

## PRIB 2007 Program

### Day 1: Oct 1 2007

8.30am – 8.50am	<i>Opening Ceremony</i>  Guest of Honor: Prof Bertil Andersson Provost, Nanyang Technological University	
8.50am – 9.50am	Keynote 1: Prof Nikhil R. Pal Identification of biomarkers from expression data: Linear and nonlinear methods	
9.50am – 10.10am	<i>Coffee Break</i>	
10.10am – 12.10pm	Oral session O1AM1 Prediction of Protein Structure, Interaction and Localization	Oral Session O1AM2 Gene Expression Analysis
12.10pm – 1.20pm	<i>Lunch</i>	
1.20pm – 2.30pm	Poster session P1	
2.30pm – 3.30pm	Keynote 2: Dr. Gary B. Fogel Computational Intelligence Approaches for Pattern Discovery in Biological Systems	
3.30pm – 3.50pm	<i>Coffee Break</i>	
3.50pm – 5.50pm	Oral Session O1PM1 Special Session on Residue-wise Protein Interaction Prediction	Oral Session O1PM2 Special Session on Information Theoretical Approaches to Microarray Data Analysis

## Day 2: Oct 2 2007

8.30am – 9.30am	Keynote 3: Dr. Glenn Tesler Distribution of Segment Lengths in Genome Rearrangements	
9.30am – 9.50am	<i>Coffee Break</i>	
9.50am – 11.50pm	Oral session O2AM1 Sequence Analysis	Oral Session O2AM2 Pathway Analysis
11.50am – 1.00pm	<i>Lunch</i>	
1.00pm – 2.00pm	Posters session P2	
2.00pm – 4.00pm	Oral Session O2PM1 Bioimaging	Oral Session O2PM2 Medical Informatics
4.00pm – 4.20pm	<i>Coffee Break</i>	
4.20pm – 5.20pm	Keynote 4: Prof Raj Acharya Information fusion techniques in bioinformatics	
5.20pm – 5.40pm	<i>Award Ceremony and Closing</i>	

## **Session O1AM1: Prediction of Protein Structure, Interaction and Localization**

### **Monday, Oct 1, 10.10am – 12.10pm, Ball Room 1**

*Session Chair: TBA*

10.10am – 10.30am: Finding Useful Building Blocks for Construction of Protein 3-D Structures Using a Structural Variant of Mountain Clustering Method (#159, *EMBM*)

*Ken-Li Lin<sup>1,2</sup>, Chin-Teng Lin<sup>1</sup>, Nikhil R. Pal<sup>3,4</sup>, Sudepta Ojha<sup>5</sup>*

<sup>1</sup>Department of Electrical and Control Engineering, National Chiao-Tung University, Taiwan

<sup>2</sup> Computer Center, Chung-Hua University, Taiwan; College of Computer Science, National Chiao-Tung University, Taiwan

<sup>3</sup>Indian Statistical Institute, Calcutta, India

<sup>4</sup>Hong Kong and Shanghai Banking Corporation Ltd, India

10.30am – 10.50am: Wavelet Variance Features for Identification and Classification of GPCRs using SVM (#192, *EMBM*)

*Ravi Gupta<sup>1</sup>, Ankush Mittal<sup>1</sup>, Kuldip Singh<sup>1</sup>, Vipin Narang<sup>2</sup>, Sujoy Roy<sup>3</sup>*

<sup>1</sup>Department of Electronics and Computer Engineering, Indian Institute of Technology Roorkee, India

<sup>2</sup>Department of Computer Science Engineering, National University of Singapore, Singapore

<sup>3</sup>Institute of Infocomm Research, Singapore

10.50am – 11.10am: Using Decision Templates to Predict Subcellular Localization of Protein (#166, *LNBI*)

*Jianyu Shi<sup>1</sup>, Shaowu Zhang<sup>2</sup>, Quan Pan<sup>2</sup>, Yanning Zhang<sup>1</sup>*

<sup>1</sup>School of Computer Science and Engineering, Northwestern Polytechnical University, China

<sup>2</sup>School of Automation, Northwestern Polytechnical University, China

11.10am – 11.30am: Generalized Schemata Theorem Incorporating Twin Removal for Protein Structure Prediction (#201, *LNBI*)

