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	Nota di contenuto	Recomb Retrospectives -- The Second Decade of the International Conference on Research in Computational Molecular Biology (RECOMB) -- Extended Abstracts -- A MAD-Bayes Algorithm for State-space Inference and Clustering with Application to Querying Large Collections of ChIP-Seq Data Sets -- Accurate Recovery of Ribosome Positions Reveals Slow Translation of Wobble-Pairing Codons in Yeast -- Multitask matrix completion for learning protein interactions across diseases -- pathTiMEx: Joint Inference of Mutually Exclusive Cancer Pathways and their Dependencies in Tumor Progression -- Clonality inference from single tumor samples using low coverage sequence data -- Flexible Modelling of Genetic Effects on Function-Valued Traits -- MetaFlow: Metagenomic profiling based on whole-genome coverage

analysis with min-cost flows -- LUTE (Local Unpruned Tuple Expansion): Accurate continuously flexible protein design with general energy functions and rigid-rotamerlike efficiency -- Improving Bloom filter performance on sequence data using k-mer Bloom filters.-Safe and complete contig assembly via omnitigs -- Long single-molecule reads can resolve the complexity of the Influenza virus composed of rare, closely related mutant variants.-Structural variation detection with read pair information { An improved null-hypothesis reduces bias -- On Computing Breakpoint Distances for Genomes with Duplicate Genes -- New Genome Similarity Measures based on Conserved Gene Adjacencies -- Fast Phylogenetic Biodiversity Computations Under a Non-Uniform Random Distribution -- Short Abstracts -- SLICER: Inferring Branched, Nonlinear Cellular Trajectories from Single Cell RNA-seq Data -- Multi-track modeling for genome-scale reconstruction of 3D chromatin structure from Hi-C data -- Revealing the Genetic Basis of Immune Traits in the Absence of Experimental Immunophenotyping -- Shall we dense? Comparing design strategies for time series expression experiments -- Enabling Privacy-Preserving GWAS in Heterogeneous Human Populations -- Efficient Privacy-Preserving Read Mapping Using Locality Sensitive Hashing and Secure Kmer Voting -- Finding Mutated Subnetworks Associated with Survival Time in Cancer -- Multi-State Perfect Phylogeny Mixture Deconvolution and Applications to Cancer Sequencing -- Tree inference for single-cell data -- mLDM: a new hierarchical Bayesian statistical model for sparse microbial association discovery -- Low-density locality-sensitive hashing boosts metagenomic binning -- metaSPAdes: a new versatile de novo metagenomics assembler -- Distributed Gradient Descent in Bacterial Food Search.-AptaTRACE: Elucidating Sequence-Structure Binding Motifs by Uncovering Selection Trends in HT-SELEX Experiments -- Fast Bayesian Inference of Copy Number Variants using Hidden Markov Models with Wavelet Compression -- Allele-Specific Quantification of Structural Variations in Cancer Genomes -- Assembly of Long Error-Prone Reads Using de Bruijn Graphs -- Locating a Tree in a Reticulation-Visible Network in Cubic Time -- Joint alignment of multiple protein-protein interaction networks via convex optimization -- Complexes Detection in Biological Networks via Diversified Dense Subgraphs Mining.

Sommario/riassunto	This book constitutes the proceedings of the 20th Annual Conference on Research in Computational Molecular Biology, RECOMB 2016, held in Santa Monica, CA, USA, in April 2016. The 15 regular papers presented in this volume were carefully reviewed and selected from 172 submissions. 20 short abstracts are included in the back matter of the volume. They report on original research in all areas of computational molecular biology and bioinformatics.