Coulson first described a reliable, efficient method for DNA sequencing in 1975 (Sanger and Coulson, 1975), they made possible the full sequencing of both genes and entire genomes. Although the method was resource-intensive, many institutions invested in the necessary equipment, and Sanger sequencing remained the standard for the next 30 years. Refinement of the process increased read lengths from around 25 to 2 Mohlere, Wang, and Manyam almost 750 base pairs (Schadt et al., 2010, fig. 1). While this greatly increased efficiency and reliability, the Sanger method still required not only large equipment but significant human investment, as the process requires the work of several people. This prompted researchers and companies such as Applied Biosystems to seek improved sequencing techniques and instruments. Starting in the late 2000s, new instruments came on the market that, although they actually decreased read length, lessened run time and could be operated more easily with fewer human resources (Schadt et al., 2010). Despite discoveries that have illuminated new therapeutic targets, clarified the role of specific mutations in clinical response, and yielded new methods for diagnosis and predicting prognosis (Chin et al., 2011), the initial promise of genomic data has largely remained so far unfulfilled. The difficulties are numerous"--

The Most Comprehensive and Cutting-Edge Guide to Statistical Applications in Biomedical Research With the increasing use of biotechnology in medical research and the sophisticated advances in computing, it has become essential for practitioners in the biomedical sciences to be fully educated on the role statistics plays in ensuring the accurate analysis of research findings. Statistical Advances in the Biomedical Sciences explores the growing value of statistical knowledge in the management and comprehension of medical research and, more specifically, provides an accessible introduction to the contemporary methodologies used to understand complex problems in the four major areas of modern-day biomedical science: clinical trials, epidemiology, survival analysis, and bioinformatics. Composed of contributions from eminent researchers in the field, this volume discusses the application of statistical techniques to various aspects of modern medical research and illustrates how these methods ultimately prove to be an indispensable part of proper data collection and analysis. A structural uniformity is maintained across all chapters, each beginning with an introduction that discusses general concepts and the biomedical problem under focus and is followed by specific details on the associated methods, algorithms, and applications. In addition, each chapter provides a summary of the main ideas and offers a concluding remarks section that presents novel ideas, approaches, and challenges for future research. Complete with detailed references and insight on the future directions of

biomedical research, Statistical Advances in the Biomedical Sciences provides vital statistical guidance to practitioners in the biomedical sciences while also introducing statisticians to new, multidisciplinary frontiers of application. This text is an excellent reference for graduate- and PhD-level courses in various areas of biostatistics and the medical sciences and also serves as a valuable tool for medical researchers, statisticians, public health professionals, and biostatisticians.

Advances in computers and biotechnology have had a profound impact on biomedical research, and as a result complex data sets can now be generated to address extremely complex biological questions. Correspondingly, advances in the statistical methods necessary to analyze such data are following closely behind the advances in data generation methods. The statistical methods required by bioinformatics present many new and difficult problems for the research community. This book provides an introduction to some of these new methods. The main biological topics treated include sequence analysis, BLAST, microarray analysis, gene finding, and the analysis of evolutionary processes. The main statistical techniques covered include hypothesis testing and estimation, Poisson processes, Markov models and Hidden Markov models, and multiple testing methods. The second edition features new chapters on microarray analysis and on statistical inference, including a discussion of ANOVA, and discussions of the statistical theory of motifs and methods based on the hypergeometric distribution. Much material has been clarified and reorganized. The book is written so as to appeal to biologists and computer scientists who wish to know more about the statistical methods of the field, as well as to trained statisticians who wish to become involved with bioinformatics. The earlier chapters introduce the concepts of probability and statistics at an elementary level, but with an emphasis on material relevant to later chapters and often not covered in standard introductory texts. Later chapters should be immediately accessible to the trained statistician. Sufficient mathematical background consists of introductory courses in calculus and linear algebra. The basic biological concepts that are used are explained, or can be understood from the context, and standard mathematical concepts are summarized in an Appendix. Problems are provided at the end of each chapter allowing the reader to develop aspects of the theory outlined in the main text. Warren J. Ewens holds the Christopher H. Brown Distinguished Professorship at the University of Pennsylvania. He is the author of two books, Population Genetics and Mathematical Population Genetics. He is a senior editor of Annals of Human Genetics and has served on the editorial boards of Theoretical Population Biology, GENETICS, Proceedings of the Royal Society B and SIAM Journal in Mathematical Biology. He is a fellow of the Royal Society and the Australian Academy of Science. Gregory R. Grant is a senior bioinformatics researcher in the University of Pennsylvania Computational Biology and Informatics Laboratory. He obtained his Ph.D. in number theory from the University of Maryland in 1995 and his Masters in Computer Science from the University of Pennsylvania in 1999. Comments on the first edition: "This book would be an ideal text for a postgraduate course...[and] is equally well suited to individual study.... I would recommend the book highly." (Biometrics) "Ewens and Grant have given us a very welcome introduction to what is behind those pretty [graphical user] interfaces." (Naturwissenschaften) "The authors do an excellent job of presenting the essence of the material without getting bogged down in mathematical details." (Journal American Statistical Association) "The authors have restructured classical material to a great extent and the new organization of the different topics is one of the outstanding services of the book." (Metrika)

This unified volume is a collection of invited chapters presenting recent developments in the field of data analysis, with applications to reliability and inference, data mining, bioinformatics, lifetime data, and neural networks. The book is a useful reference for graduate students, researchers, and practitioners in statistics, mathematics, engineering, economics, social science, bioengineering, and bioscience.

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Papers presented at the conference, held during 23-27 Nov. 2003, at Banaras Hindu University, Varanasi.

A far-reaching course in practical advanced statistics for biologists using R/Bioconductor, data exploration, and simulation.

This book gathers papers presented at the 13th International Conference on Genetic and Evolutionary Computing (ICGEC 2019), which was held in Qingdao, China, from 1st to 3rd, November 2019. Since it was established, in 2006, the ICGEC conference series has been devoted to new approaches with a focus on evolutionary computing. Today, it is a forum for the researchers and professionals in all areas of computational intelligence including evolutionary computing, machine learning, soft computing, data mining, multimedia and signal processing, swarm intelligence and security. The book appeals to policymakers, academics, educators, researchers in pedagogy and learning theory, school teachers, and other professionals in the learning industry, and further and continuing education.

This book is comprised of the presentations delivered at the 25th ICSA Applied Statistics Symposium held at the Hyatt Regency Atlanta, on June 12-15, 2016. This symposium attracted more than 700 statisticians and data scientists working in academia, government, and industry from all over the world. The theme of this conference was the “ Challenge of Big Data and Applications of Statistics, ” in recognition of the advent of big data era, and the symposium offered opportunities for learning, receiving inspirations from old research ideas and for developing new ones, and for promoting further research collaborations in the data sciences. The invited contributions addressed rich topics closely related to big data analysis in the data sciences, reflecting recent advances and major challenges in statistics, business statistics, and biostatistics. Subsequently, the six editors selected 19 high-quality presentations and invited the speakers to prepare full chapters for this book, which showcases new methods in statistics and data sciences, emerging theories, and case applications from statistics, data science and interdisciplinary fields. The topics covered in the book are timely and have great impact on data sciences, identifying important directions for future research, promoting advanced statistical methods in big data science, and facilitating future collaborations across disciplines and between theory and practice.