*Md Tamjidul Hoque, Madhu Chetty, Laurence S Dooley*

Gippsland School of Information Technology, Monash University, Australia

11.30am – 11.50am: Using Fuzzy Support Vector Machine Network to Predict Low Homology Protein Structural Classes (#153, *LNBI*)

*Tongliang Zhang<sup>1</sup>, Rong Wei<sup>3</sup>, Yongsheng Ding<sup>1,2</sup>*

<sup>1</sup>College of Information Sciences and Technology, China

<sup>2</sup>Donghua University, China

<sup>3</sup>College of Sciences, Hebei Polytechnic University, China

11.50am – 12.10pm: SVM-BetaPred: Prediction of Right-Handed  $\beta$ -Helix Fold from Protein Sequence Using SVM (#197, *LNBI*)

*Siddharth Singh<sup>1</sup>, Krishnan Hajela<sup>2</sup>, Ashwini Kumar Ramani<sup>1</sup>*

<sup>1</sup>School of Computer Science, Devi Ahilya University, India

<sup>2</sup>School of Life Science, Devi Ahilya University, India

## **Session O1AM2: Gene Expression Analysis**

### **Monday, Oct 1, 10.10am – 12.10pm, Ball Room 2**

*Session Chair: TBA*

10.10am – 10.30am: Ant-Based Association Rule Mining on Gene Expression Data Classification (#141, *EMBM*)

*Yulan He, Siu-Cheung Hui, Hock Siang Toh*

School of Computer Engineering, Nanyang Technological University, Singapore

10.30am – 10.50am: APMA Database for Affymetrix Target Sequences Mapping, Quality Assessment and Expression Data Mining (#205, *LNBI*)

*Yuriy Orlov<sup>1</sup>, Jiangtao Zhou<sup>1</sup>, Joanne Chen<sup>2</sup>, Atif Shahab<sup>1,2</sup>, Vladimir Kuznetsov<sup>1</sup>*

<sup>1</sup>Genome Institute of Singapore, Singapore

<sup>2</sup>Bioinformatics Institute, Singapore

10.50am – 11.10am: Ensemble of Dissimilarity Based Classifiers for Cancerous Samples Classification (#195, *LNBI*)

*Ángela Blanco<sup>1</sup>, Manuel Martín-Merino<sup>1</sup>, Javier de las Rivas<sup>2</sup>*

<sup>1</sup>Universidad Pontificia de Salamanca, Spain

<sup>2</sup>Cancer Research Center of Salamanca, Spain

11.10am – 11.30am: Gene Expression Analysis of Leukemia Samples Using Visual Interpretation of Small Ensembles: A Case Study (#150, *LNBI*)

*Gregor Stiglic<sup>1</sup>, Nawaz Khan<sup>2</sup>, Mateja Verlic<sup>1</sup>, Peter Kokol<sup>1</sup>*

<sup>1</sup>University of Maribor, Slovenia

<sup>2</sup>School of Computing Science, Middlesex University, United Kingdom

11.30am – 11.50am: Ant-MST: an Ant-Based Minimum Spanning Tree for Gene Expression Data Clustering (#160, *LNBI*)

*Deyu Zhou, Yulan He, Chee Keong Kwoh, Hao Wang*

School of Computer Engineering, Nanyang Technological University, Singapore

11.50am – 12.10pm: Integrating Gene Expression Data from Microarrays using the Self-Organising Map and the Gene Ontology (#152, *LNBI*)

*Ken McGarry, Mohammad Sarfraz, John MacIntyre,*

School of Computing and Technology, University of Sunderland, St Peters Campus, UK

## Poster Session P1

### Monday, Oct 1, 1.20pm – 2.30pm

Rough Sets and Fuzzy Sets Theory Applied to the Sequential Medical Diagnosis (#137, *LNBI*)

*Andrzej Zolnierrek, Marek Kurzynski*

Faculty of Electronics, Wroclaw University of Technology, Poland

TollML – a User-Editable Database for Toll-like Receptors and Ligands (#231, *Supplemental*)

*Jing Gong<sup>1</sup>, Tiandi Wei<sup>1</sup>, Ferdinand Jamitzky<sup>1,2</sup>, Wolfgang M. Heckl<sup>1,3</sup>, Shaila C. Rössle<sup>1</sup>*

<sup>1</sup>Department of Earth and Environmental Sciences, University of Munich, Germany

<sup>2</sup>Max-Planck-Institute for Extraterrestrial Physics, Germany

<sup>3</sup>Deutsches Museum, Germany.

