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PMSB'06 Decisions

Accepted as oral presentations:

Authors	Title
Blockeel, Schietgat, Struyf, Clare, Dzeroski	Hierarchical Multilabel Classification Trees for Gene Function Prediction
Geurts, Touleimat, Dutreix, d'Alche-Buc	Completion of biological networks : the output kernel trees approach
Girolami	Bayesian Data Fusion with Gaussian Process Priors : An Application to Protein Fold Recognition
Gopalacharyulu, Lindfors, Bounsaythip, Oresic	Context dependent visualization of protein function
Kato, Seki, Kasami	RNA Structure Prediction Including Pseudoknots Based on Stochastic Multiple Context-Free Grammar
Landwehr, Mielikäinen, Eronen, Toivonen, Mannila	Constrained Hidden Markov Models for Population-based Haplotyping
Nagl, Williams, Williamson	Objective Bayesian Nets for Breast Cancer Prognosis
Oja, Peltonen, Kaski	Estimation of human endogenous retrovirus activities from expressed sequence databases
Pelckmans, Van Vooren, Coessens, Suykens, De Moor	Mutual Spectral Clustering: Microarray Experiments Versus Text Corpus
Rogers, Khanin, Girolami	Model based identification of transcription factor activity from microarray data
Roth, Fischer	Improved Functional Prediction of Proteins by Learning Kernel Combinations in Multilabel Setting
Rätsch, Sonnenburg, Srinivasan, Witte, Muller, Sommer, Schölkopf	Improving the Caenorhabditis elegans Genome Annotation using Machine Learning
Vehtari, Mäkinen, Soininen, Ingman, Mäkelä, Savolainen,	A Novel Bayesian Approach for Uncovering Potential Spectroscopic Counterparts for Clinical Variables in 1H NMR Metabonomic Applications
Hannuksela, Kaski, Ala-Korpela	Predicting co-evolving pairs in Pfam using information theory where entropy is determined by phylogenetic mutation events
Willis	

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Accepted as poster presentations:

Bertoni, Valentini	Model order selection for clustered bio-molecular data
Best, Hegerl, Nickell, Baumeister	Visual proteomics: Machine learning and pattern recognition problems in three-dimensional cryo-electron tomography
Dix, Powell, Allison, Jaeger, Bernal, Stern	Exploring Long DNA Sequences by Information Content
Gevaert, Van Vooren, De Moor	Prior Distributions for Learning Genetic Networks
Greco, Somervuo, Raitila, Nitsch, Auvinen	Comprehensive gene expression profiling of normal human tissues in massive meta-analysis of Affymetrix experiments
Hallivuori, Kumar, Heikkonen	Using Kalman Filters to Model Gene Regulatory Networks
Kim, Lee, Park	Regression Based Gene Regulatory Networks
Korpela, Hollmen	Extending an Algorithm for Clustering Gene Expression Time Series
Lambros, Panagiotis, Spiridon	A comparison of Machine Learning Algorithms for MicroRNA Genes Prediction
Maetschke, Boden, Gallagher	Predicting the subcellular localization of transmembrane proteins
Naumoff	Development Of A Hierarchical Classification Of The Tim-Barrel Type Glycoside Hydrolases
Nikkilä, Honkela, Kaski	Exploring the independence of gene regulatory modules
Okun, Priisalu	Multi-class Cancer Classification Using Ensembles of Classifiers: Preliminary Results
Opgen-Rhein	A VAR-process approach to infer large-scale gene association networks from microarray time series data
Oresic	Normalization of metabolomics data using multiple internal standards
Purutcuoglu, Wit	Stochastic Simulation and Statistical Inference of the MAPK Signalling Pathway
Turkett	Static Bayesian Modeling of Biological Time-Series Data
Van den Bulcke, Van Leemput, Dholander, De Moor, van	
Remortel, Marchal	Assessing characteristics of gene network inference algorithms using synthetic gene expression data
Yoon, Lee, Park	Robust estimation method for missing value imputation in microarray gene expression data