1.

Record Nr.	UNINA9910140740003321
Autore	Israelsen Craig L
Titolo	7 twelve [[electronic resource]] : a diversified investment portfolio with a plan / / Craig L. Israelsen
Pubbl/distr/stampa	Hoboken, N.J., : Wiley, c2010
ISBN	0-470-64987-9 1-119-20018-0 1-282-70786-8 9786612707865 0-470-64985-2
Descrizione fisica	1 online resource (227 p.)
Disciplina	332.6
Soggetti	Portfolio management Investments Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Includes index.
Nota di contenuto	7Twelve: A Diversified Investment Portfolio with a Plan; CONTENTS; FOREWORD; PREFACE; ACKNOWLEDGMENTS; CHAPTER 1: A RECIPE FOR SUCCESS; CHAPTER 2: LINING UP THE INGREDIENTS; CHAPTER 3: THE MORE INGREDIENTS, THE BETTER; CHAPTER 4: GROWTH OF MONEY; CHAPTER 5: COMBINING INGREDIENTS THAT ZIG ZAG; CHAPTER 6: STIRRING THE MIX; CHAPTER 7: ADJUSTING THE SECRET SAUCE; CHAPTER 8: HOW LONG WILL MY NEST EGG LAST?; CHAPTER 9: SHOULD I TILT TOWARD VALUE OR GROWTH?; CHAPTER 10: SHOULD I JUMP IN OR LET THE POT SIMMER?; CHAPTER 11: A BETTER 401(K); CHAPTER 12: THE PROBLEM OF UNDERSAVING CHAPTER 13: OF STOCKS, BONDS, AND RISKCHAPTER 14: ASSEMBLING YOUR PORTFOLIO; CHAPTER 15: 3 SECRETS + 4 PRINCIPLES = 7TWELVE PERFECTION; ABOUT THE AUTHOR; INDEX
Sommario/riassunto	A proven way to put together a portfolio that enhances performance and reduces risk Professor Craig Israelsen of Brigham Young University is an important voice in the area of asset allocation. The reason? He keeps things simple. Now, in 7Twelve, he shows you how to do the

	same, and demonstrates how his approach to investing can help you grow your money as well as protect it. 7Twelve outlines a multi-asset balanced portfolio that is a logical starting point when assembling a portfolio-either as the blueprint for the entire portfolio or as a significant building block. P

2.

Record Nr.	UNICAMPANIAVAN0006172
Autore	Crisafulli, Vezio
Titolo	2.1: L'ordinamento costituzionale italiano : le fonti normative / Vezio Crisafulli
Pubbl/distr/stampa	Padova, : CEDAM, 1993
ISBN	88-13-17842-5
Edizione	[6. ed. aggiornata]
Descrizione fisica	XII, 247 p. ; 24 cm + 1 fasc. - Tit. del fasc.: Appendice di aggiornamento, a cura di Francesco Crisafulli.
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia

3. Record Nr.	UNINA9910484023403321
Titolo	Algorithms in Bioinformatics : 10th International Workshop, WABI 2010, Liverpool, UK, September 6-8, 2010, Proceedings / / edited by Vincent Moulton, Mona Singh
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	1-280-38845-5 9786613566379 3-642-15294-5
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (XII, 376 p. 94 illus.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 6293
Classificazione	570
Altri autori (Persone)	MoultonVincent SinghMona
Disciplina	570.285
Soggetti	Life sciences Algorithms Computer science Artificial intelligence Database management Bioinformatics Life Sciences Theory of Computation Artificial Intelligence Database Management Computational and Systems Biology
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	International conference proceedings.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Biomolecular Structure: RNA, Protein and Molecular Comparison -- A Worst-Case and Practical Speedup for the RNA Co-folding Problem Using the Four-Russians Idea -- Sparse Estimation for Structural Variability -- Data Structures for Accelerating Tanimoto Queries on Real Valued Vectors -- Sparsification of RNA Structure Prediction Including Pseudoknots -- Prediction of RNA Secondary Structure Including Kissing Hairpin Motifs -- Reducing the Worst Case Running

	Times of a Family of RNA and CFG Problems, Using Valiant’s Approach -- Comparative Genomics -- Reconstruction of Ancestral Genome Subject to Whole Genome Duplication, Speciation, Rearrangement and Loss -- Genomic Distance with DCJ and Indels -- Listing All Sorting Reversals in Quadratic Time -- Haplotype and Genotype Analysis -- Discovering Kinship through Small Subsets -- Fixed-Parameter Algorithm for Haplotype Inferences on General Pedigrees with Small Number of Sites -- Haplotypes versus Genotypes on Pedigrees -- Haplotype Inference on Pedigrees with Recombinations and Mutations -- High-throughput Data Analysis: Next Generation Sequencing and Flow Cytometry -- Identifying Rare Cell Populations in Comparative Flow Cytometry -- Fast Mapping and Precise Alignment of AB SOLiD Color Reads to Reference DNA -- Design of an Efficient Out-of-Core Read Alignment Algorithm -- Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data -- Networks -- Improved Orientations of Physical Networks -- Enumerating Chemical Organisations in Consistent Metabolic Networks: Complexity and Algorithms -- Efficient Subgraph Frequency Estimation with G-Tries -- Phylogenetics -- Accuracy Guarantees for Phylogeny Reconstruction Algorithms Based on Balanced Minimum Evolution -- The Complexity of Inferring a Minimally Resolved Phylogenetic Supertree.-Reducing Multi-state to Binary Perfect Phylogeny with Applications to Missing, Removable, Inserted, and Deleted Data -- An Experimental Study of Quartets MaxCut and Other Supertree Methods -- An Efficient Method for DNA-Based Species Assignment via Gene Tree and Species Tree Reconciliation -- Sequences, Strings and Motifs -- Effective Algorithms for Fusion Gene Detection -- Swiftly Computing Center Strings -- Speeding Up Exact Motif Discovery by Bounding the Expected Clump Size -- Pair HMM Based Gap Statistics for Re-evaluation of Indels in Alignments with Affine Gap Penalties -- Quantifying the Strength of Natural Selection of a Motif Sequence.
Sommario/riassunto	We are pleased to present the proceedings of the 10th Workshop on Algorithms in Bioinformatics (WABI 2010) which took place in Liverpool, UK, Sept- ber 6-8, 2010. The WABI 2010 workshop was part of the four ALGO 2010 conference meetings, which, in addition to WABI, included ESA, ATMOS, and WAOA. WABI 2010 was hosted by the University of Liverpool Department of Computer Science, and sponsored by the European Association for Theoretical Computer Science (EATCS) and the International Society for Computational Biology(ISCB). Seehttp: //algo2010.csc.liv.ac.uk/wabi/for more details. The Workshop in Algorithms in Bioinformatics highlights research in alrithmicworkforbioinformatics,computationalbiologyandsystemsbiology. The emphasis is mainly on discrete algorithms and machine-learning methods that address important problems in molecular biology, that are founded on sound models, that are computationally efficient, and that havebeen implemented and tested in simulations and on real datasets. The goal is to present recent research results, including significant work-in-progress,and to identify and explore dir- tions of future research.