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Nota di contenuto	Cancer panomics: Computational methods and infrastructure for integrative analysis of cancer high-throughput "OMICS" data. Session introduction / Soren Brunak ... [et al.] -- Tumor haplotype assembly algorithms for cancer genomics / Derek Aguiar, Wendy S.W. Wong, Sorin Istrail -- Extracting significant sample-specific cancer mutations using their protein interactions / Liviu Badea -- The stream algorithm: Computationally efficient ridge-regression via Bayesian model averaging, and applications to pharmacogenomic prediction of cancer cell line sensitivity / Elias Chaibub Neto ... [et al.] -- Sharing information to reconstruct patient-specific pathways in heterogeneous diseases / Anthony Gitter ... [et al.] -- Detecting statistical interaction between somatic mutational events and germline variation from next-generation sequence data / Hao Hu, Chad D. Huff -- Systematic assessment of analytical methods for drug sensitivity prediction from cancer cell line data / In Sock Jang ... [et al.] -- Integrative analysis of two cell lines derived from a non-small-lung cancer patient - A panomics approach / Oleg Mayba ... [et al.] -- An integrated approach

to blood-based cancer diagnosis and biomarker discovery / Martin Renqiang Min ... [et al.] -- Multiplex meta-analysis of medulloblastoma expression studies with external controls / Alexander A. Morgan ... [et al.] -- Computational approaches to drug repurposing and pharmacology. Session introduction / S. Joshua Swamidass ... [et al.] -- Challenges in secondary analysis of high throughput screening data / Aurora S. Blucher, Shannon K. McWeeney -- Drug intervention response predictions with paradigm (DIRPP) identifies drug resistant cancer cell lines and pathway mechanisms of resistance / Douglas Brubaker ... [et al.] -- Anti-infectious drug repurposing using an integrated chemical genomics and structural systems biology approach / Clara Ng ... [et al.] -- Drug-target interaction prediction by integrating chemical, genomic, functional and pharmacological data / Fan Yang, Jinbo Xu, Jianyang Zeng -- Prediction of off-target drug effects through data fusion / Emmanuel R. Yera, Ann E. Cleves, Ajay N. Jain -- Exploring the pharmacogenomics knowledge base (PharmGKB) for repositioning breast cancer drugs by leveraging web ontology language (OWL) and cheminformatics approaches / Qian Zhu ... [et al.] -- Detecting and characterizing pleiotropy: New methods for uncovering the connection between the complexity of genomic architecture and multiple phenotypes. Session introduction / Anna L. Tyler, Dana C. Crawford, Sarah A. Pendergrass -- Using the bipartite human phenotype network to reveal pleiotropy and epistasis beyond the gene / Christian Darabos, Samantha H. Harmon, Jason H. Moore -- Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield personalized medicine research project biobank / Molly A. Hall ... [et al.] -- Dissection of complex gene expression using the combined analysis of pleiotropy and epistasis / Vivek M. Philip, Anna L. Tyler, Gregory W. Carter -- Personalized medicine: From genotypes and molecular phenotypes towards therapy. Session introduction / Jennifer Listgarten ... [et al.] -- PATH-SCAN: A reporting tool for identifying clinically actionable variants / Roxana Daneshjou ... [et al.] -- Imputation-based assessment of next generation rare exome variant arrays / Alicia R. Martin ... [et al.] -- Utilization of an EMR-biorepository to identify the genetic predictors of calcineurin-inhibitor toxicity in heart transplant recipients/ Matthew Oetjens ... [et al.] -- Robust reverse engineering of dynamic gene networks under sample size heterogeneity / Ankur P. Parikh, Wei Wu, Eric P. Xing -- Variant priorization and analysis incorporating problematic regions of the genome / Anil Patwardhan ... [et al.] -- Bags of words models of epitope sets: HIV viral load regression with counting grids / Alessandro Perina, Pietro Lovato, Nebojsa Jojic -- Joint association discovery and diagnosis of Alzheimer's disease by supervised heterogeneous multiview learning / Shandian Zhe ... [et al.] -- Text and data mining for biomedical discover. Session introduction / Graciela H. Gonzalez ... [et al.] -- Vector quantization kernels for the classification of protein sequences and structures / Wyatt T. Clark, Predrag Radivojac -- Combining Heterogenous data for prediction of disease related and pharmacogenes / Christopher S. Funk, Lawrence E. Hunter, K. Bretonnel Cohen -- A novel profile biomarker diagnosis for mass spectral proteomics / Henry Han -- Towards pathway curation through literature mining - A case study using PharmGKB / Ravikumar K.E., Kavishwar B. Wagholikar, Hongfang Liu -- Sparse generalized functional linear model for predicting remission status of depression patients / Yashu Liu ... [et al.] -- Development of a data-mining algorithm to identify ages at reproductive milestones in electronic medical records / Jennifer Malinowski, Eric Farber-Eger, Dana C. Crawford -- An efficient algorithm to integrate network and attribute

	data for gene function prediction / Shankar Vembu, Quaid Morris -- Matrix factorization-based data fusion for gene function prediction in Baker's yeast and slime mold / Marinka Zitnik, Blaz Zupan -- Workshops. Applications of bioinformatics to non-coding RNAs in the era of next-generation sequencing / Chao Cheng, Jason Moore, Casey Greene -- Building the next generation of quantitative biologists / Kristine A. Pattin ... [et al.] -- Uncovering the etiology of autism spectrum disorders: Genomics, bioinformatics, environment, data collection and exploration, and future possibilities / Sarah A. Pendergrass, Santhosh Girirajan, Scott Selleck.
Sommario/riassunto	$a The Pacific Symposium on Biocomputing (PSB) 2014 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 2014 will be held from January 3 – 7, 2014 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2014 will bring together top researchers from the US, the Asian Pacific nations, and 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 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.