Single Cell Rna Analysis

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Essentials of Single-Cell Analysis John Wiley & Sons
RNA-seq offers unprecedented information about transcriptome, but harnessing this information with bioinformatics tools is typically a bottleneck. This self-contained guide enables researchers to examine differential expression at gene, exon, and transcript level and to discover novel genes, transcripts, and whole transcriptomes. Each chapter starts with theoretical background, followed by descriptions of relevant analysis tools. The book also provides examples using command line tools and the R statistical environment. For non-programming scientists, the same examples are covered using open source software with a graphical user interface.
Handbook of Statistical Genomics Springer Nature
A timely update of a highly popular handbook on statistical genomics This new, two-volume edition of a classic text provides a thorough introduction to statistical genomics, a vital resource for advanced graduate students, early-career researchers and new entrants to the field. It introduces new and updated information on developments that have occurred since the 3rd edition. Widely regarded as the reference work in the field, it features new chapters focusing on statistical aspects of data generated by new sequencing technologies, including sequence-based functional assays. It expands on previous coverage of the many processes between genotype and phenotype, including gene expression and epigenetics, as well as metabolomics. It also examines population genetics and evolutionary models and

inference, with new chapters on the multi-species coalescent, admixture and ancient DNA, as well as genetic association studies including causal analyses and variant interpretation. The Handbook of Statistical Genomics focuses on explaining the main ideas, analysis methods and algorithms, citing key recent and historic literature for further details and references. It also includes a glossary of terms, acronyms and abbreviations, and features extensive cross-referencing between chapters, tying the different areas together. With heavy use of up-to-date examples and references to web-based resources, this continues to be a must-have reference in a vital area of research. Provides much-needed, timely coverage of new developments in this expanding area of study Numerous, brand new chapters, for example covering bacterial genomics, microbiome and metagenomics Detailed coverage of application areas, with chapters on plant breeding, conservation and forensic genetics Extensive coverage of human genetic epidemiology, including ethical aspects Edited by one of the leading experts in the field along with rising stars as his co-editors Chapter authors are world-renowned experts in the field, and newly emerging leaders. The Handbook of Statistical Genomics is an excellent introductory text for advanced graduate students and early-career researchers involved in statistical genetics.

Stem Cell Transcriptional Networks Humana Press

Since the invention of next-generation RNA sequencing (RNA-seq) technologies, they have become a powerful tool to study the presence and quantity of RNA molecules in biological samples and have revolutionized transcriptomic studies on bulk tissues. Recently, the emerging single-cell RNA sequencing (scRNA-seq) technologies enable the investigation of transcriptomic landscapes at a single-cell resolution, providing a chance to characterize stochastic heterogeneity within a cell population. The analysis of bulk and single-cell RNA-seq data at four different levels (samples, genes, transcripts, and exons) involves multiple statistical and computational questions, some of which remain challenging up to date. The first part of this dissertation focuses on the statistical challenges in the transcript-level analysis of bulk RNA-seq data. The next-generation RNA-seq technologies have been widely used to assess full-length RNA isoform structure and abundance in a high-throughput manner, enabling us to better understand the alternative splicing process and transcriptional regulation mechanism. However, accurate isoform identification and quantification from RNA-seq data are challenging due to the information loss in sequencing experiments. In Chapter 2, given the fast accumulation of multiple RNA-seq datasets from the same biological condition, we develop a statistical method, MSIQ, to achieve more accurate isoform quantification by integrating multiple RNA-seq samples under a Bayesian framework. The MSIQ method aims to (1) identify a consistent group of samples with homogeneous quality and (2) improve isoform quantification accuracy by jointly modeling multiple RNA-seq samples and allowing for higher weights on the consistent group. We show that MSIQ provides a consistent estimator of isoform abundance, and we demonstrate the accuracy of MSIQ compared with alternative methods through both simulation and real data studies. In Chapter 3, we introduce a novel method, AIDE, the first approach that directly controls false isoform discoveries by implementing the statistical model selection principle. Solving the

