

Phylogenetic Trees Made Easy A How To 3 Rd

This book offers the first comprehensive, in-depth treatment of microbial diversity for undergraduate and graduate students. Using a global approach, *Microbial Diversity* illustrates the impact of microorganisms on ecological and Earth system phenomena. Accompanied by a devoted website with resources for both instructors and students: www.blackwellpublishing.com/ogunseit Uses key ecological and global phenomena to show the continuity of microbial contribution. Illustrates the importance of microbial diversity for the understanding of global physiochemical and biological processes. Presents analyses of microscopic, culture, molecular, and phylogenetic systematic methods. Shows the relevance of microbial diversity to global environmental problems, such as climate change and ozone depletion. Features numerous illustrations, including over 60 4-color photographs of microbes.

This authoritative text/reference presents a review of the history, current status, and potential future directions of computational biology in molecular evolution. Gathering together the unique insights of an international selection of prestigious researchers, this must-read volume examines the latest developments in the field, the challenges that remain, and the new avenues emerging from the growing influx of sequence data. These viewpoints build upon the pioneering work of David Sankoff, one of the founding fathers of computational biology, and mark the 50th anniversary of his first scientific article. The broad spectrum of rich contributions in this essential collection will appeal to all computer scientists, mathematicians and biologists involved in comparative genomics, phylogenetics and related areas.

An introduction to biological networks and methods for their analysis *Analysis of Biological Networks* is the first book of its kind to provide readers with a comprehensive introduction to the structural analysis of biological networks at the interface of biology and computer science. The book begins with a brief overview of biological networks and graph theory/graph algorithms and goes on to explore: global network properties, network centralities, network motifs, network clustering, Petri nets, signal transduction and gene regulation networks, protein interaction networks, metabolic networks, phylogenetic networks, ecological networks, and correlation networks. *Analysis of Biological Networks* is a self-contained introduction to this important research topic, assumes no expert knowledge in computer science or biology, and is accessible to professionals and students alike. Each chapter concludes with a summary of main points and with exercises for readers to test their understanding of the material presented. Additionally, an FTP site with links to author-provided data for the book is available for deeper study. This book is suitable as a resource for researchers in computer science, biology, bioinformatics, advanced biochemistry, and the life sciences, and also serves as an ideal reference text for graduate-level courses in bioinformatics and biological research.

Principles of Virology, the leading virology textbook in use, is an extremely valuable and highly informative presentation of virology at the interface of modern cell biology and immunology. This text utilizes a uniquely rational approach by highlighting common principles and processes across all viruses. Using a set of representative viruses to illustrate the breadth of viral complexity, students are able to understand viral reproduction and pathogenesis and are equipped with the necessary tools for future encounters with new or understudied viruses. This fifth edition was updated to keep pace with the ever-changing field of virology. In addition to the beloved full-color illustrations, video interviews with leading scientists, movies, and links to exciting blogposts on relevant topics, this edition includes study questions and active learning puzzles in each chapter, as well as short descriptions regarding the key messages of references of special interest. Volume I: Molecular Biology focuses on the molecular processes of viral reproduction, from entry through release. Volume II: Pathogenesis and Control addresses the interplay between viruses and their host organisms, on both the micro- and macroscale, including chapters on public health, the immune response, vaccines and other antiviral strategies, viral evolution, and a brand new chapter on the therapeutic uses of viruses. These two volumes can be used for separate courses or together in a single course. Each includes a unique appendix, glossary, and links to internet resources. Principles of Virology, Fifth Edition, is ideal for teaching the strategies by which all viruses reproduce, spread within a host, and are maintained within populations. This edition carefully reflects the results of extensive vetting and feedback received from course instructors and students, making this renowned textbook even more appropriate for undergraduate and graduate courses in virology, microbiology, and infectious diseases.

