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Applied Computer & Applied Computational Science

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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 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

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

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

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

Plenary Lecture 1

Mathematics of Bioinformatics: Theory, Practice, and Applications



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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.

Authors Index

Akkoyunlu, C.	23	Huang, X.	161	Osman, M. A.	67
Andreu, J.	117	Hwang, S.-C.	153	Osorio, M. A.	37
Bagheri, M.	123	Idrus, R.	67	Pan, B.-C.	55
Ballagi, A.	208	Iseri, M.	27	Park, J. H.	141, 153
Batyrsin, I.	196	Ismail, R.	215	Park, Y. C.	136, 141
Bernabe, B.	37	Jiang, L.	167	Park, Y. C.	149, 157
Botzheim, J.	202	Jitthammapirom, P.	85	Rahman, M. N. A.	215
Caglar, H.	23, 27	Jung, J. H.	136	Sanchez, A.	37
Caglar, N.	23, 27	Kamitani, S.	60	Shin, I.	126
Cano, S.	117	Kang, S.-M.	157	Slaby, A.	96
Chan, J.-Y.	55	Kim, D. K.	136	Son, H.-J.	149
Chen, C.-L.	100	Kim, J.-K.	149	Song, X.	31
Chen, C.-S.	55	Kim, S. K.	149	Song, X.-G.	136, 157
Chen, I.-J.	111	Koczy, L. T.	196, 202, 208	Song, Y. S.	141
Chen, J.-J.	44	Kuo, C.-W.	50	Tan, S.-Y.	67
Cheng, W.-J.	55	Lee, H. S.	136	Tian, Q.	161
Chiang, J. K.	50	Lee, Ji.-H.	153	Tsai, C.-H.	111
Chittayasothorn, S.	85	Lee, Jo. H.	141, 157	Udin, N.	215
Choi, J. J.	141	Lee, K.-H.	149, 153	Wahab, F. A.	215
Chung, R.-G.	100	Li, C.-W.	100	Wang, H.	31
Dundar, D.	23	Li, J. Z.	17	Wang, S.-L.	80
El-Bakry, H. M.	191	Li, M.	130	Wu, C.-H.	80
El-Razek, S. M. A.	191	Li, Sha.	31, 74	Yan, Y.-H.	80
El-Wahed, Q. F. A.	191	Li, Shu.	17	Yang, H.-E.	55
Farkas, M.	202	Li, Z.-W.	106	Yang, L.	74
Foldesi, P.	202	Lin, C.-H.	44	Ye, Q.	167
Gal, L.	196	Lin, Y.	167	Yen, J.-C.	111
Ghasrodashti, S.	123	Lin, Y.-H.	185	Yi, S.-C.	44
Gonzalez, R.	37	Lovassy, R.	196	Yih, J.-M.	174, 180
Guo, Y.-M.	60	Lu, C.-W.	90	Yilmaz, S.	27
He, H.	17	Maly, F.	96	Yu, L.-W.	167
Hooi, L. Y.	67	Mao, J.	161	Zavala, A. H.	196
Hoseinzadeh, F.	123	Mastorakis, N.	191	Zhang, X.	31, 74
Huang, S.-F.	180	Nieto, O. C.	196	Zhu, M.	106