Practical Computing Biologists Steven Haddock

Revision of California SeaGrant 1986 book, "Blue Water Diving Guidelines" to include updated information on equipment and procedures.

A concise introduction to key computing skills for biologists While biological data continues to grow exponentially in size and quality, many of today's biologists are not trained adequately in the computing skills necessary for leveraging this information deluge. In Computing Skills for Biologists, Stefano Allesina and Madlen Wilmes present a valuable toolbox for the effective analysis of biological data. Based on the authors' experiences teaching scientific computing at the University of Chicago, this textbook emphasizes the automation of repetitive tasks and the construction of pipelines for data organization, analysis, visualization, and publication. Stressing practice rather than theory, the book's examples and exercises are drawn from actual biological data and solve cogent problems spanning the entire breadth of biological disciplines, including ecology, genetics, microbiology, and molecular biology. Beginners will benefit from the many examples explained step-by-step, while more seasoned researchers will learn how to combine tools to make biological data analysis robust and reproducible. The book uses free software and code that can be run on any platform. Computing Skills for Biologists is ideal for scientists wanting to improve their technical skills and instructors looking to teach the main computing tools essential for biology research in the twenty-first century. Excellent resource for acquiring comprehensive computing skills Both novice and experienced scientists will increase efficiency by building automated and reproducible pipelines for biological data analysis Code examples based on published data spanning the breadth of biological disciplines Detailed solutions provided for exercises in each chapter Extensive companion website

Concepts in Bioinformatics and Genomics takes a conceptual approach to its subject, balancing biology, mathematics, and programming while highlighting relevant real-world applications and providing students with the tools to compute and analyze biological data. It presents many thought-provoking exercises to stretch students' imaginations, giving them a deeper understanding of the molecular biology, basic probability, software programs, and program-codingmethodology underpinning this exciting field.

To help with the increasingly large data sets that many scientists deal with, this book illustrates how to use many freely available computing tools to work more powerfully and effectively. The book was born out of the authors' experiences developing tools for their research and to fix other biologist's computational problems.

More physicists today are taking on the role of software developer as part of their research, but software development isn't always easy or obvious, even for physicists. This practical book teaches essential software development skills to help you automate and accomplish nearly any aspect of research in a physics-based field. Written by two PhDs in nuclear engineering, this book includes practical examples drawn from a working knowledge of physics concepts. You'll learn how to use the Python programming language to perform everything from collecting and analyzing data to building software and publishing your results. In four parts, this book includes: Getting Started: Jump into Python, the command line, data containers, functions, flow control and logic, and classes and objects Getting It Done: Learn about regular expressions, analysis and visualization, NumPy, storing data in files and HDF5, important data structures in physics, computing in parallel, and deploying software Getting It Right: Build pipelines and software, learn to use local and remote version control, and debug and test your code Getting It Out There: Document your code, process and publish your findings, and collaborate efficiently; dive into software licenses, ownership, and copyright procedures

Powerful, flexible, and easy to use, Python is an ideal language for building software tools and applications for life science research and development. This unique book shows you how to program with Python, using code examples taken directly from bioinformatics. In a short time, you'll be using sophisticated techniques and Python modules that are particularly effective for bioinformatics programming. Bioinformatics Programming Using Python is perfect for anyone involved with bioinformatics -- researchers, support staff, students, and software developers interested in writing bioinformatics applications. You'll find it useful whether you already use Python, write code in another language, or have no programming experience at all. It's an excellent self-instruction tool, as well as a handy reference when facing the challenges of real-life programming tasks. Become familiar with Python's fundamentals, including ways to develop simple applications Learn how to use Python modules for pattern matching, structured text processing, online data retrieval, and database access Discover generalized patterns that cover a large proportion of how Python code is used in bioinformatics Learn how to apply the principles and techniques of object-oriented programming Benefit from the "tips and traps" section in each chapter

The sixteenth volume in the Aubrey/Maturin series, and Patrick O'Brian's first bestseller in the United States. At the outset of this adventure filled with disaster and delight, Jack Aubrey and Stephen Maturin pursue an American privateer through the Great South Sea. The strange color of the ocean reminds Stephen of Homer's famous description, and portends an underwater volcanic eruption that will create a new island overnight and leave an indelible impression on the reader's imagination. Their ship, the Surprise, is now also a privateer, the better to escape diplomatic complications from Stephen's mission, which is to ignite the revolutionary tinder of South America. Jack will survive a desperate open boat journey and come face to face with his illegitimate black son; Stephen, caught up in the aftermath of his failed coup, will flee for his life into the high, frozen wastes of the Andes; and Patrick O'Brian's brilliantly detailed narrative will reunite them at last in a breathtaking chase through stormy seas and icebergs south of Cape Horn, where the hunters suddenly become the hunted.

