

Statistical Analysis Of Next Generation Sequencing Data Frontiers In Probability And The Statistical Sciences

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Statistical Analysis of Next Generation Sequencing Data Provides statistical tools for working with the latest research data in NGS Contains chapters written by leading statisticians in the field of NGS Useful for students and researchers that work in biomedical research and genomic medicine

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Next Generation Sequencing (NGS) is the latest high throughput technology to revolutionize genomic research. NGS generates massive genomic datasets that play a key role in the big data phenomenon that surrounds us today. To extract signals from high-dimensional NGS data and make valid statistical inferences and predictions, novel data analytic and statistical techniques are needed.

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Statistical Analysis of Next Generation Sequencing Data Somnath Datta , Dan Nettleton (eds.) Next Generation Sequencing (NGS) is the latest high throughput technology to revolutionize genomic research.

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Source: Metzker ML. Sequencing technologies - the next generation. Nat Rev Genet. 2010 Source: Whiteford et al. Swift: primary data analysis for the Illumina Solexa sequencing platform. Bioinformatics. 2009 Source: Metzker ML. Sequencing technologies - the next generation. Nat Rev Genet. 2010 name sequence quality scores x 100s of millions

Statistical Methods for Next Generation Sequencing

Next generation sequencing (NGS) is a revolutionary technology for biomedical research. One highly cost-efficient application of NGS is to detect disease association based on pooled DNA samples. However, several key issues need to be addressed for pooled NGS.

Design and Statistical Analysis of Pooled Next Generation ...

The boom of next generation sequencing (NGS) technology and its applications to a wide range of biomedical fields has brought about many computational and statistical challenges. The NHGRI funded small conference "Statistical Analysis for NGS" was held September 26th-27th 2011 in Birmingham, AL, USA, to discuss these statistical challenges and strategies to tackle them.

Statistics for Next Generation Sequencing - Meeting Report

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Statistical Analysis of Next Generation Sequencing Data ...

This proposal is to develop advanced statistical methods for analyzing large next generation sequencing data in genetic cancer epidemiological studies. The genomic era provides an unprecedented promise of understanding multifactorial diseases, such as cancer, and of identifying specific targets that can be used to develop patient-tailored therapies.

Project 3: Statistical Methods for Analysis of Next ...

Abstract We develop a statistical tool SNVer for calling common and rare variants in analysis of pooled or individual next-generation sequencing (NGS) data. We formulate variant calling as a hypothesis testing problem and employ a binomial-binomial model to test the significance of observed allele frequency against sequencing error.

SNVer: a statistical tool for variant calling in analysis ...

Chapter 1 Statistical Analyses of Next Generation Sequencing Data: An Overview Altmetric Badge. Chapter 2 Using RNA-seq Data to Detect Differentially Expressed Genes ... Chapter 19 Statistical Methods for the Analysis of Next Generation Sequencing Data from Paired Tumor-Normal Samples Altmetric Badge.

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Next-Generation Sequencing Data Analysis | Taylor ...

Next-Generation Data Storage Market size is poised to grow at a double digit CAGR from 2019 to 2025 propelled by massive growth in digital data volumes. With the increase in globalization and digitalization, there is a massive increase in the volume of file and unstructured data.

Next Generation Sequencing (NGS) is the latest high throughput technology to revolutionize genomic research. NGS generates massive genomic datasets that play a key role in the big data phenomenon that surrounds us today. To extract signals from high-dimensional NGS data and make valid statistical inferences and predictions, novel data analytic and statistical techniques are needed. This book contains 20 chapters written by prominent statisticians working with NGS data. The topics range from basic preprocessing and analysis with NGS data to more complex genomic applications such as copy number variation and isoform expression detection. Research statisticians who want to learn about this growing and exciting area will find this book useful. In addition, many chapters from this book could be included in graduate-level classes in statistical bioinformatics for training future biostatisticians who will be expected to deal with genomic data in basic biomedical research, genomic clinical trials and personalized medicine. About the editors: Somnath Datta is Professor and Vice Chair of Bioinformatics and Biostatistics at the University of Louisville. He is Fellow of the American Statistical Association, Fellow of the Institute of Mathematical Statistics and Elected Member of the International Statistical Institute. He has contributed to numerous research areas in Statistics, Biostatistics and Bioinformatics. Dan Nettleton is Professor and Laurence H. Baker Endowed Chair of Biological Statistics in the Department of Statistics at Iowa State University. He is Fellow of the American Statistical Association and has published research on a variety of topics in statistics, biology and bioinformatics.

