Dynamic Prediction In Clinical Survival Analysis Chapman Hallcrc Monographs On Statistics Applied Probability

Cancer is a major healthcare burden across the world and impacts not only the people diagnosed with various cancers but also their families, carers, and healthcare systems. With advances in the diagnosis and treatment, more people are diagnosed early and receive treatments for a disease where few treatments options were previously available. As a result, the survival of patients with cancer has steadily improved and, in most cases, patients who are not cured may receive multiple lines of treatment, often with financial consequences for the patients, insurers and healthcare systems. Although many books exist that address economic evaluation, Economic Evaluation of Cancer Drugs using Clinical Trial and Real World Data is the first unified text that specifically addresses the economic evaluation of cancer drugs. The authors discuss how to perform cost-effectiveness analyses while emphasising the strategic importance of designing cost-effectiveness into cancer trials and building robust economic evaluation models that have a higher chance of reimbursement if truly cost-effective. They cover the use of real-world data using cancer registries and discuss how such data can support or complement clinical trials with limited follow up. Lessons learned from failed reimbursement attempts, factors predictive of successful reimbursement and the different payer requirements across major countries including US, Australia, Canada, UK, Germany,

France and Italy are also discussed. The book includes many detailed practical examples, case studies and thought-provoking exercises for use in classroom and seminar discussions. Iftekhar Khan is a medical statistician and health economist and a lead statistician at Oxford Unviersity's Center for Statistics in Medicine. Professor Khan is also a Senior Research Fellow in Health Economics at University of Warwick and is a Senior Statistical Assessor within the Licensing Division of the UK Medicine and Health Regulation Agency. Ralph Crott is a former professor in Pharmacoeconomics at the University of Montreal in Quebec, Canada and former head of the EORTC Health Economics Unit and former senior health economist at the Belgian HTA organization. Zahid Bashir has over twelve years experience working in the pharmaceutical industry in medical affairs and oncology drug development where he is involved in the design and execution of oncology clinical trials and development of reimbursement dossiers for HTA submission.

Bankruptcy prediction is one of the most important research areas in corporate finance. Bankruptcies are an indispensable element of the functioning of the market economy, and at the same time generate significant losses for stakeholders. Hence, this book was established to collect the results of research on the latest trends in predicting the bankruptcy of enterprises. It suggests models developed for different countries using both traditional and more advanced methods. Problems connected with predicting bankruptcy during periods of prosperity and recession, the selection of appropriate explanatory variables, as well as the dynamization of models are presented. The reliability of financial data and the validity of the audit are also referenced. Thus, I hope that this book will inspire you to undertake new research in the field of forecasting the risk of bankruptcy.

There is a huge amount of literature on statistical models for the prediction of survival after diagnosis of a wide range of diseases like cancer, cardiovascular disease, and chronic kidney disease. Current practice is to use prediction models based on the Cox proportional hazards model and to present those as static models for remaining lifetime after diagnosis or treatment. In contrast, Dynamic Prediction in Clinical Survival Analysis focuses on dynamic models for the remaining lifetime at later points in time, for instance using landmark models. Designed to be useful to applied statisticians and clinical epidemiologists, each chapter in the book has a practical focus on the issues of working with real life data. Chapters conclude with additional material either on the interpretation of the models, alternative models, or theoretical background. The book consists of four parts: Part I deals with prognostic models for survival data using (clinical) information available at baseline, based on the Cox model Part II is about prognostic models for survival data using (clinical) information available at baseline, when the proportional hazards assumption of the Cox model is violated Part III is dedicated to the use of time-dependent information in dynamic prediction Part IV explores dynamic prediction models for survival data using genomic data Dynamic Prediction in Clinical Survival Analysis summarizes cutting-edge research on the dynamic use of predictive models with traditional and new approaches. Aimed at applied statisticians who actively analyze clinical data in collaboration with clinicians, the analyses of the different data sets throughout the book demonstrate how predictive models can be obtained from proper data sets.

This book trains the next generation of scientists representing different disciplines to leverage the data generated during routine patient care. It formulates a more complete lexicon of evidence-based recommendations and support shared, ethical decision making by doctors with

their patients. Diagnostic and therapeutic technologies continue to evolve rapidly, and both individual practitioners and clinical teams face increasingly complex ethical decisions. Unfortunately, the current state of medical knowledge does not provide the guidance to make the majority of clinical decisions on the basis of evidence. The present research infrastructure is inefficient and frequently produces unreliable results that cannot be replicated. Even randomized controlled trials (RCTs), the traditional gold standards of the research reliability hierarchy, are not without limitations. They can be costly, labor intensive, and slow, and can return results that are seldom generalizable to every patient population. Furthermore, many pertinent but unresolved clinical and medical systems issues do not seem to have attracted the interest of the research enterprise, which has come to focus instead on cellular and molecular investigations and single-agent (e.g., a drug or device) effects. For clinicians, the end result is a bit of a “data desert” when it comes to making decisions. The new research infrastructure proposed in this book will help the medical profession to make ethically sound and well informed decisions for their patients.