This book constitutes the refereed proceedings of the 7th International Conference on Artificial Immune Systems, ICARIS 2008, held in Phuket, Thailand, in August 2008. The 40 revised full papers presented were carefully reviewed and selected from 67 submissions. The papers are organized in topical sections on computational immunology, applied AIS, and theoretical AIS. Position papers and conceptual papers are also included.

This edited book focuses on affordances and limitations of e-books for early language and literacy, features and design of e-books for early language and literacy, print versus e-books in early language and literacy development, and uses of and guidelines for how to use e-books in school and home literacy practices. Uniquely, this book includes critical reviews of diverse aspects of e-books (e.g., features) and e-book uses (e.g., independent reading) for early literacy as well as multiple examinations of e-books in home and school contexts using a variety of research methods and/or theoretical frames. The studies of children's engagement with diverse types of e-books in different social contexts provide readers with a contemporary and comprehensive

understanding of this topic. Research has demonstrated that ever-increasing numbers of children use digital devices as part of their daily routine. Yet, despite children's frequent use of e-books from an early age, there is a limited understanding regarding how those e-books are actually being used at home and school. As more e-books become available, it is important to examine the educational benefits and limitations of different types of e-books for children. So far, studies on the topic have presented inconsistent findings regarding potential benefits and limitations of e-books for early literacy activities (e.g., independent reading, shared reading). The studies in this book aim to fill such gaps in the literature.

Why did such highly abstract ideas as truth, knowledge, or justice become so important to us? What was the point of coming to think in these terms? Matthieu Queloz presents a method for answering such questions: pragmatic genealogy. We can make sense of these grand abstractions by identifying their roots in concrete practical concerns.

Essential Bioinformatics is a concise yet comprehensive textbook of bioinformatics, which provides a broad introduction to the entire field. Written specifically for a life science audience, the basics of bioinformatics are explained, followed by discussions of the state-of-the-art computational tools available to solve biological research problems. All key areas of bioinformatics are covered including biological databases, sequence alignment, genes and promoter prediction, molecular phylogenetics, structural bioinformatics, genomics and proteomics. The book emphasizes how computational methods work and compares the strengths and weaknesses of different methods. This balanced yet easily accessible text will be invaluable to students who do not have sophisticated computational backgrounds. Technical details of computational algorithms are explained with a minimum use of mathematical formulae; graphical illustrations are used in their place to aid understanding. The effective synthesis of existing literature as well as in-depth and up-to-date coverage of all key topics in bioinformatics make this an ideal textbook for all bioinformatics courses taken by life science students and for researchers wishing to develop their knowledge of bioinformatics to facilitate their own research.

A Primer for Computational Biology aims to provide life scientists and students the skills necessary for research in a data-rich world. The text covers accessing and using remote servers via the command-line, writing programs and pipelines for data analysis, and provides useful vocabulary for interdisciplinary work. The book is broken into three parts: Introduction to Unix/Linux: The command-line is the "natural environment" of scientific computing, and this part covers a wide range of topics, including logging in, working with files and directories, installing programs and writing scripts, and the powerful "pipe" operator for file and data manipulation. Programming in Python: Python is both a premier language for learning and a common choice in scientific software development. This part covers the basic concepts in programming (data types, if-statements and loops, functions) via examples of DNA-sequence analysis. This part also covers more complex subjects in software development such as objects and classes, modules, and APIs. Programming in R: The R language specializes in statistical data analysis, and is also quite useful for visualizing large datasets. This third part covers the basics of R as a programming language (data types, if-statements, functions, loops and when to use them) as well as techniques for large-scale, multi-test analyses. Other topics include S3 classes and data visualization with ggplot2.

Python for biologists is a complete programming course for beginners that will give you the skills you need to tackle common biological and bioinformatics problems.