Introduces readers to core algorithmic techniques for next-generation sequencing (NGS) data analysis and discusses a wide range of computational techniques and applications This book provides an in-depth survey of some of the recent developments in NGS and discusses mathematical and computational challenges in various application areas of NGS technologies. The 18 chapters featured in this book have been authored by bioinformatics experts and represent the latest work in leading labs actively contributing to the fast-growing field of NGS. The book is divided into four parts: Part I focuses on computing and experimental infrastructure for NGS analysis, including chapters on cloud computing, modular pipelines for metabolic pathway reconstruction, pooling strategies for massive viral sequencing, and high-fidelity sequencing

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protocols. Part II concentrates on analysis of DNA sequencing data, covering the classic scaffolding problem, detection of genomic variants, including insertions and deletions, and analysis of DNA methylation sequencing data. Part III is devoted to analysis of RNA-seq data. This part discusses algorithms and compares software tools for transcriptome assembly along with methods for detection of alternative splicing and tools for transcriptome quantification and differential expression analysis. Part IV explores computational tools for NGS applications in microbiomics, including a discussion on error correction of NGS reads from viral populations, methods for viral quasispecies reconstruction, and a survey of state-of-the-art methods and future trends in microbiome analysis. Computational Methods for Next Generation Sequencing Data Analysis: Reviews computational techniques such as new combinatorial optimization methods, data structures, high performance computing, machine learning, and inference algorithms Discusses the mathematical and computational challenges in NGS technologies Covers NGS error correction, de novo genome transcriptome assembly, variant detection from NGS reads, and more This text is a reference for biomedical professionals interested in expanding their knowledge of computational techniques for NGS data analysis. The book is also useful for graduate and post-graduate students in bioinformatics.

This dissertation, "Statistical Analysis of Human Gastrointestinal Microbiota Using Next Generation Sequencing Data" by Youwen, Qin, 甄文, was obtained from The University of Hong Kong (Pokfulam, Hong Kong) and is being sold pursuant to Creative Commons: Attribution 3.0 Hong Kong License. The content of this dissertation has not been altered in any way. We have altered the formatting in order to facilitate the ease of printing and reading of the dissertation. All rights not granted by the above license are retained by the author. Abstract: The human gastrointestinal tract is the niche of both commensal and pathogenic microbes which play an important role in human health. This thesis includes two independent studies relevant to analyzing next-generation sequencing data on the human gastrointestinal microbiota. The first study conducted a comparative analysis on 16S rRNA gene sequencing data obtained from gastritis and gastric cancer patients in the Hong Kong (HK) and Korean cohorts. Neisseriaceae and Lachnospiraceae were the important families in segregating gastritis and cancer samples in the HK dataset while it was Streptococcaceae in the Korean dataset. Proteobacteria, Firmicutes, Bacteroidetes, Actinobacteria and Fusobacteria were the major phyla in the two cohorts, where they made up $\geq 99\%$ of the total relative abundance. However, when narrowed down to the family level, the two datasets only shared 5 major families among the 15 and 13 major families in the HK and Korean datasets, respectively. Hierarchical clustering showed that samples were segregated into two major clusters according to the relative abundance of *Helicobacter pylori* (*H. pylori*) in the two datasets. Moreover, the cross-prediction results for gastritis versus cancer between two datasets yielded up to 3 times larger error rates compared to the prediction results within the training set. Taken together, the differences between the HK and Korean cohorts in the gastric microbiota outweighed the similarities. The second study developed a computational workflow to improve the draft genomes assembled from shotgun metagenomic sequencing data. The publicly available sequencing data of 396 human stool samples were downloaded for this purpose. Firstly, 3.9 million genes assembled from 396 samples were clustered into 7,381 co-abundance gene groups (CAGs) according to their pairwise correlations. The CAGs (741 CAGs) with more than 700 genes were defined as metagenomic species (MGSs), while the others (6,640 CAGs) were defined as metagenomic units (MGUs). In order to recover the relevant MGSs of the MGUs, the metagenomic deconvolution framework which decomposes the community-level gene content into taxon-specific gene profile was applied. Overall, 377 MGUs were assigned to 354 relevant MGSs, achieving a 9.57% mean improvement in the gene count of MGSs. Most of these MGSs were annotated to phylum Firmicutes. Specifically, the augmented results of 9 MGSs annotated to genus *Faecalibacterium* by their relative MGUs achieved average improvement of 21.08% and 17.84% in sensitivity and specificity. Importantly, MGUs included essential genes that were missed in MGSs, such as ribosomal genes, metabolism and transport system genes. Hence, the implementation of metagenomic deconvolution after binning improves the draft genomes of metagenomic species. Subjects: Gastrointestinal system - Microbiology Nucleotide sequence