Microorganisms are distributed across every ecosystem, and microbial transformations are fundamental to the operation of the biosphere. Microbial ecology is the study of this interaction between microorganisms and their environment, and arguably represents one of the most important areas of biological research. Yet for many years our study of microbial flora was severely limited: the primary method of culturing microorganisms on media allowed us to study only between 0.1 and 10% of the total microbial flora in any given environment. Molecular Microbial Ecology gives a comprehensive guide to the recent revolution in the study of microorganisms in the environment. Details are given on molecular methods for isolating some of the previously uncultured and numerically dominant microbial groups. PCR-based approaches to studying prokaryotic systematics are described, including ribosomal RNA analysis and stable isotope probing. Later chapters cover DNA hybridisation techniques (including fluorescent in situ hybridisation), as well as genomic and metagenomic approaches to microbial ecology. Gathering together some of the world's leading experts, this book provides an invaluable introduction to the modern theory and molecular methods used in studying microbial ecology.

The complete Numerical Recipes 3rd edition book/CD bundle, with a hundred new routines, two new chapters and much more.

Much of what we are comes from our ancestors. Through cultural and biological inheritance mechanisms, our genetic composition, instructions for constructing artifacts, the structure and content of languages, and rules for behavior are passed from parents to children and from individual to individual. Mapping Our Ancestors demonstrates how various genealogical or "phylogenetic" methods can be used both to answer questions about human history and to build evolutionary explanations for the shape of history. Anthropologists are increasingly turning to quantitative phylogenetic methods. These methods depend on the transmission of information regardless of mode and as such are applicable to many anthropological questions. In this way, phylogenetic approaches have the potential for building bridges among the various subdisciplines of anthropology; an exciting prospect indeed. The structure of Mapping Our Ancestors reflects the editors' goal of developing a common understanding of the methods and conditions under which ancestral relations can be derived in a range of data classes of interest to anthropologists. Specifically, this volume explores the degree to which patterns of ancestry can be determined from artifactual, genetic, linguistic, and behavioral data and how processes such as selection, transmission, and geography impact the results of phylogenetic analyses. Mapping Our Ancestors provides a solid demonstration of the potential of phylogenetic methods for studying the evolutionary history of human populations using a variety of data sources and thus helps explain how cultural material, language, and biology came to be as they are. Carl P. Lipo is assistant professor of anthropology at California State University in Long Beach. Michael O'Brien is professor of anthropology and director of the Museum of Anthropology at the University of Missouri. Mark Collard is assistant professor of anthropology at the University of British Columbia, Stephen J. Shennan is a professor and director of the Institute of Archaeology at the University College London. Niles Eldredge is a curator in the department of invertebrates at the American Museum of Natural History, and adjunct professor at the City University of New York. Symbiotic Fungi – Principles and Practice presents current protocols for the study of symbiotic fungi and their interactions with plant roots, such as techniques for analyzing nutrient transfer, ecological restoration, microbial communication, and mycorrhizal bioassays, AM inoculum procedures and mushroom technology. The protocols offer practical solutions for researchers and students involved in the study of symbiotic microorganisms. The volume will be of great use for basic research, biotechnological applications, and the development of commercial products.

Barry G. Hall helps beginners get started in creating phylogenetic trees from protein or nucleic acid sequence data.

This multidisciplinary book is at the crossroads between two major scientific fields of the 21st century: evolutionary biology and infectious diseases. The genomic revolution has upset

modern biology and has revolutionized our approach to ancient disciplines such as evolutionary studies. In particular, this revolution is profoundly changing our view on genetically driven human phenotypic diversity, and this is especially true in disease genetic susceptibility. Infectious diseases are indisputably the major challenge of medicine. When looking globally, they are the number one killer of humans and therefore the main selective pressure exerted on our species. Even in industrial countries, infectious diseases are now far less under control than 20 years ago. The first part of this book covers the main features and applications of modern technologies in the study of infectious diseases. The second part provides detailed information on a number of the key infectious diseases such as malaria, SARS, avian flu, HIV, tuberculosis, nosocomial infections and a few other pathogens that will be taken as examples to illustrate the power of modern technologies and the value of evolutionary approaches. Takes an integrated approach to infectious diseases Includes contributions from leading authorities Provides the latest developments in the field

