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B. D. Hames, Steve J. Higgins

Gene Expression Profiling Richard A. Shimkets, 2008-02-03 Leading scientists in gene expression methodology and bioinformatics data analysis describe readily reproducible methods for measuring RNA levels in cells and tissues. The techniques presented include new methods for applying the Affymetrix GeneChip®, SAR-SAGE, StaRT-PCR, SSH, the Invader Assay®, and ADGEM. The authors also provide critical bioinformatics insight and resources for data analysis and management. By distilling the basic underlying principles of many methods to a few straightforward concepts, investigators can easily choose the method most appropriate to their application.

Molecular Microbial Ecology Manual A.D. Akkermans, Jan Dirk van Elsas, F.J. de Bruijn, 2012-12-06 For a long time microbial ecology has been developed as a distinct field within Ecology. In spite of the important role of microorganisms in the environment, this group of 'invisible' organisms remained unaccessible to other ecologists. Detection and identification of microorganisms remain largely dependent on isolation techniques and characterisation of pure cultures. We now realise that only a minor fraction of the microbial community can be cultivated. As a result of the introduction of molecular methods, microbes can now be detected and identified at the DNA/RNA level in their natural environment. This has opened a new field in ecology: Molecular Microbial Ecology. In the present manual we aim to introduce the microbial ecologist to a selected number of current molecular techniques that are relevant in microbial ecology. The first edition of the manual contains 33 chapters and an equal number of additional chapters will be added this year. Since the field of molecular ecology is in a continuous progress, we aim to update and extend the Manual regularly and will invite anyone to deposit their new protocols in full detail in the next edition of this Manual.

RNA-Protein Interaction Protocols Susan R. Haynes, 2008-02-03 The molecular characterization of RNA and its interactions with proteins is an important and exciting area of current research. Organisms utilize a variety of RNA-protein interactions to regulate the expression of their genes. This is particularly true for eukaryotes, since newly synthesized messenger RNA must be extensively modified and transported to the cytoplasm before it can be used for protein synthesis. The realization that posttranscriptional processes are critical components of gene regulation has sparked an explosion of interest in both stable ribonucleoprotein (RNP) complexes and transient RNA-protein interactions. RNA is conformationally flexible and can adopt complex structures that provide diverse surfaces for interactions with proteins. The fact that short

RNA molecules (aptamers; see Chapter 16) can be selected to bind many different types of molecules is evidence of the structural variability of RNA. RNA molecules are rarely entirely single- or double-stranded, but usually contain multiple short duplexes interrupted by single-stranded loops and bulges; in some RNAs, such as tRNAs, the short duplexes stack on each other. Further variability is generated by the presence of non-Watson-Crick base pairs, modified nucleotides, and more complex structures, such as pseudoknots and triple-strand interactions.

Python Data Science Handbook Jake VanderPlas, 2016-11-21 For many researchers, Python is a first-class tool mainly because of its libraries for storing, manipulating, and gaining insight from data. Several resources exist for individual pieces of this data science stack, but only with the Python Data Science Handbook do you get them all—IPython, NumPy, Pandas, Matplotlib, Scikit-Learn, and other related tools. Working scientists and data crunchers familiar with reading and writing Python code will find this comprehensive desk reference ideal for tackling day-to-day issues: manipulating, transforming, and cleaning data; visualizing different types of data; and using data to build statistical or machine learning models. Quite simply, this is the must-have reference for scientific computing in Python. With this handbook, you'll learn how to use: IPython and Jupyter: provide computational environments for data scientists using Python NumPy: includes the ndarray for efficient storage and manipulation of dense data arrays in Python Pandas: features the DataFrame for efficient storage and manipulation of labeled/columnar data in Python Matplotlib: includes capabilities for a flexible range of data visualizations in Python Scikit-Learn: for efficient and clean Python implementations of the most important and established machine learning algorithms

Chemical Engineering Design Gavin Towler, Ray Sinnott, 2012-01-25 Chemical Engineering Design, Second Edition, deals with the application of chemical engineering principles to the design of chemical processes and equipment. Revised throughout, this edition has been specifically developed for the U.S. market. It provides the latest US codes and standards, including API, ASME and ISA design codes and ANSI standards. It contains new discussions of conceptual plant design, flowsheet development, and revamp design; extended coverage of capital cost estimation, process costing, and economics; and new chapters on equipment selection, reactor design, and solids handling processes. A rigorous pedagogy assists learning, with detailed worked examples, end of chapter exercises, plus supporting data, and Excel spreadsheet calculations, plus over 150 Patent References for downloading from the companion website. Extensive instructor resources, including 1170 lecture slides and a fully worked solutions manual are available to adopting instructors. This text is designed for chemical and biochemical engineering students (senior undergraduate year, plus appropriate for capstone design courses where taken, plus graduates) and lecturers/tutors, and professionals in industry (chemical process, biochemical, pharmaceutical, petrochemical sectors). New to this edition: Revised organization into Part I: Process Design, and Part II: Plant Design. The broad themes of Part I are flowsheet development, economic analysis, safety and environmental impact

