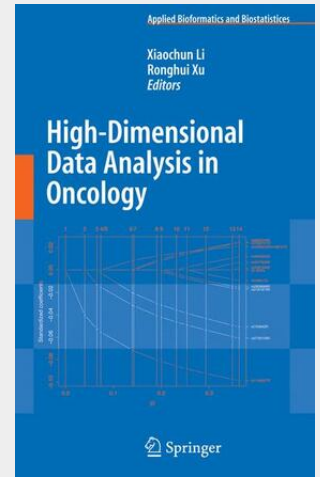


## High-Dimensional Data Analysis in Cancer Research

Multivariate analysis is a mainstay of statistical tools in the analysis of biomedical data. It concerns with associating data matrices of  $n$  rows by  $p$  columns, with rows representing samples (or patients) and columns attributes of samples, to some response variables, e.g., patients outcome. Classically, the sample size  $n$  is much larger than  $p$ , the number of variables. The properties of statistical models have been mostly discussed under the assumption of fixed  $p$  and infinite  $n$ . The advance of biological sciences and technologies has revolutionized the process of investigations of cancer. The biomedical data collection has become more automatic and more extensive. We are in the era of  $p$  as a large fraction of  $n$ , and even much larger than  $n$ . Take proteomics as an example. Although proteomic techniques have been researched and developed for many decades to identify proteins or peptides uniquely associated with a given disease state, until recently this has been mostly a laborious process, carried out one protein at a time. The advent of high throughput proteome-wide technologies such as liquid chromatography-tandem mass spectroscopy make it possible to generate proteomic signatures that facilitate rapid development of new strategies for proteomics-based detection of disease. This poses new challenges and calls for scalable solutions to the analysis of such high dimensional data. In this volume, we will present the systematic and analytical approaches and strategies from both biostatistics and bioinformatics to the analysis of correlated and high-dimensional data.

With the advent of high-throughput technologies, various types of high-dimensional data have been generated in recent years for the understanding of biological processes, especially processes that relate to disease occurrence or management of cancer. Motivated by these important applications in cancer research, there has been a dramatic growth in the development of statistical methodology in the analysis of high-dimensional data, particularly related to regression model selection, estimation and prediction. High-Dimensional Data Analysis in Cancer Research, edited by Xiaochun Li and Ronghui Xu, is a collective effort to showcase statistical innovations for meeting the challenges and opportunities uniquely presented by the analytical needs of high-dimensional data in cancer research, particularly in genomics and proteomics. All the chapters included in this volume contain interesting case studies to demonstrate the analysis methodology. High-Dimensional Data Analysis in Cancer Research is an invaluable reference for researchers, statisticians, bioinformaticians, graduate students and data analysts working in the fields of cancer research.



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