One of the pathways by which the scientific community confirms the validity of a new scientific discovery is by repeating the research that produced it. When a scientific effort fails to independently confirm the computations or results of a previous study, some fear that it may be a symptom of a lack of rigor in science, while others argue that such an observed inconsistency can be an important precursor to new discovery. Concerns about reproducibility and replicability have been expressed in both scientific and popular media. As these concerns came to light, Congress requested that the National Academies of Sciences, Engineering, and Medicine conduct a study to assess the extent of issues related to reproducibility and replicability and to offer recommendations for improving rigor and transparency in scientific research. Reproducibility and Replicability in Science defines reproducibility and replicability and examines the factors that may lead to non-reproducibility and non-replicability in research. Unlike the typical expectation of reproducibility between two computations, expectations about replicability are more nuanced, and in some cases a lack of replicability can aid the process of scientific discovery. This report provides recommendations to researchers, academic institutions, journals, and funders on steps they can take to improve reproducibility and replicability in science.

This text combines a practical, hands-on approach to programming with the introduction of sound theoretical support focused on teaching the construction of high-quality software. A major feature of the book is the use of Design by Contract.

Practical Computing for BiologistsSinauer Associates Incorporated

Bioluminescence is everywhere on earth—most of all in the ocean, from angler fish in the depths to flashing dinoflagellates at the surface. Wilson and Hastings explore the natural history, evolution, and biochemistry of the diverse array of organisms that emit light and offer an evolutionary explanation for their sporadic distribution and rarity.

Experience Sampling in Mental Health Research provides comprehensive and user-friendly guidance on when and how to apply this methodology in the assessment of clinical populations. Divided into three sections, the book offers step-by-step instruction on how to design, develop and implement an ESM study, as well as advice on how this approach might be adapted for common mental health difficulties. With an eye to the future of this type of research, the contributors also consider how ESM might be adapted for use as a form of clinical assessment and intervention. Experience Sampling in Mental Health Research combines the knowledge and expertise of leading international experts in the field, and will be helpful for students, researchers and clinicians wishing to start or develop their understanding of this methodology.

The Evolution of the Immune System: Conservation and Diversification is the first book of its kind that prompts a new perspective when describing and considering the evolution of the immune system. Its unique approach summarizes, updates, and provides new insights on the different immune receptors, soluble factors, and immune cell effectors. Helps the reader gain a modern idea of the evolution of the immune systems in pluricellular organisms Provides a complete overview of the most studied and hot topics in comparative and evolutionary immunology Reflects the organisation of the immune system (cell-based, humoral [innate], humoral [adaptive]) without introducing further and misleading levels of organization Brings concepts and ideas on the evolution of the immune system to a wide readership

The SAGE Handbook of Applied Social Research Methods, Second Edition provides students and researchers with the most comprehensive resource covering core methods, research designs, and data collection, management, and analysis issues. This thoroughly revised edition continues to place critical emphasis on finding the tools that best fit the research question given the constraints of deadlines, budget, and available staff. Each chapter offers key guidance on how to make intelligent and conscious tradeoffs so that one can refine and hone the research question as new knowledge is gained, unanticipated obstacles are encountered, or contextual shifts take place - all key elements in the iterative nature of applied research. Each chapter has been enhanced pedagogically to include more step-by-step procedures, specific, rich yet practical examples from various settings to illustrate the method, parameters to define when the method is most appropriate and when it is not appropriate, and greater use of visual aids (graphs, models, tip boxes) to provide teaching and learning tools. - twenty core chapters written by research experts that cover major methods and data analysis issues across the social and behavioral sciences, education, and management; - emphasis on applying research techniques, particularly in "real-world" settings in which there are various data, money, time, and political constraints; - new chapters on mixed methods, qualitative comparative analysis, concept mapping, and internet data collection; - a newly developed section that serves as a guide for students who are navigating through the

book and attempting to translate the chapters into action; - a new Instructor's Resources CD, with relevant journal articles, test questions, and exercises to aid the instructor in developing appropriate course materials.

This is the only book completely devoted to the popular BLAST (Basic Local Alignment Search Tool), and one that every biologist with an interest in sequence analysis should learn from.

