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This book constitutes

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**the thoroughly refereed
post-conference
proceedings of the 15th
International Meeting on
Computational
Intelligence Methods for
Bioinformatics and**

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**Biostatistics., CIBB
2018, held in Caparica,
Portugal, in September
2018. The 32 revised
full papers were
carefully reviewed and
selected from 51**

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submissions. The papers present current trends at the edge of computer and life sciences, the application of computational intelligence to a system

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**and synthetic biology
and the consequent
impact on innovative
medicine were presented.
Theoretical and
experimental biologists
also presented novel**

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**challenges and fostered
multidisciplinary
collaboration aiming to
blend theory and
practice, where the
founding theories of the
techniques used for**

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**modelling and analyzing
biological systems are
investigated and used
for practical
applications and the
supporting technologies.
Bioinformatics**

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**Algorithms: Design and
Implementation in Python**
provides a comprehensive
book on many of the most
important bioinformatics
problems, putting
forward the best

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**algorithms and showing
how to implement them.
The book focuses on the
use of the Python
programming language and
its algorithms, which is
quickly becoming the**

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**most popular language in
the bioinformatics
field. Readers will find
the tools they need to
improve their knowledge
and skills with regard
to algorithm development**

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**and implementation, and
will also uncover
prototypes of
bioinformatics
applications that
demonstrate the main
principles underlying**

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**real world applications.
Presents an ideal text
for bioinformatics
students with little to
no knowledge of computer
programming Based on
over 12 years of**

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**pedagogical materials
used by the authors in
their own classrooms
Features a companion
website with
downloadable codes and
runnable examples (such**

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as using Jupyter
Notebooks) and exercises
relating to the book
Suitable for advanced
undergraduates &
postgraduates, this book
provides a definitive

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approach & guides the
reader from first
principles through to an
understanding of the
computational techniques**

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& the key algorithms.

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broad range of topics in
deep learning, covering
mathematical and
conceptual background,
deep learning techniques**

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**used in industry, and
research perspectives.**

**“Written by three
experts in the field,
Deep Learning is the
only comprehensive book
on the subject.” –Elon**

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**Musk, cochair of OpenAI;
cofounder and CEO of
Tesla and SpaceX Deep
learning is a form of
machine learning that
enables computers to
learn from experience**

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**and understand the world
in terms of a hierarchy
of concepts. Because the
computer gathers
knowledge from
experience, there is no
need for a human**

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computer operator to formally specify all the knowledge that the computer needs. The hierarchy of concepts allows the computer to learn complicated

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concepts by building them out of simpler ones; a graph of these hierarchies would be many layers deep. This book introduces a broad range of topics in deep

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**learning. The text
offers mathematical and
conceptual background,
covering relevant
concepts in linear
algebra, probability
theory and information**

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**theory, numerical
computation, and machine
learning. It describes
deep learning techniques
used by practitioners in
industry, including deep
feedforward networks,**

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**regularization,
optimization algorithms,
convolutional networks,
sequence modeling, and
practical methodology;
and it surveys such
applications as natural**

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**language processing,
speech recognition,
computer vision, online
recommendation systems,
bioinformatics, and
videogames. Finally, the
book offers research**

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**perspectives, covering
such theoretical topics
as linear factor models,
autoencoders,
representation learning,
structured probabilistic
models, Monte Carlo**

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**methods, the partition
function, approximate
inference, and deep
generative models. Deep
Learning can be used by
undergraduate or
graduate students**

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planning careers in either industry or research, and by software engineers who want to begin using deep learning in their products or platforms. A

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supplementary material
for both readers and
instructors.**

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Computational**

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Bioinformatics and
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Design and
Implementation in Python
Bioinformatics Data
Skills**

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Bioinformatics

Algorithms

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MATLAB**

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turning large sequencing datasets
into reproducible and robust**

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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

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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

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**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**

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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

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Makefiles

Bioinformatics Algorithms: an Active Learning Approach is one of the first textbooks to emerge from the recent Massive Open Online Course (MOOC) revolution. A light-hearted and analogy-filled companion to the authors'

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acclaimed MOOC on Coursera, this book presents students with a dynamic approach to learning bioinformatics. It strikes a unique balance between practical challenges in modern biology and fundamental algorithmic ideas, thus capturing the interest of students of

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both biology and computer science. Each chapter begins with a central biological question, such as "Are There Fragile Regions in the Human Genome?" or "Which DNA Patterns Play the Role of Molecular Clocks?" and then steadily develops the algorithmic sophistication required

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to answer this question. Hundreds of exercises are incorporated directly into the text as soon as they are needed; readers can test their knowledge through automated coding challenges on the Rosalind Bioinformatics Textbook Track. A website augments the textbook by

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providing additional educational materials, including video lectures and PowerPoint slides.--Book website.

