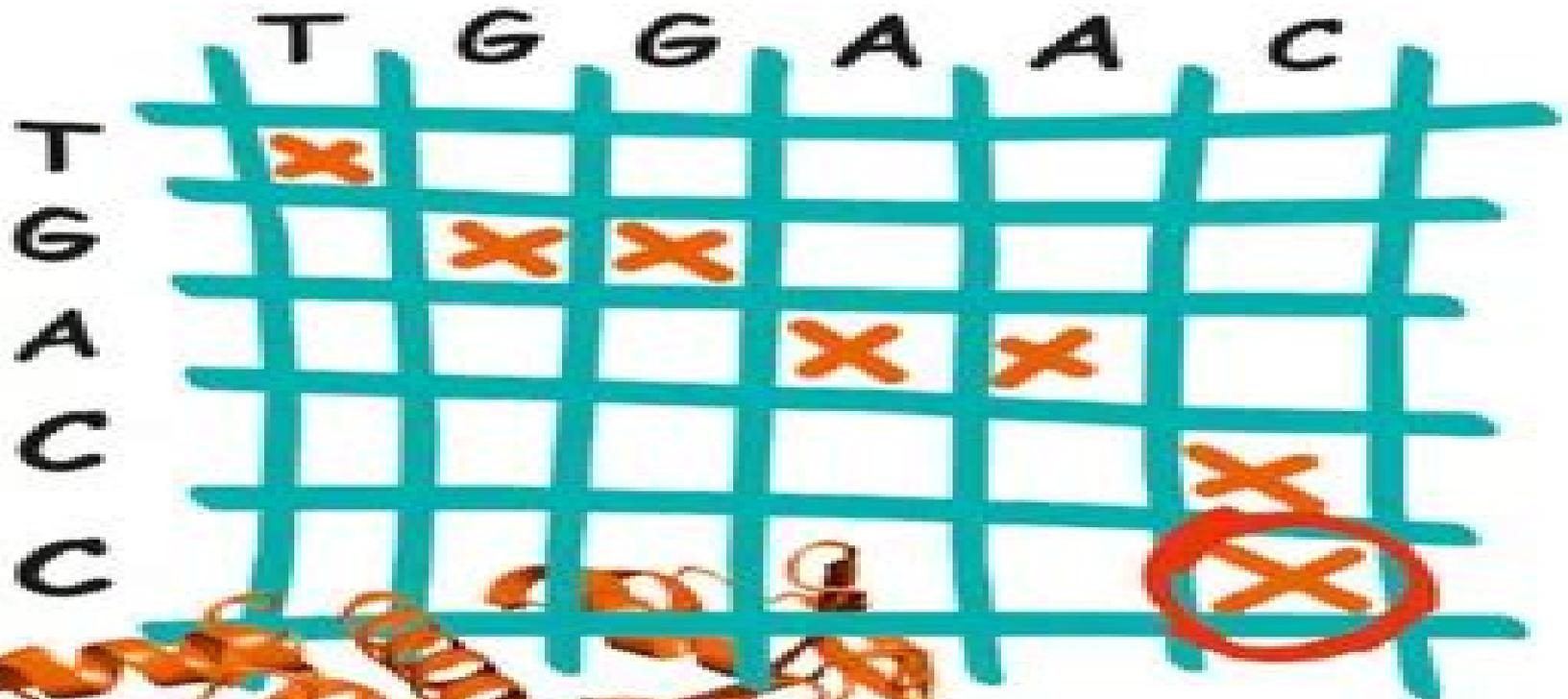


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Grundlagen, Algorithmen, Anwendungen

Rainer Merkl und Stephan Waack

2., erweiterte und neubearbeitete Auflage



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**Ute Schmid, Franziska Klügl, Diedrich
Wolter**



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KI 2003: Advances in Artificial Intelligence Andreas Günter, Rudolf Kruse, Bernd Neumann, 2003-09-09 This book constitutes the refereed proceedings of the 26th Annual German Conference on Artificial Intelligence KI 2003 held in Hamburg Germany in September 2003 The 42 revised full papers presented together with 5 invited papers were carefully reviewed and selected from 90 submissions from 22 countries The papers are organized in topical sections on logics and ontologies cognitive modeling reasoning methods machine learning neural networks reasoning under uncertainty planning and constraints spatial modeling user modeling and agent technology