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 volume reflects the current state of scientific knowledge about natural climate variability on decade-to-century time scales. It covers a wide range of relevant subjects, including the characteristics of the atmosphere and ocean environments as well as the methods used to describe and analyze them, such as proxy data and numerical models. They clearly demonstrate the range, persistence, and magnitude of climate variability as represented by many different indicators. Not only do natural climate variations have important socioeconomic effects, but they must be better understood before possible anthropogenic effects (from greenhouse gas emissions, for instance) can be evaluated. A topical essay introduces each of the disciplines represented, providing the nonscientist with a perspective on the field and linking the papers to the larger issues in climate research. In its conclusions section, the book evaluates progress in the different areas and makes recommendations for the direction and conduct of future climate research. This book, while consisting of technical papers, is also accessible to the interested layperson.

This book is the bible of bioluminescence and a must-read not only for the students but for those who work in various fields relating to bioluminescence. It summarizes current structural information on all known bioluminescent systems in nature, from well-studied ones to those that have been seldom investigated.This book remains an important source of chemical knowledge on bioluminescence and, since the second edition's publication in 2012, has been revised to include major developments in two systems: earthworm Fridericia and higher fungi whose luciferins have been elucidated and synthesized. These two new luciferins represent an essential addition to seven previously known, with fully rewritten sections covering this new subject matter.

Covering the most important developments in meta-analysis from 1990 to 2004, this text presents new patterns in research findings as well as updated information on existing topics.

Your research has generated gigabytes of data and now you need to analyse it. You hate using spreadsheets but it is all you know, so what else can you do? This book will transform how you work with large and complex data sets, teaching you powerful programming tools for slicing and dicing data to suit your needs. Written in a fun and accessible style, this step-by-step guide will inspire and inform non-programmers about the essential aspects of Unix and Perl. It shows how, with just a little programming knowledge, you can write programs that could save you hours, or even days. No prior experience is required and new concepts are introduced using numerous code examples that you can try out for yourself. Going beyond the basics, the authors touch upon many broader topics that will help those new to programming, including debugging and how to write in a good programming style.

Michael Kent...& ;A young man studying to become a priest finds love, and learns that faith can separate.& ;A university cyclist seeking Olympic gold finds tragedy, death and heroism.& ;A pastor thousands of miles from home seeks vocation and finds fatherhood.& ;& ;Sarah Hughes...& ;A young woman living abroad finds love and loses family.& ;A university student meets a faith she cannot accept.& ;An artist finds faith and learns to paint with her soul.& ;& ;Dancing Priest is the story of Michael Kent and Sarah Hughes and a love, born, separated, and reborn, in faith and hope.

Reviews the circumstances surrounding the Challenger accident to establish the probable cause or causes of the accident. Develops recommendations for corrective or other action based upon the Commission1s findings and determinations. Color photos, charts and tables.

Were you always curious about biology but were afraid to sit through long hours of dense reading? Did you like the subject when you were in high school but had other plans after you graduated? Now you can explore the human genome and analyze DNA without ever leaving your desktop! Bioinformatics For Dummies is packed with valuable information that introduces you to this exciting new discipline. This easy-to-follow guide leads you step by step through every bioinformatics task that can be done over the Internet. Forget long equations, computer-geek gibberish, and installing bulky programs that slow down your computer. You'll be amazed at all the things you can accomplish just by logging on and following these trusty directions. You get the tools you need to: Analyze all types of sequences Use all types of databases Work with DNA and protein sequences Conduct similarity searches Build a multiple sequence alignment Edit and publish alignments Visualize protein 3-D structures Construct phylogenetic trees This up-to-date second edition includes newly created and popular databases and Internet programs as well as multiple new genomes. It provides tips for using servers and places to seek resources to find out about what's going on in the bioinformatics world. Bioinformatics For Dummies will show you how to get the most out of your PC and the right Web tools so you'll be searching databases and analyzing sequences like a pro!

In this volume of 15 articles, contributors from a wide range of disciplines present their analyses of Disney movies and Disney music, which are mainstays of popular culture. The power of the Disney brand has heightened the need for academics to question whether Disney's films and music function as a tool of the Western elite that shapes the views of those less empowered. Given its global reach, how the Walt Disney Company handles the role of race, gender, and sexuality in social structural inequality merits serious reflection according to a number of the articles in the volume. On the other hand, other authors argue that Disney productions can help individuals cope with difficult situations or embrace progressive thinking. The different approaches to the assessment of Disney films as cultural artifacts also vary according to the theoretical perspectives guiding the interpretation of both overt and latent symbolic meaning in the movies. The authors of the 15 articles encourage readers to engage with the material, showcasing a variety of views about the good, the bad, and the best way forward.