Gene Arrangement for Cell Division Cycle Microarray Experiments without Sinusoidal Fittings (#234, *Supplemental*)

*Kazuhisa Makabe<sup>1</sup>, Y-h. Taguchi<sup>1,2</sup>*

<sup>1</sup>Faculty of Science and Technology, Chuo University, Japan

<sup>2</sup>Institute for Science and Technology, Chuo University, Japan

Error-Correcting Output Code Based on Feature Selection in Multiclass Learning Problems (#235, *Supplemental*)

*Young Bun Kim, Jung Hun Oh, Jean Gao*

Computer Science and Engineering Department, University of Texas, USA

Considering Syntax for Genome-Wide Genetic Analysis (#238, *Supplemental*)

*Richard Cowper-Sallari, Jason H. Moore*

Computational Genetics Laboratory, Dartmouth College, USA

Combination of Computational and Biological Approaches for Cis-regulatory Element Recognition in Glutamine Synthetase Sequences (#239, *Supplemental*)

*Tieming Ji<sup>1</sup>, Bindu Simon<sup>2</sup>, Desh Ranjan<sup>1</sup>, Champa Sengupta-Gopalan<sup>2</sup>*

<sup>1</sup>Department of Computer Science, New Mexico State University, USA

<sup>2</sup>Department of Plant and Environmental Sciences, New Mexico State University, USA

A Fuzzy Inference Scheme for SNP Identification (#242, *Supplemental*)

Elizabeth Sherly<sup>1</sup>, Sanil Shanker<sup>2</sup>

<sup>1</sup>Indian Institute of Information Technology and Management Kerala, India

<sup>2</sup>Department of Computer Science, University of Kerala, India

Critical Role of Tetra Proline Repeats in Osteoarthritis and Rheumatoid Arthritis (#243, *Supplemental*)

Kumar Amit, Naveen S, Shambhavi Srivastava, Amita Sinha

Department of Bioinformatics, DNA Research Centre, India

Critical Role of Proline and Glycine Conservation with Repeats in Neurodegenerative Disorders (#244, *Supplemental*)

Amit Kumar, Shambhavi Srivastava, Vivek Keshore, Karan Chengappa, Amita Sinha, Ravikant Kumar, Aryasekhar Sanyal

Department of Bioinformatics, DNA Research Centre, India

Bibliography Extraction Framework and Visualizer (#241, *Supplemental*)

Chia Bin Siak<sup>1</sup>, Chum Mok Pua<sup>2</sup>, James Michael Hogan<sup>3</sup>, Peter Timms<sup>4</sup>

<sup>1</sup>School of Media and Info Communications Technology, Singapore Polytechnic, Singapore

<sup>2</sup>Centre for Biomedical & Life Sciences, Singapore Polytechnic, Singapore

<sup>3</sup>School of Software Engineering and Data Communications, Queensland University of Technology, Australia

<sup>4</sup>School of Life Sciences, Queensland University of Technology, Australia

Conservation of “Mfcag” and “Aahc” Patterns in Insulin Resistance Syndrome and Other Coagulation Factor Disorders (#252, *Supplemental*)

Neetu Jabalia, Amit Kumar, Neelajali Srivastav, Jatinder Kaur

Department of Bioinformatics, DNA Research Centre, India

Involvement of TGKF & FTYDQ Pattern Conservation in Diabetes and Obesity (#253, *Supplemental*)

Manisha.Bhala, Amit Kumar, Ravikant Kumar, Vijayalakshmi.Kasu

Department of Bioinformatics, DNA Research Centre, India

A Comparison of Methods for Detection of Horizontal Gene Transfer, with Reference to Resistance Determinant Genes in *Staphylococcus aureus* (#255)

Zhang Tian You<sup>1</sup>, Kwoh Chee Keong<sup>2</sup>, Lim Chu Sing<sup>1</sup>

<sup>1</sup>Biomedical Engineering Research Center, Nanyang Technological University, Singapore

<sup>2</sup>School of Computer Engineering, Nanyang Technological University, Singapore

Predicting Plant microRNA Targets Using Hidden Markov Model (#258, *Supplemental*)

