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Nota di contenuto	PREFACE; CONTENTS; INTEGRATIVE -OMICS FOR TRANSLATIONAL SCIENCE; TOWARDS INTEGRATIVE GENE PRIORITIZATION IN ALZHEIMER'S DISEASE; SYSTEMS BIOLOGY ANALYSES OF GENE EXPRESSION AND GENOME WIDEASSOCIATION STUDY DATA IN OBSTRUCTIVE SLEEP APNEA; FINDING MOST LIKELY HAPLOTYPES IN GENERAL PEDIGREESTHROUGH PARALLEL SEARCH WITH DYNAMIC LOAD BALANCING; DYNAMIC, MULTI-LEVEL NETWORK MODELS OF CLINICAL TRIALS; MINING FUNCTIONALLY RELEVANT GENE SETS FOR ANALYZINGPHYSIOLOGICALLY NOVEL CLINICAL EXPRESSION DATA; GENOTYPE PHENOTYPE MAPPING IN RNA VIRUSES - DISJUNCTIVENORMAL FORM LEARNING GENOME-WIDE ASSOCIATION MAPPING AND RARE ALLELES: FROMPOPULATION GENOMICS TO PERSONALIZED MEDICINEAN APPLICATION AND EMPIRICAL COMPARISON OF STATISTICAL ANALYSISMETHODS FOR ASSOCIATING RARE VARIANTS TO A COMPLEX PHENOTYPE; HAPLOTYPHE PHASING BY MULTI-ASSEMBLY OF SHAREDHAPLOTYPES: PHASE-DEPENDENT INTERACTIONS BETWEEN RARE VARIANTS; AN EVALUATION OF POWER TO DETECT LOW-

FREQUENCY VARIANT ASSOCIATIONS USING ALLELE-MATCHING TESTS THAT ACCOUNT FOR UNCERTAINTY; PENALIZED REGRESSION FOR GENOME-WIDE ASSOCIATION SCREENING OF SEQUENCE DATA; MICROBIOME STUDIES: PSB 2011 SPECIAL SESSION INTRODUCTION ESTIMATING THE NUMBER OF SPECIES WITH CATCHALLA FRAMEWORK FOR ANALYSIS OF METAGENOMIC SEQUENCING DATA; VISUALIZATION AND STATISTICAL COMPARISONS OF MICROBIAL COMMUNITIES USING R PACKAGES ON PHYLOCHIP DATA; HUMAN MICROBIOME VISUALIZATION USING 3D TECHNOLOGY; COMPARING BACTERIAL COMMUNITIES INFERRED FROM 16S rRNA GENE SEQUENCING AND SHOTGUN METAGENOMICS; MULTI-SCALE MODELLING OF BIOSYSTEMS: FROM MOLECULAR TO MESOSCALE; COMPUTATIONAL GENERATION INHIBITOR-BOUND CONFORMERS OF P38 MAPKINASE AND COMPARISON WITH EXPERIMENTS
MOLECULAR DYNAMICS SIMULATIONS OF THE FULL TRIPLE HELICAL REGION OF COLLAGEN TYPE I PROVIDE AN ATOMIC SCALE VIEW OF THE PROTEIN'S REGIONAL HETEROGENEITY STRUCTURAL INSIGHTS INTO PRE-TRANSLOCATION RIBOSOME MOTIONS; NEW CONFORMATIONAL SEARCH METHOD USING GENETICALGORITHM AND KNOT THEORY FOR PROTEINS; PERSONAL GENOMICS; THE REFERENCE HUMAN GENOME DEMONSTRATES HIGH RISK OF TYPE 1 DIABETES AND OTHER DISORDERS; MATCHING CANCER GENOMES TO ESTABLISHED CELL LINES FOR PERSONALIZED ONCOLOGY
USE OF BIOLOGICAL KNOWLEDGE TO INFORM THE ANALYSIS OF GENE-GENE INTERACTIONS INVOLVED IN MODULATING VIROLOGIC FAILURE WITH THE HAVIRENZ-CONTAINING TREATMENT REGIMENS IN ART-NAIVE ACTG CLINICAL TRIALS PART C VISUAL INTEGRATION OF RESULTS FROM A LARGE DNA BIOBANK (BIOVU) USING SYNTHESIS-VIEW; MULTIVARIATE ANALYSIS OF REGULATORY SNPS: EMPOWERING PERSONAL GENOMICS BY CONSIDERING CIS-EPISTASIS AND HETEROGENEITY; HAPLOTYPE INFERENCE FROM SHORT SEQUENCE READS USING A POPULATION GENEALOGICAL HISTORY MODEL; REVERSE ENGINEERING AND SYNTHESIS OF BIOMOLECULAR SYSTEMS; BINARY COUNTING WITH CHEMICAL REACTIONS
DEFINING THE PLAYERS IN HIGHER-ORDER NETWORKS: PREDICTIVE MODELING FOR REVERSE ENGINEERING FUNCTIONAL INFLUENCE NETWORKS

Sommario/riassunto

The Pacific Symposium on Biocomputing (PSB) 2011 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 2011" will be held on January 3 - 7, 2011 in Kohala Coast, Hawaii. Tutorials and workshops will be offered prior to the start of the conference. PSB 2011 will bring together top researchers from the US, Asia Pacific, and around the world to exchan
