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Nota di contenuto	Identification of aberrant pathway and network activity from high-throughput data. Session introduction / Rachel Karchin ... [et al.]. SSLPred : predicting synthetic sickness lethality / Nirmalya Bandyopadhyayy, Sanjay Ranka, and Tamer Kahveci. Predicting the effects of copy-number variation in double and triple mutant combinations / Gregory W. Carter ... [et al.]. Integrative network analysis to identify aberrant pathway networks in ovarian cancer / Li Chen ... [et al.] -- Role of synthetic genetic interactions in understanding functional interactions among pathways / Shahin Mohammadi, Giorgos Kollias, and Ananth Grama -- Discovery of mutated subnetworks associated with clinical data in cancer / Fabio Vandin ... [et al.] -- Intrinsically disordered proteins : analysis, prediction, simulation, and biology. Session introduction / Jianhan Chen, Jianlin Cheng, and A. Keith Dunker. Quasi-anharmonic analysis reveals intermediate states in the nuclear co-activator receptor binding domain ensemble / Virginia M. Burger ... [et al.]. Efficient construction of disordered protein ensembles in a Bayesian framework with optimal selection of conformations / Charles K. Fisher, Orly Ullman, and Collin M. Stultz. Correlation between posttranslational modification and intrinsic disorder in protein / Jianjiong Gao and Dong Xu. Intrinsic disorder within and flanking the DNA-binding domains of human transcription factors / Xin Guo, Martha L. Bulyk, and Alexander J.

Hartemink. Intrinsic protein disorder and protein-protein interactions / Wei-Lun Hsu ... [et al.]. Subclassifying disordered proteins by the CH-CDF plot method / Fei Huang ... [et al.]. Coevolved residues and the functional association for intrinsically disordered proteins / Chan-Seok Jeong and Dongsup Kim. Cryptic disorder: an order-disorder transformation regulates the function of nucleophosmin / Diana M. Mitrea and Richard W. Kriwacki. Functional annotation of intrinsically disordered domains by their amino acid content using IDD navigator / Ashwini Patil ... [et al.]. On the complementarity of the consensus-based disorder prediction / Zhenling Peng and Lukasz Kurgan. Modulating protein-DNA interactions by post-translational modifications at disordered regions / Dana Vuzman, Yonit Hoffman, and Yaakov Levy -- Microbiome studies: analytical tools and techniques. Session introduction / James A. Foster ... [et al.]. Estimating population diversity with unreliable low frequency counts / John Bunge ... [et al.]. Comparisons of distance methods for combining covariates and abundances in microbiome studies / Julia Fukuyama ... [et al.]. Proteotyping of microbial communities by optimization of tandem mass spectrometry data interpretation / Alys Hugo ... [et al.]. phyloseq: a bioconductor package for handling and analysis of high-throughput phylogenetic sequence data / Paul J. McMurdie and Susan Holmes. SEPP: SATe-enabled phylogenetic placement / Siavash Mirarab, Nam Nguyen, and Tandy Warnow. Artificial functional difference between microbial communities caused by length difference of sequencing reads / Quan Zhang, Thomas G. Doak, and Yuzhen Ye. MetaDomain: a profile HMM-based protein domain classification tool for short sequences / Yuan Zhang and Yanni Sun.

Modeling host-pathogen interactions: computational biology and bioinformatics for infectious disease research. Session introduction / Jason E. Mcdermott ... [et al.]. Structural models for host-pathogen protein-protein interactions: assessing coverage and bias / Eric A. Franzosa and Yu Xia. Identification of cell cycle-regulated, putative hyphal genes in Candida Albicans / Raluca Gordan, Saumyadipta Pyne, and Martha L. Bulyk. Determining confidence of predicted interactions between HIV-1 and human proteins using conformal method / Ilia Nouretdinov ... [et al.] -- Personalized medicine: from genotypes and molecular phenotypes towards computed therapy. Session introduction / Oliver Stegle ... [et al.]. Finding genome-transcriptome-phenome associations with structured association mapping and visualization in GenAMap / Ross E. Curtis ... [et al.]. Interpretome: a freely available, modular, and secure personal genome interpretation engine / Konrad J. Karczewski ... [et al.]. A kinase inhibition map approach for tumor sensitivity prediction and combination therapy design for targeted drugs / Ranadip Pal and Noah Berlow. Mixture model for sub-phenotyping in GWAS / David Warde-Farley ... [et al.] -- Text and knowledge mining for pharmacogenomics: genotypephenotype-drug relationships. Session introduction / Kevin Bretonnel Cohen ... [et al.]. The extraction of pharmacogenetic and pharmacogenomic relations - A case study using PharmGKB / Ekaterina Buyko, Elena Beisswanger, and Udo Hahn. Linking PharmGKB to phenotype studies and animal models of disease for drug repurposing / Robert Hoehndorf ... [et al.]. Integrating VA's NDF-RT drug terminology with PharmGKB: preliminary results / Jyotishman Pathak ... [et al.]. Discovery and explanation of drug-drug interactions via text mining / Bethany Percha, Yael Garten, and Russ B. Altman. Ranking gene-drug relationships in biomedical literature using latent Dirichlet allocation / Yonghui Wu ... [et al.] -- Workshops. The structure and function of chromatin and chromosomes / William Stafford Noble ... [et al.]. Law, bioethics and the current status

	of ownership, privacy, informed consent in the genomic age / Greg Hampikian and Eric M. Meslin. Systems pharmacogenomics-bridging the gap / Marylyn Ritchie ... [et al.].
Sommario/riassunto	The Pacific Symposium on Biocomputing (PSB) 2012 is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application of computational methods in the problems of biological significance. Presentations are rigorously peer-reviewed and are published in an archival proceedings volume. PSB 2012 will be held on January 3 - 7, 2012 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2012 will bring together top researchers from the US, the Asian Pacific nations, and countries around the world to exchange research results and address open 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 the applications in the 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.