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RECENT ADVANCES IN BIOMEDICAL ELECTRONICS AND BIOMEDICAL INFORMATICS

PROCEEDINGS OF THE 2ND WSEAS INTERNATIONAL CONFERENCE ON BIOMEDICAL ELECTRONICS AND BIOMEDICAL INFORMATICS (BEBI'09)

Moscow, Russia, August 20-22, 2009

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Preface

This year the 2nd WSEAS International Conference on BIOMEDICAL ELECTRONICS and BIOMEDICAL INFORMATICS (BEBI '09) was held in Moscow, Russia, in August 20-22, 2009. The Conference remains faithful to its original idea of providing a platform to discuss biomedical circuits, biomedical devices, biomedical electronics, biomedical signal processing, biomedical applied electromagnetics, biomedical informaticsa etc. with participants from all over the world, both from academia and from industry.

Its success is reflected in the papers received, with participants coming from several countries, allowing a real multinational multicultural exchange of experiences and ideas.

The accepted papers of this conference are published in this Book that will be indexed by ISI. Please, check it: www.worldses.org/indexes as well as in the CD-ROM Proceedings. They will be also available in the E-Library of the WSEAS. The best papers will be also promoted in many Journals for further evaluation.

A Conference such as this can only succeed as a team effort, so the Editors want to thank the International Scientific Committee and the Reviewers for their excellent work in reviewing the papers as well as their invaluable input and advice.

The Editors

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Plenary Lecture 1

Present Situation and Future Trends of Omics-Based Medicine and Systems Pathology



Professor Hiroshi Tanaka School of Biomedical Sciences Tokyo Medical and Dental University JAPAN

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Abstract: A new perspective for personalized and predictive care which clinical omics and bioinformatics cooperatively open will be presented, with emphasis on promising possibilities which "omics-based personalized care" is thought to bring about. In doing so, we take it into consideration that, along the rapid progress of the omics and bioinformatics, the contents of "genome/omics-based personalized care" have evolved, mainly through three generations. The first generation is personalized care based on (1) the polymorphism of the "germline" genome sequences, such as personalized medication depending on the individual genetic differences concerning the pharmacodynamics/phamarcokinetics or estimation of genotype relative risk for individual's disease occurrence, the second generation is that based on (2) the information pattern of vast amount of omics data of diseased "somatic" cell, which brings about detailed classification, early diagnosis and prognosis of the disease, and the third generation is that based on (3) the system level understanding of complex diseases which enables wholistic comprehension of the mechanism of diseases, with special reference to disease pathway.

Brief Biography of the Speaker:

Date of birth: September 15, 1949

Home address: 4-29-14 Hakusan, Bunkyo-ku, Tokyo, Japan 112-0001

Affiliation: Professor, Department of computational biology, School of Biomedical sciences, Department of

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Education

1974: Graduated from Department of Mathematical Engineering Faculty of Engineering, University of Tokyo

1976: Received Master of Engineering from the Graduate School of Engineering, University of Tokyo

1981: Received Doctor of Medical Science from Graduate School of Medicine, University of Tokyo

1983: Received Ph.D. from Graduate School of Engineering, University of Tokyo

Academic career

1982-1987: Assistant Professor at the Institute for Medical Electronics, School of Medicine, University of Tokyo

1982-1984: Visiting Scientist, at Uppsala University and Linkoping University, Sweden

1987-1991: Associate Professor, Hamamatsu University School of Medicine

1990: Visiting scientist in MIT Laboratory of Computer Science

1991-2003: Professor of bioinformatics, Medical Research Institute, Tokyo Medical and Dental University

1995-now: Director of Information center for Medicine, Tokyo Medical and Dental University

2003-now: Professor of computational biology, School of Biomedical Sciences, Tokyo Medical and Dental University

Plenary Lecture 2 Complexity Analysis of Signals and Images in Biomedicine



Professor Tuan D. Pham

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Abstract: Measuring the complexity of a pattern expressed either in time or space has been introduced to quantify its information content, which can then be applied for classification. Such information measures are particularly useful for the understanding of systems complexity in many fields of sciences, business and engineering. This talk presents recent work on the concepts of geostatistical entropy and fuzzy fractals as the measures of pattern complexity and similarity in bio-signals, molecular and biomedical images. These measures can be useful tools for extracting temporal signatures of biological and physiological time series data, and quantifying morphological changes in cell and brain images.

Brief Biography of the Speaker: Tuan D. Pham received his PhD degree in 1995 from the University of New South Wales. His current research interests include image processing, molecular and medical image analysis, pattern recognition, bioinformatics, biomedical informatics, fuzzy-set algorithms, genetic algorithms, neural networks, geostatistics, signal processing, fractals and chaos. His research has been funded by the Australian Research Council, academic institutions, and industry. Dr. Pham is an editorial board member of several journals and book series including Pattern Recognition (Elsevier), Current Bioinformatics (Bentham), Recent Patents on Computer Science (Bentham), Proteomics Insights (open access journal, Libertas Academica Press), Book Series on Bioinformatics and Computational Biolmaging (Artech House), invited Regional Editor of International Journal of Computer Aided Engineering and Technology (Inderscience Publishers), and invited Editor-in-Chief of WSEAS Transaction on Biology and Biomedicine. He has been serving as chair and technical committee member of more than 30 international conferences in the fields of image processing, pattern recognition, computational intelligence, and computational life sciences.

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