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Collana	Lecture Notes in Bioinformatics ; ; 9683
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Soggetti	Bioinformatics Data mining Pattern recognition Biomathematics Artificial intelligence Computational Biology/Bioinformatics Data Mining and Knowledge Discovery Pattern Recognition Mathematical and Computational Biology Artificial Intelligence
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Next generation sequencing data analysis -- An Efficient Algorithm for finding all pairs k-mismatch maximal common substrings -- Poisson-Markov Mixture Model and Parallel Algorithm for Binning Massive and Heterogenous DNA Sequencing Reads -- FSG: Fast String Grap Construction for De Novo Assembly of reads data 25 -- OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads -- High performance sensing of DNA hybridization on surface of self-organized MWCNT-arrays decorated by organometallic complexes -- Towards a more accurate error model for BioNano optical maps -- Haplso : An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads -- Protein-protein

interactions and networks -- Genome-Wide Structural Modeling of Protein-Protein Interactions -- Identifying essential proteins by purifying protein interaction networks -- Differential functional analysis and change motifs in gene networks to explore the role of anti-sense transcription -- Predicting MicroRNA-disease associations by random walking on multiple networks -- Progression Reconstruction from Unsynchronized Biological Data using Cluster Spanning Trees -- Protein and RNA structure -- Consistent visualization of multiple rigid domain decompositions of Proteins -- A Multiagent Ab Initio Protein Structure Prediction Tool for Novices and Experts -- Filling a protein scaffold with a reference -- Phylogenetics -- Mean values of gene duplication and loss cost functions -- The SCJ small parsimony problem for weighted gene adjacencies -- Path-Difference Median Trees -- NEMo: An Evolutionary Model with Modularity for PPI Networks -- Multi-Genome Scaffold Co-Assembly Based on the Analysis of Gene Orders and Genomic Repeats -- Sequence and image analysis -- Selectoscope: a modern web-app for positive selection analysis of genomic data -- Methods for Genome-wide Analysis of MDR and XDR Tuberculosis from Belarus -- Haplotype Inference for Pedigrees with Few Recombinations -- Improved detection of 2D gel electrophoresis spots by using Gaussian mixture model -- Abridged Track 2 abstracts -- Predicting Combinative Drug Pairs via Integrating Heterogeneous Features for both Known and New Drugs -- SkipCPP-Pred: Promising Prediction Method for Cell-Penetrating Peptides Using Adaptive k-skip-n-gram Features on a High-quality Dataset -- CPredictor2.0: Effectively Detecting Both Small and Large Complexes from Protein-Protein Interaction Networks -- Structural Insights into Antiapoptotic Activation of Bcl-2 and Bcl-xL -- Mediated by FKBP38 and tBid -- VALiBS: a visual aligner for bisulfite sequences -- MegaGTA: a sensitive and accurate metagenomic Gene-Targeted Assembler using iterative de Bruijn graphs -- EnhancerDBN: An Enhancer Prediction Method Based on Deep Belief Network -- An improved burden-test pipeline for cancer sequencing data -- Modeling and Simulation of Specific Production of Trans10, cis12-Conjugated Linoleic Acid in the Biosynthetic Pathway -- Dynamic protein complex identification in uncertain protein-protein interaction networks -- Predicting lncRNA-Protein Interactions Based on Protein-Protein Similarity Network Fusion -- DCJ-RNA: Double Cut and Join for RNA Secondary Structures Using a Component-Based Representation -- Improve Short Read Homology Search using Paired-End Read Information -- Framework for integration of genome and exome data for more accurate identification of somatic variants -- Semantic Biclustering: a New Way to Analyze and Interpret Gene Expression Data -- Epistasis Analysis of microRNAs in Colon Cancer Using Empirical Bayesian Elastic Nets -- Tractable Kinetics of RNA-Ligand Interaction -- MitoDel: A Method to Detect and Quantify Mitochondrial DNA Deletions from Next-Generation Sequence Data -- TRANScendence: transposable elements database and de-novo mining tool allows inferring TEs activity chronology -- Phylogeny Reconstruction from Whole-Genome Data using Variable Length Binary Encoding.

Sommario/riassunto

This book constitutes the proceedings of the 12th International Symposium on Bioinformatics Research and Applications, ISBRA 2016, held in Minsk, Belarus, in June 2016. The 25 papers presented in this volume were carefully reviewed and selected from 77 submissions. They were organized in topical sections named: next generation sequencing data analysis; protein-protein interactions and networks; protein and RNA structure; phylogenetics; sequence analysis; and statistical methods.
