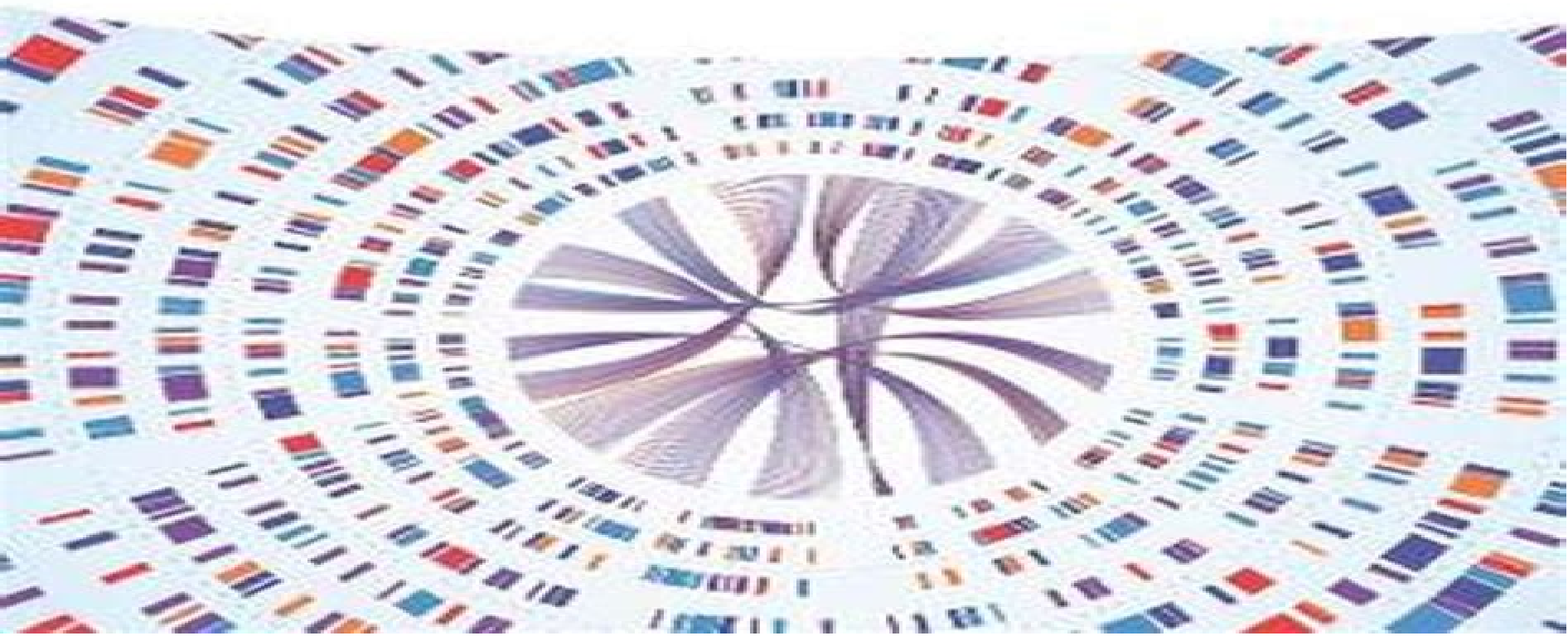


Rainer Merkl

Bioinformatik

Grundlagen, Algorithmen, Anwendungen

Vierte Auflage



Bioinformatik Algorithmen Anwendungen Rainer Merkl

Rosina Ehmann



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Bioinformatik Rainer Merkl, 2022-08-15 Bioinformatik Der Markt f hrt bei den Bioinformatiklehrb chern in neuer Auflage und mit dem neuen Thema Molekulardynamik Bioinformatik ist eine Kerndisziplin in den modernen Biowissenschaften von der Biotechnologie ber die Biochemie und Molekularbiologie bis zur Molekulargenetik und Molekularmedizin Sie ist eine essenzielle Grundlage f r alle omics Technologien f r die Strukturbioogie die Systembiologie sowie die synthetische Biologie Bioinformatik Grundlagen Algorithmen Anwendungen bietet eine umfassende Einf hrung in die wichtigsten Methoden der Bioinformatik Der Autor erkl rt 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 F r 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 einschlie lich mehr als 120 bungsaufgaben zum Teil mit L sungen Eine perfekte Einf hrung f r alle Studenten der Lebenswissenschaften oder Informatik die einen Einblick in die g ngigen Methoden der Bioinformatik ben tigen sowie ein wertvoller Begleiter f r alle die bereits bioinformatische Werkzeuge nutzen und die zugrundeliegenden Konzepte verstehen m chten

Bioinformatik Interaktiv Rainer Merkl, Stephan Waack, 2013-12-09 The second edition of this successful textbook completely revised and largely expanded In particular the section on the analysis of genome data is covered in much greater depth and chapters added on machine learning Bayesian networks protein and enzyme designs as well as the evaluation of microarrays Furthermore an attractive website with supplementary material and problems is available WWW WILEY VCH DE HOME BIOINFORMATIK

Strukturen im Sprachraum Alfred Lameli, 2013-10-14 Die Strukturierung des Sprachraums ist ein zentraler Gegenstand der Variationsforschung dessen Komplexit t bis heute nicht vollst ndig erfasst ist Ausgangspunkt des Buches ist die Erstellung eines datenbasierten regionalsprachlichen Modells der historischen Dialekte in Deutschland das aus verschiedenen Perspektiven ausgewertet und erweitert wird Auf diese Weise gelingt eine neue Sicht auf die raumstrukturellen Bedingungen der Dialekte v a im 19 Jahrhundert Eine Besonderheit stellt der Einsatz von Methoden aus Bioinformatik und Geostatistik dar die in der Regionalsprachenforschung weithin unber cksichtigt geblieben sind Im Ergebnis tr gt das Vorgehen zum Verst ndnis zahlreicher sprachgeographischer und sprachhistorischer Ph nomene bei etwa mit Blick auf den Ausgleich der Dialekte oder die Genese der deutschen Schriftsprache Zudem werden neue Kriterien zur intersubjektiven Definition der Dialektlandschaft geliefert die in ihrer Verkn pfung mit au ersprachlichen Daten einen Br ckenschlag zu kulturwissenschaftlichen Themenfeldern leisten Die Studie begr ndet darauf aufbauend neue Forschungsans tze zur Erkl rung r umlicher Handlungsmuster in Vergangenheit und

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Patentverletzungen in der Biotechnologie Isumo Bergmann, 2011-06-03 Isumo Bergmann entwickelt semantische Patentanalysen die die Ähnlichkeiten zwischen Patenten aufdecken sollen. Er gestaltet den Patentrecherche- und Analyseprozess für biotechnologische Fragestellungen neu und wertet ausgewählte Patentverletzungsfälle in der Biotechnologie aus.

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.

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 hervorragende auf das Textbuch abgestimmten Übungen 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.

Einführung in die Bioinformatik Rainer Merkl, 2003

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b 6.10
c 18.10
d 9.10
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