Strategic health planning, the cornerstone of initiatives designed to achieve health improvement goals around the world, requires an understanding of the comparative burden of diseases and injuries, their corresponding risk factors and the likely effects of invervention options. The Global Burden of Disease framework, originally published in 1990, has been widely adopted as the preferred method for health accounting and has become the standard to guide the setting of health research priorities. This publication sets out an updated assessment of the situation, with an analysis of trends observed since 1990 and a chapter on the sensitivity of GBD estimates to various sources of uncertainty in methods and data.

The aim of this book is to bridge the gap between standard textbook models and a range of models where the dynamic structure of the data manifests itself fully. The common denominator of such models is stochastic processes. The authors show how counting processes, martingales, and stochastic integrals fit very nicely with censored data. Beginning with standard analyses such as Kaplan-Meier plots and Cox regression, the presentation progresses to the additive hazard model and recurrent event data. Stochastic processes are also used as natural models for individual frailty; they allow sensible interpretations of a number of surprising artifacts seen in population data. The stochastic process framework is naturally connected to causality. The authors show how dynamic path analyses can incorporate many modern causality ideas in a framework that takes the time aspect seriously. To make the material accessible to the reader, a large number of practical examples, mainly from medicine, are developed in detail. Stochastic processes are introduced in an intuitive and non-technical manner. The book is aimed at investigators who use event history methods and want a better understanding of the statistical concepts. It is suitable as a textbook for graduate courses in statistics and biostatistics.

Dynamic Prediction in Clinical Survival AnalysisCRC Press

Ever-greater computing technologies have given rise to an exponentially growing volume of data. Today massive data sets (with potentially thousands of variables) play an important role in almost every branch of modern human activity, including networks, finance, and genetics. However, analyzing such data has presented a challenge for statisticians

This book provides a groundbreaking introduction to the likelihood inference for correlated survival data via the hierarchical (or h-) likelihood in order to obtain the (marginal) likelihood

and to address the computational difficulties in inferences and extensions. The approach presented in the book overcomes shortcomings in the traditional likelihood-based methods for clustered survival data such as intractable integration. The text includes technical materials such as derivations and proofs in each chapter, as well as recently developed software programs in R (“frailtyHL”), while the real-world data examples together with an R package, “frailtyHL” in CRAN, provide readers with useful hands-on tools. Reviewing new developments since the introduction of the h-likelihood to survival analysis (methods for interval estimation of the individual frailty and for variable selection of the fixed effects in the general class of frailty models) and guiding future directions, the book is of interest to researchers in medical and genetics fields, graduate students, and PhD (bio) statisticians.

Disease Modelling and Public Health, Part A, Volume 36 addresses new challenges in existing and emerging diseases with a variety of comprehensive chapters that cover Infectious Disease Modeling, Bayesian Disease Mapping for Public Health, Real time estimation of the case fatality ratio and risk factor of death, Alternative Sampling Designs for Time-To-Event Data with Applications to Biomarker Discovery in Alzheimer's Disease, Dynamic risk prediction for cardiovascular disease: An illustration using the ARIC Study, Theoretical advances in type 2 diabetes, Finite Mixture Models in Biostatistics, and Models of Individual and Collective Behavior for Public Health Epidemiology. As a two part volume, the series covers an extensive range of techniques in the field. It present a vital resource for statisticians who need to access a number of different methods for assessing epidemic spread in population, or in formulating public health policy. Presents a comprehensive, two-part volume written by leading subject experts Provides a unique breadth and depth of content coverage Addresses the most cutting-

edge developments in the field Includes chapters on Ebola and the Zika virus; topics which have grown in prominence and scholarly output

"This is truly an outstanding book. [It] brings together all of the latest research in clinical trials methodology and how it can be applied to drug development.... Chang et al provide applications to industry-supported trials. This will allow statisticians in the industry community to take these methods seriously." Jay Herson, Johns Hopkins University The pharmaceutical industry's approach to drug discovery and development has rapidly transformed in the last decade from the more traditional Research and Development (R & D) approach to a more innovative approach in which strategies are employed to compress and optimize the clinical development plan and associated timelines. However, these strategies are generally being considered on an individual trial basis and not as part of a fully integrated overall development program. Such optimization at the trial level is somewhat near-sighted and does not ensure cost, time, or development efficiency of the overall program. This book seeks to address this imbalance by establishing a statistical framework for overall/global clinical development optimization and providing tactics and techniques to support such optimization, including clinical trial simulations. Provides a statistical framework for achieve global optimization in each phase of the drug development process. Describes specific techniques to support optimization including adaptive designs, precision medicine, survival-endpoints, dose finding and multiple testing. Gives practical approaches to handling missing data in clinical trials using SAS. Looks at key controversial issues from both a clinical and statistical perspective. Presents a generous number of case studies from multiple therapeutic areas that help motivate and illustrate the statistical methods introduced in the book. Puts great emphasis on software implementation of

the statistical methods with multiple examples of software code (both SAS and R). It is important for statisticians to possess a deep knowledge of the drug development process beyond statistical considerations. For these reasons, this book incorporates both statistical and "clinical/medical" perspectives.

