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This essential text provides a readable yet sophisticated overview of the basic concepts of information technologies as they apply in healthcare.

Spanning areas as diverse as the electronic medical record,

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searching, protocols, and
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communications as well as the
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Internet, Enrico Coiera has
And Computational Biology
succeeded in making this vast
and complex area accessible
an

Provides a collection of medical

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IT research in topics such as clinical knowledge management, medical informatics, mobile health and service delivery, and gene expression.

The State of the Art in

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Transcriptome Analysis
RNA sequencing (RNA-seq) data offers unprecedented information about the transcriptome, but harnessing this information with bioinformatics tools is typically

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a bottleneck. RNA-seq Data
Analysis: A Practical Approach
enables researchers to
examine differential expression
at gene, exon, and transcript le
Despite what you may have
read in the popular press and

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in social media, Precision Medicine is not devoted to finding unique treatments for individuals, based on analyzing their DNA. To the contrary, the goal of Precision Medicine is to find general treatments that

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are highly effective for large numbers of individuals who fall into precisely diagnosed groups. We now know that every disease develops over time, through a sequence of defined biological steps, and

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that these steps may differ among individuals, based on genetic and environmental conditions. We are currently developing rational therapies and preventive measures, based on our precise

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understanding of the steps
leading to the clinical
expression of diseases.

Precision Medicine and the
Reinvention of Human Disease
explains the scientific
breakthroughs that have

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changed the way that we understand diseases, and reveals how medical scientists are using this new knowledge to launch a medical revolution. Clarifies the foundational concepts of Precision Medicine,

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distinguishing this field from its predecessors such as genomics, pharmacogenetics, and personalized medicine.

Gathers the chief conceptual advances in the fields of genetics, pathology, and

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Healthcare Programming In bioinformatics, and synthesizes a coherent narrative for the field of Precision Medicine.

Delivers its message in plain language, and in a relaxed, conversational writing style, making it easy to understand

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the complex subject matter.

Guides the reader through a coherent and logical narrative, gradually providing expertise and skills along the way.

Covers the importance of data sharing in Precision Medicine,

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and the many data-related challenges that confront this fragile new field.

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Structure, Function, and Motion, Second Edition

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Volume 2: Deductions Based
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Classification Made Relevant
Fundamentals of Healthcare
Programming in Perl, Python,
and Ruby

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Repurposing Legacy Data:

Innovative Case Studies takes a look at how data scientists have repurposed legacy data, whether their own, or legacy data that has been donated to the public domain. Most of the data stored worldwide is

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legacy data—data created some time in the past, for a particular purpose, and left in obsolete formats. As with keepsakes in an attic, we retain this information thinking it may have value in the future, though we have no current use for it. The case

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studies in this book, from such diverse fields as cosmology, quantum physics, high-energy physics, microbiology, psychiatry, medicine, and hospital administration, all serve to demonstrate how innovative people

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draw value from legacy data. By following the case examples, readers will learn how legacy data is restored, merged, and analyzed for purposes that were never imagined by the original data creators.

Discusses how combining existing

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data with other data sets of the same kind can produce an aggregate data set that serves to answer questions that could not be answered with any of the original data Presents a method for re-analyzing original data sets using alternate or improved

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methods that can provide outcomes more precise and reliable than those produced in the original analysis

Explains how to integrate

heterogeneous data sets for the purpose of answering questions or developing concepts that span

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several different scientific fields

Physical oncology has the potential
to revolutionize cancer research and
treatment. The fundamental

rationale behind this approach is that
physical processes, such as transport
mechanisms for drug molecules

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within tissue and forces exchanged by cancer cells with tissue, may play an equally important role as biological processes in influencing progression and treatment outcome. This book introduces the emerging field of physical oncology to a

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general audience, with a focus on recent breakthroughs that help in the design and discovery of more effective cancer treatments. It

describes how novel mathematical models of physical transport processes incorporate patient tissue

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and imaging data routinely produced in the clinic to predict the efficacy of many cancer treatment approaches, including chemotherapy and radiation therapy. By helping to identify which therapies would be most beneficial for an individual

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patient, and quantifying their effects prior to actual implementation in the clinic, physical oncology allows doctors to design treatment regimens customized to each patient's clinical needs, significantly altering the current clinical approach to cancer

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treatment and improving the outcomes for patients.

Demystifies Biomedical and Biological Big Data Analyses Big Data Analysis for Bioinformatics and Biomedical Discoveries provides a practical guide to the nuts

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and bolts of Big Data, enabling you
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to quickly and effectively harness
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the power of Big Data to make
And Computational Biology
groundbreaking biological
discoveries, carry out translational
medical research, and implement
personalized genomic medicine.

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Contributing to the NIH Big Data to Knowledge (BD2K) initiative, the book enhances your computational and quantitative skills so that you can exploit the Big Data being generated in the current omics era.

