The advancements of computational and informational techniques have enabled in silico testing of many lab-based experiments in life sciences before performing them in vitro or in vivo. Though computational techniques are not capable of mimicking all wet-lab experiments, bioinformatics will inevitably play a major role in future medical practice. For example, in the pursuit of new drugs it can reduce the costs and complexity involved in expensive wet-lab experiments. It is expected that by 2010, sequencing of individual genomes will be affordable generating an unprecedented increase of life sciences data, in the form of sequences, expressions, networks, images, literature. Pattern recognition techniques lie at the heart of discovery of new insights into biological knowledge, as the presence of particular patterns or structure is often an indication of its function.

The aim of the workshop series Pattern Recognition in Bioinformatics (PRIB) is to bring pattern recognition scientists and life scientists together to promote pattern recognition applications to solve life sciences problems. This volume presents the proceedings of the 2nd IAPR Workshop PRIB 2007 held in Singapore, October 1–2, 2007. It includes 38 technical contributions that were selected by the International Program Committee from 125 submissions. Each of these rigorously reviewed papers was presented orally at the workshop. The proceedings consists of six parts. Part 1: Sequence Analysis; Part 2: Prediction of Protein Structure, Interaction, and Localization; Part 3: Gene Expression Analysis; Part 4: Pathway Analysis; Part 5: Medical Informatics; and Part 6: Bioimaging.

Part 1 of the proceedings contains seven chapters on sequence analysis. Tang et al. propose a new design of BLAST-based gene ontology (GO) term annotator which incorporates data mining techniques and rough sets to deduce biological functions from DNA sequences. A design of ClustalW, using field programmable gate arrays (FPGA) is developed by Aung et al. to perform sequence alignment in real-time applications. Stepanova, Lin, and Lin develop a two-phase artificial neural network, and present its FPGA implementation, for genome-wide detection of response elements in steroid hormone receptors. Greene, Bill, and Moore propose an expert knowledge-guided mutation operator for the detection of genome-wide variations of DNA, using genetic programming. Luthra et al. find a conserved motif PMNYM of the transmembrane TM5 domain involved in dimerization of the A2a receptor, with a PROSITE search. Deng, Deng, and Havukkala find a strong GC and AT skew correlation in the chicken genome, using a novel visualization technique. Pearson et al. compare interval mapping to a hierarchical Bayesian method for quantitative trait loci analysis on Arabidopsis thaliana.

Part 2 of the proceedings contains nine chapters on the prediction of protein structure, interaction, and localization. Shi et al. propose multiple support vector machines (SVM) to handle different features and then decision templates to combine predictions so as to detect protein subcellular localization. Hoque, Chetty, and Dooley
propose a generalized schemata theorem incorporating twin removal for genetic algorithms (GA) to predict protein structure. Zhang, Wei, and Ding use a fuzzy SVM to improve the prediction of structural classes of low-homology proteins. Singh and Ramani demonstrate a method to predict right-handed $\beta$-helix fold from protein sequences using SVM and report improved performance measures.

Taguchi and Gromiha investigate several amino acid features and find amino acid occurrences improve the recognition of protein fold recognition significantly over the other features. Ou, Shao, and Chen propose an efficient RBF network to identify interface residues of interacting proteins, based on PSSM profiles and biochemical properties. Ahmad presents dynamic outlier exclusion training algorithm for neural networks to enhance sequence-based predictions in residue level protein properties. Gromiha analyzes amino acid sequences of transmembrane $\beta$-barrel proteins (TMBs) and finds a significantly higher occurrence of Ser, Asn and Gln in TMBs than in globular proteins. Ahmed estimates the evolutionary average hydrophobicity profile from a family of protein sequences.

