

Statistics for Biology and Health

**Warren J. Ewens
Gregory R. Grant**

**Statistical
Methods in
Bioinformatics**

An Introduction

Second Edition

 Springer

Statistical Methods In Bioinformatics Statistics For Biology And Health

David G. Kleinbaum, Mitchel Klein



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Statistical Methods in Bioinformatics Warren J. Ewens, Gregory R. Grant, 2004 **Statistical Methods in Bioinformatics** Warren J. Ewens, 1989 Statistical Methods in Bioinformatics Warren J. Ewens, Gregory R.

Grant, 2008-11-01 Advances in computers and biotechnology have had a profound impact on biomedical research and as a result complex data sets can now be generated to address extremely complex biological questions Correspondingly advances in the statistical methods necessary to analyze such data are following closely behind the advances in data generation methods The statistical methods required by bioinformatics present many new and difficult problems for the research community This book provides an introduction to some of these new methods The main biological topics treated include sequence analysis BLAST microarray analysis gene finding and the analysis of evolutionary processes The main statistical techniques covered include hypothesis testing and estimation Poisson processes Markov models and Hidden Markov models and multiple testing methods The second edition features new chapters on microarray analysis and on statistical inference including a discussion of ANOVA and discussions of the statistical theory of motifs and methods based on the hypergeometric distribution Much material has been clarified and reorganized The book is written so as to appeal to biologists and computer scientists who wish to know more about the statistical methods of the field as well as to trained statisticians who wish to become involved with bioinformatics The earlier chapters introduce the concepts of probability and statistics at an elementary level but with an emphasis on material relevant to later chapters and often not covered in standard introductory texts Later chapters should be immediately accessible to the trained statistician Sufficient mathematical background consists of introductory courses in calculus and linear algebra The basic biological concepts that are used are explained or can be understood from the context and standard mathematical concepts are summarized in an Appendix Problems are provided at the end of each chapter allowing the reader to develop aspects of the theory outlined in the main text Warren J Ewens holds the Christopher H Brown Distinguished Professorship at the University of Pennsylvania He is the author of two books Population Genetics and Mathematical Population Genetics He is a senior editor of Annals of Human Genetics and has served on the editorial boards of Theoretical Population Biology GENETICS Proceedings of the Royal Society B and SIAM Journal in Mathematical Biology He is a fellow of the Royal Society and the Australian Academy of Science Gregory R Grant is a senior bioinformatics researcher in the University of Pennsylvania Computational Biology and Informatics Laboratory He obtained his Ph D in number theory from the University of Maryland in 1995 and his Masters in Computer Science from the University of Pennsylvania in 1999 Comments on the first edition This book would be an ideal text for a postgraduate course and is equally well suited to individual study I would recommend the book highly Biometrics Ewens and Grant have given us a very welcome introduction to what is behind those pretty graphical user interfaces Naturwissenschaften The authors do an excellent job of presenting the essence of the material without getting bogged down in mathematical details Journal

American Statistical Association The authors have restructured classical material to a great extent and the new organization of the different topics is one of the outstanding services of the book **Metrika**

The Evaluation of Surrogate Endpoints Geert Molenberghs, Tomasz Burzykowski, Marc Buyse, 2005-02-28 Covers the latest research on a sensitive and controversial topic in a professional and well researched manner Provides practical outlook as well as model guidelines and software tools that should be of interest to people who use the software tools described and those who do not Related title by Co author Geert Molenbergh has sold more than 3500 copies world wide Provides dual viewpoints from scientists in the industry as well as regulatory authorities

Probability Models for DNA Sequence Evolution Rick Durrett, 2013-03-09 Our basic question is Given a collection of DNA sequences what underlying forces are responsible for the observed patterns of variability To approach this question we introduce and analyze a number of probability models the Wright Fisher model the coalescent the infinite alleles model and the infinite sites model We study the complications that come from nonconstant population size recombination population subdivision and three forms of natural selection directional selection balancing selection and background selection These theoretical results set the stage for the investigation of various statistical tests to detect departures from neutral evolution The final chapter studies the evolution of whole genomes by chromosomal inversions reciprocal translocations and genome duplication Throughout the book the theory is developed in close connection with data from more than 60 experimental studies from the biology literature that illustrate the use of these results This book is written for mathematicians and for biologists alike We assume no previous knowledge of concepts from biology and only a basic knowledge of probability a one semester undergraduate course and some familiarity with Markov chains and Poisson processes Rick Durrett received his Ph D in operations research from Stanford University in 1976 He taught in the UCLA mathematics department before coming to Cornell in 1985 He is the author of six books and 125 research papers and is the academic father of more than 30 Ph D students His current interests are the use of probability models in genetics and ecology and decreasing the mean and variance of his golf

Analyzing Ecological Data Alain Zuur, Elena N. Ieno, Graham M. Smith, 2007-08-29 Which test should I apply During the many years of working with ecologists biologists and other environmental scientists this is probably the question that the authors of this book hear the most often The answer is always the same and along the lines of What are your underlying questions What do you want to show The answers to these questions provide the starting point for a detailed discussion on the ecological background and purpose of the study This then gives the basis for deciding on the most appropriate analytical approach Therefore a better starting point for an ecologist is to avoid the phrase test and think in terms of analysis A test refers to something simple and unified that gives a clear answer in the form of a p value something rarely appropriate for ecological data In practice one has to apply a data exploration check assumptions validate the models perhaps apply a series of methods and most importantly interpret the results in terms of the underlying ecology and the ecological questions being investigated Ecology is a quantitative science

trying to answer difficult questions about the complex world we live in Most ecologists are aware of these complexities but few are fully equipped with the statistical sophistication and understanding to deal with them **Scan Statistics** Joseph

Glaz,Joseph Naus,Sylvan Wallenstein,2013-03-09 In many statistical applications the scientists have to analyze the occurrence of observed clusters of events in time or space The scientists are especially interested to determine whether an observed cluster of events has occurred by chance if it is assumed that the events are distributed independently and uniformly over time or space Applications of scan statistics have been recorded in many areas of science and technology including geology geography medicine minefield detection molecular biology photography quality control and reliability theory and radio optics **Cancer Mortality and Morbidity Patterns in the U.S. Population** K.G. Manton,Igor

Akushevich,Julia Kravchenko,2008-12-28 The purpose of this book is to examine the etiology of cancer in large human populations using mathematical models developed from an inter disciplinary perspective of the population epidemiological biodemographic genetic and physiological basis of the mechanisms of cancer initiation and progression In addition an investigation of how the basic mechanism of tumor initiation relates to general processes of senescence and to other major chronic diseases e g heart disease and stroke will be conducted Survival Analysis David G. Kleinbaum,Mitchel Klein,2005

This text on survival analysis provides a straightforward and easy to follow introduction to the main concepts and techniques of the subject It is based on numerous courses given by the author to students and researchers in the health sciences and is written with such readers in mind Throughout there is an emphasis on presenting each new topic motivated with real examples of a survival analysis investigation and then presenting thorough analyses of real data sets Each chapter concludes with practice exercises to help readers reinforce their understanding of the concepts covered in the chapter **Modeling**

Survival Data: Extending the Cox Model Terry M. Therneau,Patricia M. Grambsch,2000-08-11 Extending the Cox Model is aimed at researchers practitioners and graduate students who have some exposure to traditional methods of survival analysis The emphasis is on semiparametric methods based on the proportional hazards model The inclusion of examples with SAS and S PLUS code will make the book accessible to most working statisticians

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