The book explores many significant

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topics of Big Data analyses in an easily understandable format. It describes popular tools and software for Big Data analyses and explains next-generation DNA sequencing data analyses. It also discusses comprehensive Big Data analyses of

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several major areas, including the integration of omics data, pharmacogenomics, electronic health record data, and drug discovery. Accessible to biologists, biomedical scientists, bioinformaticians, and computer

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data analysts, the book keeps

complex mathematical deductions

and jargon to a minimum. Each

chapter includes a theoretical

introduction, example applications,

data analysis principles, step-by-step

tutorials, and authoritative

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Mathematical Models of Plant-Herbivore Interactions addresses mathematical models in the study of practical questions in ecology, particularly factors that affect herbivory, including plant defense,

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herbivore natural enemies, and adaptive herbivory, as well as the effects of these on plant community dynamics. The result of extensive research on the use of mathematical modeling to investigate the effects of plant defenses on plant-herbivore

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dynamics, this book describes a toxin-determined functional response model (TDFRM) that helps explains field observations of these interactions. This book is intended for graduate students and researchers interested in

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mathematical biology and ecology.

Precision Medicine and the

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RNA-seq Data Analysis

Computational Intelligence and

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Principles of Biomedical

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Health and Medical Informatics

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Education in Europe

And Computational Biology
Preparing, Sharing, and Analyzing
Complex Information

AI techniques are being successfully used
in the fields of health to increase the

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efficacy of therapies and avoid the risks of false diagnosis, therapeutic decision-making, and outcome prediction in many clinical cases, thanks to the rapid advancement of technology. The acquisition, analysis, and application of a vast amount of information required to solve complex problems is a challenge for

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modern health therapies. The 21 chapters in this integrate several aspects of computational intelligence like machine learning and deep learning from diversified perspectives. The purpose of the book is to endow to different communities with their innovative advances in theory, analytical approaches,

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Healthcare Programming In numerical simulation, statistical analysis, modeling, advanced deployment, case studies, analytical results, computational structuring and significance progress in healthcare applications.

The success of individualized medicine, advanced crops, and new and sustainable energy sources requires thoroughly

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annotated genomic information and the integration of this information into a coherent model. A thorough overview of this field, Genome Annotation explores automated genome analysis and annotation from its origins to the challenges of next-generation sequencing data analysis. The book initially takes you

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through the last 16 years since the sequencing of the first complete microbial genome. It explains how current analysis strategies were developed, including sequencing strategies, statistical models, and early annotation systems. The authors then present visualization techniques for displaying integrated results as well as

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state-of-the-art annotation tools, including MAGPIE, Ensembl, Bluejay, and Galaxy.

They also discuss the pipelines for the analysis and annotation of complex, next-generation DNA sequencing data. Each chapter includes references and pointers to relevant tools. As very few existing genome annotation pipelines are capable

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of dealing with the staggering amount of DNA sequence information, new strategies must be developed to accommodate the needs of today's genome researchers. Covering this topic in detail, Genome Annotation provides you with the foundation and tools to tackle this challenging and evolving area. Suitable

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for both students new to the field and professionals who deal with genomic information in their work, the book offers two genome annotation systems on an accompanying CD-ROM.

Essentials of Clinical Informatics provides a concise and user-friendly overview on important topics such as technical

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Chapter: Health, Mathematical
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infrastructure, team members and their roles, informatics methods, policies and laws, implementation, and operations. With increased interest in training and expertise in order to participate in all aspects of medical technology from basic function of electronic health record to data analytics and quality improvement to

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population health, this work serves as a foundational guide to better understand and analyze medical data. The book is separated into six parts: Part 1, "Areas of Focus", is an introduction to the healthcare system and healthcare information systems; Part 2, "The Framework", discusses the theoretical and

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Healthcare Programming In procedural infrastructure of informatics, including data, knowledge, people, policies, procedures, and regulations; Part 3, "The Foundation", covers the fundamentals of clinical informatics in detail, including data representation, computer science, logic and programming, decision-making and decision support,

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Healthcare Programming In analytics, user experience, and project management; Part 4, "Application of Informatics in Healthcare", looks at the roles of informatics in the spectrum of healthcare environments from home to hospital to population health; Part 5, "Future Trends", presents a view of future trends and methods to stay current; and

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Part 6, "Appendix", has reference data, glossary, case discussions, citations, recommendations for further reading, and self-assessment questions which may be of interest to professionals who are preparing for certification examinations. An invaluable resource for computational biologists and researchers from other

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Chromatin: Structure, Dynamics, Regulation offers comprehensive coverage of this dynamic interdisciplinary field, from the basics to the latest research. Computational methods from statistical physics and bioinformatics are detailed whenever possible without lengthy

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recourse to specialized techniques.

