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Description. Fundamental Concepts of Bioinformatics is the first textbook co-authored by a biologist and computer scientist that is specifically designed to make bioinformatics accessible to undergraduates and prepare them for more advanced work. Students learn what programs are available for analyzing data, how to understand the basic algorithms that underlie these programs, what bioinformatic research is like, and other basic concepts.

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Fundamental Concepts of Bioinformatics. (A 314 page sophomore/ junior level textbook for biology and computer science majors; ISBN 0-8053-4633-3) Pearson Education, Inc., publishing as Benjamin Cummings, San Francisco, CA.

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Fundamental Concepts of Bioinformatics by Dan E. Krane

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Fundamental Concepts of Bioinformatics : Dan E. Krane ...

Dan Krane, professor of biological sciences, has been named interim dean of Wright State University–Lake Campus, effective Aug. 1.A search for a permanent Lake Campus dean will begin in the fall. “I’m very happy to have the opportunity to support the faculty and staff of Lake Campus,” Krane said.

Wright State Newsroom – Dan Krane named interim dean of ...

Bioinformatics and Molecular Evolution by Higgs and Attwood - good hybrid of basic concepts in molecular evolution and how they connect to bioinformatics. ... Fundamental Concepts of Bioinformatics by Dan Krane et.al. Essential Bioinformatics by Jin Xiong. ADD REPLY • link written 8.7 years ago by Wou • 2.8k. 3. 9.4 years ago by.

Recommend Your Favorite Bioinformatics Books

I am looking for personal experiences and short opinions regarding bioinformatics books. So far I have noticed the following trend: many books titled _Bioinformatics with Perl/Python/Java/R_ etc end up being introductions into the programming language in question, often only minor code examples are related to bioinformatics.

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Information flows easily from one topic to the next, with enough detail to support the major concepts without overwhelming students.”--BOOK JACKET.

This book constitutes the refereed proceedings of the Third International Symposium on Bioinformatics Research and Applications, ISBRA 2007, held in Atlanta, GA, USA in May 2007. The 55 revised full papers presented together with three invited talks cover a wide range of topics, including clustering and classification, gene expression analysis, gene networks, genome analysis, motif finding, pathways, protein structure prediction, protein domain interactions, phylogenetics, and software tools.

Offers a structured approach to biological data and the computer tools needed to analyze it, covering UNIX, databases, computation, Perl, data mining, data visualization, and tailoring software to suit specific research needs.

This latest version of Information Resources in Toxicology (IRT) continues a tradition established in 1982 with the publication of the first edition in presenting an extensive itemization, review, and commentary on the information infrastructure of the field. This book is a unique wide-ranging, international, annotated bibliography and compendium of major resources in toxicology and allied fields such as environmental and occupational health, chemical safety, and risk assessment. Thoroughly updated, the current edition analyzes technological changes and is rife with online tools and links to Web sites. IRT-IV is highly structured, providing easy access to its information. Among the “hot topics covered are Disaster Preparedness and Management, Nanotechnology, Omics, the Precautionary Principle, Risk Assessment, and Biological, Chemical and Radioactive Terrorism and Warfare are among the designated. • International in scope, with contributions from over 30 countries • Numerous key references and relevant Web links • Concise narratives about toxicologic sub-disciplines • Valuable appendices such as the IUPAC Glossary of Terms in Toxicology • Authored by experts in their respective sub-disciplines within toxicology

Comprehensively presents the foundations and leading application research in medical informatics/biomedicine. The concepts and techniques are illustrated with detailed case studies. Authors are widely recognized professors and researchers in Schools of Medicine and Information Systems from the University of Arizona, University of Washington, Columbia University, and Oregon Health & Science University. Related Springer title, Shortliffe: Medical Informatics, has sold over 8000 copies The title will be positioned at the upper division and graduate level Medical Informatics course and a reference work for practitioners in the field.

The Fourth Edition of the compendium pools together the knowledge and experience of experts from all over the world, who are engaged in teaching and research in the field of biochemistry, medical sciences and allied disciplines. Comprising 20 sections, the present edition of the book has been substantially revised incorporating the latest research and achievements in the field. Beginning appropriately with chemical architecture of the living systems, role and significance of biochemical reactions, organization of specialised tissues, and importance of food and nutrition, the book explores beyond traditional boundaries of biochemistry. The knowledge of various organ systems has been expanded covering their normal function, ailments and dysfunction. A chapter on Eye and Vision explaining molecular basis of cataract and glaucoma have been added. Also, the book introduces stem cells and regenerative therapy and defines molecules associated with pleasure, happiness, stress and anxiety. A Section on Gastrointestinal and Biliary System elaborates on physiology and dysfunction including fatty liver and its implications, and hepatitis viruses. The knowledge of Human Genetics and Biochemical Basis of Inheritance has been appropriately expanded to reflect the latest advances in various domains. Besides DNA fingerprinting for identity establishment, the Section discusses epigenetics, micro-RNA and siRNA including their role in gene expression, chromatin modification and its association with human diseases, and genetic engineering. It also explores emerging areas such as metabolomics and proteomics; synthetic biology; and dual use technology in bioterrorism. Due emphasis has been given to the Section on Cell Replication and Cancer. Emergence of the use of probiotics in human health has also been highlighted. Besides, an entire Section has been devoted to male and female reproductive systems, fertilization, implantation, pregnancy, lactation, and assisted reproductive technology. Immunology, including vaccines and immunization, has been given due attention with latest updates in this fast growing area. Modern medicine, despite its stupendous advances cannot provide cure for all ailments. Thus, the new edition provides knowledge of alternative medicine systems—Ayurveda, Homeopathy, Unani, Yoga and Herbal Medicine. Incorporating vast information on the latest and emerging areas, the book will be of immense value to the students of medical sciences not only in their preclinical years, but also in all phases of medical course including postgraduate education and practice. Besides, it will also serve as a valuable source to the students of biochemistry and human bi