Summary Machine Learning in Action is unique book that blends the foundational theories of machine learning with the practical

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realities of building tools for everyday data analysis. You'll use the flexible Python programming language to build programs that implement algorithms for data classification, forecasting, recommendations, and higher-level features like summarization and

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simplification. About the Book A machine is said to learn when its performance improves with experience. Learning requires algorithms and programs that capture data and ferret out the interesting or useful patterns. Once the specialized domain of analysts

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and mathematicians, machine learning is becoming a skill needed by many. Machine Learning in Action is a clearly written tutorial for developers. It avoids academic language and takes you straight to the techniques you'll use in your day-to-day work. Many (Python)

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examples present the core algorithms of statistical data processing, data analysis, and data visualization in code you can reuse. You'll understand the concepts and how they fit in with tactical tasks like classification, forecasting, recommendations, and higher-level

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features like summarization and simplification. Readers need no prior experience with machine learning or statistical processing. Familiarity with Python is helpful. Purchase of the print book comes with an offer of a free PDF, ePub, and Kindle eBook from Manning.

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Also available is all code from the book. What's Inside

- A no-nonsense introduction**
- Examples showing common ML tasks**
- Everyday data analysis**
- Implementing classic algorithms like Apriori and Adaboos**

Table of Contents PART 1

CLASSIFICATION Machine learning

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basics Classifying with k-Nearest Neighbors Splitting datasets one feature at a time: decision trees Classifying with probability theory: naïve Bayes Logistic regression Support vector machines Improving classification with the AdaBoost meta algorithm PART 2

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**FORECASTING NUMERIC VALUES
WITH REGRESSION** Predicting
numeric values: regression Tree-
based regression **PART 3**
UNSUPERVISED LEARNING
Grouping unlabeled items using k-
means clustering Association
analysis with the Apriori algorithm

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Efficiently finding frequent itemsets with FP-growth PART 4

ADDITIONAL TOOLS Using principal component analysis to simplify data Simplifying data with the singular value decomposition Big data and MapReduce Effective SQL brings together the

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hands-on solutions and practical insights you need to solve a wide range of complex problems with SQL, and to design databases that make it far easier to manage data in the future. Leveraging the proven format of the best-selling Effective series, it focuses on providing

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clear, practical explanations, expert tips, and plenty of realistic examples -- all in full color. Drawing on their immense experience as consultants and instructors, three world-class database experts identify specific challenges, and distill each solution into five pages

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or less. Throughout, they provide well-annotated SQL code designed for all leading platforms, as well as code for specific implementations ranging from SQL Server to Oracle and MySQL, wherever these vary or permit you to achieve your goal more efficiently. Going beyond

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mere syntax, the authors also show how to avoid poor database design that makes it difficult to write effective SQL, how to improve suboptimal designs, and how to work around designs you can't change. You'll also find detailed sections on filtering and finding

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data, aggregation, subqueries, and metadata, as well as specific solutions for everything from listing products to scheduling events and defining data hierarchies. Simply put, if you already know the basics of SQL, Effective SQL will help you become a world-class SQL problem-

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solver.

Bioinformatics for Everyone
From Theory to Algorithms
Reproducible and Robust Research
with Open Source Tools
Fundamentals of Bioinformatics
and Computational Biology
The Machine Learning Approach

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Introduction to Computational Molecular Biology

Basic concepts of molecular biology.

Strings, graphs, and algorithms. Sequence
comparasion and database search.

Fragment assembly of DNA. Physical
mapping of DNA. Phylogenetic trees.

Genome rearrangements. Molecular

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structure prediction. epilogue: computing with DNA. Answers to selected exercises. References. index.

Thoroughly revised and updated, *Exploring Bioinformatics: A Project-Based Approach, Second Edition* is intended for an introductory course in bioinformatics at the undergraduate level.

