

1. Record Nr.	UNISA996200343903316
Titolo	Research in Computational Molecular Biology [[electronic resource]] : 19th Annual International Conference, RECOMB 2015, Warsaw, Poland, April 12-15, 2015, Proceedings / / edited by Teresa M. Przytycka
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2015
ISBN	3-319-16706-5
Edizione	[1st ed. 2015.]
Descrizione fisica	1 online resource (XVII, 368 p. 110 illus., 98 illus. in color.)
Collana	Lecture Notes in Bioinformatics ; ; 9029
Disciplina	570.285
Soggetti	Bioinformatics Biomathematics Data mining Algorithms Computational Biology/Bioinformatics Mathematical and Computational Biology Data Mining and Knowledge Discovery Algorithm Analysis and Problem Complexity
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 and index.
Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Efficient Alignment Free Sequence Comparison with Bounded Mismatches -- 1 Introduction -- 2 Key Concepts and Properties -- 3 An Overview of Our Algorithm -- 4 Constructing Sk -- 4.1 Analysis -- 5 Processing Sk -- 5.1 Proof of Lemma 6 -- 6 Conclusions -- A Ordering of Pairs -- References -- DockStar: A Novel ILP Based Integrative Method for Structural Modelling of Multimolecular Protein Complexes (Extended Abstract) -- References -- CRISPR Detection from Short Reads Using Partial Overlap Graphs -- 1 Introduction -- 2 Methods -- 2.1 Algorithm Overview -- 2.2 Identifying Frequent k-Mers -- 2.3 Analysis of Frequent k-Mers: Basic Observation -- 2.4 Data Indexing -- 2.5 Partial Construction of Overlap Graph -- 2.6 k-Mer Clustering -- 2.7 Repeat Consensus Derivation -- 3 Results -- 3.1 Simulated Reads Data -- 3.2 Real Reads Data -- 4 Conclusions and Future Work -- References -- HapTree-X: An

Integrative Bayesian Framework for Haplotype Reconstruction from Transcriptome and Genome Sequencing Data -- References -- Read Clouds Uncover Variation in Complex Regions of the Human Genome -- 1 Background -- 2 Method -- 3 Results -- References -- Learning Microbial Interaction Networks from Metagenomic Count Data -- 1 Introduction -- 2 Materials and Methods -- 2.1 Preliminaries -- 2.2 The Model -- Model Learning. -- Model Initialization. -- Model Selection. -- 2.3 Synthetic Experiment -- 2.4 Artificial Community Experiment -- 2.5 In vitro Coplating Validation Experiments -- 3 Results -- 3.1 Synthetic Experiment -- 3.2 Artificial Community Experiment -- 4 Discussion -- References -- Immunoglobulin Classification Using the Colored Antibody Graph -- 1 Introduction -- 2 Methods -- 3 Results -- 4 Discussion -- References -- CIDANE: Comprehensive Isoform Discovery and Abundance Estimation -- References.

Diffusion Component Analysis: Unraveling Functional Topology in Biological Networks -- 1 Introduction -- 2 Methods -- 3 Results -- References -- Fragmentation Trees Reloaded -- 1 Introduction -- 2 Fragmentation Trees -- 3 Maximum a Posteriori Estimation -- 3.1 Prior Probability of the Tree -- 3.2 Likelihood of the Tree -- 3.3 Posterior Probability of the Tree -- 3.4 Hypothesis-Driven Recalibration. -- 4 Results -- 5 Conclusion -- References -- KGSrna: Efficient 3D Kinematics-Based Sampling for Nucleic Acids -- 1 Introduction -- 2 Methods -- 2.1 Construction of the Tree -- 2.2 Modeling the Conformational Flexibility of Pentameric Rings -- 2.3 Null Space Perturbations -- 2.4 Rebuild Perturbations -- 2.5 Experimental Design -- 3 Results and Discussion -- 3.1 Broad and Accurate Atomic-Scale Sampling of the Native Ensemble -- 3.2 Large Scale Deformations -- 3.3 KGSrna as an Alternative to NMA -- 4 Conclusion -- A Benchmark Set -- B Ensemble Backbone Torsional Distributions -- C Video Files -- References -- Locating a Tree in a Phylogenetic Network in Quadratic Time -- 1 Introduction -- 2 Concepts and Notions -- 3 How Many Reticulations in a Network? -- 4 A Quadratic-Time Algorithm for the TCP -- 5 Conclusion -- References -- Constructing Structure Ensembles of Intrinsically Disordered Proteins from Chemical Shift Data -- 1 Introduction -- 2 Methods -- 2.1 Overview -- 2.2 Constructing the Initial Structure Pool -- 2.3 Selecting Representative Structures from the Initial Pool -- 2.4 Obtaining the Chemical Shifts of Backbone Atoms -- 2.5 Calculating the Corresponding Weights of the Selected Structures -- 2.6 Implementation -- 3 Results -- 3.1 Validation through A Reference Ensemble Approach -- 3.2 Tests on Real Data -- 3.3 Case Study -- 4 Conclusions -- References.