isoform discovery problem in a stepwise manner, AIDE prioritizes the annotated isoforms and precisely identifies novel isoforms whose addition significantly improves the explanation of observed RNA-seq reads. Our results demonstrate that AIDE has the highest precision compared to the state-of-the-art methods, and it is able to identify isoforms with biological functions in pathological conditions. The second part of this dissertation discusses two statistical methods to improve scRNA-seq data analysis, which is complicated by the excess missing values, the so-called dropouts due to low amounts of mRNA sequenced within individual cells. In Chapter 5, we introduce scImpute, a statistical method to accurately and robustly impute the dropouts in scRNA-seq data. The scImpute method automatically identifies likely dropouts, and only performs imputation on these values by borrowing information across similar cells. Evaluation based on both simulated and real scRNA-seq data suggests that scImpute is an effective tool to recover transcriptome dynamics masked by dropouts, enhance the clustering of cell subpopulations, and improve the accuracy of differential expression analysis. In Chapter 6, we propose a flexible and robust simulator, scDesign, to optimize the choices of sequencing depth and cell number in designing scRNA-seq experiments, so as to balance the exploration of the depth and breadth of transcriptome information. It is the first statistical framework for researchers to quantitatively assess practical scRNA-seq experimental design in the context of differential gene expression analysis. In addition to experimental design, scDesign also assists computational method development by generating high-quality synthetic scRNA-seq datasets under customized experimental settings.

Tumor Immunology and Immunotherapy - Cellular Methods Part B Humana Press

This detailed book provides state-of-art computational approaches to further explore the exciting opportunities presented by single-cell technologies. Chapters each detail a computational toolbox aimed to overcome a specific challenge in single-cell analysis, such as data normalization, rare cell-type identification, and spatial transcriptomics analysis, all with a focus on hands-on implementation of computational methods for analyzing experimental data. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and cutting-edge, Computational Methods for Single-Cell Data Analysis aims to cover a wide range of tasks and serves as a vital handbook for single-cell data analysis.

A Single-cell RNA-sequencing Training and Analysis Suite Using the Galaxy Framework Cold Spring Harbor, N.Y. : Cold Spring Harbor Laboratory Press

To thrive, every living cell must continuously gauge and respond to changes in its environment. These changes are ultimately implemented by modulating gene expression, a process that relies on transcription by Nature’s most multivalent molecular machine, the RNA polymerase. This book covers progress made over the past decade understanding how this machine functions to compute the cellular state, from the atomistic structural level responsible for chemistry to the integrative level at which RNA

polymerase interacts with the other key molecular machineries of the cell.

Transcriptome Analysis Springer

3' RNA sequencing provides an alternative to whole transcript analysis. However, we do not know a priori the relative advantage of each method. Thus, a comprehensive comparison between the whole transcript and the 3' method is needed to determine their relative merits. Single cell RNA sequencing (scRNA-seq) enables the profiling of the transcriptomes of individual cells. Cell type identification is one of the major goals in scRNA-seq. Current methods for assigning cell types have several limitations, such as unwanted sources of variation that influence clustering and a lack of canonical markers for certain cell types. Thus, new methods need to be developed. We first used two commercially available library preparation kits, the KAPA Stranded mRNA-seq kit (traditional method) and the Lexogen QuantSeq 3' mRNA-seq kit (3' method), to determine the advantages and disadvantages of these two approaches. We found that the 3' RNA-seq method detected more short transcripts than the whole transcript method. With regard to differential expression analysis, we found that the whole transcript method detected more differentially expressed genes, regardless of the level of sequencing depth. We then developed ACTINN (Automated Cell Type Identification using Neural Networks), which employs a neural network to predicts cell types for scRNA-seq datasets. We trained and tested ACTINN on multiple datasets, the results showed that ACTINN is fast and accurate, and should therefore be a useful tool to complement existing scRNA-seq pipelines. Lastly, we performed scRNA-seq to study gene networks associated with host defense comparing lesions from reversal reaction vs. lepromatous lesions from leprosy patients. We constructed an antimicrobial ecosystem by integrating the IFNG and IL1B antimicrobial targets with the cell-cell co-abundance in lesions, which revealed that the interaction of dendritic cells, macrophages, T cells, keratinocytes and fibroblasts contributes to the capacity of granulomas to eliminate the pathogen in leprosy.