Multi-State Survival Models for Interval-Censored Data introduces methods to describe stochastic processes that consist of transitions between states over time. It is targeted at researchers in medical statistics, epidemiology, demography, and social statistics. One of the applications in the book is a three-state process for dementia and survival in the older population. This process is described by an illness-death model with a dementia-free state, a dementia state, and a dead state. Statistical modelling of a multi-state process can investigate potential associations between the risk of moving to the next state and variables such as age, gender, or education. A model can also be used to predict the multi-state process. The methods are for longitudinal data subject to interval censoring. Depending on the definition of a state, it is possible that the time of the transition into a state is not observed exactly. However, when longitudinal data are available the transition time may be known to lie in the time interval defined by two successive observations. Such an interval-censored observation scheme can be taken into account in the statistical inference. Multi-state modelling is an elegant combination of statistical inference and the theory of stochastic processes. Multi-State Survival Models for Interval-Censored Data shows that the statistical modelling is versatile and allows for a wide range of applications.

In longitudinal studies it is often of interest to investigate how a marker that is repeatedly measured in time is associated with a time to an event of interest, e.g., prostate cancer studies

where longitudinal PSA level measurements are collected in conjunction with the time-to-recurrence. Joint Models for Longitudinal and Time-to-Event Data: With Applications in R provides a full treatment of random effects joint models for longitudinal and time-to-event outcomes that can be utilized to analyze such data. The content is primarily explanatory, focusing on applications of joint modeling, but sufficient mathematical details are provided to facilitate understanding of the key features of these models. All illustrations put forward can be implemented in the R programming language via the freely available package JM written by the author. All the R code used in the book is available at: http://jmr.r-forge.r-project.org/

The high-level language of R is recognized as one of the most powerful and flexible statistical software environments, and is rapidly becoming the standard setting for quantitative analysis, statistics and graphics. R provides free access to unrivalled coverage and cutting-edge applications, enabling the user to apply numerous statistical methods ranging from simple regression to time series or multivariate analysis. Building on the success of the author's bestselling Statistics: An Introduction using R, The R Book is packed with worked examples, providing an all inclusive guide to R, ideal for novice and more accomplished users alike. The book assumes no background in statistics or computing and introduces the advantages of the R environment, detailing its applications in a wide range of disciplines. Provides the first comprehensive reference manual for the R language, including practical guidance and full coverage of the graphics facilities. Introduces all the statistical models covered by R, beginning with simple classical tests such as chi-square and t-test. Proceeds to examine more advance methods, from regression and analysis of variance, through to generalized linear models, generalized mixed models, time series, spatial statistics, multivariate statistics and much more.

The R Book is aimed at undergraduates, postgraduates and professionals in science, engineering and medicine. It is also ideal for students and professionals in statistics, economics, geography and the social sciences.

Design and Analysis of Clinical Trials for Predictive Medicine provides statistical guidance on conducting clinical trials for predictive medicine. It covers statistical topics relevant to the main clinical research phases for developing molecular diagnostics and therapeutics—from identifying molecular biomarkers using DNA microarrays to confirming their clinical utility in randomized clinical trials. The foundation of modern clinical trials was laid many years before modern developments in biotechnology and genomics. Drug development in many diseases is now shifting to molecularly targeted treatment. Confronted with such a major break in the evolution toward personalized or predictive medicine, the methodologies for design and analysis of clinical trials is now evolving. This book is one of the first attempts to contribute to this evolution by laying a foundation for the use of appropriate statistical designs and methods in future clinical trials for predictive medicine. It is a useful resource for clinical biostatisticians, researchers focusing on predictive medicine, clinical investigators, translational scientists, and graduate biostatistics students.

A guide for everyone involved in medical decision making to plot a clear course through complex and conflicting benefits and risks.

Survival analysis arises in many fields of study including medicine, biology, engineering, public health, epidemiology, and economics. This book provides a comprehensive treatment of Bayesian survival analysis. It presents a balance between theory and applications, and for each class of models discussed, detailed examples and analyses from case studies are

presented whenever possible. The applications are all from the health sciences, including cancer, AIDS, and the environment.