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Classifications and Ontologies

Big Data Analysis for Bioinformatics and

Biomedical Discoveries

Taming Information With Open Source

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Introduction to Mathematical Oncology

Principles and Practice of Big Data

After the success of the first two books

with the proceedings of the newly established series of European conferences in Health Telematics

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Healthcare Programming In Education the third one gives a new dimension in the field of Health and Medical Informatics Education in Europe. It deals with the needs and the current status in Health Telematics Education in Europe, with curriculum development in Health-

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Medical and Nursing Informatics, with development of courseware

material, computer based training and computer assisted learning. Also

distance learning and Internet applications, training in using

Hospital Information Systems (HIS)

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and Departmental Information Systems, Inter-University programmes and accreditation of courses are discussed.

Exome and genome sequencing are revolutionizing medical research and diagnostics, but the computational

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analysis of the data has become an extremely heterogeneous and often challenging area of bioinformatics.

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Computational Exome and Genome

Analysis provides a practical introduction to all of the major areas in the field, enabling readers to

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develop a comprehensive understanding of the sequencing

process and the entire computational analysis pipeline.

In today's data driven biology, programming knowledge is essential in turning ideas into testable

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hypothesis. Based on the author's extensive experience, Python for Bioinformatics, Second Edition helps biologists get to grips with the basics of software development. Requiring no prior knowledge of programming-related concepts, the book focuses on

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the easy-to-use, yet powerful, Python computer language. This new edition is updated throughout to Python 3 and is designed not just to help scientists master the basics, but to do more in less time and in a reproducible way. New developments added in this

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edition include NoSQL databases, the Anaconda Python distribution, graphical libraries like Bokeh, and the use of Github for collaborative development.

Too often, healthcare workers are led to believe that medical informatics is a

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complex field that can only be mastered by teams of professional programmers. This is simply not the case. With just a few dozen simple algorithms, easily implemented with open source programming languages, you can fully utilize the medical

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information contained in clini

Repurposing Legacy Data

Innovative Case Studies

Statistical Modeling and Machine

Learning for Molecular Biology

Computational Exome and Genome

Analysis

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Principles of Big Data

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Guide to Health Informatics

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This book comprises select peer-reviewed proceedings of the

International Conference on

Advances in Materials Research

(ICAMR 2019). The contents

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cover latest research in materials and their applications relevant to composites, metals, alloys, polymers, energy and phase change. The indigenous properties of materials including mechanical, electrical, thermal,

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optical, chemical and biological
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functions are discussed. The
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book also elaborates the
And Computational Biology
properties and performance
enhancement and/or
deterioration in order of the
modifications in atomic particles

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and structure. This book will be useful for both students and professionals interested in the development and applications of advanced materials.

Principles of Big Data helps readers avoid the common

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mistakes that endanger all Big Data projects. By stressing simple, fundamental concepts, this book teaches readers how to organize large volumes of complex data, and how to achieve data permanence when

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the content of the data is constantly changing. General methods for data verification and validation, as specifically applied to Big Data resources, are stressed throughout the book.

The book demonstrates how

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adept analysts can find relationships among data objects held in disparate Big Data resources, when the data objects are endowed with semantic support (i.e., organized in classes of uniquely identified

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data objects). Readers will learn how their data can be integrated with data from other resources, and how the data extracted from Big Data resources can be used for purposes beyond those imagined by the data creators.

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Learn general methods for specifying Big Data in a way that is understandable to humans and to computers Avoid the pitfalls in Big Data design and analysis Understand how to create and use Big Data safely

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and responsibly with a set of laws, regulations and ethical standards that apply to the acquisition, distribution and integration of Big Data resources From the spontaneous rapid firing of cortical neurons to the

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spatial diffusion of disease

epidemics, biological systems

exhibit rich dynamic behaviour

over a vast range of time and

space scales. Unifying many of

these diverse phenomena,

Dynamics of Biological Systems

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provides the computational and mathematical platform from which to understand the underlying processes of the phenomena. Through an extensive tour of various biological systems, the text

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introduces computational methods for simulating spatial diffusion processes in excitable media, such as the human heart, as well as mathematical tools for dealing with systems of nonlinear ordinary and partial differential

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equations, such as neuronal
activation and disease diffusion.
The mathematical models and
computer simulations offer
insight into the dynamics of
temporal and spatial biological
systems, including cardiac

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pacemakers, artificial electrical defibrillation, pandemics, pattern formation, flocking behaviour, the interaction of autonomous agents, and hierarchical and structured network topologies.

Tools from complex systems and

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complex networks are also presented for dealing with real phenomenological systems. With exercises and projects in each chapter, this classroom-tested text shows students how to apply a variety of mathematical and

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Healthcare Programming In computational techniques to model and analyze the temporal and spatial phenomena of biological systems. MATLAB® implementations of algorithms and case studies are available on the author's website.