Machine Learning Methods for Single-cell RNA-sequencing Data Analysis Frontiers Media SA

Transcriptome analysis is the study of the transcriptome, of the complete set of RNA transcripts that are produced under specific circumstances, using high-throughput methods. Transcription profiling, which follows total changes in the behavior of a cell, is used throughout diverse areas of biomedical research, including diagnosis of disease, biomarker discovery, risk assessment of new drugs or environmental chemicals, etc. Transcriptome analysis is most commonly used to compare specific pairs of samples, for example, tumor tissue versus its healthy counterpart. In this volume, Dr. Pyo Hong discusses the role of long RNA sequences in transcriptome analysis, Dr. Shinichi describes the next-generation single-cell sequencing technology developed by his team, Dr. Prasanta presents transcriptome analysis applied to rice under various environmental factors, Dr. Xiangyuan addresses the reproductive systems of flowering plants and Dr. Sadovsky compares codon usage in conifers.

Single Cell Methods SIAM

The volume focuses on the genomics, proteomics, metabolomics, and bioinformatics of a single cell, especially lymphocytes and on

understanding the molecular mechanisms of systems immunology. Based on the author’s personal experience, it provides revealing insights into the potential applications, significance, workflow, comparison, future perspectives and challenges of single-cell sequencing for identifying and developing disease-specific biomarkers in order to understand the biological function, activation and dysfunction of single cells and lymphocytes and to explore their functional roles and responses to therapies. It also provides detailed information on individual subgroups of lymphocytes, including cell characters, function, surface markers, receptor function, intracellular signals and pathways, production of inflammatory mediators, nuclear receptors and factors, omics, sequencing, disease-specific biomarkers, bioinformatics, networks and dynamic networks, their role in disease and future prospects. Dr. Xiangdong Wang is a Professor of Medicine, Director of Shanghai Institute of Clinical Bioinformatics, Director of Fudan University Center for Clinical Bioinformatics, Director of the Biomedical Research Center of Zhongshan Hospital, Deputy Director of Shanghai Respiratory Research Institute, Shanghai, China.

Distortion in Dimensionality Reduction and Implications for the Analysis of Single Cell RNA-Sequencing Data Springer Science & Business Media

Analysis of single cell RNA sequencing (scRNA-seq) datasets is a complex and time-consuming process, requiring both biological knowledge and technical skill. With the rapid growth in scRNA-seq datasets and the increasing number of biological applications, there is a need to simplify and systematize this process. In order to systematize and simplify this process, we introduce three tools to aid : UNCURL, CellMeSH, and UNCURL-App. UNCURL is a preprocessing tool that assists in dimensionality reduction and clustering of scRNA-seq data. CellMeSH is a database and associated query method that allows for the easy identification of cell types present in single cell data. UNCURL-App is an online GUI-based interactive web app which integrates multiple stages of the data analysis pipeline into a single interface, including dimensionality reduction, clustering, differential expression, and cell type identification. Together, these tools encompass all stages of the scRNA-seq cell type annotation pipeline into a single user-friendly interface.

Computational Methods for Single-Cell Data Analysis CRC Press

Next-generation DNA and RNA sequencing has revolutionized biology and medicine. With sequencing costs continuously dropping and our ability to generate large datasets rising, data analysis becomes more important than ever. Next-Generation Sequencing Data Analysis walks readers through next-generation sequencing (NGS) data analysis step by step for a wide range of NGS applications. For each NGS application, this book covers topics from experimental design, sample processing, sequencing strategy formulation, to sequencing read quality control, data preprocessing, read mapping or assembly, and more advanced stages that are specific to each application. Major applications include: RNA-seq: Both bulk and single cell (separate chapters) Genotyping and variant discovery through whole genome/exome sequencing Clinical sequencing and detection of actionable variants De novo genome assembly ChIP-seq to map protein-DNA interactions Epigenomics through DNA methylation sequencing Metagenome sequencing for microbiome analysis Before