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Through hands-on projects, students are introduced to current biological problems and then explore and develop bioinformatic solutions to these issues. Each chapter presents a key problem, provides basic biological concepts, introduces computational techniques to address the problem, and guides students

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through the use of existing web-based tools and software solutions. This progression prepares students to tackle the On-Your-Own Project, where they develop their own software solutions. Topics such as antibiotic resistance, genetic disease, and genome sequencing provide context and relevance to capture

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student interest.

Bioinformatics for Everyone provides a brief overview on currently used technologies in the field of bioinformatics—interpreted as the application of information science to biology— including various online and offline bioinformatics tools and softwares.

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The book presents valuable knowledge in a simplified way to help students and researchers easily apply bioinformatics tools and approaches to their research and lab routines. Several protocols and case studies that can be reproduced by readers to suit their needs are also included.

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tools available in a didactic manner so that readers can easily apply them to their research Includes several protocols that can be used in different types of research work or in lab routines Discusses upcoming technologies and their impact on biological/biomedical sciences
Data Structures & Theory of Computation

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Machine Learning Approaches to

Bioinformatics

Bioinformatics

Effective SQL

Biological Sequence Analysis

Machine Learning in Action

Computational Genome Analysis

An introductory text that

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emphasizes the underlying algorithmic ideas that are driving advances in bioinformatics. This introductory text offers a clear exposition of the algorithmic principles driving advances in bioinformatics. Accessible to students in both biology and

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computer science, it strikes a unique balance between rigorous mathematics and practical techniques, emphasizing the ideas underlying algorithms rather than offering a collection of apparently unrelated problems. The book introduces

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biological and algorithmic ideas together, linking issues in computer science to biology and thus capturing the interest of students in both subjects. It demonstrates that relatively few design techniques can be used to solve a large number of practical

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problems in biology, and presents this material intuitively. An Introduction to Bioinformatics Algorithms is one of the first books on bioinformatics that can be used by students at an undergraduate level. It includes a dual table of contents, organized

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by algorithmic idea and biological idea; discussions of biologically relevant problems, including a detailed problem formulation and one or more solutions for each; and brief biographical sketches of leading figures in the field. These interesting vignettes offer

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students a glimpse of the inspirations and motivations for real work in bioinformatics, making the concepts presented in the text more concrete and the techniques more approachable. Power Point presentations, practical

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bioinformatics problems, sample code, diagrams, demonstrations, and other materials can be found at the Author's website.

Lucidly Integrates Current Activities Focusing on both fundamentals and recent advances, Introduction to

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Machine Learning and Bioinformatics presents an informative and accessible account of the ways in which these two increasingly intertwined areas relate to each other. Examines Connections between Machine Learning &

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Bioinformatics The book begins with a brief historical overview of the technological developments in biology. It then describes the main problems in bioinformatics and the fundamental concepts and algorithms of machine learning. After forming this

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foundation, the authors explore how machine learning techniques apply to bioinformatics problems, such as electron density map interpretation, biclustering, DNA sequence analysis, and tumor classification. They also include exercises at the end of some

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chapters and offer supplementary materials on their website. Explores How Machine Learning Techniques Can Help Solve Bioinformatics Problems Shedding light on aspects of both machine learning and bioinformatics, this text shows

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how the innovative tools and techniques of machine learning help extract knowledge from the deluge of information produced by today's biological experiments.

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ALGORITHMS IN BIOINFORMATICS
Explore a comprehensive and
insightful treatment of the
practical application of
bioinformatic algorithms in a
variety of fields **Algorithms in
Bioinformatics: Theory and
Implementation** delivers a

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fulsome treatment of some of the main algorithms used to explain biological functions and relationships. It introduces readers to the art of algorithms in a practical manner which is linked with biological theory and interpretation. The book covers

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many key areas of bioinformatics, including global and local sequence alignment, forced alignment, detection of motifs, Sequence logos, Markov chains or information entropy. Other novel approaches are also described, such as Self-Sequence

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**alignment, Objective Digital
Stains (ODSs) or Spectral
Forecast and the Discrete
Probability Detector (DPD)
algorithm. The text incorporates
graphical illustrations to
highlight and emphasize the
technical details of**