Le Lu, Jinming Li

School of Biological Sciences, Nanyang Technological University, Singapore

Recognition of Endogenous Features in Genome-wide Probe Selection (#266, *Supplemental*)

Angela Jean, Feng Lin

School of Computer Engineering, Nanyang Technological University, Singapore

## **Session O1PM1: Special Session on Residue-wide Prediction of Protein Structure Prediction**

**Monday, Oct 1, 3.50pm – 5.50pm, Ball Room 1**

*Session Organizers: Shandar Ahamad, Michael Gromiha*

3.50pm – 4.10pm: Secondary structure-based classification of protein-protein and protein-DNA interfaces (#257, *Supplemental*)-(Invited Talk)

Pinak Chakrabarti<sup>1</sup>, Mainak Guharoy<sup>2</sup>, Sumit Biswas<sup>2</sup>,

<sup>1</sup>Department of Biochemistry and Bioinformatics Centre, Bose Institute, India

<sup>2</sup>Department of Biochemistry, Bose Institute, India

4.10pm – 4.30pm: Protein Fold Recognition based upon the Amino Acid Occurrence (#210, *LNBI*)

*Y-h. Taguchi<sup>1</sup>, M. Michael Gromiha<sup>2</sup>,*

<sup>1</sup>Department of Physics, Chuo University, Japan

<sup>2</sup>National Institute of Advanced Industrial Science and Technology, Japan

4.30pm – 4.50pm: Using Efficient RBF Network to Identify interface residues based on PSSM profile and Biochemical Properties (#216, *LNBI*)

*Yu-Yen Ou<sup>1</sup>, Shu-An Chen<sup>1</sup>, Chung-Lu Shao<sup>2</sup>, and Hao-Geng Hung<sup>2</sup>*

<sup>1</sup>Graduate School of Biotechnology and Bioinformatics, Yuan-Ze University, Taiwan

<sup>2</sup>Department of Computer Science and Information Engineering, National Taiwan University, Taiwan

4.50pm – 5.10pm: Dynamic Outlier Exclusion training algorithm for sequence based predictions in proteins using neural network (#211, *LNBI*)

*Shandar Ahmad*

National Institute of Biomedical Innovation, Japan

5.10pm – 5.30pm: Bioinformatics on beta-barrel Membrane Proteins: Sequence and Structural Analysis, Discrimination and Prediction (#212, *LNBI*)

*M. Michael Gromiha*

National Institute of Advanced Industrial Science and Technology, Japan

5.30pm – 5.50pm: Estimation of Evolutionary Average Hydrophobicity Profile from a Family of Protein Sequences (#219, *LNBI*)

*Said Hassan Ahmed, Tor Flå*

Department of Mathematics and Statistics, University of Tromsø, Norway

## **Session O1PM2: Information theoretic approaches to microarray data analysis** **Monday, Oct 1, 3.50pm – 5.50pm, Ball Room 2**

*Session Organizers: Madhu Chetty and Ramesh Ram*

3.50pm – 4.10pm: Predicting the Optimal Degree of Differential Prioritization for Molecular Classification (#155, *EMBM*)

*Chia Huey Ooi, Madhu Chetty, Shyh Wei Teng*

Gippsland School of Information Technology, Monash University, Australia

4.10pm – 4.30pm: A Data-Driven Method of Identification of Essential Genes and Gene Pairs Associated with Survival Time of Cancer Patients (#228, *EMBM*)

*Efthimios Motakis, Anna V. Ivshina, Vladimir Kuznetsov*

Genome Institute of Singapore, Singapore

4.30pm – 4.50pm: Order Preserving Clustering by Finding Frequent Order in Gene Expression Data (#140, *LNBI*)

*Li Teng, Lai-Wan Chan*

Department of Computer Science and Engineering, the Chinese University of Hong Kong, Hong Kong

4.50pm – 5.10pm: Correlation-based Relevancy and Redundancy Measures for Efficient Gene Selection (#151, *LNBI*)

*Kezhi Mao, Wenyin Tang*

School of Electrical and Electronic Engineering, Nanyang Technological University, Singapore

5.10pm – 5.30pm: SVM-RFE with Relevancy and Redundancy Criteria for Gene Selection (#225, *LNBI*)

*Piyushkumar A. Mundra<sup>1</sup>, Jagath C. Rajapakse<sup>1,2</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>Singapore-MIT Alliance, Singapore.