detailing the analytic steps for each of these applications, the book presents introductory cellular and molecular biology as a refresher mostly for data scientists, the ins and outs of widely used NGS platforms, and an overview of computing needs for NGS data management and analysis. The book concludes with a chapter on the changing landscape of NGS technologies and data analytics. The second edition of this book builds on the well-received first edition by providing updates to each chapter. Two brand new chapters have been added to meet rising data analysis demands on single-cell RNA-seq and clinical sequencing. The increasing use of long-read sequencing has also been reflected in all NGS applications. This book discusses concepts and principles that underlie each analytic step, along with software tools for implementation. It highlights key features of the tools while omitting tedious details to provide an easy-to-follow guide for practitioners in life sciences, bioinformatics, biostatistics, and data science. Tools introduced in this book are open source and freely available.

RNA-seq Data Analysis Academic Press

Tumor Immunology and Immunotherapy - Cellular Methods Part BAcademic Press

Statistical Power Analysis for Single-cell RNA-sequencing CRC Press

The Mouse Nervous System provides a comprehensive account of the central nervous system of the mouse. The book is aimed at molecular biologists who need a book that introduces them to the anatomy of the mouse brain and spinal cord, but also takes them into the relevant details of development and organization of the area they have chosen to study. The Mouse Nervous System offers a wealth of new information for experienced anatomists who work on mice. The book serves as a valuable resource for researchers and graduate students in neuroscience. Systematic consideration of the anatomy and connections of all regions of the brain and spinal cord by the authors of the most cited rodent brain atlases A major section (12 chapters) on functional systems related to motor control, sensation, and behavioral and emotional states A detailed analysis of gene expression during development of the forebrain by Luis Puelles, the leading researcher in this area Full coverage of the role of gene expression during development and the new field of genetic neuroanatomy using site-specific recombinases Examples of the use of mouse models in the study of neurological illness

Computer and Information Sciences - ISCIS 2005 Springer

This book provides an overview of single-cell isolation, separation, injection, lysis and dynamics analysis as well as a study of their heterogeneity using different miniaturized devices. As an important part of single-cell analysis, different techniques including electroporation, microinjection, optical trapping, optoporation, rapid electrokinetic patterning and optoelectronic tweezers are described in detail. It presents different fluidic systems (e.g. continuous micro/nano-fluidic devices, microfluidic cytometry) and their integration with sensor technology, optical and hydrodynamic stretchers etc., and demonstrates the applications of single-cell analysis in systems biology, proteomics, genomics, epigenomics, cancer transcriptomics, metabolomics, biomedicine and drug delivery systems. It also discusses the future challenges for single-cell analysis, including the advantages and limitations. This book is enjoyable reading