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This book covers the fundamentals of IoT and healthcare systems for carrying out system architectures, protocols, wearable devices, and interoperability. It explores major challenges in artificial

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Healthcare Programming In intelligence (AI) and smart computing in resource-constrained IoT-based applications along with cost, energy efficiency, and the availability of quality service.

Healthcare Systems and Health

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Healthcare Programming In Informatics: Using Internet of

Things explores the role of AI and smart computing in health

informatics and healthcare with an emphasis on clinical data

management and analysis for precise prediction and prompt

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action. It presents cutting-edge tracking, monitoring, real-time assistance, and security for IoT in healthcare and broadly discusses wearable sensors and IoT devices and their role in smart living assistance. The

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book goes on to describe a system model and architecture

for a clear picture of energy conservation-based IoT in

healthcare and explains the challenges and opportunities with IoT-based healthcare

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industries. A study of the threats and impacts, along with the need for information security, is also included. The chapters are written by experts in the field, and this book provides a comprehensive description of the

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important aspects of IoT and
health from a beginner- to
advanced-level perspective and
is ideal for researchers,
academicians, students, persons
in industry, technologists, and
entrepreneurs.

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Evolution's Clinical Guidebook

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Information Technology

Professionals (Sixth Edition)

***Too often, healthcare
workers are led to
believe that medical
informatics is a complex***

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field that can only be mastered by teams of professional programmers. This is simply not the case. With just a few dozen simple algorithms,

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easily implemented with open source programming languages, you can fully utilize the medical information contained in clinical and research datasets. The common

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***computational tasks of
medical informatics are
accessible to anyone
willing to learn the
basics. Methods in
Medical Informatics:
Fundamentals of***

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Healthcare Programming In Perl Python And Ruby
Healthcare Programming in Perl, Python, and Ruby demonstrates that biomedical professionals with fundamental programming knowledge can master any kind of

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data collection.

Providing you with

access to data,

nomenclatures, and

programming scripts and

languages that are all

free and publicly

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available, this book --
Describes the structure
of data sources used,
with instructions for
downloading Includes a
clearly written
explanation of each

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*algorithm Offers
equivalent scripts in
Perl, Python, and Ruby,
for each algorithm Shows
how to write short,
quickly learned scripts,
using a minimal*

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selection of commands

Perl Python And Ruby
Teaches basic

informatics methods for
retrieving, organizing,

merging, and analyzing

data sources Provides

case studies that detail

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***the kinds of questions
that biomedical***

***scientists can ask and
answer with public data***

and an open source

programming language

Requiring no more than a

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*working knowledge of
Perl, Python, or Ruby,*

Methods in Medical

Informatics will have

you writing powerful

programs in just a few

minutes. Within its

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chapters, you will find descriptions of the basic methods and implementations needed to complete many of the projects you will encounter in your

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A European wide survey on the EDUCTRA (Education and Training in Health Informatics) Concerted Action, was commenced in 1992 under

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the auspices of the AIM
(Advanced Informatics in
Medicine in Europe)
programme. This book
consists of four parts.
The first chapter
reproduces the original

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EC Recommendation and outlines the concerted European efforts in education and training in health telematics made by the European Commission, DG XIII

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Health Telematics office. The second part provides the general guidelines for European curricula in health informatics as they were developed and elaborated

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***by the members of the
EDUCTRA Concerned Action
(1992-1994). The third
part of this volume
entails the detailed
descriptions and
applications of***

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informatics in European
states. The fourth part
consists of a glossary
of terms and acronyms
used in current research
and practice of health*

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informatics. The work provides a comprehensive overview of the current needs in health informatics in Europe but also the necessary guidelines, materials,

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tools and applications
for improving education
and training within the
near future. Readers:
medicine and health care
professionals,
administrators, health

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professionals, teachers
and trainers. "The work
provides not only a
comprehensive overview
of the current needs in
health informatics in
Europe, but also the

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***necessary guidelines,
materials, tools and
applications for
improving education and
training within the near
future." Health
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November 1995, p. 15***

***Praise for the first
edition "This book***

***captures, in a very
accessible way, a***

growing body of

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***literature on the
structure, function and
motion of proteins [...]
[This is] a superb
publication that would
be very useful to
undergraduates, graduate***

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*students, postdoctoral
researchers, and
instructors involved in
structural biology or
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relationships." –David Sheehan, ChemBioChem,

2011 "Introduction to Proteins is an

excellent, state-of-the-art choice for students, faculty, or researchers

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***needing a monograph on
protein structure. [...] this is an immensely
informative, thoroughly
researched, up-to-date
text, with broad
coverage and remarkable***

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depth. Introduction to Proteins would provide an excellent basis for an upper-level or graduate course on protein structure, and a valuable addition to the

