

Statistics for Biology and Health

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

**Statistical
Methods in
Bioinformatics**

An Introduction

Second Edition

 Springer

Statistical Methods In Bioinformatics An Introduction

Huangqi Zhang



Statistical Methods In Bioinformatics An Introduction:

Statistical Methods in Bioinformatics Warren J. Ewens, Gregory R. Grant, 2013-03-09 Advances in computers and biotechnology have had an immense impact on the biomedical fields with broad consequences for humanity Correspondingly new areas of probability and statistics are being developed specifically to meet the needs of this area There is now a necessity for a text that introduces probability and statistics in the bioinformatics context This book also describes some of the main statistical applications in the field including BLAST gene finding and evolutionary inference much of which has not yet been summarized in an introductory textbook format This book grew out of the bioinformatics courses given at the University of Pennsylvania The material is however organized to appeal to biologists or 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 in bioinformatics The earlier chapters introduce the concepts of probability and statistics at an elementary level Later chapters should be immediately accessible to the trained statistician Sufficient mathematics background consists of courses in calculus and linear algebra The basic biological concepts that are used are explained or can be understood from the context

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

Statistical Methods In Bioinformatics: An Introduction, 2E Ewens,2006-08-01 **Statistical Bioinformatics** Jae K. Lee,2011-09-20 This book provides an essential understanding of statistical concepts necessary for the analysis of genomic and proteomic data using computational techniques The author presents both basic and advanced topics focusing on those that are relevant to the computational analysis of large data sets in biology Chapters begin with a description of a statistical concept and a current example from biomedical research followed by more detailed presentation discussion of limitations and problems The book starts with an introduction to probability and statistics for genome wide data and moves into topics such as clustering classification multi dimensional visualization experimental design statistical resampling and statistical network analysis Clearly explains the use of bioinformatics tools in life sciences research without requiring an advanced background in math statistics Enables biomedical and life sciences researchers to successfully evaluate the validity of their results and make inferences Enables statistical and quantitative researchers to rapidly learn novel statistical concepts and techniques appropriate for large biological data analysis Carefully revisits frequently used statistical approaches and highlights their limitations in large biological data analysis Offers programming examples and datasets Includes chapter problem sets a glossary a list of statistical notations and appendices with references to background mathematical and technical material Features supplementary materials including datasets links and a statistical package available online Statistical Bioinformatics is an ideal textbook for students in medicine life sciences and bioengineering aimed at researchers who utilize computational tools for the analysis of genomic proteomic and many other emerging high throughput molecular data It may also serve as a rapid introduction to the bioinformatics science for statistical and computational students and audiences who have not experienced

such analysis tasks before **Journal of the American Statistical Association** ,2007 **Proceedings of the ... Annual International Conference on Research in Computational Molecular Biology** ,2003 **Genome Research** ,2001 **Proceedings of the Pakistan Academy of Sciences** Pakistan Academy of Sciences,2003 Parametric Modelling of Genomic Sequences Distance Aluísio de Souza Pinheiro,2002 **Pacific Symposium on Biocomputing** ,2008

RECOMB 2003 Webb Miller,2003 We study haplotype reconstruction under the Mendelian law of inheritance and the minimum recombination principle on pedigree data We prove that the problem of finding a minimum recombinant haplotype configuration MRHC is in general NP hard This is the first complexity result concerning the problem to our knowledge An iterative algorithm based on blocks of consecutive resolved marker loci called block extension is proposed It is very efficient and can be used for large pedigrees with a large number of markers especially for those data sets requiring few recombinants or recombination events A polynomial time exact algorithm for haplotype reconstruction without recombinants is also presented This algorithm first identifies all the necessary constraints based on the Mendelian law and the zero recombinant assumption and represents them using a system of linear equations over the cyclic group Z_2 By using a simple method based on Gaussian elimination we could obtain all possible feasible haplotype configurations We have tested the block extension algorithm on simulated data generated on three pedigree structures The results show that the algorithm performs very well on both multi allelic and biallelic data especially when the number of recombinants is small **American Book Publishing Record** ,2005 **Encyclopedia of Database Technologies and Applications** Rivero, Laura C.,Doorn, Jorge Horacio,Ferraggine, Viviana E.,2005-06-30 Addresses the evolution of database management technologies and applications along with the progress and endeavors of new research areas P xiii **Nanotechnology** M. H. Fulekar,2010 Nanotechnology Importance Applications highlights the latest developments and advances in the field of nanoscience and nanotechnology and their wide applications in design and development of Material Science and Devices Energy Drug Delivery Cosmetics Biology Biotechnology Tissue Engineering Bioinformatics Information Technology Agriculture and Food Environmental Protection Health Risk Ethics Regulations and future prospects This book will be useful to both Undergraduate and Postgraduate students teachers and researchers scientists and industrial personnel working in the field of Nanoscience and Nanotechnology AUUGN ,2003-09 **Historical Records of Australian Science** ,2005 Comparison of Genomic Sequences Using the Hamming Distance Hildete Prisco Pinheiro,2002 Probatat '02 ,2003

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