Ecological Genetics addresses the fundamental problems of which of the many molecular markers should be used and how the resulting data should be analysed in clear, accessible language, suitable for upper-level undergraduates through to research-level professionals. A very accessible straightforward text to deal with this difficult topic - applying modern molecular techniques to ecological processes. Written by active researchers and teachers within the field. There will be an accompanying web site managed by the authors, comprising of worked examples, test data sets and hyperlinks to relevant web pages.

Mammalogy is the study of mammals from the diverse biological viewpoints of structure, function, evolutionary history, behavior, ecology, classification, and economics. Thoroughly updated, the Sixth Edition of Mammalogy explains and clarifies the subject as a unified whole. The text begins by defining mammals and summarizing their origins. It moves on to discuss the orders and families of mammals with comprehensive coverage on the fossil history, current distribution, morphological characteristics, and basic behavior and ecology of each family of mammals. The third part of the text progresses to discuss special topics such as mammalian echolocation, physiology, behavior, ecology, and zoogeography. The text concludes with two additional chapters, previously available online, that cover mammalian domestication and mammalian disease and zoonoses.

Multimedia services are now commonly used in various activities in the daily lives of humans. Related application areas include services that allow access to large depositories of information, digital libraries, e-learning and e-education, e-government and e-governance, e-commerce and e-auctions, e-entertainment, e-health and e-medicine, and e-legal services, as well as their mobile counterparts (i.e., m-services). Despite the tremendous growth of multimedia services over the recent years, there is an increasing demand for their further development. This demand is driven by the ever-increasing desire of society for easy accessibility to information in friendly, personalized and adaptive environments. In this book at hand, we examine recent Recommendation Services. Recommendation services appear in the mobile environment, medicine/biology, tourism, education, and so on. The book includes ten chapters, which present various recently developed recommendation services. This research book is directed to professors, researchers, application engineers and students of all disciplines who are interested in learning more about recommendation services, advancing the corresponding state of the art and developing innovative recommendation services.

The Darwinian theory of evolution is itself evolving and this book presents the details of the core of modern Darwinism and its latest developmental directions. The authors present current scientific work addressing theoretical problems and challenges in four sections, beginning with the concepts of evolution theory, its processes of variation, heredity, selection, adaptation and function, and its patterns of character, species, descent and life. The second part of this book scrutinizes Darwinism in the philosophy of science and its usefulness in understanding

ecosystems, whilst the third section deals with its application in disciplines beyond the biological sciences, including evolutionary psychology and evolutionary economics, Darwinian morality and phylolinguistics. The final section addresses anti-Darwinism, the creationist view and issues around teaching evolution in secondary schools. The reader learns how current experimental biology is opening important perspectives on the sources of variation, and thus of the very power of natural selection. This work examines numerous examples of the extension of the principle of natural selection and provides the opportunity to critically reflect on a rich theory, on the methodological rigour that presides in its extensions and exportations, and on the necessity to measure its advantages and also its limits. Scholars interested in modern Darwinism and scientific research, its concepts, research programs and controversies will find this book an excellent read, and those considering how Darwinism might evolve, how it can apply to the human sciences and other disciplines beyond its origins will find it particularly valuable. Originally produced in French (*Les Mondes Darwiniens*), the scope and usefulness of the book have led to the production of this English text, to reach a wider audience. This book is a milestone in the impressive penetration by Francophone scholars into the world of Darwinian science, its historiography and philosophy over the last two decades. Alex Rosenberg, R. Taylor Cole Professor of Philosophy, Duke University Until now this useful and comprehensive handbook has only been available to francophones. Thanks to this invaluable new translation, this collection of insightful and original essays can reach the global audience it deserves. Tim Lewens, University of Cambridge