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***libraries of
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in this centrally
important field." -Eric
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Molecular Biology
Education, 2012***

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be analyzed in multiple
ways. It refers to the
roles of proteins and
enzymes in diverse
contexts and everyday

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biophysical methods for
studying proteins,
including fully
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function relationship***

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intrinsically
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***This open access book
comprehensively covers
the fundamentals of
clinical data science,
focusing on data
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and clinical applications. Topics covered in the first section on data collection include: data sources, data at scale (big data), data

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***stewardship (FAIR data)
and related privacy
concerns. Aspects of
predictive modelling
using techniques such as
classification,
regression or***

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clustering, and prediction model validation will be covered in the second section. The third section covers aspects of (mobile) clinical

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decision support systems, operational

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Fundamentals of Clinical

Data Science is an

essential resource for

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intending to develop and
refine their skills in
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promise is "no math, no code"and will explain

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Molecular biologists are performing increasingly large and complicated experiments, but often have little background in data analysis. The book is devoted to teaching the statistical

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and computational techniques molecular biologists need to analyze their data. It explains the big-picture concepts in data analysis using a wide variety of real-world molecular biological examples such as eQTLs, ortholog identification, motif finding, inference of population structure,

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protein fold prediction and many more. The book takes a pragmatic approach, focusing on techniques that are based on elegant mathematics yet are the simplest to explain to scientists with little background in computers and statistics.

Data Simplification: Taming Information

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Healthcare Programming In Perl Python And Ruby With Open Source Tools addresses the simple fact that modern data is too big and complex to analyze in its native form. Data simplification is the process whereby large and complex data is rendered usable. Complex data must be simplified before it can be analyzed, but the process of data simplification is

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anything but simple, requiring a specialized set of skills and tools. This book provides data scientists from every scientific discipline with the methods and tools to simplify their data for immediate analysis or long-term storage in a form that can be readily repurposed or integrated with other

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data. Drawing upon years of practical experience, and using numerous examples and use cases, Jules Berman discusses the principles, methods, and tools that must be studied and mastered to achieve data simplification, open source tools, free utilities and snippets of code that can

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be reused and repurposed to simplify data, natural language processing and machine translation as a tool to simplify data, and data summarization and visualization and the role they play in making data useful for the end user. Discusses data simplification principles, methods, and tools that

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must be studied and mastered

Provides open source tools, free utilities, and snippets of code that can be reused and repurposed to simplify data Explains how to best utilize indexes to search, retrieve, and analyze textual data Shows the data scientist how to apply ontologies,

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classifications, classes, properties, and
instances to data using tried and true
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computations with Python scripts in the
Chimera environment. It focuses on the
three core areas needed to study
structural bioinformatics: biochemistry,
mathematics, and computation.*

*Understand Important Concepts of
Structural Bioinformatics The book
covers topics that deal primarily with*

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protein structure and includes many exercises that are grounded in biological problems at the molecular level. The text encourages mathematical analysis by providing a firm foundation for computations. It analyzes numerous Python scripts for the Chimera environment, with the

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Healthcare Programming In Perl, Python, And Ruby. Scripts and other material available on a supplementary website. Build Python Scripts to Extend the Capabilities of Chimera Through more than 60 exercises that involve the development of Python scripts, the book gives you concrete guidance on using the scripting capabilities of Chimera. You'll

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gain experience in solving real problems as well as understand the various applications of linear algebra. You can also use the scripts as starting points for the development of similar applications and use classes from the StructBio toolkit for computations, such as structure

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overlap, data plotting, scenographics, and display of residue networks.

Quantitative methods are revolutionizing modern molecular and cellular biology. Groundbreaking technical advances are fueling the rapid expansion in our ability to observe, as seen in multidisciplinary

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studies that integrate theory, computation, experimental assays, and the control of microenvironments.

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foundation for starting work in this field. The book is organized into three sections: *Fundamental Concepts* covers bold ideas that inspire novel approaches in modern quantitative biology. It offers perspectives on evolutionary dynamics, system design principles, chance and memory, and

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information processing in biology.

Methods describes recently developed or improved techniques that are transforming biological research. It covers experimental methods for studying single-molecule biochemistry, small-angle scattering from biomolecules, subcellular localization

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of proteins, and single-cell behavior. It also describes theoretical methods for synthetic biology and modeling random variations among cells. Molecular and Cellular Systems focuses on specific biological systems where modern quantitative biology methods are making an impact. It incorporates case

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studies of biological systems for which new concepts or methods are increasing our understanding.