This unique book addresses the statistical modelling and analysis of microbiome data using cutting-edge R software. It includes real-world data from the authors' research and from the public domain, and discusses the implementation of R for data analysis step by step. The data and R computer programs are publicly available, allowing readers to replicate the model development and data analysis presented in each chapter, so that these new methods can be readily applied in their own research. The book also discusses recent developments in statistical modelling and data analysis in microbiome research, as well as the latest advances in next-generation sequencing and big data in methodological development and applications. This timely book will greatly benefit all readers involved in microbiome, ecology and microarray data analyses, as well as other fields of research.

A Practical Guide to the Highly Dynamic Area of Massively Parallel Sequencing The development of genome and transcriptome sequencing technologies has led to a paradigm shift in life science research and disease diagnosis and prevention. Scientists are now able to see how human diseases and phenotypic changes are connected to DNA mutation, polymorphi

This textbook for courses on function data analysis and shape data analysis describes how to define, compare, and mathematically represent shapes, with a focus on statistical modeling and inference. It is aimed at graduate students in analysis in statistics, engineering, applied mathematics, neuroscience, biology, bioinformatics, and other related areas. The interdisciplinary nature of the broad range of ideas covered—from introductory theory to algorithmic implementations and some statistical case studies—is meant to familiarize graduate students with an array of tools that are relevant in developing computational solutions for shape and related analyses. These tools, gleaned from geometry, algebra, statistics, and computational science, are traditionally scattered across different courses, departments, and disciplines; Functional and Shape Data Analysis offers a unified, comprehensive solution by integrating the registration problem into shape analysis, better preparing graduate students for handling future scientific challenges. Recently, a data-driven and application-oriented focus on shape analysis has been trending. This text offers a self-contained treatment of this new generation of methods in shape analysis of curves. Its main focus is shape analysis of functions and curves—in one, two,

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and higher dimensions—both closed and open. It develops elegant Riemannian frameworks that provide both quantification of shape differences and registration of curves at the same time. Additionally, these methods are used for statistically summarizing given curve data, performing dimension reduction, and modeling observed variability. It is recommended that the reader have a background in calculus, linear algebra, numerical analysis, and computation.

Recent improvements in the efficiency, quality, and cost of genome-wide sequencing have prompted biologists and biomedical researchers to move away from microarray-based technology to ultra high-throughput, massively parallel genomic sequencing (Next Generation Sequencing, NGS) technology. In *Next Generation Microarray Bioinformatics: Methods and Protocols*, expert researchers in the field provide techniques to bring together current computational and statistical methods to analyze and interpreting both microarray and NGS data. These methods and techniques include resources for microarray bioinformatics, microarray data analysis, microarray bioinformatics in systems biology, next generation sequencing data analysis, and emerging applications of microarray and next generation sequencing. Written in the highly successful *Methods in Molecular Biology*TM series format, the chapters include the kind of detailed description and implementation advice that is crucial for getting optimal results in the laboratory. Authoritative and practical, *Next Generation Microarray Bioinformatics: Methods and Protocols* seeks to aid scientists in the further study of this crucially important research into the human DNA.

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