"...a must-read text that provides a historical lens to see how ubicomp has matured into a multidisciplinary endeavor. It will be an essential reference to researchers and those who want to learn more about this evolving field." -From the Foreword, Professor Gregory D. Abowd, Georgia Institute of Technology First introduced two decades ago, the term

ubiquitous computing is now part of the common vernacular. Ubicomp, as it is commonly called, has grown not just quickly but broadly so as to encompass a wealth of concepts and technology that serves any number of purposes across all of human endeavor. While such growth is positive, the newest generation of ubicomp practitioners and researchers, isolated to specific tasks, are in danger of losing their sense of history and the broader perspective that has been so essential to the field's creativity and brilliance. Under the guidance of John Krumm, an original ubicomp pioneer, Ubiquitous Computing Fundamentals brings together eleven ubiquitous computing trailblazers who each report on his or her area of expertise. Starting with a historical introduction, the book moves on to summarize a number of self-contained topics. Taking a decidedly human perspective, the book includes discussion on how to observe people in their natural environments and evaluate the critical points where ubiquitous computing technologies can improve their lives. Among a range of topics this book examines: How to build an infrastructure that supports ubiquitous computing applications Privacy protection in systems that connect personal devices and personal information Moving from the graphical to the ubiquitous computing user interface Techniques that are revolutionizing the way we determine a person's location and understand other sensor measurements While we needn't become expert in every sub-discipline of ubicomp, it is necessary that we appreciate all the perspectives that make up the field and understand how our work can influence and be influenced by those perspectives. This is important, if we are to encourage future generations to be as successfully innovative as the field's originators.

Praise for previous editions: "Gandrud has written a great outline of how a fully reproducible research project should look from start to finish, with brief explanations of each tool that he uses along the way... Advanced undergraduate students in mathematics, statistics, and similar fields as well as students just beginning their graduate studies would benefit the most from reading this book. Many more experienced R users or second-year graduate students might find themselves thinking, 'I wish I'd read this book at the start of my studies, when I was first learning R!'...This book could be used as the main text for a class on reproducible research ..." (The American Statistician) Reproducible Research with R and R Studio, Third Edition brings together the skills and tools needed for doing and presenting computational research. Using straightforward examples, the book takes you through an entire reproducible research workflow. This practical workflow enables you to gather and analyze data as well as dynamically present results in print and on the web. Supplementary materials and example are available on the author's website. New to the Third Edition Updated package recommendations, examples, URLs, and removed technologies no longer in regular use. More advanced R Markdown (and less LaTeX) in discussions of markup languages and examples. Stronger focus on reproducible working directory tools. Updated discussion of cloud storage services and persistent reproducible material citation. Added discussion of Jupyter notebooks and reproducible practices in industry. Examples of data manipulation with Tidyverse tibbles (in addition to standard data frames) and pivot_longer() and pivot_wider() functions for pivoting data. Features Incorporates the most important advances that have been developed since the editions were published Describes a complete reproducible research workflow, from data gathering to the presentation of results Shows how to automatically generate tables and figures using R Includes instructions on formatting a presentation document via markup languages Discusses cloud storage and versioning services, particularly Github Explains how to use Unix-like shell programs for working with large research projects

Computing is revolutionizing the practice of biology. This book, which assumes no prior computing experience, provides students with the tools to write their own Python programs and to understand fundamental concepts in computational biology and bioinformatics. Each major part of the book begins with a compelling biological question, followed by the algorithmic ideas and programming tools necessary to explore it: the origins of pathogenicity are examined using gene finding, the evolutionary history of sex determination systems is studied using sequence alignment, and the origin of modern humans is addressed using phylogenetic methods. In addition to providing general programming skills, this book explores the design of efficient algorithms, simulation, NP-hardness, and the maximum likelihood method, among other key concepts and methods. Easy-to-read and designed to equip students with the skills to write programs for solving a range of biological problems, the book is accompanied by numerous programming exercises, available at www.cs.hmc.edu/CFB.