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Examples include protein kinase at the molecular level, the genetic switch of phage lambda at the regulatory system level, and Escherichia coli chemotaxis at the cellular level. In short,

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*Quantitative Biology presents practical
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systems from the molecular to the
cellular levels.*

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*Fundamentals and Applications
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Over the years, medical informatics has matured into a true scientific discipline. Fundamental and applied

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aspects are now taught in various fields of health, including medicine, dentistry, pharmacy, nursing and public health. Medical informatics is also often included in the curricula of many other disciplines, including the life sciences, engineering and

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economics. Medical informatics is a complex and rapidly changing discipline. Relatively few books have been published on the subject, and they rapidly become obsolete. This book is the fruit of a collaborative effort between authors teaching

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medical informatics in France and
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others who are conducting research
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in this field. In addition, an
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international perspective was
pursued, as reflected in the inclusion
of various developments and actions
in both the USA and Europe. This

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book is divided into 18 chapters, all of which include learning objectives, recommendations for further reading, exercises and bibliographic references.

**Evolution's Clinical Guidebook:
Translating Ancient Genes into**

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Precision Medicine demonstrates, through well-documented examples, how an understanding of the phylogenetic ancestry of humans allows us to make sense out of the flood of genetic data streaming from modern laboratories and how it can

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**lead us to new ways to prevent,
diagnose and treat diseases. Topics
cover evolution and human genome,
meiosis and other recombinants
events, embryology, speciation,
phylogeny, rare and common
diseases, and the evolution of aging.**

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This book is a valuable source for bioinformaticians and those in the biomedical field who need knowledge, down to gene level, to fully comprehend currently available data. Offers an innovative approach, focusing on how disease-associated

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pathways evolved Explains how the
fields of phylogeny and embryology
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have become closely tied to the fields
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of genetics and bioinformatics
And Computational Biology

**Demonstrates how students and
biomedical professionals can apply
the knowledge obtained in this book**

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to the theory and practice of precision medicine

Principles and Practice of Big Data: Preparing, Sharing, and Analyzing Complex Information, Second Edition updates and expands on the first edition, bringing a set of

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Healthcare Programming In techniques and algorithms that are tailored to Big Data projects. The book stresses the point that most data analyses conducted on large, complex data sets can be achieved without the use of specialized suites of software (e.g., Hadoop), and

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without expensive hardware (e.g., supercomputers). The core of every algorithm described in the book can be implemented in a few lines of code using just about any popular programming language (Python snippets are provided). Through the

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use of new multiple examples, this edition demonstrates that if we understand our data, and if we know how to ask the right questions, we can learn a great deal from large and complex data collections. The book will assist students and professionals

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from all scientific backgrounds who are interested in stepping outside the traditional boundaries of their chosen academic disciplines.

Presents new methodologies that are widely applicable to just about any project involving large and complex

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**datasets Offers readers informative
new case studies across a range
scientific and engineering disciplines
Provides insights into semantics,
identification, de-identification,
vulnerabilities and regulatory/legal
issues Utilizes a combination of**

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pseudocode and very short snippets
of Python code to show readers how
they may develop their own projects
without downloading or learning
new software

All too often, individuals engaged in
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numeric data must be left to the proper authorities (e.g., statisticians and data analysts) who are trained to apply sophisticated mathematical algorithms to sets of data. This is a terrible mistake. Individuals with keen observational skills, regardless

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of their mathematical training, are in the best position to draw correct inferences from their own data and to guide the subsequent implementation of robust, mathematical analyses. Volume 2 of Logic and Critical Thinking in the

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readers with a repertoire of
deductive non-mathematical
methods that will help them draw
useful inferences from their own
data. Volumes 1 and 2 of Logic and
Critical Thinking in the Biomedical

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Sciences are written for biomedical scientists and college-level students engaged in any of the life sciences, including bioinformatics and related data sciences. Demonstrates that a great deal can be deduced from quantitative data, without applying

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any statistical or mathematical analyses Provides readers with

simple techniques for quickly

reviewing and finding important

relationships hidden within large

and complex sets of data Using

examples drawn from the biomedical

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Informatics in Europe

As director of a training program in medical informatics, I have found that one of the most frequent inquiries from graduate students is, "Although I am happy with my research focus and the work I have

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done, how can I design and carry out a practical evaluation that proves the value of my contribution?" Informatics is a multifaceted, interdisciplinary field with research that ranges from theoretical developments to projects

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that are highly applied and intended for near-term use in clinical settings. The implications of "proving" a research claim accordingly vary greatly depending on the details of an individual student's goals and thesis state ment. Furthermore, the

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dissertation work leading up to an evaluation plan is often so time-consuming and arduous that attempting the "perfect" evaluation is frequently seen as impractical or as diverting students from central programming or implementation

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issues that are their primary areas of interest. They often ask what compromises are possible so they can provide persuasive data in support of their claims without adding another two to three years to their graduate student life. Our

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students clearly needed help in dealing more effectively with such dilemmas, and it was therefore fortuitous when, in the autumn of 1991, we welcomed two superb visiting professors to our laboratories.