material while at the same time providing essential information to scientists in academia and professionals in industry working on different aspects of single-cell analysis. Dr. Fan-Gang Tseng is a Distinguished Professor of Engineering and System Science at the National Tsing Hua University, Taiwan. Dr. Tuhin Subhra Santra is a Research Associate at the California Nano Systems Institute, University of California at Los Angeles, USA.
Springer
This book presents recent methods for Systems Genetics (SG) data analysis, applying them to a suite of simulated SG benchmark datasets. Each of the chapter authors received the same datasets to evaluate the performance of their method to better understand which algorithms are most useful for obtaining reliable models from SG datasets. The knowledge gained from this benchmarking study will ultimately allow these algorithms to be used with confidence for SG studies e.g. of complex human diseases or food crop improvement. The book is primarily intended for researchers with a background in the life sciences, not for computer scientists or statisticians.
Single-cell RNA Sequencing (scRNA-seq) in Liver Cancer Springer Nature
This volume provides an overview of RNA bioinformatics methodologies, including basic strategies to predict secondary and tertiary structures, and novel algorithms based on massive RNA sequencing. Interest in RNA bioinformatics has rapidly increased thanks to the recent high-throughput sequencing technologies allowing scientists to investigate complete transcriptomes at single nucleotide resolution. Adopting advanced computational technics, scientists are now able to conduct more in-depth studies and present them to you in this book. Written in the highly successful Methods of Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and equipment, step-by-step, readily reproducible bioinformatics protocols, and key tips to avoid known pitfalls. Authoritative and practical, RNA Bioinformatics seeks to aid scientists in the further study of bioinformatics and computational biology of RNA.
Single Molecule and Single Cell Sequencing Humana
The State of the Art in Transcriptome AnalysisRNA sequencing (RNA-seq) data offers unprecedented information about the transcriptome, but harnessing this information with bioinformatics tools is typically a bottleneck. RNA-seq Data Analysis: A Practical Approach enables researchers to examine differential expression at gene, exon, and transcript le
Single Cell Sequencing and Systems Immunology Humana
This three-volume set LNAI 11670, LNAI 11671, and LNAI 11672 constitutes the thoroughly refereed proceedings of the 16th Pacific Rim Conference on Artificial Intelligence, PRICAI 2019, held in Cuvu, Yanuca Island, Fiji, in August 2019. The 111 full papers and 13 short papers presented in these volumes were carefully reviewed and selected from 265 submissions. PRICAI covers a wide range of topics such as AI theories, technologies and their applications in the areas of social and economic importance for countries in the Pacific Rim.
Multimodal and Integrative Analysis of Single-Cell or Bulk Sequencing Data Tumor Immunology and Immunotherapy - Cellular Methods Part B
Tumor Immunology and Immunotherapy - Cellular Methods Part

B, Volume 632, the latest release in the Methods in Enzymology series, continues the legacy of this premier serial with quality chapters authored by leaders in the field. Topics covered include Quantitation of calreticulin exposure associated with immunogenic cell death, Side-by-side comparisons of flow cytometry and immunohistochemistry for detection of calreticulin exposure in the course of immunogenic cell death, Quantitative determination of phagocytosis by bone marrow-derived dendritic cells via imaging flow cytometry, Cytofluorometric assessment of dendritic cell-mediated uptake of cancer cell apoptotic bodies, Methods to assess DC-dependent priming of T cell responses by dying cells, and more. Contains content written by authorities in the field Provides a comprehensive view on the topics covered Includes a high level of detail

Single Cell Transcriptomics Frontiers Media SA

This book presents an overview of the recent technologies in single molecule and single cell sequencing. These sequencing technologies are revolutionizing the way of the genomic studies and the understanding of complex biological systems. The PacBio sequencer has enabled extremely long-read sequencing and the MinION sequencer has made the sequencing possible in developing countries. New developments and technologies are constantly emerging, which will further expand sequencing applications. In parallel, single cell sequencing technologies are rapidly becoming a popular platform. This volume presents not only an updated overview of these technologies, but also of the related developments in bioinformatics. Without powerful bioinformatics software, where rapid progress is taking place, these new technologies will not realize their full potential. All the contributors to this volume have been involved in the development of these technologies and software and have also made significant progress on their applications. This book is intended to be of interest to a wide audience ranging from genome researchers to basic molecular biologists and clinicians.

CpG Islands Academic Press

There are trillions of cells, which make up hundreds of different cell types, found in the human body. These cells make up not only tissues but dictate the functions of those tissues. In diseased tissues, cell types can have a profound impact on the outcome of a patient. For these reasons, having a comprehensive understanding of cell types is important. In the past 10 years, single cell RNA sequencing has profoundly impacted our understanding of known and previously unknown cell types. Along with the numerous single cell datasets, a multitude of bulk expression datasets, multi-omic datasets, and curated information also exist. All of these data sources must be leveraged together to most improve our understanding of human tissues and diseases at the single cell level. We developed methodologies, frameworks, and algorithms that leverage multiple diverse datasets simultaneously to better understand single cell RNA sequencing data and as a result tissue heterogeneity as a whole.

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