# **Editorial**

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Biographical notes: Mohammed J. Zaki is an Associate Professor of Computer Science at RPI. He received his PhD Degree in Computer Science from the University of Rochester in 1998. His research interests focus on developing novel data mining techniques, especially in bioinformatics. He has published over 100 papers on data mining, and he is a co-editor of the book "Data Mining in Bioinformatics", Springer-London, 2005. He is currently an Associate Editor for IEEE Transactions on Knowledge and Data Engineering, Action Editor for Data Mining and Knowledge Discovery, and on the Editorial Board for Scientific Programming, International Journal of Data Warehousing and Mining, and International Journal of Data Mining and Bioinformatics. He has received the US NSF and DOE Career Awards, as well as service awards from the ACM and IEEE.

Akifumi Makinouchi received the BE (Bachelor of Engineering) Degree in Electronics Engineering from Kyoto University, Kyoto, Japan in 1968, and the Docteur Ingeneur Degree from the University of Grenoble, Grenoble, France, in 1970. He got DE Degree from Kyoto University in 1985. He is currently a Professor of the Graduate School of Information Science and Electrical Engineering, Kyushu University, Kyushu, Japan. His research interests include database applications for biomedical engineering and spatial databases.

Shunsuke Uemura is a Professor at the Graduate School of Information Science, Nara Institute of Science and Technology, Japan. He has been a member of the Research Staff at MITI's Electrotechnical Laboratory, a Visiting Researcher at MIT's Electronic Systems Laboratory and a Professor at the Tokyo University of Agriculture and Technology. He received a BE, an ME

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#### 1 Introduction

Modern electronic computers were invented around 1945, and the DNA double helix structure was discovered in 1953. This century promises to integrate these areas, computer science and biology, to understand the mystery of life. *The First International Workshop on Biomedical Data Engineering* was held in Tokyo in conjunction with IEEE International Conference on Data Engineering, 2005. The workshop focused on data engineering aspects of life science and medical data, and on related areas such as image processing and pattern recognition. One of its goals was to facilitate collaboration between researchers and engineers in the data engineering field and the ones in bioinformatics and medical fields. Papers were solicited on topics such as: bioinformatics, biomedical literature mining, data mining, DB migration, DB integration, digital human DB, graph data analysis, high-performance computing, human body simulation, image analysis, image databases, indexing and retrieval techniques, medical databases, medical image diagnostic, pattern recognition and visualisation.

The workshop attracted 32 submissions, out of which 19 were selected for presentation. After the workshop, three papers were selected for inclusion in this special issue on the best papers of the *International Workshop on Biomedical Data Engineering*.

### 2 Papers in this special issue

The paper by Parvini and Shahabi (2006) describes a new approach to recognise both static and dynamic hand gestures. They collect raw data from sensors attached to human hands, and extract unique signatures for various static and dynamic gestures across different users. Their approach is calibration-free and training-tree. They show how to recognise gestures from the American Sign Language, resulting in over 75% accuracy.

Morse et al. (2006) motivate the need for a new kind of indexing structure called the Target Tree, which enables efficient results for the so-called radial queries, which retrieve all objects that intersect rays emanating from a central target point. They show that for radial queries, traditional index structures like  $R^*$ -trees and quad-trees do not work as well as the target tree. They apply the new index structure for surgical planning applications in neurosurgery.

In the paper by Cheung et al. (2006), they address the problem of mining coherent clusters from micro-array gene expression datasets. They propose a new algorithm for mining order preserving sub-matrices, which can be generalised to several approaches for mining pattern-based biclusters. They demonstrate the effectiveness of their approach on several real datasets.

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