5.30pm – 5.50pm: Digital Expression Profiles of Human Endogenous Retroviruses (#172, *LNBI*)

*Merja Oja*

Helsinki Institute for Information Technology, Helsinki University of Technology, Finland

## **Session O2AM1: Sequence Analysis**

### **Tuesday, Oct 2, 9.50am – 11.50am, Ball Room 1**

*Session Chair: TBA*

9.50am – 10.10am: Knowledge Discovery from Highly Genetically Diverse and Mosaic Genome Sequences (#263, *Supplemental*) -(*Invited Talk*)

*Saman K. Halgamuge<sup>1</sup>, Jason Li<sup>1</sup>, Sen-Lin Tang<sup>2</sup>*

<sup>1</sup>Dynamic Systems & Control, University of Melbourne, Australia

<sup>2</sup>Research Center for Biodiversity, Academia Sinica, Taiwan

10.10am – 10.30am: Automated Methods of Predicting The Function of Biological Sequences Using GO and Rough Set (#121, *LNBI*)

*Xu-Ning Tang<sup>1</sup>, Zhi-Chao Lian<sup>2</sup>, Zhi-Li Pei<sup>2,3</sup>, Yan-Chun Liang<sup>2</sup>*

<sup>1</sup>College of Software, Jilin University, China

<sup>2</sup>College of Computer Science and Technology, Jilin University, China

<sup>3</sup>College of Mathematics and Computer Science, Inner Mongolia University for Nationalities, China

10.30am – 10.50am: C-based Design Methodology for FPGA Implementation of ClustalW MSA (#122, *LNBI*)

*Yan Lin Aung<sup>1</sup>, Douglas L. Maskell<sup>1</sup>, Timothy F. Oliver<sup>1</sup>, Bertil Schmidt<sup>2</sup>, William Bong<sup>3</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore,

<sup>2</sup>Division of Engineering, Science and Technology, The University of New South Wales Asia, Singapore,

<sup>3</sup>Network Storage Technology Division, A\*STAR Data Storage Institute, Singapore,

10.50am – 11.10am: A Two-phase ANN Method for Genome-wide Detection of Hormone Response Elements (#206, *LNBI*)

*Maria Stepanova<sup>1</sup>, Feng Lin<sup>2</sup>, Valerie Lin<sup>3</sup>*

<sup>1</sup>BioInformatics Research Center, Nanyang Technological University, Singapore

<sup>2</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>3</sup>School of Biological Sciences, Nanyang Technological University, Singapore

11.10am – 11.30am: An Expert Knowledge-Guided Mutation Operator for Genome-Wide Genetic Analysis using Genetic Programming (#199, *LNBI*)

*Casey S. Greene, Bill C. White, Jason H. Moore*

Dartmouth College, USA

11.30am – 11.50am: Comparative Analysis of a Hierarchical Bayesian Method for Quantitative Trait Loci Analysis for the Arabidopsis Thaliana (#217, *LNBI*)

*Caroline Pearson<sup>1</sup>, Susan J. Simmons<sup>1</sup>, Karl Ricanek Jr.<sup>2</sup>, and Edward L. Boone<sup>3</sup>*

<sup>1</sup>Department of Mathematics and Statistics, University of North Carolina Wilmington, USA

<sup>2</sup>Department of Computer Science, University of North Carolina Wilmington, USA

<sup>3</sup>Department of Statistical Sciences and Operations Research, Virginia Commonwealth University, USA

## **Session O2AM2: Pathway Analysis**

### **Tuesday, Oct 2, 9.50am – 11.50am, Ball Room 2**

*Session Chair: TBA*

9.50am – 10.10am: Variable-Length Haplotype Construction for Gene-Gene Interaction Studies (#168, *EMBM*)

*Anunchai Assawamakin<sup>1</sup>, Nachol Chaiyaratana<sup>2</sup>, Saravudh Sinsomros<sup>2</sup>, Prakarnkiat Youngkong<sup>2</sup>*

<sup>1</sup>Faculty of Medicine Siriraj Hospital, Mahidol University, Thailand

<sup>2</sup>Faculty of Engineering, King Mongkut's Institute of Technology North Bangkok, Thailand

10.10am – 10.30am: Multicellular Pattern Formation: Parameter Estimation for ODE based Gene Regulatory Networks (#175, *EMBM*)