Comets (Constrained Optimization of Multistate Energies by Tree Search): A Provable and Efficient Algorithm to Optimize Binding Affinity and Specificity with Respect to Sequence -- 1 Introduction -- 2 Methods -- 2.1 Problem Formulation -- 2.2 A\* Over Sequences -- 2.3 Starting and Finishing the Calculation -- 3 Results -- 3.1 Measurement of Efficiency -- 3.2 Differences in Sequences Returned by Multistate Designs and Single-state Proxies -- 4 Conclusions -- References -- Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure -- 1 Introduction -- 2 Results -- 2.1 Correcting for Population Structure in Multivariate Analysis -- 2.2 GAMMA Corrects for Population Structure and Accurately Identifies Genetic Variances in a Simulated Study -- 2.3 GAMMA Identifies Regulatory Hotspots Related to Regulatory Elements of a Yeast Dataset -- 2.4 GAMMA Identifies Variants that Associated with a Gut Microbiome -- 3 Discussion -- 4 Materials and Methods -- 4.1 Linear Mixed Models -- 4.2 Multiple-Phenotypes Analysis -- 4.3

Correcting for Population Structure -- 4.4 Implementation -- 4.5  
Simulated Dataset -- 4.6 Real Datasets -- References -- BWM\*: A Novel, Provable, Ensemble-Based Dynamic Programming Algorithm for Sparse Approximations of Computational Protein Design -- 1  
Introduction -- 1.1 Design with Sparse Energy Functions -- 2  
Background -- 2.1 Sparse Residue Interaction Graphs -- 2.2 Branch-Decomposition in Protein Design -- 3 Methods -- 3.1 Total Effective Search Space -- 3.2 Algorithm: Preprocessing and Enumeration -- 3.3 Sparse Error Bounds -- 4 Computational Experiments -- 4.1 Experimental Methods -- 4.2 Total Effective Search Space Predictions -- 4.3 Ensemble Enumeration Time -- 5 Conclusion -- References.  
An Efficient Nonlinear Regression Approach for Genome-Wide Detection of Marginal and Interacting Genetic Variations -- 1  
Introduction -- 2 Methods -- 2.1 Piecewise Linear Model-Based Group Lasso -- Randomization -- Stability Selection. -- 2.2 Piecewise Linear Model-Based Screening -- 2.3 System Implementation of Piecewise Linear Model-Based Screening -- 3 Simulation Study -- 3.1 Power to Detect True Casual SNPs and SNP Pairs Under False Positive Control -- 3.2 Scalability of Screening Implementation -- 4 Association Analysis of Late-Onset Alzheimer's Disease Data -- 4.1 Marginal Effects in Late-Onset Alzheimer's Disease Dataset -- 4.2 Interaction Effects in Late-Onset Alzheimer's Disease Dataset -- 5 Conclusions -- S1 Simulation Study -- S1.1 Generation of Simulation Data -- S1.2 Benefits of Using a Piecewise Linear Model for Screening -- S1.3 Comparison of Different Methods for the Detection of SNP Pairs with Interaction Effects -- Comparison with Different Minor Allele Frequencies. -- Comparison with Different Association Strengths. -- References -- Exploration of Designability of Proteins Using Graph Features of Contact Maps: Beyond Lattice Models -- 1 Introduction -- 2 Methods -- 2.1 Selection of Datasets -- 2.2 Calculating Designabilities of Structures Using Binary Energy Functions -- 2.3 Generation of Contact Graphs and Graph Features that Describe Them -- 2.4 Regression Analysis -- 2.5 Naive Bayes Prediction -- 3 Results and Discussion -- References -- CoMEt: A Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer -- 1 Introduction -- 2 Methods -- 3 Results -- References -- Deep Feature Selection: Theory and Application to Identify Enhancers and Promoters -- 1 Introduction -- 2 Method -- 2.1 Deep Feature Selection -- 2.2 Learning Model Parameter -- 2.3 Shallow DFS is not Equivalent to LASSO.  
3 Applying DFS to Enhancer-Promoter Classification -- 3.1 Data -- 3.2 Comparing Test Accuracy and Computing Time -- 3.3 Feature Analysis -- 4 Conclusion -- References -- Protein Contact Prediction by Integrating Joint Evolutionary Coupling Analysis and Supervised Learning -- References -- ScaffMatch: Scaffolding Algorithm Based on Maximum Weight Matching -- References -- A Symmetric Length-Aware Enrichment Test -- 1 Introduction -- 2 The Model -- 3 The Asymmetry Problem -- 4 Computing the p-Value of the Symmetric Test -- 5 Comparison of the Symmetric p-Value Approximation Schemes -- 6 Discussion -- 6.1 Normal Approximation - Exact Computation of the Conditional Moments -- 6.2 The Saddlepoint Approximation (Details) -- References -- Functional Alignment of Metabolic Networks -- 1 Introduction -- 2 Preliminaries -- 2.1 Metabolic Modeling -- 2.2 Problem Definition -- 3 The Alignment Algorithm -- 3.1 Similarity Computation -- 3.2 Alignment Computation -- 3.3 Media Selection and the Final Alignment -- 4 Results -- 4.1 Performance Evaluation -- 4.2 Aligning Similar Models -- 4.3 Aligning the Yeast and Human Models -- 5 Conclusions -- References -- Joint Inference of Genome Structure and Content in Heterogeneous Tumor Samples -- References -- Ultra-

Large Alignments Using Ensembles of Hidden Markov Models -- 1  
Introduction and Motivation -- 2 UPP: Ultra-Large Alignment Using Phylogeny-aware Profiles -- References -- Topological Signatures for Population Admixture -- 1 Background -- 1.1 Problem Setting -- 2 Topology Model -- 3 Experiments -- 3.1 Experiments on Avocado Germplasm -- 4 Conclusion -- References -- Haplotype Allele Frequency (HAF) Score: Predicting Carriers of Ongoing Selective Sweeps Without Knowledge of the Adaptive Allele -- References -- Gap Filling as Exact Path Length Problem -- 1 Introduction and Related Work.  
2 Gap Filling as Exact Path Length Problem.

---

#### Sommario/riassunto

This book constitutes the refereed proceedings of the 19th Annual International Conference on Research in Computational Molecular Biology, RECOMB 2015, held in Warsaw, Poland, in April 2015. The 36 extended abstracts were carefully reviewed and selected from 170 submissions. They report on original research in all areas of computational molecular biology and bioinformatics.

---