1.	Record Nr.	UNINA9910484339903321
	Autore	Hermanni Alfred-Joachim
	Titolo	Business Guide für strategisches Management : 50 Tools zum geschäftlichen Erfolg / / von Alfred-Joachim Hermanni
	Pubbl/distr/stampa	Wiesbaden : , : Springer Fachmedien Wiesbaden : , : Imprint : Springer Gabler, , 2016
	ISBN	3-658-12521-7
	Edizione	[1st ed. 2016.]
	Descrizione fisica	1 online resource (IX, 345 S. 5 Abb.)
	Disciplina	658.4092
	Soggetti	Leadership Success in business Careers Business Strategy/Leadership Careers in Business and Management
	Lingua di pubblicazione	Tedesco
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di bibliografia	Includes bibliographical references and index.
	Nota di contenuto	Alleinstellungsmerkmal -- Allianzen -- Best Practice-Lösungen -- Business Modelling -- Business Networks -- Businessplan -- Change Management -- Controlling -- Demut -- Digitalisierung -- Empathie -- Eventmarketing -- Finanzierung -- Finanzplanung -- Führung -- Geschäftsidee -- Gesundheitsmanagement -- Innovation -- Internet -- Kontinuität -- Kreativität -- Kunden -- Managementinstrumente -- Marke -- Marketing -- Nachhaltigkeit -- Preisfindung -- Public Relations -- Querdenken -- Redekunst -- Ressourcen -- Scheitern -- Social Media -- Soziales Gewissen -- Storytelling -- Strategie -- Suchmaschinen -- Teamwork -- Unternehmenskultur.- Verhandlungsstrategie -- Verkaufen -- Vernetzung -- Wissensmanagement -- Werbung -- Wettbewerb -- Zeitgeist -- Zeitmanagement -- Zielgruppe.
	Sommario/riassunto	Dieses Buch folgt dem Credo „Don´t work hard – work smart". Smart im Sinne von Cleverness, systematischer Organisation von Arbeit und Zeit sowie Weitsichtigkeit zur Erschließung geschäftlicher Perspektiven. In 50 Kapiteln werden Erfolgsfaktoren, Methoden und Strategien vorgestellt, die helfen Marktpositionen zu stärken und Strategien neu

auszurichten. Das Buch richtet sich an Manager, Führungskräfte und Selbstständige, die ihre wertvollsten Ressourcen nachhaltig und bewusst einsetzen wollen , um Produkte und Dienstleistungen zu entwickeln, die die Kunden auch wirklich wollen. Tipps am Ende der Kapitel ermöglichen die direkte Umsetzung in die Praxis. Über 100 nationale und internationale Fallbeispiele liefern zudem einen hohen Nutzwert. Der Autor So umfassend und abwechslungsreich wie das Buch ist auch der Autor, Prof. Dr. Alfred-Joachim Hermanni. In seinem Lebenslauf finden sich Stationen als Chefredakteur, Geschäftsführer, PR-Manager, Medienpolitiker, Unternehmensberater, Filmproduzent und Buchautor. Seit 2014 ist er zudem ordentlicher Professor für Medienentwicklung und –management an der SRH Fernhochschule Riedlingen.

2.	Record Nr.	UNINA9910143894203321
	Titolo	Algorithms in Bioinformatics : Second International Workshop, WABI 2002, Rome, Italy, September 17-21, 2002, Proceedings / / edited by Roderic Guigo, Dan Gusfield
	Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2002
	ISBN	3-540-45784-4
	Edizione	[1st ed. 2002.]
	Descrizione fisica	1 online resource (X, 554 p.)
	Collana	Lecture Notes in Computer Science, , 0302-9743 ; ; 2452
	Disciplina	572.80285
	Soggetti	Computer programming
		Biochemistry
		Algorithms
		Computers
		Data structures (Computer science)
		Numerical analysis
		Programming Techniques
		Biochemistry, general
		Algorithm Analysis and Problem Complexity
		Computation by Abstract Devices
		Data Structures
		Numeric Computing
	Lingua di pubblicazione	Inglese

Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	Simultaneous Relevant Feature Identification and Classification in High-Dimensional Spaces -- Pooled Genomic Indexing (PGI): Mathematical Analysis and Experiment Design -- Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem -- Methods for Inferring Block-Wise Ancestral History from Haploid Sequences -- Finding Signal Peptides in Human Protein Sequences Using Recurrent Neural Networks -- Generating Peptide Candidates from Amino-Acid Sequence Databases for Protein Identification via Mass Spectrometry -- Improved Approximation Algorithms for NMR Spectral Peak Assignment -- Efficient Methods for Inferring Tandem Duplication History -- Genome Rearrangement Phylogeny Using Weighbor -- Segment Match Refinement and Applications -- Extracting Common Motifs under the Levenshtein Measure: Theory and Experimentation -- Fast Algorithms for Finding Maximum-Density Segments of a Sequence with Applications to Bioinformatics -- FAUST: An Algorithm for Extracting Functionally Relevant Templates from Protein Structures -- Efficient Unbound Docking of Rigid Molecules -- A Method of Consolidating and Combining EST and mRNA Alignments to a Genome to Enumerate Supported Splice Variants -- A Method to Improve the Performance of Translation Start Site Detection and Its Application for Gene Finding -- Comparative Methods for Gene Structure Prediction in Homologous Sequences -- MultiProt — A Multiple Protein Structural Alignment Algorithm -- A Hybrid Scoring Function for Protein Multiple Alignment -- Functional Consequences in Metabolic Pathways from Phylogenetic Profiles -- Finding Founder Sequences from a Set of Recombinants -- Estimating the Deviation from a Molecular Clock -- Exploring the Set of All Minimal Sequences of Reversals — An Application to Test the Replication-Directed Reversal Hypothesis -- Approximating the Expected Number of Inversions Given the Number of Breakpoints -- Invited Lecture — Accelerating Smith-Waterman Searches -- Sequence-Length Requirements for Phylogenetic Methods -- Fast and Accurate Phylogeny Reconstruction Algorithms Based on the Minimum-Evolution Principle -- NeighborNet: An Agglomerative Method for the Construction of Planar Phylogenetic Networks -- On the Control of Hybridization Noise in DNA Sequencing-by-Hybridization -- Restricting SBH Ambiguity via Restriction Enzymes -- Invited Lecture — Molecule as Computation: Towards an Abstraction of Biomolecular Systems -- Fast Optimal Genome Tiling with Applications to Microarray Design and Homology Search -- Rapid Large-Scale Oligonucleotide Selection for Microarrays -- Border Length Minimization in DNA Array Design* -- The Enhanced Suffix Array and Its Applications to Genome Analysis -- The Algorithmic of Gene Teams -- Combinatorial Use of Short Probes for Differential Gene Expression Profiling -- Designing Specific Oligonucleotide Probes for the Entire S. cerevisiae Transcriptome -- K-ary Clustering with Optimal Leaf Ordering for Gene Expression Data -- Inversion Medians Outperform Breakpoint Medians in Phylogeny Reconstruction from Gene-Order Data -- Modified Mincut Supertrees.
Sommario/riassunto	We are pleased to present the proceedings of the Second Workshop on Al- rithms in Bioinformatics (WABI 2002), which took place on September 17-21, 2002 in Rome, Italy. The WABI workshop was part of a three-conference me- ing, which, in addition to WABI, included the

ESA and APPROX 2002. The three conferences are jointly called ALGO 2002, and were hosted by the F- ulty of Engineering, University of Rome "La Sapienza". Seehttp://www.dis. uniroma1.it/~algo02 for more details. The Workshop on Algorithms in Bioinformatics covers research in all areas of algorithmic work in bioinformatics and computational biology. The emphasis is on discrete algorithms that address important problems in molecular biology, genomics,andgenetics, thatarefoundedonsoundmodels,thatarecomputati- ally e?cient, and that have been implemented and tested in simulations and on real datasets. The goal is to present recent research results, including signi?cant work in progress, and to identify and explore directions of future research. Original research papers (including signi?cant work in progress) or sta- of-the-art surveys were solicited on all aspects of algorithms in bioinformatics, including, but not limited to: exact and approximate algorithms for genomics, genetics, sequence analysis, gene and signal recognition, alignment, molecular evolution, phylogenetics, structure determination or prediction, gene expression and gene networks, proteomics, functional genomics, and drug design.