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KI 2020: Advances in Artificial Intelligence Ute Schmid, Franziska Klügl, Diedrich Wolter, 2020-09-08 This book constitutes the refereed proceedings of the 43rd German Conference on Artificial Intelligence KI 2020 held in Bamberg Germany in September 2020 The 16 full and 12 short papers presented together with 6 extended abstracts in this volume were carefully reviewed and selected from 62 submissions As well established annual conference series KI is dedicated to research on theory and applications across all methods and topic areas of AI research KI 2020 had a special focus on human centered AI with highlights on AI and education and explainable machine learning Due to the Corona pandemic KI 2020 was held as a virtual event

Programmieren für Ingenieure und Naturwissenschaftler Sebastian Dörn, 2018-01-15 Ziel des Buches ist es Ingenieuren oder Naturwissenschaftlern die Programmierung als Schlüsselqualifikation mit zahlreichen Anwendungsmöglichkeiten vorzustellen Der Autor erläutert algorithmische Methoden die heute hinter digitalen Produkten und Dienstleistungen stehen Zentrale Anwendungen sind die Künstliche Intelligenz das Data Mining die Predictive Analytics die Industrie 4.0 oder das Internet der Dinge Die digitale Datenanalyse mit den zugehörigen Algorithmen ist die zentrale Grundlage vieler neuer IT-Technologien Hierzu werden große Datenmengen verschiedenster Anwendungsfelder verarbeitet und auf gewisse Muster analysiert um die relevanten Informationen zu extrahieren Diese sogenannten intelligenten Verfahren sind die Basis für nahezu alle Innovationen in unserer digitalisierten Welt Mit Hilfe dieser Art der Informationsverarbeitung werden durch die Kombination von mathematischen Modellen und algorithmischen Verfahren neue digitale Geschäftsmodelle erschaffen

Molekularbiologie Alexander McLennan, Andy Bates, Phil Turner, Mike White, 2013 Molekularbiologie ist das maßgeschneiderte Kurzlehrbuch für 14er Studenten die auf der Suche nach einer knappen Einführung in dieses grundlegende Fachgebiet sind und die sich optimal für 14er eine entsprechende Prüfung vorbereiten wollen