A guide to state-of-the-art molecular tools for monitoring and managing the toxigenicity of cyanobacteria Runaway eutrophication and climate change has made the monitoring and management of toxigenic organisms in the world's bodies of water more urgent than ever. In order to influence public policy regarding the detection and quantification of those organisms, it is incumbent upon scientists to raise the awareness of policy makers concerning the increased occurrence of toxigenic cyanobacteria and the threats they pose. As molecular methods can handle many samples in short time and help identify toxigenic organisms, they are reliable, cost-effective tools available for tracking toxigenic cyanobacteria worldwide. This volume arms scientists with the tools they need to track toxigenicity in surface waters and food supplies and, hopefully, to develop new techniques for managing the spread of toxic cyanobacteria. This handbook offers the first comprehensive treatment of molecular tools for monitoring toxigenic cyanobacteria. Growing out of the findings of the landmark European Cooperation in Science and Technology Cyanobacteria project (CYANOCOST), it provides detailed, practical coverage of the full array of available molecular tools and protocols, from water sampling, nucleic acid extraction, and downstream analysis—including PCR and qPCR based methods—to genotyping (DGGE), diagnostic microarrays, and community characterization using next-gen sequencing techniques. Offers an overview of the latest trends in the field, while providing a foundation for understanding and applying the tools and techniques described Provides detailed coverage of the full range of molecular tools currently available, with expert guidance on the analysis and interpretation of results Includes step-by-step guidance on standard operational procedures, including molecular tests used in environmental monitoring, with individual chapters devoted to each procedure Complements the published Handbook of Cyanobacterial Monitoring and Cyanotoxin Analysis from the CyanoCOST project This handbook is an indispensable working resource for scientists, lab technicians, and water management professionals and an excellent text/reference for graduate students and supervisors who use molecular tools. It will also be of great value to environmental health and protection officials and policy makers. With more than 60 applied exercises to choose from in this unique manual, students will quickly acquire the scientific skills essential for a career working with mammals. The set LNCS 2723 and LNCS 2724 constitutes the refereed proceedings of the Genetic and Evolutionary Computation Conference, GECCO 2003, held in

Chicago, IL, USA in July 2003. The 193 revised full papers and 93 poster papers presented were carefully reviewed and selected from a total of 417 submissions. The papers are organized in topical sections on a-life adaptive behavior, agents, and ant colony optimization; artificial immune systems; coevolution; DNA, molecular, and quantum computing; evolvable hardware; evolutionary robotics; evolution strategies and evolutionary programming; evolutionary scheduling routing; genetic algorithms; genetic programming; learning classifier systems; real-world applications; and search based software engineering.

A first source for traditional methods of microbiology as well as commonly used modern molecular microbiological methods. • Provides a comprehensive compendium of methods used in general and molecular microbiology. • Contains many new and expanded chapters, including a section on the newly important field of community and genomic analysis. • Provides step-by-step coverage of procedures, with an extensive list of references to guide the user to the original literature for more complete descriptions. • Presents methods for bacteria, archaea, and for the first time a section on mycology. • Numerous schematics and illustrations (both color and black and white) help the reader to easily understand the topics presented.

The ability to use DNA evidence is revolutionizing our understanding of the past. This book introduces archaeologists to the basics of DNA research so they can understand the powers and pitfalls of using DNA data in archaeological analysis and interpretation. By concentrating on the principles and applications of DNA specific to archaeology, the authors allow archaeologists to collect DNA samples properly and interpret the laboratory results with greater confidence. The volume is replete with case examples of DNA work in a variety of archaeological contexts and is an ideal teaching tool for archaeologists and their students.