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computational algorithms found within, to further the reader's understanding and retention of the material. Throughout, the book is written in an accessible and practical manner, showing how algorithms can be implemented and used in

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**JavaScript on Internet Browsers.
The author has included more
than 120 open-source
implementations of the material,
as well as 33 ready-to-use
presentations. The book contains
original material that has been
class-tested by the author and**

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numerous cases are examined in a biological and medical context. Readers will also benefit from the inclusion of: A thorough introduction to biological evolution, including the emergence of life, classifications and some known theories and

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molecular mechanisms A detailed presentation of new methods, such as Self-sequence alignment, Objective Digital Stains and Spectral Forecast A treatment of sequence alignment, including local sequence alignment, global sequence alignment and forced

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sequence alignment with full implementations Discussions of position-specific weight matrices, including the count, weight, relative frequencies, and log-likelihoods matrices A detailed presentation of the methods related to Markov Chains as well

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as a description of their implementation in Bioinformatics and adjacent fields An examination of information and entropy, including sequence logos and explanations related to their meaning An exploration of the current state of

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bioinformatics, including what is known and what issues are usually avoided in the field A chapter on philosophical transactions that allows the reader a broader view of the prediction process Native computer implementations in the

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context of the field of Bioinformatics Extensive worked examples with detailed case studies that point out the meaning of different results Perfect for professionals and researchers in biology, medicine, engineering, and information

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technology, as well as upper level undergraduate students in these fields, Algorithms in Bioinformatics: Theory and Implementation will also earn a place in the libraries of software engineers who wish to understand how to implement

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**bioinformatic algorithms in their
products.**

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**Probabilistic Models of Proteins
and Nucleic Acids**
Understanding Machine Learning
Active Learning

*An introduction to machine learning
methods and their applications to
problems in bioinformatics Machine
learning techniques are increasingly*

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being used to address problems in computational biology and bioinformatics. Novel computational techniques to analyze high throughput data in the form of sequences, gene and protein expressions, pathways, and images are becoming vital for understanding diseases and future

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drug discovery. Machine learning techniques such as Markov models, support vector machines, neural networks, and graphical models have been successful in analyzing life science data because of their capabilities in handling randomness and uncertainty of data noise and in

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generalization. From an internationally recognized panel of prominent researchers in the field, Machine Learning in Bioinformatics compiles recent approaches in machine learning methods and their applications in addressing contemporary problems in bioinformatics. Coverage includes:

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feature selection for genomic and proteomic data mining; comparing variable selection methods in gene selection and classification of microarray data; fuzzy gene mining; sequence-based prediction of residue-level properties in proteins; probabilistic methods for long-range

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features in biosequences; and much more. Machine Learning in Bioinformatics is an indispensable resource for computer scientists, engineers, biologists, mathematicians, researchers, clinicians, physicians, and medical informaticists. It is also a valuable reference text for computer

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science, engineering, and biology courses at the upper undergraduate and graduate levels.

Numerous fascinating breakthroughs in biotechnology have generated large volumes and diverse types of high throughput data that demand the development of efficient and

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appropriate tools in computational statistics integrated with biological knowledge and computational algorithms. This volume collects contributed chapters from leading researchers to survey the many active research topics and promote the visibility of this research area. This

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volume is intended to provide an introductory and reference book for students and researchers who are interested in the recent developments of computational statistics in computational biology.

Presents algorithmic techniques for solving problems in bioinformatics,

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including applications that shed new light on molecular biology This book introduces algorithmic techniques in bioinformatics, emphasizing their application to solving novel problems in post-genomic molecular biology. Beginning with a thought-provoking discussion on the role of algorithms in

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twenty-first-century bioinformatics education, Bioinformatics Algorithms covers: General algorithmic techniques, including dynamic programming, graph-theoretical methods, hidden Markov models, the fast Fourier transform, seeding, and approximation algorithms Algorithms

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and tools for genome and sequence analysis, including formal and approximate models for gene clusters, advanced algorithms for non-overlapping local alignments and genome tilings, multiplex PCR primer set selection, and sequence/network motif finding Microarray design and

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analysis, including algorithms for microarray physical design, missing value imputation, and meta-analysis of gene expression data Algorithmic issues arising in the analysis of genetic variation across human population, including computational inference of haplotypes from genotype

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*data and disease association search in case/control epidemiologic studies
Algorithmic approaches in structural and systems biology, including topological and structural classification in biochemistry, and prediction of protein-protein and domain-domain interactions Each chapter begins with*

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a self-contained introduction to a computational problem; continues with a brief review of the existing literature on the subject and an in-depth description of recent algorithmic and methodological developments; and concludes with a brief experimental study and a discussion of open

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research challenges. This clear and approachable presentation makes the book appropriate for researchers, practitioners, and graduate students alike.

