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	Nota di contenuto	Session 1: Microarray and Systems Biology I (Networks) -- Bayesian Inference of Gene Regulatory Networks Using Gene Expression Time Series Data -- Biological Network Inference Using Redundancy Analysis -- A Novel Graph Optimisation Algorithm for the Extraction of Gene Regulatory Networks from Temporal Microarray Data -- Session 2: Microarray and Systems Biology II -- Analysing Periodic Phenomena by

Circular PCA -- Identification of Cold-Induced Genes in Cereal Crops and Arabidopsis Through Comparative Analysis of Multiple EST Sets -- Mining Spatial Gene Expression Data for Association Rules -- Session 3: Medical, SNPs, Genomics I -- Individualized Predictions of Survival Time Distributions from Gene Expression Data Using a Bayesian MCMC Approach -- Comparing Logic Regression Based Methods for Identifying SNP Interactions -- Stochastical Analysis of Finite Point Sampling of 3D Chromatin Fiber in Interphase Cell Nuclei -- Session 4: Medical, SNPs, Genomics II -- Structural Screening of HIV-1 Protease/Inhibitor Docking by Non-parametric Binomial Distribution Test -- satDNA Analyzer 1.2 as a Valuable Computing Tool for Evolutionary Analysis of Satellite-DNA Families: Revisiting Y-Linked Satellite-DNA Sequences of Rumex (Polygonaceae) -- A Soft Hierarchical Algorithm for the Clustering of Multiple Bioactive Chemical Compounds -- Session 5: Systems Biology -- A Novel Method for Flux Distribution Computation in Metabolic Networks -- Inverse Bifurcation Analysis of a Model for the Mammalian G 1/S Regulatory Module -- Weighted Cohesiveness for Identification of Functional Modules and Their Interconnectivity -- Modelling and Simulation of the Genetic Phenomena of Additivity and Dominance via Gene Networks of Parallel Aggregation Processes -- Session 6: Sequence Analysis I (Coding) -- Protein Remote Homology Detection Based on Binary Profiles -- Biological Sequences Encoding for Supervised Classification -- Fast Search Algorithms for Position Specific Scoring Matrices -- Session 7: Sequence Analysis II -- A Markovian Approach for the Segmentation of Chimpanzee Genome -- Synthetic Protein Sequence Oversampling Method for Classification and Remote Homology Detection in Imbalanced Protein Data -- Stem Kernels for RNA Sequence Analyses -- Prediction of Structurally-Determined Coiled-Coil Domains with Hidden Markov Models -- Session 8: Proteomics I -- Patch Prediction of Protein Interaction Sites: Validation of a Scoring Function for an Online Server -- Statistical Inference on Distinct RNA Stem-Loops in Genomic Sequences -- Interpretation of Protein Subcellular Location Patterns in 3D Images Across Cell Types and Resolutions -- Session 9: Proteomics II (Measurements) -- Bayesian Inference for 2D Gel Electrophoresis Image Analysis -- SimShiftDB: Chemical-Shift-Based Homology Modeling -- Annotation of LC/ESI-MS Mass Signals -- Session 10: Proteomics III (Structure) -- Stochastic Protein Folding Simulation in the d-Dimensional HP-Model -- Enhancing Protein Disorder Detection by Refined Secondary Structure Prediction -- Joining Softassign and Dynamic Programming for the Contact Map Overlap Problem -- Session 11: Databases, Web and Text Analysis -- An Evaluation of Text Retrieval Methods for Similarity Search of Multi-dimensional NMR-Spectra -- Ontology-Based MEDLINE Document Classification -- Integrating Mutations Data of the TP53 Human Gene in the Bioinformatics Network Environment -- Efficient and Scalable Indexing Techniques for Biological Sequence Data.

Sommario/riassunto

This volume contains the papers which were selected for oral presentation at the first Bioinformatics Research and Development (BIRD) conference held in Berlin, Germany during March 12-14, 2007. BIRD covers a wide range of topics related to bioinformatics like microarray data, genomics, single nucleotide polymorphism, sequence analysis, systems biology, medical applications, proteomics, information systems. The conference was very competitive. From about 140 submissions only 36 were selected by the Program Committee for oral presentation at BIRD and for publication in these proceedings. The acceptance rate was 1/4. The decisions of the Program Committee were guided by the recommendations of several reviewers for each paper. It

should be mentioned that these proceedings have companion proceedings published by the Austrian Computer Society where selected poster presentations of the BIRD conference are included. The invited talk titled "From Flies to Human Disease" by Josef Penninger, one of the leading researcher in genetic experiments for investigating disease pathogenesis, was very inspiring and gave new insights into future bioinformatics challenges.