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For more than 100 years, Henry's Clinical Diagnosis and Management by Laboratory Methods has been recognized as the premier text in clinical laboratory medicine, widely used by both clinical pathologists and laboratory technicians. Leading

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experts in each testing discipline clearly explain procedures and how they are used both to formulate clinical diagnoses and to plan patient medical care and long-term management. Employing a multidisciplinary approach, it

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authoritative text on every aspect of
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the clinical laboratory and the
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application of today's complete
range of laboratory tests. Updates
include current hot topics and
advances in clinical laboratory

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practices, including new and extended applications to diagnosis and management. New content covers next generation mass spectroscopy (MS), coagulation testing, next generation sequencing (NGS), transfusion medicine,

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test selection. Includes a chapter on Toxicology and Therapeutic Drug Monitoring that discusses the necessity of testing for therapeutic drugs that are more frequently being abused by users.

Classification Made Relevant

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explains how classifications and ontologies are designed, and how they are used to analyze scientific information. It is through our description of the relationships among classes of objects that we are able to simplify knowledge and

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explore the ways in which individual classified objects behave. The book begins by describing the fundamentals of classification and leads up to a description of how computer scientists use object-oriented programming languages to

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model classifications and ontologies.

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Numerous examples are chosen from the Classification of Life, the

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Periodic Table of the Elements, and

the symmetry relationships

contained within the Classification

Theorem of Finite Simple Groups.

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When these three classifications are tied together, they provide a relational hierarchy connecting all of the natural sciences. This book is intended to reach a multidisciplinary audience of students and professionals working in the data

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Healthcare Programming In sciences, the library sciences, and all of the STEM sciences. The chapters introduce and describe general concepts that can be understood by any intelligent reader. With each new concept, there follow practical examples selected from various

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Healthcare Programming In scientific disciplines. In these cases, technical points and specialized vocabulary are linked to glossary items, where the item is clarified and expanded. Technical terms in the data sciences often have different meanings, depending on the reader's

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specific discipline. The word

“ontology has so many meanings, it has become meaningless. Skeptics can google on the word “ontology to quickly confirm the inchoate status of this subject. In such cases, the glossary describes the different

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way the term has been used and will clarify its meaning within the book's context. For the benefit of computer scientists, the glossary contains short scripts written in Perl or Python or Ruby. Non-programmers will be spared from reading computer code,

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without missing out on the concepts covered in each chapter. By using the glossary links, every reader experiences a version of this book tailored to their personal needs and preferences. Explains the theory and the practice of classification.

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Emphasizes the importance of classifications and ontologies to the modern fields of mathematics, physics, chemistry, biology, and medicine. Includes numerous real-world examples demonstrating how bad construction technique can

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destroy the value of classifications and ontologies Explains how we define and understand the relationships among the classes within a classification, and how the properties of a class are inherited by its subclasses. Describes ontologies,

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and how they differ from classifications. Explains those conditions under which ontologies are useful. Explains how statements of meaning are properly expressed as triples. Shows how triples can be specified by popular semantic

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languages. Explains how triplestores (large collections of triples) can be usefully linked to classifications and ontologies. Demonstrates how classifications, ontologies, and triplestores are modeled by modern object-oriented languages.

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Oncology presents biologically well-motivated and mathematically

tractable models that facilitate both

a deep understanding of cancer

biology and better cancer treatment

designs. It covers the medical and

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biological background of the diseases, modeling issues, and existing methods and their

limitations. The authors introduce mathematical and programming tools, along with analytical and numerical studies of the models.

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They also develop new mathematical tools and look to future improvements on dynamical models. After introducing the general theory of medicine and exploring how mathematics can be essential in its understanding, the

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text describes well-known, practical, and insightful mathematical models of avascular tumor growth and mathematically tractable treatment models based on ordinary differential equations. It continues the topic of avascular tumor growth

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in the context of partial differential equation models by incorporating

the spatial structure and

physiological structure, such as cell size. The book then focuses on the

recent active multi-scale modeling efforts on prostate cancer growth

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and treatment dynamics. It also examines more mechanistically formulated models, including cell quota-based population growth models, with applications to real tumors and validation using clinical data. The remainder of the text

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presents abundant additional historical, biological, and medical background materials for advanced and specific treatment modeling efforts. Extensively classroom-tested in undergraduate and graduate courses, this self-contained book

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allows instructors to emphasize specific topics relevant to clinical cancer biology and treatment. It can be used in a variety of ways, including a single-semester undergraduate course, a more ambitious graduate course, or a full-

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Imaging: Integrated Analysis***

