



**APPLIED COMPUTER & APPLIED COMPUTATIONAL SCIENCE**

**Editors:**

**Prof. Shengyong Chen, Zhejiang University of Technology, China**  
**Prof. Hongkuan Wu, China Jiliang University, China**

# **Applied Computer & Applied Computational Science**

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**Proceedings of the 9<sup>th</sup> WSEAS International Conference on  
Applied Computer and Applied Computational Science  
(ACACOS '10)**

**Hangzhou, China, April 11-13, 2010**

**Electrical and Computer Engineering Series  
A Series of Reference Books and Textbooks**

**ISBN: 978-960-474-173-1**  
**ISSN: 1790-5117**

**Published by WSEAS Press**  
**[www.wseas.org](http://www.wseas.org)**







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All papers of the present volume were peer reviewed by two independent reviewers. Acceptance was granted when both reviewers' recommendations were positive.  
See also: <http://www.worldses.org/review/index.html>

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**Preface**

This year the 9th WSEAS International Conference on APPLIED COMPUTER and APPLIED COMPUTATIONAL SCIENCE (ACACOS '10) was held in Hangzhou, China, April 11-13, 2010. The conference remains faithful to its original idea of providing a platform to discuss programming languages, software methodologies, educational software, mobile and wireless computing, broadband networks, fault tolerance, artificial intelligence, wireless communications, blue-tooth technologies, satellite communications, law aspects related to informatics 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](http://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



# Table of Contents

<b><u>Plenary Lecture 1: Mathematics of Bioinformatics: Theory, Practice, and Applications</u></b>	15
<i>Matthew He</i>	
<b><u>A Web-Enabled Intelligent Approach Towards Digital Marketing Planning: The Integrated System and its Effectiveness</u></b>	17
<i>Shuliang Li, Jim Zheng Li, Hong He</i>	
<b><u>The Numerical Solution of the Singular Two-Point Boundary Value Problems by using Non-Polynomial Spline Functions</u></b>	23
<i>Hikmet Caglar, Canan Akkoyunlu, Nazan Caglar, Durmus Dunder</i>	
<b><u>A Non-Polynomial Spline Solution of the One-Dimensional Wave Equation Subject to an Integral Conservation Condition</u></b>	27
<i>Hikmet Caglar, Serhat Yilmaz, Nazan Caglar, Muge Iseri</i>	
<b><u>Spatial Clustering and Outlier Analysis for the Regionalization of Maize Cultivation in China</u></b>	31
<i>Hu Wang, Xiaodong Zhang, Shaoming Li, Xiaomei Song</i>	
<b><u>On the Use of Multistage Scenario Trees for Optimal Portfolios in the BMV</u></b>	37
<i>Maria A. Osorio, Abraham Sanchez, Beatriz Bernabe, Rogelio Gonzalez</i>	
<b><u>High Speed Multiplier Based on the Algorithm of Chinese Abacus</u></b>	44
<i>Chien-Hung Lin, Shu-Chung Yi, Jin-Jia Chen</i>	
<b><u>The Preliminary Study of Ubiquitous Infrastructure of Museum Service Applications in National Palace Museum</u></b>	50
<i>Chen-Wo Kuo, Johannes K. Chiang</i>	
<b><u>Applying an Extended E-S-Qual Scale to Assess the Effects of E-service Quality on Online Loyalty with Customer Satisfaction and Perceived Value as Mediators</u></b>	55
<i>Hao-Erl Yang, Wei-Jen Cheng, Jia-Ying Chan, Bo-Chuan Pan, Chia-Shing Chen</i>	
<b><u>The Forging Analysis by Using the Rigid-Plastic Hybrid PCM/FEM</u></b>	60
<i>Yong-Ming Guo, Shunpei Kamitani</i>	
<b><u>Acceptance Level of Push Technology-based On-line Shopping Widget among Malaysians: Application of Technology Acceptance Theory</u></b>	67
<i>Lee Yean Hooi, Mohd Azam Osman, Rosnah Idrus, Tan Shiang-Yen</i>	
<b><u>Study on the Maize Varieties Combination Model of Influence of Multi-factor and System Implement</u></b>	74
<i>Lin Yang, Xiaodong Zhang, Shaoming Li</i>	
<b><u>Using a Projective Technique to Investigate Students' Mental Models toward E-Learning</u></b>	80
<i>Chun-Hui Wu, Shiow-Luan Wang, Yih-Her Yan</i>	
<b><u>Toward MLS Database System with Write Downs</u></b>	85
<i>Piya Jitthammapirom, Suphamit Chittayasothorn</i>	