*Tim Hohm, Eckart Zitzle*

Computer Engineering, Swiss Federal Institute of Technology Zurich, Switzerland

10.30am – 10.50am: A Framework for Path Analysis in Gene Regulatory Networks (#215, *LNBI*)

*Ramesh Ram, Madhu Chetty*

Gippsland School of Information Technology, Monash University, Australia

10.50am – 11.10am: Transcriptional Gene Regulatory Network Reconstruction through Cross Platform Gene Network Fusion (#162, *LNBI*)

*Muhammad Shoaib B. Sehgal<sup>1,3</sup>, Iqbal Gondal<sup>1,3</sup>, Laurence Dooley<sup>1</sup>, Ross Coppel<sup>2,3</sup>, Goh Kiah Mok<sup>4</sup>*

<sup>1</sup>Faculty of Information Technology, Monash University, Australia.

<sup>2</sup>Department of Microbiology, Monash University, Australia

<sup>3</sup>Victorian Bioinformatics Consortium, Australia

<sup>4</sup>SIMTech Institute of Technology, Singapore

11.10am – 11.30am: Reconstruction of Protein-Protein Interaction Pathways by Mining Subject-Verb-Objects Intermediates (#163, *LNBI*)

*Maurice HT Ling<sup>1,2</sup>, Christophe Lefevre<sup>3</sup>, Kevin R. Nicholas<sup>2</sup>, Feng Lin<sup>1</sup>*

<sup>1</sup>Bioinformatics Research Centre, Nanyang Technological University, Singapore

<sup>2</sup>Department of Zoology, The University of Melbourne, Australia

<sup>3</sup>Victorian Bioinformatics Consortium, Monash University, Australia

11.30am – 11.50am: Validation of gene regulatory networks from protein-protein interaction data: application to cell-cycle regulation (#227)

*Iti Chaturvedi<sup>1,2</sup>, Meena Kishore Sakharkar<sup>2</sup>, Jagath C. Rajapakse<sup>1</sup>*

<sup>1</sup>Bioinformatics Research Center, Nanyang Technological University, Singapore

<sup>2</sup>Adams Lab, MAE, Nanyang Technological University, Singapore

## Poster Session P2

### Tuesday, Oct 2, 1pm – 2pm

Predicting Binding Peptides with Simultaneous Optimization of Entropy and Evolutionary Distance (#223, *Supplemental*)

*Menaka Rajapakse<sup>1</sup>, Lin Feng<sup>2</sup>*

<sup>1</sup>Institute for Infocomm Research, Singapore

<sup>2</sup>School of Computer Engineering, Nanyang Technological University, Singapore

Strong GC and AT Skew Correlation in Chicken Genome (#147, *Supplemental*)

*Xuegong Deng<sup>1</sup>, Xuemei Deng<sup>2</sup>, Ilkka Havukkala<sup>3</sup>*

<sup>1</sup>College of Science, Northeastern University, China

<sup>2</sup>Department of Animal Genetics and Breeding & National Key Lab, China Agricultural University, China

<sup>3</sup>Knowledge Engineering and Discovery Research Institute, Auckland University of Technology, New Zealand

Grid Implementation for Comparative Genomics to Identify Conserved Non-Coding Regions (#224, *Supplemental*)

*Jagath C. Rajapakse<sup>1,2</sup>, Pooja<sup>1</sup>, Chunxi Chen<sup>1</sup>, Ho Sy Loi<sup>1</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>Singapore-MIT Alliance, Singapore

Machine Recognition of Printed Malayalam Characters Using Wavelets (#229, *Supplemental*)

*M Abdul Rahiman<sup>1</sup>, K Revathy<sup>2</sup>*

<sup>1</sup>LBS Institute of Technology for Women, Thiruvananthapuram, India

<sup>2</sup>Department of Computer Science, University of Kerala, India

3D Multi-object Segmentation, Tracking and Visualization in Fluorescence Microscopy using Active Meshes (#233, *Supplemental*)

*Alexandre Dufour<sup>1,2</sup>, Nicole Vincen<sup>2</sup>, Auguste Genovesio<sup>1</sup>*



<sup>1</sup>Image Mining group, Institute Pasteur Korea, South Korea

<sup>2</sup>Intelligent Perception Systems team, Paris Descartes University, France

