

Introduction to Special Issue on Bioinformatics

This special issue presents a selection of the latest research on data mining applications in bioinformatics. The call for submissions attracted 22 papers which were reviewed by three anonymous referees. Out of these, we selected 5 papers for inclusion in this special issue.

The first article, *Compositional Mining of Multirelational Biological Datasets* by Ying Jin, T.M. Murali, and Naren Ramakrishnan, presents a compositional framework over redescription mining and biclustering primitives to create a chain of inferences, moving from one “vocabulary” to the next. Applications in gene ontology matching and cell stress response show the effectiveness of their approach. In the article, *Discovering Semantic Biomedical Relations Utilizing the Web*, Saurav Sahay, Sougata Mukherjea, Eugene Agichtein, Ernest V. Garcia, Shamkant B. Navathe, and Ashwin Ram describe automated methods to discover relations between biomedical resources on the Web. These relations have applications in constructing and augmenting ontologies and other knowledge bases and in enabling the vision of the Semantic Web for life sciences. The article, *Developmental Stage Annotation of Drosophila Gene Expression Pattern Images via an Entire Solution Path for LDA* by Jieping Ye, Jianhui Chen, Ravi Janardan, and Sudhir Kumar, looks at the problem of finding patterns in temporal gene expression data from fruit fly embryos during development. The goal is to extract patterns of cell differentiation via LdaPath, a novel formulation of Linear Discriminant Analysis (LDA). In the article, *Adaptive Discriminant Analysis for Microarray-based Classification* by Yijuan Lu, Qi Tian, Jennifer Neary, Feng Liu, and Yufeng Wang, the authors propose the Adaptive Discriminant Analysis approach to combine the positive elements of LDA as well as biased discriminant analysis. The new approach allows the discovery of a good discriminative subspace, and they apply the technique to lifecycle microarray data taken from Yeast and Malaria parasites. Finally, in *A New Efficient Probabilistic Model for Mining Labeled Ordered Trees Applied to Glycobiology*, Kosuke Hashimoto, Kiyoko Aoki-Kinoshita, Nobuhisa Ueda, Minoru Kanehisa, and Hiroshi Mamitsuka model Glycans (Carbohydrate sugar chains) as labeled ordered trees. They propose a new probabilistic ordered tree Markov model and show how to perform efficient likelihood computation, model estimation, and state transition inference. They apply the new model in classifying two kinds of Glycans.

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