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Get complete instructions for manipulating, processing, cleaning, and crunching datasets in Python. Updated for Python 3.6, the second edition of this hands-on guide is packed with practical case studies that show you how to solve a broad set of data analysis problems effectively. You ' ll learn the latest versions of pandas, NumPy, IPython, and Jupyter in the process. Written by Wes McKinney, the creator of the Python pandas project, this book is a practical, modern introduction to data science tools in Python. It ' s ideal for analysts new to Python and for Python programmers new to data science and scientific computing. Data files and related material are available on GitHub. Use the IPython shell and Jupyter notebook for exploratory computing Learn basic and advanced features in NumPy (Numerical Python) Get started with data analysis tools in the pandas library Use flexible tools to load, clean, transform, merge, and reshape data Create informative visualizations with matplotlib Apply the pandas groupby facility to slice, dice, and summarize datasets Analyze and manipulate regular and irregular time series data Learn how to solve real-world data analysis problems with thorough, detailed examples

This Dictionary covers information and communication technology (ICT), including hardware and software; information networks, including the Internet and the World Wide Web; automatic control; and ICT-related computer-aided fields. The Dictionary also lists abbreviated names of relevant organizations, conferences, symposia and workshops. This reference is important for all practitioners and users in the areas mentioned above, and those who consult or write technical material. This Second Edition

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contains 10,000 new entries, for a total of 33,000.

A unique interdisciplinary approach to disaster risk research, including global hazards and case-studies, for researchers, graduate students and professionals.

Due to its data handling and modeling capabilities as well as its flexibility, R is becoming the most widely used software in bioinformatics. R Programming for Bioinformatics explores the programming skills needed to use this software tool for the solution of bioinformatics and computational biology problems. Drawing on the author ' s first-hand experiences as an expert in R, the book begins with coverage on the general properties of the R language, several unique programming aspects of R, and object-oriented programming in R. It presents methods for data input and output as well as database interactions. The author also examines different facets of string handling and manipulations, discusses the interfacing of R with other languages, and describes how to write software packages. He concludes with a discussion on the debugging and profiling of R code. With numerous examples and exercises, this practical guide focuses on developing R programming skills in order to tackle problems encountered in bioinformatics and computational biology.

The five-volume set LNCS 7971-7975 constitutes the refereed proceedings of the 13th International Conference on Computational Science and Its Applications, ICCSA 2013, held in Ho Chi Minh City, Vietnam in June 2013. The 248 revised papers presented in five tracks and 33 special sessions and workshops were carefully reviewed and

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selected. The 46 papers included in the five general tracks are organized in the following topical sections: computational methods, algorithms and scientific applications; high-performance computing and networks; geometric modeling, graphics and visualization; advanced and emerging applications; and information systems and technologies. The 202 papers presented in special sessions and workshops cover a wide range of topics in computational sciences ranging from computational science technologies to specific areas of computational sciences such as computer graphics and virtual reality.

Written by recognized experts in the study of proteins, *Proteomics for Biological Discovery* begins by discussing the emergence of proteomics from genome sequencing projects and a summary of potential answers to be gained from proteome-level research. The tools of proteomics, from conventional to novel techniques, are then dealt with in terms of underlying concepts, limitations and future directions. An invaluable source of information, this title also provides a thorough overview of the current developments in post-translational modification studies, structural proteomics, biochemical proteomics, microfabrication, applied proteomics, and bioinformatics relevant to proteomics. Presents a comprehensive and coherent review of the major issues faced in terms of technology development, bioinformatics, strategic approaches, and applications. Chapters offer a rigorous overview with summary of limitations, emerging approaches, questions, and realistic future industry and basic science applications. Discusses higher level integrative aspects, including technical challenges and applications for

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drug discovery Accessible to the novice while providing experienced investigators essential information Proteomics for Biological Discovery is an essential resource for students, postdoctoral fellows, and researchers across all fields of biomedical research, including biochemistry, protein chemistry, molecular genetics, cell/developmental biology, and bioinformatics.

This volume constitutes the proceedings of the Third European Symposium on Research in Computer Security, held in Brighton, UK in November 1994. The 26 papers presented in the book in revised versions were carefully selected from a total of 79 submissions; they cover many current aspects of computer security research and advanced applications. The papers are grouped in sections on high security assurance software, key management, authentication, digital payment, distributed systems, access control, databases, and measures.

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