Bio-Imaging and Bio-Informatics

"Biomedical Engineering integrates physical, chemical, mathematical, medical science, and engineering principles for the study of biology, medicine, behavior and health, and the development of tools and devices for surgical operations."

"Bio-Informatics combines computer science, biology, physical and chemical principles, and tools for analysis and modeling of large set of biological data, the managing of chronic diseases the study of molecular computing, cloning, and the development of training tools of bio-computing systems." by the National Institute of Health.

Bio-Imaging (Bioimaging) and *Bio-Informatics* (or Bioinformatics) are two very active and attractive research fields with a significant impact in the new technological developments. Bioimaging is the field of methodologies and devices for processing analysis and understanding of biological and in general, medical images. Bioinformatics is the field, where methodologies and devices from computer science, chemistry, and biology are used for processing, analysis and the understanding of the genetic code and its implications into the lives of human beings.

Both Bioimaging and Bioinformatics are very important and very active research areas that offer promising solutions to complex medical and biological problems, as well as, practical applications to other professions in industry and government.

These areas have rapidly increasing impact on our society (important health issues) and commercial applications (drugs design, diseases diagnosis, etc.). In response to this demand, a number of related papers have been published worldwide. This special issue is coming to address to important "point" of collaborative existence of both these two fields, where bioimaging methodologies and devices are going to play a very valuable role in the representation, processing, analysis and understanding of large set of bio-data. This issue covers these two fields as Part I and Part II.

The papers of this special issue have gone through several stages of review. From 94 full papers, in particular, submitted in the IEEE Symposium on BIBE-2000, 38 papers were selected for a second review for the IEEE T-SMCB special issue. From these papers only ten made the final list after peer review process with two to three referees assigned per paper.

The Bioimaging Part I includes seven papers. The paper by F. Kagalwala and T. Kanade describes the reconstructing specimens using DIC microscope images. The paper by W. Wee, Y. Tang, X. Wang, and L. He presents a model based contour searching and contour extraction deformable method. R. Chbeir and F. Favetta paper discusses a global description of medical images with high precision. The paper by R. Yager and F. Quek deals with the surface parameterization in volumetric images for feature classification. The paper by N. Bourbakis and M. Awad describes a 3-D visualization for image navigated brain surgery. Finally in Part I, S. Mertoguno and N. Bourbakis paper presents a human retina-like vision processor.

The Bioinformatics Part II includes four papers. The paper by M. A. Zaki, S. Jin, and C. Bystroff deals with mining residue contacts in proteins using local structure predictions. The paper by M. Raymer, T. Doom, L. Kuhn, and W. Punch discusses the knowledge discovery in medical and biological datasets using a hybrid Bayes classifier/evolutionary algorithm. B. Parvin, G. Cong, G. Fontenay, J. Taylor, R. Henshall and M. Barcellos-Hoff Describe a bioinformatics system for studying the mechanism of inter-cell signaling. Finally the last paper of the Part II, by J. Aracena, S. Lamine, M. Mermet, O. Cohen and J. Demongeot, deals with the mathematical modeling in genetic networks: relationships between the genetic expression and both chromosomic breakage and positive circuits.

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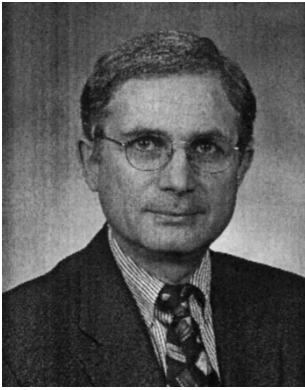
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