<<生物统计学和生物信息学最新进展>>

图书基本信息

书名：<<生物统计学和生物信息学最新进展>>

13位ISBN编号：9787040247558

10位ISBN编号：7040247550

出版时间：2008-12

出版时间：高等教育出版社

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页数：269

前言

The first eight years of the twenty-first century has witted the explosion of datacollection, with relatively low costs. Data with curves, images and movies are fre-quently collected in molecular biology, health science, engineering, geology, clima-tology, economics, finance, and humanities. For example, in biomedical research,MRI, fMRI, microarray, and proteomics data are frequently collected for eachsubject, involving hundreds of subjects; in molecular biology, massive sequencingdata are becoming rapidly available; in natural resource discovery and agricul-ture, thousands of high-resolution images are collected; in business and finance,millions of transactions are recorded every day. Frontiers of science, engineering,and humanities differ in the problems of their concerns, but nevertheless share acommon theme: massive or complex data have been collected and new knowledgeneeds to be discovered. Massive data collection and new scientific research havestrong impact on statistical thinking, methodological development, and theoreti-cal studies. They have also challenged traditional statistical theory, methods, andcomputation. Many new insights and phenomena need to be discovered and newstatistical tools need to be developed.With this background, the Center for Statistical Research at the ChineseAcademy of Science initiated the conference series "International Conference onthe Frontiers of Statistics" in 2005. The aim is to provide a focal venue for re-searchers to gather, interact, and present their new research findings, to discussand outline emerging problems in their fields, to lay the groundwork for future col-laborations, and to engage more statistical scientists in China to conduct researchin the frontiers of statistics. After the general conference in 2005, the 2006 Inter-national Conference on the Frontiers of Statistics, held in Changchun, focused onthe topic "Biostatistics and Bioinformatics". The conference attracted many topresearchers in the area and was a great success. However, there are still a lot ofChinese scholars, particularly young researchers and graduate students, who werenot able to attend the conference. This hampers one of the purposes of the con-ference series. However, an Mternative idea was born: inviting active researchersto provide a bird-eye view on the new developments in the frontiers of statistics,on the theme topics of the conference series. This will broaden significantly thebenefits of statistical research, both in China and worldwide. The edited books inthis series aim at promoting statistical research that has high societal impacts andprovide not only a concise overview on the recent developments in the frontiers ofstatistics, but also useful references to the literature at large, leading readers trulyto the frontiers of statistics.

内容概要

《生物统计学和生物信息学最新进展》主要内容：presents an overview of recent developments in biostatistics and bioinformatics. Written by active researchers in these emerging areas, it is intended to give graduate students and new researchers an idea of where the frontiers of biostatistics and bioinformatics are as well as a forum to learn common techniques in use, so that they can advance the fields via developing new techniques and new results. Extensive references are provided so that researchers can follow the threads to learn more comprehensively what the literature is and to conduct their own research. In particulars, the book covers three important and rapidly advancing topics in biostatistics: analysis of survival and longitudinal data, statistical methods for epidemiology.

书籍目录

章节摘录

插图：We assume that patients can be divided into twogroups based on an assay of a biomarker. This biomarker could be a compositeof hundreds of molecular and genetic factors, for example, but in this case wesuppose that a cutoff value has been determined that dichotomizes these values.In our example the biomarker is the expression of guanylyl cyclase C （GCC） in thelymph nodes of patients. We assume that we have an estimate of the sensitivityand specificity of the biomarker assay. The variable of patient response is takento be continuous-valued; it could represent a measure of toxicity to the patient,quality of life, uncensored survival time, or a composite of several measures. Inour example we take the endpoint to be three-year disease recurrence.We consider five study designs, each addressing its own set of scientific ques-tions, to study how patients in each marker group fare with each treatment. Al-though consideration of which scientific questions are to be addressed by the studyshould supersede consideration of necessary sample size, we give efficiency com-parisons here for those cases in which more than one design would be appropriate.One potential goal is to investigate how treatment assignment and patient markerstatus affect outcome, both separately and interactively. The marker under con-sideration is supposedly predictive: it modifies the treatment effect. We may wantto verify its predictive value and to assess its prognostic value, that is, how wellit divides patients receiving the same treatment into different risk groups. Eachstudy design addresses different aspects of these overarching goals.This paper is organized as follows:1. Definition of study designs2. Test of hypotheses3. Sample size calculation4. Numerical comparison of efficiency5. Conclusions2 Definition of study designsThe individual study designs are as follows.2.1 Traditional designTo assess the safety and efficacy of the novel treatment, the standard design （Fig. 1） is to register patients, then randomize thorn with ratio ~~ to receive treatment Aor B. We compare the response variable across the two arms of the trial withoutregard for the marker status of the patients.In our example, we would utilize this design if we wanted only to compare therecurrence rates of colorectal cancer in the two treatment groups independent ofeach patient's biomarker status.

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