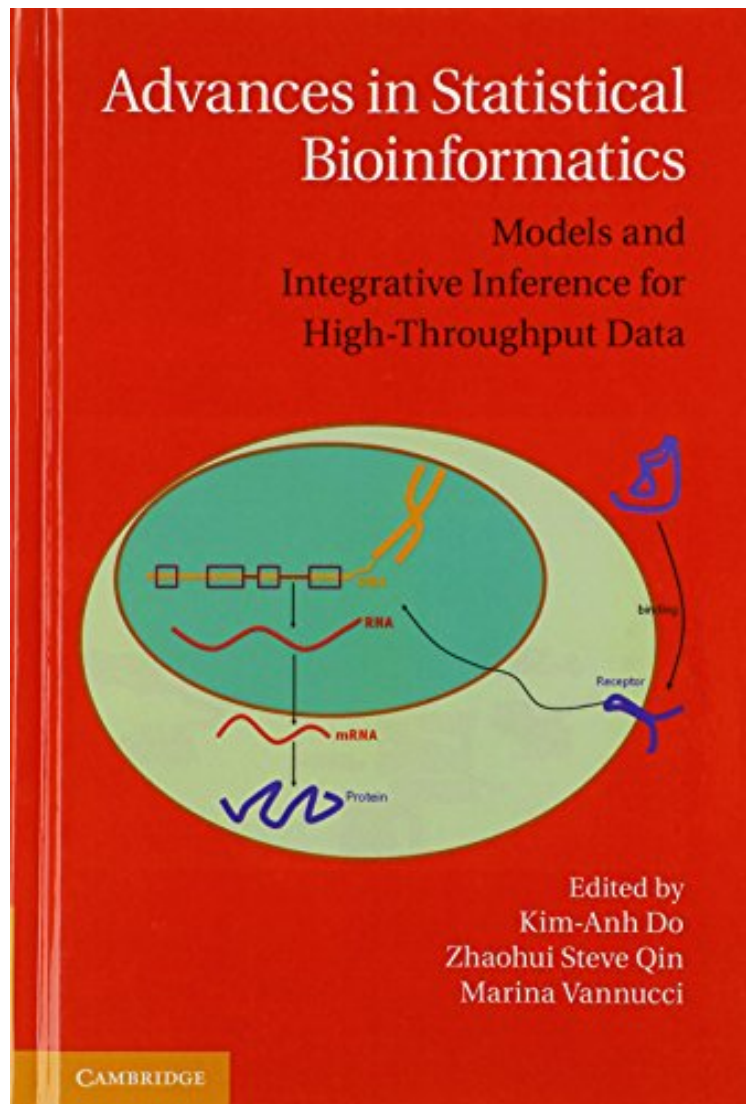


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Advances in Statistical Bioinformatics: Models and Integrative Inference for High-Throughput Data

From Kim Anh Do

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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.

About the Author Dr Kim-Anh Do is a Professor of Biostatistics, ad interim Head of the Division of Quantitative Sciences, and ad interim Chair of the Department of Biostatistics at the University of Texas MD Anderson Cancer Center. Zhaohui Steve Qin is an Associate Professor in the Department of Biostatistics and Bioinformatics at the Rollins School of Public Health, Emory University. Dr Marina Vannucci is currently a Professor in the Department of Statistics and Director of the Interinstitutional Graduate Program in Biostatistics at Rice University and an adjunct faculty member of the University of Texas MD Anderson Cancer Center.