The computational methods of bioinformatics are being used more and more to process the large volume

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of current biological data. Promoting an understanding of the underlying biology that produces this data, Pattern Discovery in Bioinformatics: Theory and Algorithms provides the tools to study regularities in biological data. Taking a systema Theory and Implementation

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*Advanced AI Techniques and
Applications in Bioinformatics*

Handbook of Statistical Bioinformatics

Algorithms in Bioinformatics

Deep Learning

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*This book is the first one specifically
dedicated to the structural*

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bioinformatics of membrane proteins. With a focus on membrane proteins from the perspective of bioinformatics, the present work covers a broad spectrum of topics in evolution, structure, function, and bioinformatics of membrane proteins focusing on the most recent

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experimental results. Leaders in the field who have recently reported breakthrough advances cover algorithms, databases and their applications to the subject. The increasing number of recently solved membrane protein structures makes the expert coverage presented here

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very timely. Structural bioinformatics of membrane proteins has been an active area of research over the last three decades and proves to be a growing field of interest.

The key idea behind active learning is that a machine learning algorithm can perform better with less training

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if it is allowed to choose the data from which it learns. An active learner may pose "queries," usually in the form of unlabeled data instances to be labeled by an "oracle" (e.g., a human annotator) that already understands the nature of the problem. This sort of approach is

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well-motivated in many modern machine learning and data mining applications, where unlabeled data may be abundant or easy to come by, but training labels are difficult, time-consuming, or expensive to obtain. This book is a general introduction to active learning. It outlines several

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scenarios in which queries might be formulated, and details many query selection algorithms which have been organized into four broad categories, or "query selection frameworks." We also touch on some of the theoretical foundations of active learning, and conclude with an

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overview of the strengths and weaknesses of these approaches in practice, including a summary of ongoing work to address these open challenges and opportunities. Table of Contents: Automating Inquiry / Uncertainty Sampling / Searching Through the Hypothesis Space /

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Minimizing Expected Error and Variance / Exploiting Structure in Data / Theory / Practical Considerations

Thoroughly Describes Biological Applications, Computational Problems, and Various Algorithmic Solutions Developed from the

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*author's own teaching material,
Algorithms in Bioinformatics: A
Practical Introduction provides an in-
depth introduction to the algorithmic
techniques applied in bioinformatics.
For each topic, the author clearly
details the bi
This is the first book primarily*

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dedicated to clustering using multiobjective genetic algorithms with extensive real-life applications in data mining and bioinformatics. The authors first offer detailed introductions to the relevant techniques - genetic algorithms, multiobjective optimization, soft

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computing, data mining and bioinformatics. They then demonstrate systematic applications of these techniques to real-world problems in the areas of data mining, bioinformatics and geoscience. The authors offer detailed theoretical and statistical notes, guides to future

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*research, and chapter summaries.
The book can be used as a textbook
and as a reference book by graduate
students and academic and industrial
researchers in the areas of soft
computing, data mining,
bioinformatics and geoscience.
An Introduction to Bioinformatics*

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Machine Learning in Bioinformatics

*Machine Learning in Non-Stationary
Environments*

Theory & Algorithms

*Applications in Data Mining and
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61 Specific Ways to Write Better SQL

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Computational Genomics with R provides a starting point for beginners in genomic data analysis and also guides more advanced practitioners to sophisticated data analysis techniques in genomics. The book covers topics from R programming, to machine

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learning and statistics, to the latest genomic data analysis techniques. The text provides accessible information and explanations, always with the genomics context in the background. This also contains practical and well-documented

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examples in R so readers can analyze their data by simply reusing the code presented. As the field of computational genomics is interdisciplinary, it requires different starting points for people with different backgrounds. For example,

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a biologist might skip sections on basic genome biology and start with R programming, whereas a computer scientist might want to start with genome biology. After reading: You will have the basics of R and be able to dive right into specialized uses of R

