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Altri autori (Persone)	MorishitaShinichi <1960-> YiSang-yop <1964-> SakakibaraYasubumi
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Nota di contenuto	Predicting protein-protein relationships from literature using latent topics / T. Aso & K. Eguchi -- Evaluation of DNA intramolecular interactions for nucleosome positioning in yeast / M. Fernandez ... [et al.] -- Quality control and reproducibility in DNA microarray experiments / A. Fujita ... [et al.] -- Comparative analysis of topological patterns in different mammalian networks / B. Goemann ... [et al.] -- Tools for investigating mechanisms of antigenic variation : new extensions to varDB / C. N. Hayes ... [et al.] -- Localized suffix array and its application to genome mapping problems for paired-end short reads / K. Kimura & A. Koike -- Comparative analysis of aerobic and anaerobic prokaryotes to identify correlation between oxygen requirement and gene-gene functional association patterns / Y. Lin & H. Wu -- Calculation of protein-ligand binding free energy using Smooth Reaction Path Generation (SRPG) method : a comparison of the explicit water model, GB/SA model and docking score function / D. Mitomo ... [et al.] -- Structural insights into the enzyme mechanism of a new family of D-2-hydroxyacid dehydrogenases, a close homolog of

2-Ketopantoate reductase / S. Mondal & K. Mizuguchi -- Comprehensive analysis of sequence-structure relationships in the loop regions of proteins / S. Nakamura & K. Shimizu -- The prediction of local modular structures in a co-expression network based on gene expression datasets / Y. Ogata ... [et al.] -- Gradient-based optimization of hyperparameters for base-pairing profile local alignment kernels / K. Sato, Y. Saito & Y. Sakakibara -- A method for efficient execution of bioinformatics workflows / J. Seo ... [et al.] -- Development of a new meta-score for protein structure prediction from seven all-atom distance dependent potentials using support vector regression / M. Shirota, T. Ishida & K. Kinoshita -- Refining Markov clustering for protein complex prediction by incorporating core-attachment structure / S. Srihari, K. Ning & H. W. Leong -- An assessment of prediction algorithms for nucleosome positioning / Y. Tanaka & K. Nakai -- Cancer classification using single genes / X. Wang & O. Gotoh -- RECOUNT : expectation maximization based error correction tool for next generation sequencing data / E. Wijaya ... [et al.] -- A new generation of homology search tools based on probabilistic inference / S. R. Eddy -- Representation and analysis of molecular networks involving diseases and drugs / M. Kanehisa -- Systems biotechnology / S. Y. Lee -- Strategies toward CNS-regeneration using induced pluripotent stem cells / H. Okano -- Thinking laterally about genomes / M. A. Ragan.

#### Sommario/riassunto

This volume contains papers presented at the 20th International Conference on Genome Informatics (GIW 2009) held at the Pacifico Yokohama, Japan from December 14 to 16, 2009. The GIW Series provides an international forum for the presentation and discussion of original research papers on all aspects of bioinformatics, computational biology and systems biology. Its scope includes biological sequence analysis, protein structure prediction, genetic regulatory networks, bioinformatic algorithms, comparative genomics, and biomolecular data integration and analysis. Boasting a history of 20 years, GIW is the longest-running international bioinformatics conference. A total of 18 contributed papers were selected for presentation at GIW 2009 and for inclusion in this book. In addition, this book contains abstracts from the five invited speakers: Sean Eddy (HHMI's Janelia Farm, USA), Minoru Kanehisa (Kyoto University, Japan), Sang Yup Lee (KAIST, Korea), Hideyuki Okano (Keio University, Japan) and Mark Ragan (University of Queensland, Australia).