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Frontiers in Natural Product Chemistry is an Ebook series devoted to publishing monographs that highlight important advances in natural product chemistry. The Ebook series covers all aspects of research in the chemistry and biochemistry of naturally occurring compounds including coverage of work on natural substances of land and sea and of plants, microbes and animals. Reviews of structure elucidation, biological activity, organic and experimental synthesis of natural products as well as developments of new methods are included. The second volume of the series brings seven reviews covering polyphenols of various types, Sambucus nigra as a health promoter, corrinoids in food samples, flavonoids in infected plants and much more.

Combining biology, computer science, mathematics, and statistics, the field of bioinformatics has become a hot new discipline with profound impacts on all aspects of biology and industrial application. Now, Computational Intelligence in Bioinformatics offers an introduction to the topic, covering the most relevant and popular CI methods, while also encouraging the implementation of these

methods to readers' research.

This new volume of *Methods in Enzymology* continues the legacy of this premier serial by containing quality chapters authored by leaders in the field. The third of 3 volumes covering Natural product biosynthesis by microorganisms and plants. This new volume continues the legacy of this premier serial Contains quality chapters authored by leaders in the field The third of 3 volumes, it has chapters on such topics as metabolic pathways in *Aspergillus oryzae*, heterologous gene clusters and cyanobacteria as a source of natural products

The biological sciences cover a broad array of literature types, from younger fields like molecular biology with its reliance on recent journal articles, genomic databases, and protocol manuals to classic fields such as taxonomy with its scattered literature found in monographs and journals from the past three centuries. Using the *Biological Literature: A Practical Guide, Fourth Edition* is an annotated guide to selected resources in the biological sciences, presenting a wide-ranging list of important sources. This completely revised edition contains numerous new resources and descriptions of all entries including textbooks. The guide emphasizes current materials in the English language and includes retrospective references for historical perspective and to provide access to the taxonomic literature. It covers both print and electronic resources including monographs, journals, databases, indexes and abstracting tools, websites, and associations—providing users with listings of authoritative informational resources of both classical and recently published works. With chapters devoted to each of the main fields in the basic biological sciences, this book offers a guide to the best and most up-to-date resources in biology. It is appropriate for anyone interested in searching the biological literature, from undergraduate students to faculty, researchers, and librarians. The guide includes a supplementary website dedicated to keeping URLs of electronic and web-based resources up to date, a popular feature continued from the third edition.

A comprehensive handbook outlining state-of-the-art analytical techniques used in geomicrobiology, for advanced students, researchers and professional scientists.

One of the leading textbooks in its field, *Bringing Fossils to Life* applies paleobiological principles to the fossil record while detailing the evolutionary history of major plant and animal phyla. It incorporates current research from biology, ecology, and population genetics, bridging the gap between purely theoretical paleobiological textbooks and those that describe only invertebrate paleobiology and that emphasize cataloguing live organisms instead of dead objects. For this third edition Donald R. Prothero has revised the art and research throughout, expanding the coverage of invertebrates and adding a discussion of new methodologies and a chapter on the origin and early evolution of life. Comparison is fundamental to evolutionary anthropology. When scientists study chimpanzee cognition, for example, they compare chimp performance on cognitive tasks to the performance of human children on the same tasks. And

when new fossils are found, such as those of the tiny humans of Flores, scientists compare these remains to other fossils and contemporary humans. Comparison provides a way to draw general inferences about the evolution of traits and therefore has long been the cornerstone of efforts to understand biological and cultural diversity. Individual studies of fossilized remains, living species, or human populations are the essential units of analysis in a comparative study; bringing these elements into a broader comparative framework allows the puzzle pieces to fall into place, creating a means of testing adaptive hypotheses and generating new ones. With this book, Charles L. Nunn intends to ensure that evolutionary anthropologists and organismal biologists have the tools to realize the potential of comparative research. Nunn provides a wide-ranging investigation of the comparative foundations of evolutionary anthropology in past and present research, including studies of animal behavior, biodiversity, linguistic evolution, allometry, and cross-cultural variation. He also points the way to the future, exploring the new phylogeny-based comparative approaches and offering a how-to manual for scientists who wish to incorporate these new methods into their research.