and optimization. Part II contains chapters on equipment design and selection that can be used as supplements to a lecture course or as essential references for students or practicing engineers working on design projects. New discussion of conceptual plant design, flowsheet development and revamp design Significantly increased coverage of capital cost estimation, process costing and economics New chapters on equipment selection, reactor design and solids handling processes New sections on fermentation, adsorption, membrane separations, ion exchange and chromatography Increased coverage of batch processing, food, pharmaceutical and biological processes All equipment chapters in Part II revised and updated with current information Updated throughout for latest US codes and standards, including API, ASME and ISA design codes and ANSI standards Additional worked examples and homework problems The most complete and up to date coverage of equipment selection 108 realistic commercial design projects from diverse industries A rigorous pedagogy assists learning, with detailed worked examples, end of chapter exercises, plus supporting data and Excel spreadsheet calculations plus over 150 Patent References, for downloading from the companion website Extensive instructor resources: 1170 lecture slides plus fully worked solutions manual available to adopting instructors

Nitric Oxide Protocols M. A Titheradge,2008-02-05 Michael Titheradge provides both the experienced researcher and the newcomer with time-tested techniques to cover all aspects of NO synthase and metabolism. Topics range from the cloning and expression of the different isoforms of NO synthase to the role of NO in DNA damage and apoptosis and include indirect and direct measurements of NO production, measurement on NO synthase mRNA both in situ and in vitro, and Western blotting and immunohistochemical localization of different isoforms of NO synthase. A variety of alternative techniques are described to enable researchers to set up an assay using either the simplest equipment or the most expensive EPR machines.

Methods in Nucleic Acids Research Gregory W. Warr,James D. Karam, Lee Chao,1990-11-26 Methods in Nucleic Acids Research provides extensively referenced overviews of chapter topics, in addition to step-by-step laboratory protocols. Topics include discussions regarding the preparation and assay of antibodies against oligopeptides, RNA footprinting, gel-retardation assays for nucleic acid binding proteins, in vitro transcription and translation assays for studies of eukaryotic gene expression, human genome mapping, forensic analysis of DNA polymorphism, in situ hybridization for the detection of specific RNA, and other methods. Biochemists, molecular biologists, immunologists, cell biologists, and geneticists will find this book invaluable for their research.

Plant Molecular Biology Manual Stanton Gelvin,2012-12-06 During the past ten years, great advances have been made in the area of plant molecular biology. Such formerly esoteric techniques as gene transfer and plant regeneration are now routinely performed, making the dissection of regulatory elements of genes a common practice in many laboratories. Along with this new technology has come an almost bewildering array of rapidly changing techniques, often making it

difficult for the novice to select and perform the technique most appropriate for answering a given biological question. In 1986, some of us felt that many of these techniques had become routine enough to warrant the publication of a laboratory manual. The manual is designed both for advanced college level laboratory courses and as a 'bench guide' for use in the scientific laboratory. Recognizing the rapidly changing nature of plant molecular biology technology, the editors have designed a laboratory manual that is both easy to use in the laboratory and which will be updated as the techniques change and new technologies are devised. Additional chapters that can replace or be added to this first edition will be published periodically. The editors recognize that many of the techniques described in this manual depend upon specialized plant genetic material, microbial strains, or recombinant plasmids. Those people desiring such material should contact the relevant authors directly. A list of the various contributors to this manual, including their addresses, is included.

RNA-Protein Interactions : A Practical Approach Christopher W.J. Smith, 1998-07-09 RNA-protein interactions play a fundamental role in gene expression and protein synthesis. Recent research into the role of RNA in cells has elucidated many more vital interactions with proteins. This book provides an up-to-date and comprehensive guide to a wide range of laboratory procedures to investigate the interactions between RNA and proteins. - ;RNA-protein interactions play a vital role in gene transcription and protein expression. Interactions such as the synthesis of mRNA by RNA polymerases, to the essential modification of RNA by the proteins of the spliceosome complex, and the highly catalytic action of the ribosome in protein synthesis, are established as being fundamental to the function of RNA. Recent research into, for example, the role of RNA as a catalyst, has elucidated many more interactions with proteins that are vital to cell function. RNA - Protein Interactions: A Practical Approach provides a clear and comprehensive guide to the experimental procedures used in studying RNA - protein interactions. The approaches covered range from those initially used to detect a novel RNA-protein interaction, various biochemical and genetic approaches to purifying and cloning RNA binding proteins, through to methods for an in depth analysis of the structural basis of the interaction. The volume includes a number of procedures that have not previously been covered in this type of manual. These include the production of site-specifically modified RNAs by enzymatic and chemical methods and in vivo screening for novel RNA - protein interactions in yeast and E. coli . This is the first volume to gather in one place this wide array of approaches for studying RNA - protein interactions. As is customary for the Practical Approach series, the writing is characterized by a clear explanatory style with many detailed protocols. This informative book will be a valuable aid to laboratory workers in biochemistry and molecular biology - graduate students, postdoctoral and senior scientists - whose research encompasses this field. -