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for computational genomics such as using Bioconductor packages. You will be familiar with statistics, supervised and unsupervised learning techniques that are important in data modeling, and exploratory analysis of high-dimensional data. You will

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understand genomic intervals and operations on them that are used for tasks such as aligned read counting and genomic feature annotation. You will know the basics of processing and quality checking high-throughput sequencing data. You will be able to

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do sequence analysis, such as calculating GC content for parts of a genome or finding transcription factor binding sites. You will know about visualization techniques used in genomics, such as heatmaps, meta-gene plots, and genomic track

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visualization. You will be familiar with analysis of different high-throughput sequencing data sets, such as RNA-seq, ChIP-seq, and BS-seq. You will know basic techniques for integrating and interpreting multi-omics datasets. Altuna Akalin is a

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group leader and head of the Bioinformatics and Omics Data Science Platform at the Berlin Institute of Medical Systems Biology, Max Delbrück Center, Berlin. He has been developing computational methods for analyzing and

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integrating large-scale genomics data sets since 2002. He has published an extensive body of work in this area. The framework for this book grew out of the yearly computational genomics courses he has been organizing and teaching since 2015.

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This book presents the foundations of key problems in computational molecular biology and bioinformatics. It focuses on computational and statistical principles applied to genomes, and introduces the mathematics and

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statistics that are crucial for understanding these applications. The book features a free download of the R software statistics package and the text provides great crossover material that is interesting and accessible to students in biology, mathematics,

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statistics and computer science. More than 100 illustrations and diagrams reinforce concepts and present key results from the primary literature. Exercises are given at the end of chapters.

This book offers comprehensive

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coverage of all the core topics of bioinformatics, and includes practical examples completed using the MATLAB bioinformatics toolbox™. It is primarily intended as a textbook for engineering and computer science students attending advanced

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undergraduate and graduate courses in bioinformatics and computational biology. The book develops bioinformatics concepts from the ground up, starting with an introductory chapter on molecular biology and genetics. This chapter will

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enable physical science students to fully understand and appreciate the ultimate goals of applying the principles of information technology to challenges in biological data management, sequence analysis, and systems biology. The first part of the

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book also includes a survey of existing biological databases, tools that have become essential in today's biotechnology research. The second part of the book covers methodologies for retrieving biological information, including fundamental algorithms for

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sequence comparison, scoring, and determining evolutionary distance.

The main focus of the third part is on modeling biological sequences and patterns as Markov chains. It presents key principles for analyzing and searching for sequences of significant

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motifs and biomarkers. The last part of the book, dedicated to systems biology, covers phylogenetic analysis and evolutionary tree computations, as well as gene expression analysis with microarrays. In brief, the book offers the ideal hands-on reference

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guide to the field of bioinformatics and computational biology.

Bioinformatics Algorithms: an Active Learning Approach is one of the first textbooks to emerge from the recent Massive Online Open Course (MOOC) revolution. A light-hearted

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and analogy-filled companion to the authors' acclaimed online course (<http://coursera.org/course/bioinformatics>), this book presents students with a dynamic approach to learning bioinformatics. It strikes a unique balance between practical challenges

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in modern biology and fundamental algorithmic ideas, thus capturing the interest of students of biology and computer science students alike. Each chapter begins with a central biological question, such as "Are There Fragile Regions in the Human

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Genome?" or "Which DNA Patterns Play the Role of Molecular Clocks?" and then steadily develops the algorithmic sophistication required to answer this question. Hundreds of exercises are incorporated directly into the text as soon as they are

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needed; readers can test their knowledge through automated coding challenges on Rosalind (<http://rosalind.info>), an online platform for learning bioinformatics. The textbook website (<http://bioinformaticsalgorithms.org>)

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*directs readers toward additional
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*Structural Bioinformatics of
Membrane Proteins*

Semi-Supervised Learning

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Computational Genomics with R
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One of Springer ' s renowned Major
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comprehensive set of solutions to important algorithmic problems for students and researchers interested in quickly locating useful information. This first edition of the reference focuses on high-impact solutions from the most recent decade, while later editions will widen the scope of the

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work. All entries have been written by experts, while links to Internet sites that outline their research work are provided. The entries have all been peer-reviewed. This defining reference is published both in print and on line. Learning Algorithms Through Programming and Puzzle Solving is