This book introduces readers to copula-based statistical methods for analyzing survival data involving dependent censoring. Primarily focusing on likelihood-based methods performed under copula models, it is the first book solely devoted to the problem of dependent censoring. The book demonstrates the advantages of the copula-based methods in the context of medical research, especially with regard to cancer patients' survival data. Needless to say, the statistical methods presented here can also be applied to many other branches of science, especially in reliability, where survival analysis plays an important role. The book can be used as a textbook for graduate coursework or a short course aimed at (bio-) statisticians. To deepen readers' understanding of copula-based approaches, the book provides an accessible introduction to basic survival analysis and explains the mathematical foundations of copula-based survival models.

Randomised Response-Adaptive Designs in Clinical Trials presents methods for the randomised allocation of treatments to patients in sequential clinical trials. Emphasizing the practical application of clinical trial designs, the book is designed for medical and applied statisticians, clinicians, and statisticians in training. After introducing clinical trials in drug development, the authors assess a simple adaptive design for binary responses without covariates. They discuss randomisation and covariate balance in normally distributed responses and cover

many important response-adaptive designs for binary responses. The book then develops response-adaptive designs for continuous and longitudinal responses, optimum designs with covariates, and response-adaptive designs with covariates. It also covers response-adaptive designs that are derived by optimising an objective function subject to constraints on the variance of estimated parametric functions. The concluding chapter explores future directions in the development of adaptive designs.

This book provides an introduction to multistate event history analysis. It is an extension of survival analysis, in which a single terminal event (endpoint) is considered and the time-to-event is studied. Multistate models focus on life histories or trajectories, conceptualized as sequences of states and sequences of transitions between states. Life histories are modeled as realizations of continuous-time Markov processes. The model parameters, transition rates, are estimated from data on event counts and populations at risk, using the statistical theory of counting processes. The Comprehensive R Network Archive (CRAN) includes several packages for multistate modeling. This book is about Biograph. The package is designed to (a) enhance exploratory analysis of life histories and (b) make multistate modeling accessible. The package incorporates utilities that connect to several packages for multistate modeling, including survival, eha, Epi,

mvna,, mstate, msm, and TraMineR for sequence analysis. The book is a 'hands-on' presentation of Biograph and the packages listed. It is written from the perspective of the user. To help the user master the techniques and the software, a single data set is used to illustrate the methods and software. It is the subsample of the German Life History Survey, which was also used by Blossfeld and Rohwer in their popular textbook on event history modeling. Another data set, the Netherlands Family and Fertility Survey, is used to illustrate how Biograph can assist in answering questions on life paths of cohorts and individuals. The book is suitable as a textbook for graduate courses on event history analysis and introductory courses on competing risks and multistate models. It may also be used as a self-study book. The R code used in the book is available online. Frans Willekens is affiliated with the Max Planck Institute for Demographic Research (MPIDR) in Rostock, Germany. He is Emeritus Professor of Demography at the University of Groningen, a Honorary Fellow of the Netherlands Interdisciplinary Demographic Institute (NIDI) in the Hague, and a Research Associate of the International Institute for Applied Systems Analysis (IIASA), Laxenburg, Austria. He is a member of Royal Netherlands Academy of Arts and Sciences (KNAW). He has contributed to the modeling and simulation of life histories, mainly in the context of population forecasting.

This book introduces readers to advanced statistical methods for analyzing survival data involving correlated endpoints. In particular, it describes statistical methods for applying Cox regression to two correlated endpoints by accounting for dependence between the endpoints with the aid of copulas. The practical advantages of employing copula-based models in medical research are explained on the basis of case studies. In addition, the book focuses on clustered survival data, especially data arising from meta-analysis and multicenter analysis. Consequently, the statistical approaches presented here employ a frailty term for heterogeneity modeling. This brings the joint frailty-copula model, which incorporates a frailty term and a copula, into a statistical model. The book also discusses advanced techniques for dealing with high-dimensional gene expressions and developing personalized dynamic prediction tools under the joint frailty-copula model. To help readers apply the statistical methods to real-world data, the book provides case studies using the authors' original R software package (freely available in CRAN). The emphasis is on clinical survival data, involving time-to-tumor progression and overall survival, collected on cancer patients. Hence, the book offers an essential reference guide for medical statisticians and provides researchers with advanced, innovative statistical tools. The book also provides a concise introduction to basic multivariate survival

models.

Prediction models are important in various fields, including medicine, physics, meteorology, and finance. Prediction models will become more relevant in the medical field with the increase in knowledge on potential predictors of outcome, e.g. from genetics. Also, the number of applications will increase, e.g. with targeted early detection of disease, and individualized approaches to diagnostic testing and treatment. The current era of evidence-based medicine asks for an individualized approach to medical decision-making. Evidence-based medicine has a central place for meta-analysis to summarize results from randomized controlled trials; similarly prediction models may summarize the effects of predictors to provide individu- ized predictions of a diagnostic or prognostic outcome. Why Read This Book? My motivation for working on this book stems primarily from the fact that the development and applications of prediction models are often suboptimal in medical publications. With this book I hope to contribute to better understanding of relevant issues and give practical advice on better modelling strategies than are nowadays widely used. Issues include: (a) Better predictive modelling is sometimes easily possible; e.g. a large data set with high quality data is available, but all continuous predictors are dich- omized, which is known to have several disadvantages.