Random Forests Proximity Clustering of Sequences (#237, *Supplemental*)

*Sheng Liu, Qing Song*

School of Electrical & Electronic Engineering, Nanyang Technological University, Singapore

Extracting Degenerate Motifs Based on a Suffix Tree (#240, *Supplemental*)

*Hongshan Jiang, Ying Zhao, Wenguang Chen, and Weimin Zheng*

Department of Computer Science, Tsinghua University, China

Nonmetric Distance for Barcode of Life (#245, *Supplemental*)

*Hisamitsu Akiba<sup>1</sup>, Y-h.Taguchi<sup>1,2</sup>*

<sup>1</sup>Faculty of Science and Technology, Chuo University, Japan

<sup>2</sup>Institute for Science and Technology, Chuo University, Japan

Features for Protein Localization in Microscopic Cellular Images (#260, *Supplemental*)

*Jagath C. Rajapakse<sup>1,2</sup>, Song Liu<sup>1</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>Singapore-MIT Alliance, Singapore

Extracting Rhythms in EEG with Temporal Structure (#261, *Supplemental*)

*Kavuri Swathi Sri<sup>1</sup>, Jagath C. Rajapakse<sup>1,2</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>Singapore-MIT Alliance, Singapore

Individual Variability of Brain Connectivity from Functional MR Scans (#262, *Supplemental*)

*Zhou Juan<sup>1</sup>, Jagath C. Rajapakse<sup>1,2</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>Singapore-MIT Alliance, Singapore

Clustered Nuclei Segmentation by Marker-Controlled Watershed Algorithm (#251, *Supplemental*)

*Jierong Cheng and Jagath C. Rajapakse*

<sup>1</sup>Bioinformatics Research Center, Nanyang Technological University, Singapore

<sup>2</sup>Singapore-MIT Alliance, Singapore

Rhabdoid Tumor of Thalamus (#254, *Supplemental*)

*Amita Kumar Amit, Singh R, Shambhavi Srivastava*

Department of Bioinformatics, DNA Research Centre, India

Involvement of “Ldre” Pattern in Pemphigus Foliaceus (#256, *Supplemental*)

*Pankaj Kalra, Amit Kumar*

Department of Bioinformatics, DNA Research Centre, India

Functional Importance of HOXA1 Hypothetical Proteins through Conserved Pattern Discovery (#259, *Supplemental*)

*Gautam S. Degweker, Amit Kumar, Vijay J. Songara*

Department of Bioinformatics, DNA Research Centre, India

## **Session O2PM1: Bioimaging**

**Tuesday, Oct 2, 2.00pm – 4.00pm, Ball Room 1**

*Session Chair: TBA*

2.00pm – 2.20pm: 3D Automated Nuclear Morphometric Analysis Using Active Meshes (#177, *LNBI*)

*Alexandre Dufour<sup>1,3</sup>, JooHyun Lee<sup>2</sup>, Nicole Vincent<sup>3</sup>, Regis Grailhe<sup>2</sup> and Auguste Genovesio<sup>1</sup>*

<sup>1</sup>Image Mining Group, Institut Pasteur Korea, Korea

<sup>2</sup>Dynamic Imaging Platform, Institut Pasteur Korea, Korea

<sup>3</sup>Intelligent Perception Systems (SIP-CRIP5) team, Paris Descartes University, France

2.20pm – 2.40pm: Real-time Cellular Morphologic Analysis with Fine-grained Parallel Image Processing (#250, *Supplemental*)

*Lee Sing Cheong<sup>1</sup>, Feng Lin<sup>1</sup>, Hock Soon Seah<sup>1</sup>, Kemao Qian<sup>1</sup>, Kenneth Chin-Wen Yu<sup>1</sup>, Patricia Soo-Ping Thong<sup>2</sup>, Malini Olivo<sup>2</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>National Cancer Centre Singapore, Singapore

2.40pm – 3.00pm: Time-Frequency Method based Activation Detection in Functional MRI Time-Series (#221, *LNBI*)

*Arun Kumar<sup>1,2</sup>, Jagath C Rajapakse<sup>1,3</sup>*

<sup>1</sup>School of Computing, Nanyang Technological University, Singapore

<sup>2</sup>School of Electrical and Electronic Engineering, Singapore Polytechnic, Singapore