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one of the first textbooks to emerge from the recent Massive Open Online Course (MOOC) revolution and a companion to the authors' online specialization on Coursera and MicroMasters Program on edX. The book introduces a programming-centric approach to learning

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algorithms and strikes a unique balance between algorithmic ideas, programming challenges, and puzzle solving. Since the launch of this project on Coursera and edX, hundreds of thousands students tried to solve programming challenges and algorithmic puzzles covered in this

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book. The book is also a step towards developing an Intelligent Tutoring System for learning algorithms. In a classroom, once a student takes a wrong turn, there are limited opportunities to ask a question, resulting in a learning breakdown, or the inability to progress further

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without individual guidance. When a student suffers a learning breakdown, that student needs immediate help in order to proceed. Traditional textbooks do not provide such help, but the automated grading system described in this MOOC book does! The book is accompanied by

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additional educational materials that include the book website, video lectures, slides, FAQs, and other resources available at Coursera and EdX.

The computational education of biologists is changing to prepare students for facing the complex

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datasets of today's life science research. In this concise textbook, the authors' fresh pedagogical approaches lead biology students from first principles towards computational thinking. A team of renowned bioinformaticians take innovative routes to introduce computational

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ideas in the context of real biological problems. Intuitive explanations promote deep understanding, using little mathematical formalism. Self-contained chapters show how computational procedures are developed and applied to central topics in bioinformatics and genomics,

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such as the genetic basis of disease, genome evolution or the tree of life concept. Using bioinformatic resources requires a basic understanding of what bioinformatics is and what it can do. Rather than just presenting tools, the authors - each a leading scientist - engage the

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students' problem-solving skills, preparing them to meet the computational challenges of their life science careers.

The advanced AI techniques are essential for resolving various problematic aspects emerging in the field of bioinformatics. This book

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covers the recent approaches in artificial intelligence and machine learning methods and their applications in Genome and Gene editing, cancer drug discovery classification, and the protein folding algorithms among others. Deep learning, which is widely used in

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image processing, is also applicable in bioinformatics as one of the most popular artificial intelligence approaches. The wide range of applications discussed in this book are an indispensable resource for computer scientists, engineers, biologists, mathematicians, physicians,

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and medical informaticists. Features:
Focusses on the cross-disciplinary relation between computer science and biology and the role of machine learning methods in resolving complex problems in bioinformatics
Provides a comprehensive and balanced blend of topics and

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applications using various advanced algorithms Presents cutting-edge research methodologies in the area of AI methods when applied to bioinformatics and innovative solutions Discusses the AI/ML techniques, their use, and their potential for use in common and

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future bioinformatics applications

Includes recent achievements in AI and bioinformatics contributed by a global team of researchers

Understanding Bioinformatics

Learning Algorithms Through

Programming and Puzzle Solving

Exploring Bioinformatics

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Introduction to Covariate Shift

Adaptation

Multiobjective Genetic Algorithms for Clustering

Introduction to Machine Learning and Bioinformatics

Introduces machine learning and its algorithmic paradigms,

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***explaining the principles
behind automated learning
approaches and the
considerations underlying
their usage.***

***Probabilistic models are
becoming increasingly***

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important in analysing the huge amount of data being produced by large-scale DNA-sequencing efforts such as the Human Genome Project. For example, hidden Markov models are used for analysing

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biological sequences, linguistic-grammar-based probabilistic models for identifying RNA secondary structure, and probabilistic evolutionary models for inferring phylogenies of sequences from

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different organisms. This book gives a unified, up-to-date and self-contained account, with a Bayesian slant, of such methods, and more generally to probabilistic methods of sequence analysis. Written by

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an interdisciplinary team of authors, it aims to be accessible to molecular biologists, computer scientists, and mathematicians with no formal knowledge of the other fields, and at the

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same time present the state-of-the-art in this new and highly important field.