Interpretable Machine Learning Christoph Molnar, 2020 This book is about making machine learning models and their decisions interpretable. After exploring the concepts of interpretability, you will learn about simple, interpretable models such as decision trees, decision rules and linear regression. Later chapters focus on general model-agnostic methods for

interpreting black box models like feature importance and accumulated local effects and explaining individual predictions with Shapley values and LIME. All interpretation methods are explained in depth and discussed critically. How do they work under the hood? What are their strengths and weaknesses? How can their outputs be interpreted? This book will enable you to select and correctly apply the interpretation method that is most suitable for your machine learning project.

Radioisotopes in Biology Robert J. Slater, 2002 Provides an introduction to the use of radioactivity in the bioscience laboratory. The text covers general aspects of radioactivity, methods for the detection of radioactivity, radioisotope protocols used to study key cellular processes, and a summary of legislative requirements in the US and European Union. Guidance on safe handling and detailed recipes are provided.

Prevention of Thalassaemias and Other Haemoglobin Disorders Galanello Renzo, Thalassaemia International Federation, 2003 Volume 1 of the Prevention Book presents the principles of a programme for the prevention of the thalassaemia and other haemoglobin disorders, including a description of the various types of disorders requiring prenatal diagnosis, the strategies used for carrier screening, and a number of annexes listing upto date epidemiological and mutation data on thalassaemia. This book was written for use in combination with Volume 2, which describes many of the laboratory protocols in great detail.

RNA Methodologies Robert E. Farrell Jr., 2010-07-22 This laboratory guide represents a growing collection of tried, tested and optimized laboratory protocols for the isolation and characterization of eukaryotic RNA, with lesser emphasis on the characterization of prokaryotic transcripts. Collectively the chapters work together to embellish the RNA story, each presenting clear take-home lessons, liberally incorporating flow charts, tables and graphs to facilitate learning and assist in the planning and implementation phases of a project. RNA Methodologies, 3rd edition includes approximately 30% new material, including chapters on the more recent technologies of RNA interference including: RNAi; Microarrays; Bioinformatics. It also includes new sections on: new and improved RT-PCR techniques; innovative 5' and 3' RACE techniques; subtractive PCR methods; methods for improving cDNA synthesis. * Author is a well-recognized expert in the field of RNA experimentation and founded Exon-Intron, a well-known biotechnology educational workshop center * Includes classic and contemporary techniques * Incorporates flow charts, tables, and graphs to facilitate learning and assist in the planning phases of projects

Statistical Parametric Mapping: The Analysis of Functional Brain Images William D. Penny, Karl J. Friston, John T. Ashburner, Stefan J. Kiebel, Thomas E. Nichols, 2011-04-28 In an age where the amount of data collected from brain imaging is increasing constantly, it is of critical importance to analyse those data within an accepted framework to ensure proper integration and comparison of the information collected. This book describes the ideas and procedures that underlie the analysis of signals produced by the brain. The aim is to understand how the brain works, in terms of its functional

architecture and dynamics. This book provides the background and methodology for the analysis of all types of brain imaging data, from functional magnetic resonance imaging to magnetoencephalography. Critically, Statistical Parametric Mapping provides a widely accepted conceptual framework which allows treatment of all these different modalities. This rests on an understanding of the brain's functional anatomy and the way that measured signals are caused experimentally. The book takes the reader from the basic concepts underlying the analysis of neuroimaging data to cutting edge approaches that would be difficult to find in any other source. Critically, the material is presented in an incremental way so that the reader can understand the precedents for each new development. This book will be particularly useful to neuroscientists engaged in any form of brain mapping; who have to contend with the real-world problems of data analysis and understanding the techniques they are using. It is primarily a scientific treatment and a didactic introduction to the analysis of brain imaging data. It can be used as both a textbook for students and scientists starting to use the techniques, as well as a reference for practicing neuroscientists. The book also serves as a companion to the software packages that have been developed for brain imaging data analysis. An essential reference and companion for users of the SPM software Provides a complete description of the concepts and procedures entailed by the analysis of brain images Offers full didactic treatment of the basic mathematics behind the analysis of brain imaging data Stands as a compendium of all the advances in neuroimaging data analysis over the past decade Adopts an easy to understand and incremental approach that takes the reader from basic statistics to state of the art approaches such as Variational Bayes Structured treatment of data analysis issues that links different modalities and models Includes a series of appendices and tutorial-style chapters that makes even the most sophisticated approaches accessible