<b><u>Industry International Competitiveness-the Case of Taiwan Consumer and Commercial Transformers Firms</u></b>	90
<i>Chun-Wei Lu</i>	
<b><u>Architecture of Web Client Server Systems with Advanced Asynchronous Communications</u></b>	96
<i>Filip Maly, Antonin Slaby</i>	
<b><u>An Analysis of the Current Status of Digital Divide in Taiwan</u></b>	100
<i>Ruey-Gwo Chung, Chih-Wei Li, Chen-Liao Chen</i>	
<b><u>Breadth-First Search based Bus Transport Transfer Algorithm</u></b>	106
<i>Zhang-Wei Li, Mei Zhu</i>	
<b><u>Enhancing Learners' Performances on 3D Animation through Game-Based E-Learning</u></b>	111
<i>Chih-Hsiao Tsai, Jung-Chuan Yen, I-Jung Chen</i>	
<b><u>Using Multiple Imputation to Simulate Time Series</u></b>	117
<i>Sebastian Cano, Jordi Andreu</i>	
<b><u>New Method of the Numerical of Gauss-Lobatto Quadrature Rules With Precision Degree (2n+5)</u></b>	123
<i>Saeed Ghasrodashti, Mehdi Bagheri, Farzad Hoseinzadeh</i>	
<b><u>Reducing Computation Overhead of Flash Translation Layer with Hash</u></b>	126
<i>Ilhoon Shin</i>	
<b><u>Essay on Teletraffic Models (I)</u></b>	130
<i>Ming Li</i>	
<b><u>2-D Dynamic Analysis of a Pressure Relief Valve by CFD</u></b>	136
<i>Xue Guan Song, Ji Hoon Jung, Hyeong Seok Lee, Dong Kwan Kim, Young Chul Park</i>	
<b><u>Shape Optimization of Clutch Drum Hub Preform Using Taguchi Method</u></b>	141
<i>Yong Seok Song, Joon Hong Park, Jun Ho Lee, Jeong Ju Choi, Young Chul Park</i>	
<b><u>Structural Design Method of a Control Arm with Consideration of Strength</u></b>	149
<i>Jong-kyu Kim, Seung Kyu Kim, Hwan-Jung Son, Kwon-Hee Lee, Young-Chul Park</i>	
<b><u>Structural Design Examples Using Metamodel-Based Approximation Model</u></b>	153
<i>Jin-Hwan Lee, Seok-Cheol Hwang, Joon Hong Park, Kwon-Hee Lee</i>	
<b><u>Computational Fluid Dynamic Analysis of Flow Coefficient for Pan Check Valve</u></b>	157
<i>Joon-Ho Lee, Xue-Guan Song, Young-Chul Park, Sang-Mo Kang</i>	
<b><u>An Adaptive Moving Least Squares Method for Non-uniform Points Set Fitting</u></b>	161
<i>Xianping Huang, Qing Tian, Jianfei Mao</i>	
<b><u>Computer-Aided Craniofacial Reconstruction</u></b>	167
<i>Li Jiang, Yaolei Lin, Le-Wei Yu, Qianwei Ye</i>	
<b><u>Fuzzy Basis on Clustering of Knowledge Structure with Cognition Diagnosis for Algebra Learning</u></b>	174
<i>Jeng-Ming Yih</i>	