An unprecedented wealth of data is being generated by genome sequencing projects and other experimental efforts

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to determine the structure and function of biological molecules. The demands and opportunities for interpreting these data are expanding more than ever. Biotechnology, pharmacology,

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and medicine will be particularly affected by the new results and the increased understanding of life at the molecular level. Bioinformatics is the development and application of computer

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***methods for analysis,
interpretation, and prediction,
as well as for the design of
experiments. It has emerged
as a strategic frontier between
biology and computer science.
Machine learning approaches***

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(e.g., neural networks, hidden Markov models, and belief networks) are ideally suited for areas where there is a lot of data but little theory—and this is exactly the situation in molecular biology. As with its

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predecessor, statistical model fitting, the goal in machine learning is to extract useful information from a body of data by building good probabilistic models. The particular twist behind

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machine learning, however, is to automate the process as much as possible. In this book, Pierre Baldi and Soren Brunak present the key machine learning approaches and apply them to the computational

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problems encountered in the analysis of biological data. The book is aimed at two types of researchers and students. First are the biologists and biochemists who need to understand new data-driven

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algorithms, such as neural networks and hidden Markov models, in the context of biological sequences and their molecular structure and function. Second are those with a primary background in

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***physics, mathematics,
statistics, or computer science
who need to know more about
specific applications in
molecular biology.
Technology is moving at an
exponential pace in this era of***

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computational intelligence. Machine learning has emerged as one of the most promising tools used to challenge and think beyond current limitations. This handbook will provide readers with a leading

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edge to improving their products and processes through optimal and smarter machine learning techniques. This handbook focuses on new machine learning developments that can lead to

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newly developed applications. It uses a predictive and futuristic approach, which makes machine learning a promising tool for processes and sustainable solutions. It also promotes newer

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algorithms that are more efficient and reliable for new dimensions in discovering other applications, and then goes on to discuss the potential in making better use of machines in order to ensure

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***optimal prediction, execution,
and decision-making.***

***Individuals looking for
machine learning-based
knowledge will find interest in
this handbook. The readership
ranges from undergraduate***

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**students of engineering and
allied courses to researchers,
professionals, and application
designers.**

**Analysis of Algorithms
A Practical Introduction
Pattern Discovery in**

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Bioinformatics

Encyclopedia of Algorithms

Theory, algorithms, and applications of machine learning techniques to overcome “covariate shift” non-stationarity. As the power of computing has grown over the past few decades, the field of machine learning has

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advanced rapidly in both theory and practice. Machine learning methods are usually based on the assumption that the data generation mechanism does not change over time. Yet real-world applications of machine learning, including image recognition, natural language processing, speech

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recognition, robot control, and bioinformatics, often violate this common assumption. Dealing with non-stationarity is one of modern machine learning's greatest challenges. This book focuses on a specific non-stationary environment known as covariate shift, in which the distributions

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of inputs (queries) change but the conditional distribution of outputs (answers) is unchanged, and presents machine learning theory, algorithms, and applications to overcome this variety of non-stationarity. After reviewing the state-of-the-art research in the field, the authors discuss topics

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that include learning under covariate shift, model selection, importance estimation, and active learning. They describe such real world applications of covariate shift adaption as brain-computer interface, speaker identification, and age prediction from facial images. With this book, they aim

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to encourage future research in machine learning, statistics, and engineering that strives to create truly autonomous learning machines able to learn under non-stationarity.

A comprehensive review of an area of machine learning that deals with the use of unlabeled data in classification

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problems: state-of-the-art algorithms, a taxonomy of the field, applications, benchmark experiments, and directions for future research. In the field of machine learning, semi-supervised learning (SSL) occupies the middle ground, between supervised learning (in which all training examples are

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labeled) and unsupervised learning (in which no label data are given). Interest in SSL has increased in recent years, particularly because of application domains in which unlabeled data are plentiful, such as images, text, and bioinformatics. This first comprehensive overview of SSL presents state-of-the-

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art algorithms, a taxonomy of the field, selected applications, benchmark experiments, and perspectives on ongoing and future research. Semi-Supervised Learning first presents the key assumptions and ideas underlying the field: smoothness, cluster or low-density separation, manifold structure,

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and transduction. The core of the book is the presentation of SSL methods, organized according to algorithmic strategies. After an examination of generative models, the book describes algorithms that implement the low-density separation assumption, graph-based methods, and algorithms that

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perform two-step learning. The book then discusses SSL applications and offers guidelines for SSL practitioners by analyzing the results of extensive benchmark experiments. Finally, the book looks at interesting directions for SSL research. The book closes with a discussion of the relationship between

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semi-supervised learning and
transduction.