Part 3 of the proceedings contains nine chapters on gene expression analysis. Yuriy et al. develop an online database for Affymetrix probe mapping and annotation (APMA) for interactive access, search, and visualization of target sequences mapping and annotation. Blanco, Martin-Merino, and Rivas combine different kinds of dissimilarity-based classifiers for the identification of cancerous samples from microarray data and illustrate its efficacy over existing classifiers. Stiglic, Khan, and Kokol propose small ensemble classifiers to visually interpret microarray data for easy comprehension of their functionality. The method is illustrated in a case-study of leukemia samples. Zhou et al. propose ant-MST, an ant-based minimum spanning tree for gene expression data clustering. McGarry, Sarfraz, and McIntyre integrate GO measures to SOM classification of gene expression data to obtain biologically meaningful clusters of genes.

Teng and Chan find order preserving clusters in gene expression data by converting each gene vector into an ordered label sequence. A method is then proposed by finding the frequent orders by iteratively combining the most frequent prefixes and suffixes in a statistical way. Mao and Tang propose correlation-based relevancy and redundancy measures for efficient gene selection and show promising results in six gene expression problems. Mundra and Rajapakse present relevancy and redundancy criteria for gene selection with an SVM-recursive feature elimination (RFE) method which selects gene subsets with better classification accuracy and generalization capability compared to the SVM-RFE method. Oja obtains digital expression profiles of human endogenous retroviruses.

Part 4 of the proceedings contains four chapters on pathway analysis. Ram and Chetty propose a framework for path analysis in gene regulatory networks by first finding the network structure by causal modeling and then enhancing the network by post-processing. Sehgal et al. reconstruct transcriptional gene regulatory network reconstruction through cross-platform fusion of gene networks. Ling et al. reconstruct protein–protein interaction pathways by mining subject-verb-objects intermediates in biological texts. Chaturvedi, Sakharkar, and Rajapakse propose a validation technique for gene regulatory networks with protein–protein interaction data by using a GA.
They demonstrate the potential of the method in an application to cell-cycle regulation.

Part 5 of the proceedings contains four chapters in medical informatics. Kurzynski and Zolnierzek introduce and compare rough set- and fuzzy set-based methods for sequential medical diagnostic problems. Perumal, Lim and Sakharkar propose a comparative genomic approach for metabolic pathway analysis for in silico identification of putative drug targets in *Pseudomonas aeruginosa*. You et al. compare four methods of affinity prediction models for HLA-binding peptides and T-cell epitope identification, and find that non-liner models perform better than linear predictors. Rajapakse and Feng propose a method to identify peptides binding to MHC molecules by simultaneously optimizing entropy and evolutionary distance. Further, the binding motifs are determined by the optimal alignment of binding sites.

Part 6 of the proceedings contains five chapters on bioimaging. Dufour et al. develop an automated nuclear morphometric analysis of 3D fluorescence microscopy images by using active meshes. They also propose shape descriptors and evaluate their robustness and independence on fluorescent beads and on two cell lines. Kumar and Rajapakse propose a time-frequency-based method for detection of activation in functional MRI time-series and discuss the advantages over earlier methods. Dehzangi, Zolghadri, and Boostani develop a weighted distance neural network for high-performance classification of two imagery tasks in the cue-based brain computer interface. Zheng and Rajapakse tract the anatomical connectivity of the brain, using sequential sampling and resampling of diffusion tensor MR images. The method does not adopt fractional anisotropy as the stopping criteria and regularizes the fiber-tracking process by assigning high confidence values at low curvature points. Gong et al. develop an automated pipeline for classification of CT brain images of different head trauma, which is useful for building a content-based medical image retrieval system.

We would like to sincerely thank all authors who spent their time and effort to make important contributions to this book. Many thanks go to the reviewers whose comments have enhanced the quality of the chapters. Our gratitude also goes to the LNBI editors and the managing editor for their most kind support and help in editing this book.

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We would like to express our gratitude to all PRIB 2007 International Program Committee members and other invited reviewers for their objective and thorough reviews of the submitted papers. We fully appreciate the PRIB 2007 Organizing Committee for their time and excellent work. We thank Publicity Co-chairs, Feng Lin and Sy Loi Ho, for their hard work in getting the proceedings ready on time. We are grateful to Norhana Ahmad, PRIB 2007 secretary, for coordinating all the logistics of the workshop. Our thanks also go to Ang Linda for maintaining the workshop Web
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October 2007

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