Traces scholarly thought from the nineteenth-century birth of evolutionary biology to the mapping of the human genome through forty-eight essays, arranged in chronological order, each preceded by a one-page essay that explains the significance of the chosen work.

The most definitive manual of microbes in air, water, and soil and their impact on human health and welfare.

- Incorporates a summary of the latest methodology used to study the activity and fate of microorganisms in various environments.
- Synthesizes the latest information on the assessment of microbial presence and microbial activity in natural and artificial environments.
- Features a section on biotransformation and biodegradation.
- Serves as an indispensable reference for environmental microbiologists, microbial ecologists, and environmental engineers, as well as those interested in human diseases, water and wastewater treatment, and biotechnology.

Wiley is proud to announce the publication of the first ever broad-based textbook introduction to Bioinformatics and Functional Genomics by a trained biologist, experienced researcher, and award-winning instructor. In this new text, author Jonathan Pevsner, winner of the 2001 Johns Hopkins University "Teacher of the Year" award, explains problem-solving using bioinformatic approaches using real examples such as breast cancer, HIV-1, and retinal-binding protein throughout. His book includes 375 figures and over 170 tables. Each chapter includes: Problems, discussion of Pitfalls, Boxes explaining key techniques and math/stats principles, Summary, Recommended Reading list, and URLs for freely available software. The text is suitable for professionals and students at every level, including those with little to no background in computer science.

This review of the application of proteomic and genomic advances in clinical biology covers principles such as the application of genomics to diagnostic

bacteriology and protocols for interrogating bacterial genomes. It also provides updates on all the significant advances of genome sequencing.

The increasing availability of molecular and genetic databases coupled with the growing power of computers gives biologists opportunities to address new issues, such as the patterns of molecular evolution, and re-assess old ones, such as the role of adaptation in species diversification. In the second edition, the book continues to integrate a wide variety of data analysis methods into a single and flexible interface: the R language. This open source language is available for a wide range of computer systems and has been adopted as a computational environment by many authors of statistical software. Adopting R as a main tool for phylogenetic analyses will ease the workflow in biologists' data analyses, ensure greater scientific repeatability, and enhance the exchange of ideas and methodological developments. The second edition is completely updated, covering the full gamut of R packages for this area that have been introduced to the market since its previous publication five years ago. There is also a new chapter on the simulation of evolutionary data. Graduate students and researchers in evolutionary biology can use this book as a reference for data analyses, whereas researchers in bioinformatics interested in evolutionary analyses will learn how to implement these methods in R. The book starts with a presentation of different R packages and gives a short introduction to R for phylogeneticists unfamiliar with this language. The basic phylogenetic topics are covered: manipulation of phylogenetic data, phylogeny estimation, tree drawing, phylogenetic comparative methods, and estimation of ancestral characters. The chapter on tree drawing uses R's powerful graphical environment. A section deals with the analysis of diversification with phylogenies, one of the author's favorite research topics. The last chapter is devoted to the development of phylogenetic methods with R and interfaces with other languages (C and C++). Some exercises conclude these chapters.

The two-volume set LNCS 7066 and LNCS 7067 constitutes the proceedings of the Second International Visual Informatics Conference, IVIC 2011, held in Selangor, Malaysia, during November 9-11, 2011. The 71 revised papers presented were carefully reviewed and selected for inclusion in these proceedings. They are organized in topical sections named computer vision and simulation; virtual image processing and engineering; visual computing; and visualisation and social computing. In addition the first volume contains two keynote speeches in full paper length, and one keynote abstract.