For over one hundred years before DNA coding was discovered, the Theory of Evolution dominated biology. We can call the biology of that era as “Pre-DNA Biology”. During this era, generations of biologists inherited biological theories derived from the Theory of Evolution. Thus, these biologists cannot understand the error of the Theory of Evolution. However, science does not follow human will. The conclusions expressed by DNA coding conflict with the foundations of the Theory of Evolution. The fact that the DNA coding of all humans have consistent sequences shatters the premise of the Theory of Evolution, namely, that evolution is random. The uniqueness in the number and karyotypes of biological chromosomes prevents the production of new species through continuous and slight change. DNA coding gives new life to biology by revealing the inherent secret of living creatures. Thus, “Post-DNA Biology” must be established. In this new era of biology, the most urgent task is to understand the inherent nature of living creatures through DNA coding, which consists of DNA decoding and mathematic analysis.

Who are we? Where are we from? These questions have troubled people for centuries. The textbooks have long taught us that human beings evolved from anthropoid apes. Today, a new science, molecular anthropology, tells us this: 7 billion human beings in the world share a common grand, grand...father, the Y-chromosome Adam, and share a common grand, grand...mother, the Mitochondrial Eve. After reading information in this book, you will be convinced that human beings could not be the result of evolution, sudden mutation, or in any way related to the anthropoid apes.

This new fifth edition of Information Resources in Toxicology offers a consolidated entry portal for the study, research, and practice of toxicology. Both volumes represents a unique, wide-ranging, curated, international, annotated bibliography, and directory of major resources in toxicology and allied fields such as environmental and occupational health, chemical safety, and risk assessment. The editors and authors are among the leaders of the profession sharing their cumulative wisdom in toxicology’s subdisciplines. This edition keeps pace with the digital world in directing and linking readers to relevant websites and other online tools. Due to the increasing size of the hardcopy publication, the current edition has been divided into two volumes to make it easier to handle and consult. Volume 1: Background, Resources, and Tools, arranged in 5 parts, begins with chapters on the science of toxicology, its history, and informatics framework in Part 1. Part 2 continues with chapters organized by more specific subject such as cancer, clinical toxicology, genetic toxicology, etc. The categorization of chapters by resource format, for example, journals and newsletters, technical reports, organizations constitutes Part 3. Part 4 further considers toxicology’s presence via the Internet, databases, and software tools. Among the miscellaneous topics in the concluding Part 5 are laws and regulations, professional education, grants and funding, and patents. Volume 2: The Global Arena offers contributed chapters focusing on the toxicology contributions of over 40 countries, followed by a glossary of toxicological terms and an appendix of popular quotations related to the field. The book, offered in both print and electronic formats, is carefully structured, indexed, and cross-referenced to enable users to easily find answers to their questions or serendipitously locate useful knowledge they were not originally aware they needed. Among the many timely topics receiving increased emphasis are disaster preparedness, nanotechnology, -omics, risk assessment, societal implications such as ethics and the precautionary principle, climate change, and children’s environmental health. Introductory chapters provide a backdrop to the science of toxicology, its history, the origin and status of toxicoinformatics, and starting points for identifying resources. Offers an extensive array of chapters organized by subject, each highlighting resources such as journals, databases,organizations, and review articles. Includes chapters with an emphasis on format such as government reports, general interest publications, blogs, and audiovisuals. Explores recent internet trends, web-based databases, and software tools in a section on the online environment. Concludes with a miscellany of special topics such as laws and regulations, chemical hazard communication resources, careers and professional education, K-12 resources, funding, poison control centers, and patents. Paired with Volume Two, which focuses on global resources, this set offers the most comprehensive compendium of print, digital, and organizational resources in the toxicological sciences with over 120 chapters contributions by experts and leaders in the field.

This book will emphatically argue that human beings and chimpanzees have never shared a common ancestor, nor did humans undergo evolution or microevolution. Moreover, this book will discuss the serious mistakes and misleading guidance the book published by NAS, National Academy of Sciences, “Science, Evolution, and Creationism” makes. Their argument that human beings and chimpanzees share a common ancestor is wrong without any scientific basis. They also claim that the Theory of Evolution is “the cornerstone of modern sciences”. However, the facts shown by DNA codes proved that the Theory of Evolution is wrong. Based on a wrong viewpoint as the cornerstone, NAS suppresses and impedes the development of science. NAS members are leaders in American sciences. Therefore, they have to bear the necessary responsibility. Modern science has determined that hereditary information of all living species is totally defined by its own DNA coding sequences. Unique DNA codes define a unique species. The overall DNA coding sequences keep high fidelity during the genetic breeding of various species, thereby helping scientists find sources of any species. Since biological features of all species depend on their own DNA codes, DNA codes must be the only correct direction and method for understanding the origin of species.

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