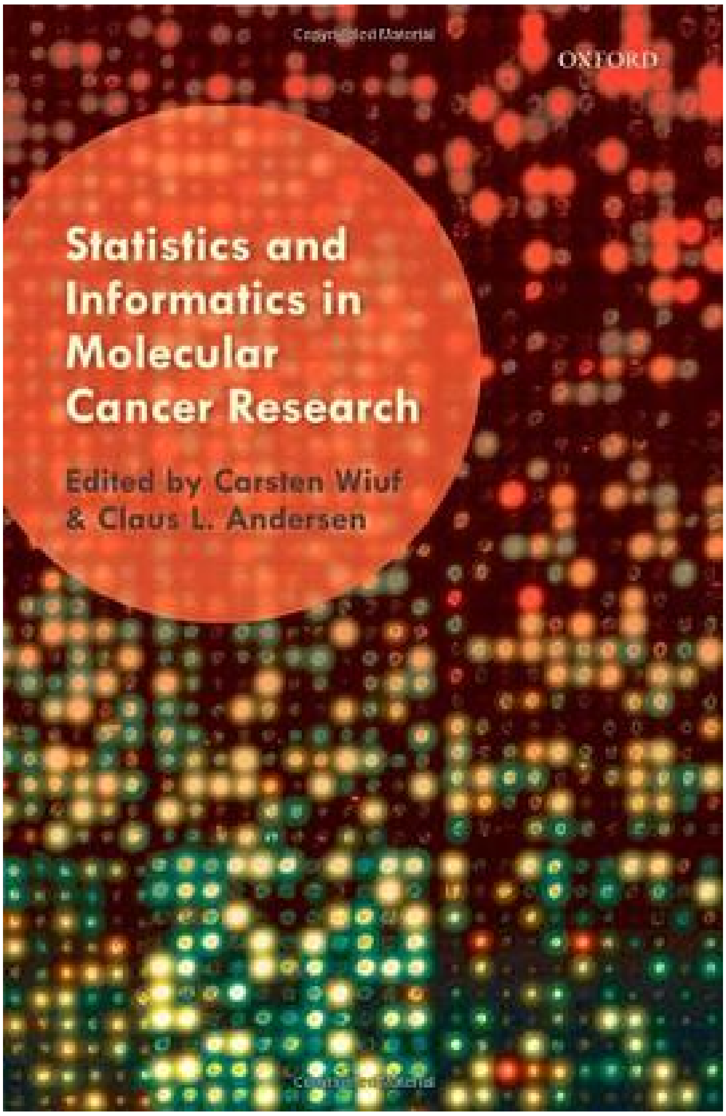
Statistics and Informatics in Molecular Cancer Research



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Molecular understanding of cancer and cancer progression is at the forefront of many research programs today. High-throughput array technologies and other modern molecular techniques produce a wealth of molecular data about the structure, and function of cells, tissues, and organisms. Correctly analyzed and interpreted these data hold the promise of bringing new markers for prognostic and diagnostic use, for new treatment schemes, and of gaining new biological insight into the evolution of cancer and its molecular, pathological, and clinical consequences. Aimed at graduates and researchers, this book discusses novel advances in informatics and statistics in molecular cancer research. Through eight chapters from carefully chosen experts it brings the reader up to date with specific topics in cancer research, how the topics give rise to development of new informatics and statistics tools, and how the tools can be applied. The focus of the book is to give the reader an understanding of key concepts and tools, rather than focusing on technical issues. A main theme is the extensive use of array technologies in modern cancer research - gene expression and exon arrays, SNP and copy number arrays, and methylation arrays - to derive quantitative and qualitative statements about cancer, its progression and aetiology, and to understand how these technologies on one hand allow us learn about cancer tissue as a complex system and on the other hand allow us to pinpoint key genes and events as crucial for the development of the disease.

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标签

评论

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