<sup>3</sup>Singapore-MIT Alliance, Singapore

3.00pm – 3.20pm: High Performance Classification of Two Imagery Tasks in the Cue-Based Brain Computer Interface (#165, *LNBI*)

*Omid Dehzangi<sup>1</sup>, Mansoor Zolghadri Jahromi<sup>2</sup>, Reza Boostani<sup>2</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>Shiraz University, Iran

3.20pm – 3.40pm: Human Brain Anatomical Connectivity Analysis using Sequential Sampling and Resampling (#226, *LNBI*)

*Bo Zheng<sup>1</sup>, Jagath C. Rajapakse<sup>1,2</sup>*

<sup>1</sup>School of Computer Engineering, Nanyang Technological University, Singapore

<sup>2</sup>Singapore-MIT Alliance, Singapore

3.40pm – 4.00pm: Classification of CT Brain Images of Head Trauma (#164, *LNBI*)

*Tianxia Gong<sup>1</sup>, Ruizhe Liu<sup>1</sup>, Chew Lim Tan<sup>1</sup>, Neda Farzad<sup>2</sup>, Cheng Kiang Lee<sup>3</sup>, Boon Chuan Pang<sup>3</sup>, Qi Tian<sup>4</sup>, Suisheng Tang<sup>4</sup>, Zhuo Zhang<sup>4</sup>*

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## **Session O2PM2: Medical Informatics**

**Tuesday, Oct 2, 2.00pm – 4.00pm, Ball Room 2**

*Session Chair: TBA*

2.00pm – 2.20pm: Pattern Recognition and Computational Simulations in Immunology and Vaccine Discovery (#264, *Supplemental*) -(Invited Talk)

*Vladimir Brusic*

Cancer Vaccine Center, Dana-Farber Cancer Institute, USA

2.20pm – 2.40pm: Characterization of MHC Class II Binding Peptides Predicted Using Multi-Objective Evolutionary Algorithm (#204, *EMBM*)

*Menaka Rajapakse<sup>1</sup>, Lin Feng<sup>2</sup>*

<sup>1</sup>Institute for Infocomm Research, Singapore

<sup>2</sup>Nanyang Technological University, Singapore

2.40pm – 3.00pm: An Application of Genetic Algorithms in Cancer Immunoinformatics (#200, *EMBM*)

*Marzio Pennisi<sup>2</sup>, Francesco Pappalardo<sup>1,2</sup>, Ping Zhang<sup>3</sup>, and Santo Motta<sup>2</sup>*

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<sup>2</sup>Department of Mathematics and Computer Science, University of Catania, Italy

<sup>3</sup>Institute for Molecular Bioscience, University of Queensland, Australia

3.00pm – 3.20pm: In Silico Identification of Putative Drug Targets in *Pseudomonas Aeruginosa* through Metabolic Pathway Analysis (#148, *LNBI*)

*Deepak Perumal<sup>1,2</sup>, Chu Sing Lim<sup>2</sup> and Meena K. Sakharkar<sup>1</sup>*

<sup>1</sup>School of Mechanical and Aerospace Engineering, Nanyang Technological University, Singapore.

<sup>2</sup>BioMedical Engineering Research Centre, Nanyang Technological University, Singapore.

3.20pm – 3.40pm: Understanding Prediction Systems for HLA-Binding Peptides and T-cell Epitope Identification (#173, *LNBI*)

*Liwen You*<sup>1,2,3</sup>, *Ping Zhang*<sup>3</sup>, *Mikael Bod'en*<sup>4</sup>, *Vladimir Brusic*<sup>3,5</sup>

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<sup>3</sup>School of Land, Crop, and Food Sciences, University of Queensland, Australia

<sup>4</sup>School of Information Technology and Electrical Engineering, University of Queensland, Australia

<sup>5</sup>Cancer Vaccine Center, Dana-Farber Cancer Institute, USA

3.40pm – 4.00pm: Cdna-Derived Amino Acid Sequence from Rat Brain A2ar Possesses Conserved Motifs PMNYM of TM 5 Domain Involved in Dimerization of A2ar. (#220, *LNBI*)

*Pratibha Mehta Luthra*<sup>1</sup>, *Sandeep Kumar Barodia*<sup>1</sup>, *Amresh Prakash*<sup>1</sup>, *Ramraghubir*<sup>2</sup>

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