NEW YORK TIMES BESTSELLER • This instant classic explores how we can change our lives by changing our habits. NAMED ONE OF THE BEST BOOKS OF THE YEAR BY The Wall Street Journal • Financial Times In The Power of Habit, award-winning business reporter Charles Duhigg takes us to the thrilling edge of scientific discoveries that explain why habits exist and how they can be changed. Distilling vast amounts of information into engrossing narratives that take us from the boardrooms of Procter & Gamble to the sidelines of the NFL to the front lines of the civil rights movement, Duhigg presents a whole new understanding of human nature and its potential. At its core, The Power of Habit contains an exhilarating argument: The key to exercising regularly, losing weight, being more productive, and achieving success is understanding how habits work. As Duhigg shows, by harnessing this new science, we can transform our businesses, our communities, and our lives. With a new Afterword by the author "Sharp, provocative, and useful."—Jim Collins "Few [books] become essential manuals for business and living. The Power of Habit is an exception. Charles Duhigg not only explains how habits are formed but how to kick bad ones and hang on to the good."—Financial Times "A flat-out great read."—David Allen, bestselling author of Getting Things Done: The Art of Stress-Free Productivity "You'll never look at yourself, your organization, or your world quite the same way."—Daniel H. Pink, bestselling author of Drive and A Whole New Mind "Entertaining . . . enjoyable . . . fascinating . . . a serious look at the science of habit formation and change."—The New York Times Book Review

R is rapidly becoming the standard software for statistical analyses, graphical presentation of data, and programming in the natural, physical, social, and engineering sciences.

Getting Started with R is now the go-to introductory guide for biologists wanting to learn how to use R in their research. It teaches readers how to import, explore, graph, and analyse data, while keeping them focused on their ultimate goals: clearly communicating their data in oral presentations, posters, papers, and reports. It provides a consistent workflow for using R that is simple, efficient, reliable, and reproducible. This second edition has been updated and expanded while retaining the concise and engaging nature of its predecessor, offering an accessible and fun introduction to the packages dplyr and ggplot2 for data manipulation and graphing. It expands the set of basic statistics considered in the first edition to include new examples of a simple regression, a one-way and a two-way ANOVA. Finally, it introduces a new chapter on the generalised linear model. Getting Started with R is suitable for undergraduates, graduate students, professional researchers, and practitioners in the biological sciences.

With its highly developed capacity to detect patterns in data, Perl has become one of the most popular languages for biological data analysis. But if you're a biologist with little or no programming experience, starting out in Perl can be a challenge. Many biologists have a difficult time learning how to apply the language to bioinformatics. The most popular Perl programming books are often too theoretical and too focused on computer science for a non-programming biologist who needs to solve very specific problems.Beginning Perl for Bioinformatics is designed to get you quickly over the Perl language barrier by approaching programming as an important new laboratory skill, revealing Perl programs and techniques that are immediately useful in the lab. Each chapter focuses on solving a particular bioinformatics problem or class of problems, starting with the simplest and increasing in complexity as the book progresses. Each chapter includes programming exercises and teaches bioinformatics by showing and modifying programs that deal with various kinds of practical biological problems. By the end of the book you'll have a solid understanding of Perl basics, a collection of programs for such tasks as parsing BLAST and GenBank, and the skills to take on more advanced bioinformatics programming. Some of the later chapters focus in greater detail on specific bioinformatics topics. This book is suitable for use as a classroom textbook, for self-study, and as a reference.The book covers: Programming basics and working with DNA sequences and strings Debugging your code Simulating gene mutations using random number generators Regular expressions and finding motifs in data Arrays, hashes, and relational databases Regular expressions and restriction maps Using Perl to parse PDB records, annotations in GenBank, and BLAST output