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and Causal Inference

addresses the recent

development of integrated

genomic, epigenomic and

imaging data analysis and

causal inference in big data

era. Despite significant

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progress in dissecting the

genetic architecture of

complex diseases by genome-

wide association studies

(GWAS), genome-wide

expression studies (GWES),

and epigenome-wide

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***association studies (EWAS),
the overall contribution of the
new identified genetic variants
is small and a large fraction of
genetic variants is still hidden.
Understanding the etiology
and causal chain of***

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mechanism underlying

complex diseases remains

elusive. It is time to bring big

data, machine learning and

causal revolution to

developing a new generation

of genetic analysis for shifting

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the current paradigm of genetic analysis from shallow association analysis to deep causal inference and from genetic analysis alone to integrated omics and imaging data analysis for unraveling

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the mechanism of complex diseases. FEATURES Provides a natural extension and companion volume to Big Data in Omic and Imaging: Association Analysis, but can be read independently.

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Introduce causal inference theory to genomic, epigenomic and imaging data analysis Develop novel statistics for genome-wide causation studies and epigenome-wide causation

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between the traditional

association analysis and

modern causation analysis

Use combinatorial

optimization methods and

various causal models as a

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image causal networks***

Present statistical methods
and computational algorithms
for searching causal paths
from genetic variant to disease

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Develop causal machine learning methods integrating causal inference and machine learning Develop statistics for testing significant difference in directed edge, path, and graphs, and for assessing

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causal relationships between two networks The book is designed for graduate students and researchers in genomics, epigenomics, medical image, bioinformatics, and data science. Topics

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covered are: mathematical

formulation of causal

inference, information

geometry for causal inference,

topology group and Haar

measure, additive noise

models, distance correlation,

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***multivariate causal inference
and causal networks, dynamic
causal networks, multivariate
and functional structural
equation models, mixed
structural equation models,
causal inference with***

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confounders, integer programming, deep learning and differential equations for wearable computing, genetic analysis of function-valued traits, RNA-seq data analysis, causal networks for genetic

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methylation analysis, gene expression and methylation deconvolution, cell –specific causal networks, deep learning for image segmentation and image analysis, imaging and

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**genomic data analysis,
integrated multilevel causal
genomic, epigenomic and
imaging data analysis.**

**Beginning with a survey of
fundamental concepts
associated with data**

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***integration, knowledge
representation, and***

***hypothesis generation from
heterogeneous data sets,***

Methods in Biomedical

Informatics provides a

practical survey of

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*methodologies used in
biological, clinical, and public
health contexts. These
concepts provide the
foundation for more advanced
topics like information
retrieval, natural language*

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*processing, Bayesian
modeling, and learning
classifier systems. The survey
of topics then concludes with
an exposition of essential
methods associated with
engineering, personalized*

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*medicine, and linking of
genomic and clinical data.*

*Within an overall context of
the scientific method, Methods
in Biomedical Informatics
provides a practical coverage
of topics that is specifically*

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designed for: (1) domain experts seeking an understanding of biomedical informatics approaches for addressing specific methodological needs; or (2) biomedical informaticians

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seeking an approachable overview of methodologies that can be used in scenarios germane to biomedical research. Contributors represent leading biomedical informatics experts:

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individuals who have demonstrated effective use of biomedical informatics methodologies in the real-world, high-quality biomedical applications Material is presented as a balance

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between foundational coverage of core topics in

biomedical informatics with practical "in-the-trenches"

scenarios. Contains

appendices that function as

primers on: (1) Unix; (2) Ruby;

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**(3) Databases; and (4) Web
Services.**

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***Principles of Biomedical
Informatics provides a
foundation for understanding
the fundamentals of
biomedical informatics, which***

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***deals with the storage,
retrieval, and use of***

***biomedical data for biological
problem solving and medical***

***decision making. It covers the
application of these principles***

to the three main biomedical

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domains of basic biology, clinical medicine, and public health. The author offers a coherent summary, focusing on the three core concept areas of biomedical data and knowledge representation:

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biomedical information access, biomedical decision making, and information and technology use in biomedical contexts. Develops principles and methods for representing biomedical data, using

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***information in context and in
decision making, and
accessing information to
assist the medical community
in using data to its full
potential Provides a series of
principles for expressing***

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***biomedical data and ideas in a
computable form to integrate
biological, clinical, and public
health applications Includes a
discussion of user interfaces,
interactive graphics, and
knowledge resources and***

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***reference material on
programming languages to
provide medical informatics
programmers with the
technical tools to develop
systems***

Health Informatics (HI) focuses

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on the application of Information Technology (IT) to the field of medicine to improve individual and population healthcare delivery, education and research. This extensively updated fifth

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*edition reflects the current
knowledge in Health*

*Informatics and provides
learning objectives, key
points, case studies and
references.*

A Pragmatic Approach

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***Using Internet of Things
From Molecular to Cellular
Systems***

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***Logic and Critical Thinking in
the Biomedical Sciences***