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with centroid estimators / Yohei Okada, Kengo Sato, Yasubumi Sakakibara. Dynamic programming algorithms for RNA structure prediction with binding sites / Unyane Poolsap, Yuki Kato, Tatsuya Akutsu. An algorithm for the energy barrier problem without pseudoknots and temporary arcs / Chris Thachuk ... [et al.] -- Dynamics of biological networks. Session introduction / Tanya Y. Berger-Wolf ... [et al.]. Local optimization for global alignment of protein interaction networks / Leonid Chindelevitch, Chung-Shou Liao, Bonnie Berger. Identification of coordinately dysregulated subnetworks in complex phenotypes / Salim A. Chowdhury, Mehmet Koyuturk. Subspace differential coexpression analysis : problem definition and a general approach / Gang Fang ... [et al.]. Estimation of protein and domain interactions in the switching motility system of *Myxococcus xanthus* ... [et al.]. Exploring biological network dynamics with ensembles of graph partitions / Saket Navlakha, Carl Kingsford. Geometric evolutionary dynamics of protein interaction networks / Natasa Przulj ... [et al.]. The steady states and dynamics of Urokinase-mediated plasmin activation / Lakshmi Venkatraman ... [et al.] -- Multi-resolution modeling of biological macromolecules. Session introduction / Samuel Flores ... [et al.]. Multi-resolution approach for interactively locating functionally linked ion binding sites by steering small molecules into electrostatic potential maps using a haptic device / Olivier Delalande ... [et al.]. Predicting RNA structure by multiple template homology modeling / Samuel C. Flores ... [et al.]. Constructing multi-resolution Markov State Models (MSMs) to elucidate RNA hairpin folding mechanisms / Xuhui Huang ... [et al.]. Multiscale dynamics of macromolecules using normal mode langevin / Jesus A. Izaguirre, Christopher R. Sweet, Vijay S. Pande. Insights into the intraring subunit order of TriC/CCT : structural and evolutionary analysis / Nir Kalisman, Michael Levitt. "Cross-graining : " Efficient multi-scale simulation via Markov state models / Peter Kasson, Vijay Pande. Toward understanding allosteric signaling mechanisms in the ATPase domain of molecular chaperones / Ying Liu, Ivet Bahar. 3D-blast : 3D protein structure alignment, comparison, and classification using spherical polar Fourier correlations / Lazaros Mavridis. David W. Ritchie. Structural prediction of protein-RNA interaction by computational docking with propensity-based statistical potentials / Laura Perez-Cano ... [et al.] -- Personal genomics. Session introduction / Can Alkan ... [et al.]. Improving the prediction of pharmacogenes using text-derived gene-drug relationships / Yael Garten, Nicholas P. Tatonetti, Russ B. Altman. Finding unique filter sets in PLATO : a precursor to efficient interaction analysis in GWAS data / Benjamin J. Grady ... [et al.]. Enabling personal genomics with an explicit test of epistasis / Casey S. Greene ... [et al.]. Loss of post-translational modification sites in disease / Shuyan Li ... [et al.]. Detecting genome-wide haplotype polymorphism by combined use of mendelian constraints and local population structure / Xin Li, Yixuan Chen, Jing Li. Sequence Feature Variant Type (SFVT) analysis of the HLA genetic association in juvenile idiopathic arthritis / Glenys Thomson ... [et al.]. Cokgen : a software for the identification of rare copy number variation from SNP microarrays / Gokhan Yavas ... [et al.] -- Reverse engineering and synthesis of biomolecular systems. Session introduction / Gil Alterovitz ... [et al.]. Co-design in synthetic biology : a system-level analysis of the development of an environmental sensing device / David A. Ball ... [et al.]. Critical analysis of transcriptional and post-transcriptional regulatory networks in multiple myeloma / Marta Biasiolo ... [et al.]. A computational model of gene expression in an inducible synthetic circuit / Francesca Ceroni, Simone Furini, Silvio Cavalcanti. Retrovirus

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Sommario/riassunto

The Pacific Symposium on Biocomputing (PSB) 2010 is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application of computational methods in problems of biological significance. Presentations are rigorously peer reviewed and are published in an archival proceedings volume. PSB 2010 will be held on January 4 - 8, 2010 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2010 will bring together top researchers from the US, Asia Pacific, and around the world to exchange research results and address pertinent issues in all aspects of computational biology. It is a forum for the presentation of work in databases, algorithms, interfaces, visualization, modeling, and other computational methods, as applied to biological problems, with emphasis on applications in data-rich areas of molecular biology. The PSB has been designed to be responsive to the need for critical mass in sub-disciplines within biocomputing. For that reason, it is the only meeting whose sessions are defined dynamically each year in response to specific proposals. PSB sessions are organized by leaders of research in biocomputing's "hot topics". In this way, the meeting provides an early forum for serious examination of emerging methods and approaches in this rapidly changing field.