auch dank der 14 über 70 Fragen und Antworten **Datenschutzrechtliche Fragen des Personenbezugs** Martin Sebastian Haase, 2015-10-27 Das Merkmal personenbezogene Daten stellt europaweit eines der wichtigsten Eingangstore für den Anwendungsbereich des Datenschutzrechts dar. Zugleich ist die Auslegung der gesetzlichen Voraussetzungen des Personenbezugs stark umstritten. Nach wie vor besteht ein hoher Entwicklungs- und Konkretisierungsbedarf. Aufbauend auf einer breiten Diskussion der bisherigen Ansätze gibt Martin Sebastian Haase neue Impulse für die Auslegung und Umschreibung des sachlichen Anwendungsbereiches des Datenschutzrechts. Er behandelt unter anderem typische Individualisierungsmerkmale der natürlichen Person, die Beurteilung von aggregierten und anonymisierten Daten, die Abgrenzung von personenbezogenen Daten zu reinen Sachdaten, den Umgang mit spezifischen Informationskombinationen, die Zurechnung von Zusatzmitteln und Zusatzwissen im Rahmen der Bestimmbarkeit einer natürlichen Person und die Einordnung technischer Repräsentanten z. B. IP-Adresse. Durch die Einbeziehung gesellschaftlicher und technischer Aspekte entwirft der Autor eine geeignete Grundlage für einen interdisziplinären Diskurs. *Ideen der Informatik* Uwe Schöningh, 2009-12-16 Dieses Buch beschreibt einen neuen Weg. Inhalte der Informatik greift teils aus dem Bereich der Theoretischen Informatik wie sie meist nur an den Universitäten mit der ganzen dahinter steckenden Tiefe und Strukturtheorie gelehrt werden werden hier für ein breiteres Publikum aufbereitet und verfügbar gemacht. Der Autor verdeutlicht, dass der Zugang zur Informatik über die formale Methode, die Grundideen und die Algorithmik viel Spaß machen kann. Effiziente praxisrelevante Lösungssansätze stehen im Vordergrund. Was Verständlichkeit und Anwendbarkeit der Ideen fördert. Durch die Vielzahl der behandelten Modelle und Konzepte wird der große Zusammenhang deutlich gemacht. Ein umfangreiches, weiterführendes Literaturverzeichnis runden die leicht lesbare und trotzdem korrekte und umfassende Darstellung ab. *Bioinformatik Interaktiv* Rainer Merkl, Stephan Waack, 2009-12-14 Die zweite Auflage dieses erfolgreichen Lehrbuchs ist vollständig bearbeitet und in großen Teilen erweitert. Insbesondere wurde die Behandlung der Genomdatenanalyse deutlich vertieft und es wurden Kapitel über maschinelles Lernen, bayessche Netzwerke sowie Protein- und Enzymdesigns und über die Auswertung von Microarrays eingefügt. Außerdem steht dem Leser jetzt eine attraktive Webseite mit Zusatzmaterial und Fragen zum Stoff zur Verfügung. Webseite mit Zusatzmaterial und Fragen WWW: WILEY-VCH/DE/HOME/BIOINFORMATIK **The British National Bibliography** Arthur James Wells, 2009 **Bioinformatik Interaktiv** Rainer Merkl, Stephan Waack, 2003-08-08 Dieses Buch bietet eine Einführung in die wichtigsten Algorithmen der Bioinformatik. Schwerpunkte sind die Methoden des Sequenzvergleichs und Verfahren zur Charakterisierung von Proteinfamilien, insbesondere Hidden Markov Modelle. Daneben werden Algorithmen zur Vorhersage der Proteinraum-Proteinsekundär- und RNA-Sekundärstruktur vorgestellt. Der Text ist in sich geschlossen, er vermittelt die für das Verständnis erforderlichen statistischen und biologischen Grundlagen sowie eine Einführung in Genetische Algorithmen und Neuronale Netze. Besonderer Wert wird auf die Vertiefung und Festigung der Kenntnisse durch praktische Übungen gelegt. Auf der Begleit-

CD sind interaktive und internetbasierte Lektionen vorbereitet deren Bearbeitung das Verständnis der relevanten Algorithmen wesentlich erleichtert Sie führen in die Verwendung der wichtigsten Methoden ein und fördern die kritische Bewertung und Analyse der Verfahren und Ergebnisse Zusätzlich können DNA und Proteinraumstrukturen interaktiv untersucht werden Der Text ist geeignet für alle die sich einen Einblick in die gängigen Bioinformatik Methoden verschaffen wollen Studenten der Biologie oder Informatik und diejenigen die bereits bioinformatische Werkzeuge nutzen und daran interessiert sind die zugrundeliegenden Konzepte zu verstehen Durch die hervorragend auf das Textbuch abgestimmten Ergänzungen auf der beiliegenden CD werden dem Leser zusätzlich Erfahrungen bezüglich der Aussagekraft dieser Methoden vermittelt Dadurch ist dieses Buch auf dem besten Weg ein Studienbegleiter für alle Einsteiger in die Welt der Genomforschung und Informatik zu werden Chemie in unserer Zeit Würzburg Heute, 2001 *Books in Print Supplement*, 2002 **Books In Print 2004-2005** Ed Bowker Staff, Staff Bowker, Ed, 2004 **Abhandlungen der**