Insect Molecular Genetics, Third Edition, summarizes and synthesizes two rather disparate disciplines—entomology and molecular genetics. This volume provides an introduction to the techniques and literature of molecular genetics; defines terminology; and reviews concepts, principles, and applications of these powerful tools. The world of insect molecular genetics, once dominated by *Drosophila*, has become much more diverse, especially with the sequencing of multiple arthropod genomes (from spider mites to mosquitoes). This introduction includes discussion

of honey bees, mosquitoes, flour beetles, silk moths, fruit flies, aphids, house flies, kissing bugs, cicadas, butterflies, tsetse flies and armyworms. This book serves as both a foundational text and a review of a rapidly growing literature. With fully revised and updated chapters, the third edition will be a valuable addition to the personal libraries of entomologists, geneticists, and molecular biologists. Up-to-date references to important review articles, websites, and seminal citations in the disciplines Well crafted and instructive illustrations integral to explaining the techniques of molecular genetics Glossary of terms to help beginners learn the vocabulary of molecular biology

The animals loosely termed fish constitute more than half of all known vertebrate species. There are approximately 27,000 described living species of bony fishes (Euteleostomi = Osteichthyes), about 70 species of hagfishes and some 34 species of lampreys. Approximately 970 species are chondrichthyans, the sharks and their relatives, which were the subject of volume 3 in this series. It is perhaps because fishes live in a buoyant medium, whether it be fresh or sea water, that they show a diversity in body shapes that is unparalleled by other vertebrates. There is also a unique diversity in the modes of reproduction, whether by external or internal fertilization, and this, with the morphology and fine structure of the reproductive system and its components, is the subject of Part A. Part B deals with complementary topics: testes, sperm, and sperm competition; endocrinology of reproduction; pheromones and reproduction; copulatory structures: taxonomic overview and the potential for sexual selection; sexual selection: signaling and courtship; adaptation and evolution of reproductive mode in copulating cottoid species; fertilization; sex determination; parental care; reproduction in relation to conservation and exploitation of marine fishes; Cryopreservation of Gametes; Embryogenesis and Development; and Molecular Genetics of Development. "The biological diversity of the planet is being rapidly depleted due to the direct and indirect consequences of human activity. As the size of wild animal and plant populations decreases and fragmentation increases, inbreeding reduces fitness and loss of genetic diversity reduces their ability to adapt to changes in the environment. Many small isolated populations are going extinct unnecessarily. In many cases, such populations can be genetically rescued by gene flow from another population within the species, but this is very rarely done. This book provides a practical guide to the genetic management of fragmented animal and plant populations"--

This is a handbook of methods and protocols for biologists. It aimed at undergraduate, graduate students and researchers originally trained in biological or medical sciences who need to know how to access the data archives of genomes, proteins, metabolites, gene expression profiles and the questions these data and tools can answer. For each chapter, the conceptual and experimental background is provided, together with specific guidelines for handling raw data, including preprocessing and analysis. The content is structured into three parts. Part one introduces basic knowledge about popular

bioinformatics tools, databases and web resources. Part two presents examples of omics bioinformatics applications. Part three provides basic statistical analysis skills and programming skills needed to handle and analyze omics datasets. Phylogenetic comparative approaches are powerful analytical tools for making evolutionary inferences from interspecific data and phylogenies. The phylogenetic toolkit available to evolutionary biologists is currently growing at an incredible speed, but most methodological papers are published in the specialized statistical literature and many are incomprehensible for the user community. This textbook provides an overview of several newly developed phylogenetic comparative methods that allow to investigate a broad array of questions on how phenotypic characters evolve along the branches of phylogeny and how such mechanisms shape complex animal communities and interspecific interactions. The individual chapters were written by the leading experts in the field and using a language that is accessible for practicing evolutionary biologists. The authors carefully explain the philosophy behind different methodologies and provide pointers – mostly using a dynamically developing online interface – on how these methods can be implemented in practice. These “conceptual” and “practical” materials are essential for expanding the qualification of both students and scientists, but also offer a valuable resource for educators. Another value of the book are the accompanying online resources (available at: <http://www.mpcm-evolution.com>), where the authors post and permanently update practical materials to help embed methods into practice.

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