Longitudinal studies often incur several problems that challenge standard statistical methods for data analysis. These problems include non-ignorable missing data in longitudinal measurements of one or more response variables, informative observation times of longitudinal data, and survival analysis with intermittently measured time-dependent covariates that are subject to measurement error and/or substantial biological variation. Joint modeling of longitudinal and time-to-event data has emerged as a novel approach to handle these issues. Joint Modeling of Longitudinal and Time-to-Event Data provides a systematic introduction and review of state-of-the-art statistical methodology in this active research field. The methods are illustrated by real data examples from a wide range of clinical research topics. A collection of data sets and software for practical implementation of the joint modeling methodologies are available through the book website. This book serves as a reference book for scientific investigators who need to analyze longitudinal and/or survival data, as well as researchers developing methodology in this field. It may also be used as a textbook for a graduate level course in biostatistics or statistics.

Handbook of Spatial Epidemiology explains how to model epidemiological problems and improve inference about disease etiology from a geographical perspective. Top epidemiologists, geographers, and statisticians share

interdisciplinary viewpoints on analyzing spatial data and space–time variations in disease incidences. These analyses can provide important information that leads to better decision making in public health. The first part of the book addresses general issues related to epidemiology, GIS, environmental studies, clustering, and ecological analysis. The second part presents basic statistical methods used in spatial epidemiology, including fundamental likelihood principles, Bayesian methods, and testing and nonparametric approaches. With a focus on special methods, the third part describes geostatistical models, splines, quantile regression, focused clustering, mixtures, multivariate methods, and much more. The final part examines special problems and application areas, such as residential history analysis, segregation, health services research, health surveys, infectious disease, veterinary topics, and health surveillance and clustering. Spatial epidemiology, also known as disease mapping, studies the geographical or spatial distribution of health outcomes. This handbook offers a wide-ranging overview of state-of-the-art approaches to determine the relationships between health and various risk factors, empowering researchers and policy makers to tackle public health problems.

Using real data sets throughout, Survival Analysis in Medicine and Genetics introduces the latest methods for analyzing high-dimensional survival data. It

provides thorough coverage of recent statistical developments in the medical and genetics fields. The text mainly addresses special concerns of the survival model. After covering the fundamentals, it discusses interval censoring, nonparametric and semiparametric hazard regression, multivariate survival data analysis, the sub-distribution method for competing risks data, the cure rate model, and Bayesian inference methods. The authors then focus on time-dependent diagnostic medicine and high-dimensional genetic data analysis. Many of the methods are illustrated with clinical examples. Emphasizing the applications of survival analysis techniques in genetics, this book presents a statistical framework for burgeoning research in this area and offers a set of established approaches for statistical analysis. It reveals a new way of looking at how predictors are associated with censored survival time and extracts novel statistical genetic methods for censored survival time outcome from the vast amount of research results in genomics.

Survival data analysis is a very broad field of statistics, encompassing a large variety of methods used in a wide range of applications, and in particular in medical research. During the last twenty years, several extensions of "classical" survival models have been developed to address particular situations often encountered in practice. This book aims to gather in a single reference the most

commonly used extensions, such as frailty models (in case of unobserved heterogeneity or clustered data), cure models (when a fraction of the population will not experience the event of interest), competing risk models (in case of different types of event), and joint survival models for a time-to-event endpoint and a longitudinal outcome. Features Presents state-of-the art approaches for different advanced survival models including frailty models, cure models, competing risk models and joint models for a longitudinal and a survival outcome Uses consistent notation throughout the book for the different techniques presented Explains in which situation each of these models should be used, and how they are linked to specific research questions Focuses on the understanding of the models, their implementation, and their interpretation, with an appropriate level of methodological development for masters students and applied statisticians Provides references to existing R packages and SAS procedure or macros, and illustrates the use of the main ones on real datasets This book is primarily aimed at applied statisticians and graduate students of statistics and biostatistics. It can also serve as an introductory reference for methodological researchers interested in the main extensions of classical survival analysis.
This book presents a systematic and unified approach for modern nonparametric treatment of missing and modified data via examples of density and hazard rate

estimation, nonparametric regression, filtering signals, and time series analysis. All basic types of missing at random and not at random, biasing, truncation, censoring, and measurement errors are discussed, and their treatment is explained. Ten chapters of the book cover basic cases of direct data, biased data, nondestructive and destructive missing, survival data modified by truncation and censoring, missing survival data, stationary and nonstationary time series and processes, and ill-posed modifications. The coverage is suitable for self-study or a one-semester course for graduate students with a prerequisite of a standard course in introductory probability. Exercises of various levels of difficulty will be helpful for the instructor and self-study. The book is primarily about practically important small samples. It explains when consistent estimation is possible, and why in some cases missing data should be ignored and why others must be considered. If missing or data modification makes consistent estimation impossible, then the author explains what type of action is needed to restore the lost information. The book contains more than a hundred figures with simulated data that explain virtually every setting, claim, and development. The companion R software package allows the reader to verify, reproduce and modify every simulation and used estimators. This makes the material fully transparent and allows one to study it interactively. Sam Efromovich is the Endowed Professor of