DICOM Structured Reporting David A. Clunie,2000

Differentially Expressed Genes In Plants Axel Kornerup Hansen,2002-09-11 The analysis of changes in gene activity in tissues and cells of plants is a way of measuring developmental and environmental responses. This volume provides detailed accounts of new and established techniques used to carry out such analyses.

Gene Transcription B. D. Hames,Steve J. Higgins,1993

A Laboratory Guide to RNA Paul A. Krieg,1996-08-15 Here is the most complete guide available to the isolation, analysis, and synthesis of RNA. It covers everything researchers and laboratory workers need to know about the study of gene expression via RNA analysis-from the theory behind the methods, to actual problem-solving techniques. Step-by-step protocols are presented for each method. A careful presentation of the experimental formalities of these protocols enables specialists and nonspecialists alike to implement the methods easily in the laboratory. Each protocol is accompanied by the theoretical background underlying the experimental procedure and most chapters contain illustrations of typical results and troubleshooting tips. A Laboratory Guide to RNA offers a straightforward detailed account of experimental procedures,

ranging from the isolation of RNA from a variety of cell and tissue types, detection analysis, and quantitation using a range of strategies, to large- and small-scale synthesis of RNA. This unique guide not only covers established procedures such as RNA blotting and nuclease protection, but also the latest protocols for quantitative PCR and differential display. Protocols addressing in situ hybridization are highlighted in an eight-page, full-color section that illustrates the power of the technique for detection of gene expression in tissues and whole organisms. Featuring contributions from leading research laboratories and the biotechnology field, *A Laboratory Guide to RNA: Isolation, Analysis, and Synthesis* provides all the methods required for RNA analysis. It is the ideal laboratory guide for research scientists, graduate students, and lab personnel who need a solid reference on the analysis of gene expression at the RNA level.

Molecular Tools for Screening Biodiversity A. Karp, D.S. Ingram, Peter G. Isaac, 2012-12-06 Mark Chase There are many literature resources available to molecular biologists wishing to assess genetic variation, but the myriad of techniques and approaches potentially available to the plant breeder and the evolutionary biologist is truly bewildering, and most have never been evaluated side-by-side on the same sets of samples. Additionally, it is often not recognized that tools that are useful for breeders can often be adapted for use in evolutionary studies and vice versa, but this is generally the case. The borderline between population genetics and phylogenetics is vague and difficult to assess, and a combination of both types of tools is best when it is not clear with which area one is dealing. Furthermore, it is not now appropriate to use just one type of marker in any kind of study; most markers have the potential to misinform under certain conditions, so it is always wise to incorporate at least two different types of assessments into any project. This volume is designed to facilitate this sort of multiple approach and provides comparative data on most currently available methods so that researchers can more intelligently select those appropriate to their area of interest, regardless of whether it is in the realm of breeding or evolutionary biology.

RNA Turnover in Bacteria, Archaea and Organelles Lynne E. Maquat, Cecilia Arraiano, 2008-12-23 Specific complexes of protein and RNA carry out many essential biological functions, including RNA processing, RNA turnover, RNA folding, as well as the translation of genetic information from mRNA into protein sequences. Messenger RNA (mRNA) decay is now emerging as an important control point and a major contributor to gene expression. Continuing identification of the protein factors and cofactors, and mRNA instability elements, responsible for mRNA decay allow researchers to build a comprehensive picture of the highly orchestrated processes involved in mRNA decay and its regulation. Covers the difference in processing of mRNA between eukaryotes, bacteria and archaea. Benefit: Processing of mRNA differs greatly between eukaryotes, bacteria and archaea and this affords researchers readily reproducible techniques to understand and study the molecular pathogenesis of disease Expert researchers introduce the most advanced technologies and techniques to identify mRNA processing, transport, localization and turnover which are central to the process of gene expression. Benefit: Keeps

MIE buyers and online subscribers up-to-date with the latest research Offers step by step lab instructions including necessary equipment and reagents. Benefit: Provides tried and tested techniques which eliminate searching through many different sources. Tested techniques are trustworthy and avoid pitfalls so the same mistakes are not made over and over

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