INSTANT NEW YORK TIMES BESTSELLER "One of the most important books I've ever read—an indispensable guide to thinking clearly about the world." – Bill Gates "Hans Rosling tells the story of 'the secret silent miracle of human progress' as only he can. But Factfulness does much more than that. It also explains why progress is so often secret and silent and teaches readers how to see it clearly." —Melinda Gates "Factfulness by Hans Rosling, an outstanding international public health expert, is a hopeful book about the potential for human progress when we work off facts rather than our inherent biases." - Former U.S. President Barack Obama Factfulness: The stress-reducing habit of only carrying opinions for which you have strong supporting facts. When asked simple questions about global trends—what percentage of the world's population live in poverty; why the world's population is increasing; how many girls finish school—we systematically get the answers wrong. So wrong that a chimpanzee choosing answers at random will consistently outguess teachers, journalists, Nobel laureates, and investment bankers. In Factfulness, Professor of International Health and global TED phenomenon Hans Rosling, together with his two long-time collaborators, Anna and Ola, offers a radical new explanation of why this happens. They reveal the ten instincts that distort our perspective—from our tendency to divide the world into two camps (usually some version of us and them) to the way we consume media (where fear rules) to how we perceive progress (believing that most things are getting worse). Our problem is that we don't know what we don't know, and even our guesses are informed by unconscious and predictable biases. It turns out that the world, for all its imperfections, is in a much better state than we might think. That doesn't mean there aren't real concerns. But when we worry about everything all the time instead of embracing a worldview based on facts, we can lose our ability to focus on the things that threaten us most. Inspiring and revelatory, filled with lively anecdotes and moving stories, Factfulness is an urgent and essential book that will change the way you see the world and empower you to respond to the crises and opportunities of the future. --- "This book is my last battle in my life-long mission to fight devastating ignorance...Previously I armed myself with huge data sets, eye-opening software, an energetic learning style and a Swedish bayonet for sword-swallowing. It wasn't enough. But I hope this book will be." Hans Rosling, February 2017.

Drawn from best practices, this casebook provides a practical road map and real-life case studies to help students develop the necessary skills to design, negotiate, and manage domestic and international alliances. Editors Jean-Louis Schaan and Micheál J. Kelly have organized this book around the four major phases in the alliance formation and management process—strategic rationale, partner selection, negotiation, and implementation.

Learn the data skills necessary for turning large sequencing datasets into reproducible and robust biological findings. With this practical guide, you'll learn how to use freely available open source tools to extract meaning from large complex biological data sets. At no other point in human history has our ability to understand life's complexities been so dependent on our skills to work with and analyze data. This intermediate-level book teaches the general computational and data skills you need to analyze biological data. If you have experience with a scripting language like Python, you're ready to get started. Go from handling small problems with messy scripts to tackling large problems with clever methods and tools Process bioinformatics data with powerful Unix pipelines and data tools Learn how to use exploratory data analysis techniques in the R language Use efficient methods to work with genomic range data and range operations Work with common genomics data file formats like FASTA, FASTQ, SAM, and BAM Manage your bioinformatics project with the Git version control system Tackle tedious data processing tasks with with Bash scripts and Makefiles

A key goal of fisheries management is to regulate extractive pressure on a resource so as to ensure social, economic and ecological sustainability. This text provides an accessible entry point for students and professionals to management science as developed in fisheries, in order to facilitate uptake of the latest ideas and methods. Traditional management approaches have relied upon a stock assessment based on existing understanding of resource status and dynamics, and a prediction of the likely future response to a static management proposal. However all such predictions include an inherent degree of uncertainty, and the last few decades have seen the emergence of an adaptive approach that uses feedback control to account for unknown future behaviour. Feedback is achieved via a control rule, which defines a relationship between perceived status of the resource and a management action. Evaluations of such rules usually include computer simulation testing across a broad range of uncertainties, so that an appropriate and robust rule can be selected by stakeholders and managers. The book focuses on this approach, which is usually referred to as Management Strategy Evaluation. The book is enriched by case study examples from different parts of the world, as well as insights into the theory and practice from those actively involved in the science of fisheries management.

This volume examines the phenomenon of fake news by bringing together leading experts from different fields within psychology and related areas, and explores what has become a prominent feature of

public discourse since the first Brexit referendum and the 2016 US election campaign. Dealing with misinformation is important in many areas of daily life, including politics, the marketplace, health communication, journalism, education, and science. In a general climate where facts and misinformation blur, and are intentionally blurred, this book asks what determines whether people accept and share (mis)information, and what can be done to counter misinformation? All three of these aspects need to be understood in the context of online social networks, which have fundamentally changed the way information is produced, consumed, and transmitted. The contributions within this volume summarize the most up-to-date empirical findings, theories, and applications and discuss cutting-edge ideas and future directions of interventions to counter fake news. Also providing guidance on how to handle misinformation in an age of "alternative facts", this is a fascinating and vital reading for students and academics in psychology, communication, and political science and for professionals including policy makers and journalists.

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