<b><u>Unsupervised Clustering Algorithm Based on Normalized Mahalanobis Distances</u></b>	180
<i>Jeng-Ming Yih, Sue-Fen Huang</i>	
<b><u>Clustering Approach to Polytomous IRS with Application in Statistics Learning for University Students</u></b>	185
<i>Yuan-Horng Lin</i>	
<b><u>Collaborative Virtual Environment Model for Medical E-Learning</u></b>	191
<i>Samir M. Abd El-Razek, Hazem M. El-Bakry, Wael F. Abd El-Wahed, Nikos Mastorakis</i>	
<b><u>Hardware Implementation of Fuzzy Flip-Flops Based on Lukasiewicz Norms</u></b>	196
<i>Rita Lovassy, Antonio Hernandez Zavala, Laszlo Gal, Oscar Camacho Nieto, Laszlo T. Koczy, Ildar Batyrshin</i>	
<b><u>Determining an Optimal Subdivision of Gene Transfer Partitions</u></b>	202
<i>Mark Farkas, Peter Foldesi, Janos Botzheim, Laszlo T. Koczy</i>	
<b><u>Fuzzy Communication in Collaboration of Intelligent Agents</u></b>	208
<i>Aron Ballagi, Laszlo T. Koczy</i>	
<b><u>Innovation Management Framework in Academic Institutions</u></b>	215
<i>M. Nordin A. Rahman, Norlina Udin, Fauziah A. Wahab, Rohana Ismail</i>	
<b><u>GPS Receiver Tracking Loop Optimization Based on a Behavioral Approach</u></b>	221
<i>He-Sheng Wang</i>	
<b><u>Authors Index</u></b>	226



## Plenary Lecture 1

### Mathematics of Bioinformatics: Theory, Practice, and Applications



#### Professor Matthew He

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**Abstract:** Historically, mathematics, probability and statistics have been widely used in biological sciences. Science has a challenge to understand a system organization of molecular genetic ensemble with its unique properties of reliability and productivity. Disclosing of key secrets of this organization means a big step in science about nature in a whole and a big step to create the most productive biotechnologies. Knowledge about this structural organization should become a part of mathematical natural science.

Recent advances of mathematical methods and techniques in bioinformatics have been rapidly growing. There is more to life than the genomic blueprint of each organism. Life functions within the natural laws that we know and the ones we do not know. Mathematics can be used to understand life from the molecular to the biosphere level. This talk is devoted to the connection and integration between fundamental mathematical methods and biological sequences, structures, and networks.

The outline of this talk includes:

1. Bioinformatics and Mathematics
2. Genetic Codes, Matrices, and Symmetrical Techniques
3. Biological Sequences, Sequence Alignment, and Statistics
4. Structures of DNA and Knot Theory
5. Protein Structures, Geometry, and Topology
6. Biological Networks and Graph Theory

#### Brief Biography of the Speaker:

Matthew He, Ph.D., is Full Professor and Director of the Division of Math, Science, and Technology of Nova Southeastern University, Florida, USA. He is Full Professor and Grand Ph.D. from the World Information Distributed University in 2004. He has been awarded as an academician of European Academy of Informatization since 2004. He received the World Academy of Sciences Achievement Award in recognition of his research contributions in the field of computing in 2003.

Matthew He received his Ph. D. in Mathematics from University of South Florida in 1991. He was a research associate at the Department of Mathematics and Theoretical Physics, Cambridge University, Cambridge, England in 1986 and at the Department of Mathematics, Eidgenossische Technische Hochschule, Zurich, Switzerland in 1987. He was also a visiting professor at National Key Research Lab of Computational Mathematics of Chinese Science of Academy and University of Rome, Italy in 1998.

Dr. Matthew He has authored/edited 8 books and published over 100 research papers in the areas of mathematics, bioinformatics, computer vision, information theory, mathematics and engineering techniques in medical and biological sciences. He is an editor of International Journal of Software Science and Computational Intelligence, International Journal of Cognitive Informatics and Natural Intelligence, International Journal of Biological Systems, and International Journal of Integrative Biology. He is an invited series editor of Biomedical and Life Sciences of Henry Stewart Talk "Using Bioinformatics in Exploration in Genetic Diversity". He is a Chairman of International Society of Symmetry in Bioinformatics and a member of International Advisory Board of "International Symmetry Association (ISA)". He is a member of American Mathematical Society (AMS), Association of Computing Machinery (ACM), IEEE Computer Society, World Association of Science Engineering (WASE), and International Advisory Board member of Bioinformatics Group of International Federation for Information Processing (IFIP). He was an international scientific committee co-chair of International Conference of Bioinformatics and its Applications (ICBA 2004), a general co-chair of International Conference of Bioinformatics Research and Applications (ISBRA 2009), and a keynote speaker of many international conferences in the areas of mathematics, bioinformatics, and information science and engineering.