Mathematical Sciences and the Head of the Actuarial Program at the University of Texas at Dallas. He is well known for his work on the theory and application of nonparametric curve estimation and is the author of Nonparametric Curve Estimation: Methods, Theory, and Applications. Professor Sam Efromovich is a Fellow of the Institute of Mathematical Statistics and the American Statistical Association.

At the intersection of computer science and healthcare, data analytics has emerged as a promising tool for solving problems across many healthcare-related disciplines. Supplying a comprehensive overview of recent healthcare analytics research, Healthcare Data Analytics provides a clear understanding of the analytical techniques currently available to solve healthcare problems. The book details novel techniques for acquiring, handling, retrieving, and making best use of healthcare data. It analyzes recent developments in healthcare computing and discusses emerging technologies that can help improve the health and well-being of patients. Written by prominent researchers and experts working in the healthcare domain, the book sheds light on many of the computational challenges in the field of medical informatics. Each chapter in the book is structured as a "survey-style" article discussing the prominent research issues and the advances made on that research topic. The book is divided into three

major categories: Healthcare Data Sources and Basic Analytics - details the various healthcare data sources and analytical techniques used in the processing and analysis of such data Advanced Data Analytics for Healthcare - covers advanced analytical methods, including clinical prediction models, temporal pattern mining methods, and visual analytics Applications and Practical Systems for Healthcare - covers the applications of data analytics to pervasive healthcare, fraud detection, and drug discovery along with systems for medical imaging and decision support Computer scientists are usually not trained in domain-specific medical concepts, whereas medical practitioners and researchers have limited exposure to the data analytics area. The contents of this book will help to bring together these diverse communities by carefully and comprehensively discussing the most relevant contributions from each domain.

Data Analysis with Competing Risks and Intermediate States explains when and how to use models and techniques for the analysis of competing risks and intermediate states. It covers the most recent insights on estimation techniques and discusses in detail how to interpret the obtained results.After introducing example studies from the biomedical and

Statistical Models and Methods for Reliability and Survival Analysis brings together contributions by specialists in statistical theory as they discuss their

applications providing up-to-date developments in methods used in survival analysis, statistical goodness of fit, stochastic processes for system reliability, amongst others. Many of these are related to the work of Professor M. Nikulin in statistics over the past 30 years. The authors gather together various contributions with a broad array of techniques and results, divided into three parts - Statistical Models and Methods, Statistical Models and Methods in Survival Analysis, and Reliability and Maintenance. The book is intended for researchers interested in statistical methodology and models useful in survival analysis, system reliability and statistical testing for censored and non-censored data. Handbook of Survival Analysis presents modern techniques and research problems in lifetime data analysis. This area of statistics deals with time-to-event data that is complicated by censoring and the dynamic nature of events occurring in time. With chapters written by leading researchers in the field, the handbook focuses on advances in survival analysis techniques, covering classical and Bayesian approaches. It gives a complete overview of the current status of survival analysis and should inspire further research in the field. Accessible to a wide range of readers, the book provides: An introduction to various areas in survival analysis for graduate students and novices A reference to modern investigations into survival analysis for more established researchers A text or

supplement for a second or advanced course in survival analysis A useful guide to statistical methods for analyzing survival data experiments for practicing statisticians

This book introduces readers to advanced statistical methods for analyzing survival data involving correlated endpoints. In particular, it describes statistical methods for applying Cox regression to two correlated endpoints by accounting for dependence between the endpoints with the aid of copulas. The practical advantages of employing copula-based models in medical research are explained on the basis of case studies. In addition, the book focuses on clustered survival data, especially data arising from meta-analysis and multicenter analysis. Consequently, the statistical approaches presented here employ a frailty term for heterogeneity modeling. This brings the joint frailty-copula model, which incorporates a frailty term and a copula, into a statistical model. The book also discusses advanced techniques for dealing with high-dimensional gene expressions and developing personalized dynamic prediction tools under the joint frailty-copula model. To help readers apply the statistical methods to real-world data, the book provides case studies using the authors' original R software package (freely available in CRAN). The emphasis is on clinical survival data, involving time-to-tumor progression and overall survival, collected on cancer

patients. Hence, the book offers an essential reference guide for medical statisticians and provides researchers with advanced, innovative statistical tools. The book also provides a concise introduction to basic multivariate survival models.