Braunschweigischen Wissenschaftlichen Gesellschaft Braunschweigische Wissenschaftliche Gesellschaft, 2007 Deutsche Nationalbibliographie und Bibliographie der im Ausland erschienenen deutschsprachigen Veröffentlichungen, 2005 Bioinformatics Thomas Dandekar, Meik Kunz, 2023-03-02 This book offers a gripping introduction to the fastest growing field of biology with easy to follow examples and a well prepared appendix for the reader to cook up and experience everything right away The book gets the reader started with the basics such as how to easily find sequence information and then analyze it In further chapters the authors go into the various analysis options from RNA DNA and proteins to entire metabolic pathways Exciting examples from biology are chosen in each chapter to illustrate the analysis Each chapter concludes with an exercise section that immediately puts what has been learned to use The subject of this book is a must for any biology student whether undergraduate or graduate as bioinformatics is now unearthing amazing insights into the molecular basis of all living things Computer science students and other students from related sciences will get a good introduction to bioinformatics as biology and current topics e.g AI are systematically introduced step by step alongside the software Discover the key to life together with the authors and learn to understand the language of life This book is a translation of the original German 2nd edition Bioinformatik by Thomas Dandekar and Meik Kunz published by Springer Verlag GmbH Germany part of Springer Nature in 2021 The translation was done with the help of artificial intelligence machine translation by the service DeepL.com A subsequent human revision was done primarily in terms of content so that the book will read stylistically differently from a conventional translation Springer Nature works continuously to further the development of tools for the production of books and on the related technologies to support the authors **Kürschners deutscher Gelehrten-Kalender**, 2009 Each volume includes Wissenschaftliche Zeitschriften *Nachrichten aus der Chemie*, 2003 *Bioinformatik* Rainer Merkl, 2022-08-15 Bioinformatik Der Marktführer bei den Bioinformatiklehrbüchern in neuer Auflage und mit dem neuen Thema Molekulardynamik Bioinformatik ist eine Kerndisziplin in den modernen

Biowissenschaften von der Biotechnologie über die Biochemie und Molekularbiologie bis zur Molekulargenetik und Molekularmedizin. Sie ist eine essenzielle Grundlage für alle omics-Technologien für die Strukturbiologie, die Systembiologie sowie die synthetische Biologie. Bioinformatik Grundlagen, Algorithmen, Anwendungen bietet eine umfassende Einführung in die wichtigsten Methoden der Bioinformatik. Der Autor erklärt dabei sowohl die mathematischen und biologischen Grundlagen als auch die wichtigsten Software-Tools und deren Anwendungsbereiche. Schwerpunkte sind Methoden zum Sequenzvergleich, Verfahren zur Charakterisierung von Proteinfamilien, Algorithmen zur Vorhersage von Protein- und RNA-Strukturen, Methoden des maschinellen Lernens und das Proteindesign. Für die 4. Auflage wurde der Text durchgehend aktualisiert und um ein Kapitel zur Molekulardynamik erweitert. Neu aufgenommene Exkurse zu Meilensteinen der Bioinformatik und aktuellen Anwendungsgebieten lockern den Text auf. Auf der ebenfalls komplett bearbeiteten Begleit-Webseite werden interaktive Lernmodule bereitgestellt, einschließlich mehr als 120 Übungsaufgaben, zum Teil mit Lösungen. Eine perfekte Einführung für alle Studenten der Lebenswissenschaften oder Informatik, die einen Einblick in die gängigen Methoden der Bioinformatik benötigen sowie ein wertvoller Begleiter für alle, die bereits bioinformatische Werkzeuge nutzen und die zugrundeliegenden Konzepte verstehen möchten.

Bioinformatics: From Nucleic Acids and Proteins to Cell Metabolism Dietmar Schomburg, Uta Lessel, 2008-09-26

Bioinformatics in this context, the application of computer science to biological problems has become an indispensable part of any research in the biosciences. Rapid developments in gene sequencing, structure determination as well as rational protein engineering and design have made it necessary for biologists, chemists and computer scientists to channel their expertise into large-scale collaborative projects. This GBF Monograph gives a general overview of the latest versatile activities in bioinformatics: Biological Data Bases, DNA and RNA, Protein Sequences and Structures, From Molecules to Cell Metabolism. The articles have been selected from contributions to a conference on Bioinformatics Computer Application in the Biosciences held in October 1995 in Braunschweig at the German National Research Center for Biotechnology.

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