M. K. Gospodarowicz, P. Hermanek, and D. E. Henson Attention to innovations in cancer treatment has tended to eclipse the importance of prognostic assessment. However, the recognition that prognostic factors often have a greater impact on outcome than available therapies and the proliferation of biochemical, molecular, and genetic markers have resulted in renewed interest in this field. The outcome in patients with cancer is determined by a combination of numerous factors. Presently, the most widely recognized are the extent of disease, histologic type of tumor, and treatment. It has been known for some time that additional factors also influence outcome. These include histologic grade, lymphatic or vascular invasion, mitotic index, performance status, symptoms, and most recently genetic and biochemical markers. It is the aim of this volume to compile those prognostic factors that have emerged as important determinants of outcome for tumors at various sites. This compilation represents the first phase of a more extensive process to integrate all prognostic factors in cancer to further enhance the prediction of outcome following treatment. Certain issues surround

ing the assessment and reporting of prognostic factors are also considered. Importance of Prognostic Factors Prognostic factors in cancer often have an immense influence on outcome, while treatment often has a much weaker effect. For example, the influence of the presence of lymph node involvement on survival of patients with metastatic breast cancer is much greater than the effect of adjuvant treatment with tamoxifen in the same group of patients [5].

Drawing on the authors' substantial expertise in modeling longitudinal and clustered data, Quasi-Least Squares Regression provides a thorough treatment of quasi-least squares (QLS) regression—a computational approach for the estimation of correlation parameters within the framework of generalized estimating equations (GEEs). The authors present a detailed evaluation of QLS methodology, demonstrating the advantages of QLS in comparison with alternative methods. They describe how QLS can be used to extend the application of the traditional GEE approach to the analysis of unequally spaced longitudinal data, familial data, and data with multiple sources of correlation. In some settings, QLS also allows for improved analysis with an unstructured correlation matrix. Special focus is given to goodness-of-fit analysis as well as new strategies for selecting the appropriate working correlation structure for QLS and GEE. A chapter on longitudinal binary data tackles recent issues raised in

the statistical literature regarding the appropriateness of semi-parametric methods, such as GEE and QLS, for the analysis of binary data; this chapter includes a comparison with the first-order Markov maximum-likelihood (MARK1ML) approach for binary data. Examples throughout the book demonstrate each topic of discussion. In particular, a fully worked out example leads readers from model building and interpretation to the planning stages for a future study (including sample size calculations). The code provided enables readers to replicate many of the examples in Stata, often with corresponding R, SAS, or MATLAB® code offered in the text or on the book's website.

Design and Analysis of Cross-Over Trials is concerned with a specific kind of comparative trial known as the cross-over trial, in which subjects receive different sequences of treatments. Such trials are widely used in clinical and medical research, and in other diverse areas such as veterinary science, psychology, sports science, and agriculture. The first edition of this book was the first to be wholly devoted to the subject. The second edition was revised to mirror growth and development in areas where the design remained in widespread use and new areas where it had grown in importance. This new Third Edition: Contains seven new chapters written in the form of short case studies that address re-estimating sample size when testing for average bioequivalence, fitting a

nonlinear dose response function, estimating a dose to take forward from phase two to phase three, establishing proof of concept, and recalculating the sample size using conditional power Employs the R package Crossover, specially created to accompany the book and provide a graphical user interface for locating designs in a large catalog and for searching for new designs Includes updates regarding the use of period baselines and the analysis of data from very small trials Reflects the availability of new procedures in SAS, particularly proc glimmix Presents the SAS procedure proc mcmc as an alternative to WinBUGS for Bayesian analysis Complete with real data and downloadable SAS code, Design and Analysis of Cross-Over Trials, Third Edition provides a practical understanding of the latest methods along with the necessary tools for implementation.

Cystic Fibrosis in the Light of New Research provides the latest research and clinical evidence that will be useful for clinicians, scientists and researchers to further their knowledge around this fascinating condition. The authors have brought along their expertise and wealth of knowledge to produce this book, including the basic science that underlies the disease, the burden of bacterial and viral infections, immunologic aspects of CF, a variety of clinical measurements to predict prognosis and novel therapies including gene therapy. This book will be

invaluable and entertaining for anyone who is involved in the care of patients with cystic fibrosis.

Medical Risk Prediction Models: With Ties to Machine Learning is a hands-on book for clinicians, epidemiologists, and professional statisticians who need to make or evaluate a statistical prediction model based on data. The subject of the book is the patient's individualized probability of a medical event within a given time horizon. Gerds and Kattan describe the mathematical details of making and evaluating a statistical prediction model in a highly pedagogical manner while avoiding mathematical notation. Read this book when you are in doubt about whether a Cox regression model predicts better than a random survival forest. Features: All you need to know to correctly make an online risk calculator from scratch Discrimination, calibration, and predictive performance with censored data and competing risks R-code and illustrative examples Interpretation of prediction performance via benchmarks Comparison and combination of rival modeling strategies via cross-validation Thomas A. Gerds is a professor at the Biostatistics Unit at the University of Copenhagen and is affiliated with the Danish Heart Foundation. He is the author of several R-packages on CRAN and has taught statistics courses to non-statisticians for many years. Michael W. Kattan is a highly cited author and Chair of the Department of Quantitative Health

Sciences at Cleveland Clinic. He is a Fellow of the American Statistical Association and has received two awards from the Society for Medical Decision Making: the Eugene L. Saenger Award for Distinguished Service, and the John M. Eisenberg Award for Practical Application of Medical Decision-Making Research.

How can analytics scholars and healthcare professionals access the most exciting and important healthcare topics and tools for the 21st century? Editors Tinglong Dai and Sridhar Tayur, aided by a team of internationally acclaimed experts, have curated this timely volume to help newcomers and seasoned researchers alike to rapidly comprehend a diverse set of thrusts and tools in this rapidly growing cross-disciplinary field. The Handbook covers a wide range of macro-, meso- and micro-level thrusts—such as market design, competing interests, global health, personalized medicine, residential care and concierge medicine, among others—and structures what has been a highly fragmented research area into a coherent scientific discipline. The handbook also provides an easy-to-comprehend introduction to five essential research tools—Markov decision process, game theory and information economics, queueing games, econometric methods, and data science—by illustrating their uses and applicability on examples from diverse healthcare settings, thus connecting tools with thrusts.

The primary audience of the Handbook includes analytics scholars interested in healthcare and healthcare practitioners interested in analytics. This Handbook: Instills analytics scholars with a way of thinking that incorporates behavioral, incentive, and policy considerations in various healthcare settings. This change in perspective—a shift in gaze away from narrow, local and one-off operational improvement efforts that do not replicate, scale or remain sustainable—can lead to new knowledge and innovative solutions that healthcare has been seeking so desperately. Facilitates collaboration between healthcare experts and analytics scholar to frame and tackle their pressing concerns through appropriate modern mathematical tools designed for this very purpose. The handbook is designed to be accessible to the independent reader, and it may be used in a variety of settings, from a short lecture series on specific topics to a semester-long course. Large sample techniques are fundamental to all fields of statistics. Mixed effects models, including linear mixed models, generalized linear mixed models, non-linear mixed effects models, and non-parametric mixed effects models are complex models, yet, these models are extensively used in practice. This monograph provides a comprehensive account of asymptotic analysis of mixed effects models. The monograph is suitable for researchers and graduate students who wish to learn about asymptotic tools and research problems in mixed effects

models. It may also be used as a reference book for a graduate-level course on mixed effects models, or asymptotic analysis.

Absolute Risk: Methods and Applications in Clinical Management and Public Health provides theory and examples to demonstrate the importance of absolute risk in counseling patients, devising public health strategies, and clinical management. The book provides sufficient technical detail to allow statisticians, epidemiologists, and clinicians to build, test, and apply models of absolute risk. Features: Provides theoretical basis for modeling absolute risk, including competing risks and cause-specific and cumulative incidence regression Discusses various sampling designs for estimating absolute risk and criteria to evaluate models Provides details on statistical inference for the various sampling designs Discusses criteria for evaluating risk models and comparing risk models, including both general criteria and problem-specific expected losses in well-defined clinical and public health applications Describes many applications encompassing both disease prevention and prognosis, and ranging from counseling individual patients, to clinical decision making, to assessing the impact of risk-based public health strategies Discusses model updating, family-based designs, dynamic projections, and other topics Ruth M. Pfeiffer is a mathematical statistician and Fellow of the American Statistical Association, with

interests in risk modeling, dimension reduction, and applications in epidemiology. She developed absolute risk models for breast cancer, colon cancer, melanoma, and second primary thyroid cancer following a childhood cancer diagnosis. Mitchell H. Gail developed the widely used "Gail model" for projecting the absolute risk of invasive breast cancer. He is a medical statistician with interests in statistical methods and applications in epidemiology and molecular medicine. He is a member of the National Academy of Medicine and former President of the American Statistical Association. Both are Senior Investigators in the Division of Cancer Epidemiology and Genetics, National Cancer Institute, National Institutes of Health.

This book is comprised of presentations delivered at the 5th Workshop on Biostatistics and Bioinformatics held in Atlanta on May 5-7, 2017. Featuring twenty-two selected papers from the workshop, this book showcases the most current advances in the field, presenting new methods, theories, and case applications at the frontiers of biostatistics, bioinformatics, and interdisciplinary areas. Biostatistics and bioinformatics have been playing a key role in statistics and other scientific research fields in recent years. The goal of the 5th Workshop on Biostatistics and Bioinformatics was to stimulate research, foster interaction among researchers in field, and offer opportunities for learning and facilitating

research collaborations in the era of big data. The resulting volume offers timely insights for researchers, students, and industry practitioners.