

The 3rd Asia-Pacific Bioinformatics Conference

Institute for Infocomm Research
21 Heng Mui Keng Terrace, Singapore 119613
Tel: +65-6874-2099

17–21 January 2005

Program Overview

Monday, 17 January 2005

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| 8.30–17.30 | Registration Lobby |
| 9.00–12.00 | Tutorial 1 Big One
Classification of Microarray Data: Recent Statistical Approaches
<i>Geoff McLachlan, Liat Ben-Tovin Jones (Univ of Queensland)</i> |
| 12.00–13.30 | Lunch Break |
| 13.30–16.30 | Tutorial 2 Big One
How to Build a Virtual Cell Through Cellware?
<i>Pawan K. Dhar, Li Ye (Bioinformatics Institute of Singapore)</i> |
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Tuesday, 18 January 2005

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| 8.30–17.30 | Registration Lobby |
| 9.00–9.15 | Opening Session Auditorium |
| 9.15–10.00 | Keynote 1 Auditorium (<i>chair: Ming Li, Univ of Waterloo</i>)
Computing the Assignment of Orthologous Genes via Genome Rearrangement, <i>Prof. Tao Jiang (UC Riverside)</i> |
| 10.00–10.30 | Tea Break Multi-Purpose Hall |

- 10.30–11.30 **Protein Structures 1** Auditorium (*chair: Tao Jiang, UC Riverside*)
- no.146 Clique Based Algorithms for Protein Threading with Profiles and Constraints, *Dukka Bahadur K.C., E. Tomita, J. Suzuki, K. Horimoto, T. Akutsu (Kyoto Univ & Univ of Electro-Communications)*
- no.161 Classification of Protein 3D Folds by Hidden Markov Learning on Sequences of Structural Alphabets, *S.-L. Wang, C.-M. Chen, M.-J. Hwang (Taiwan Univ & Academia Sinica)*
- no.236 Consensus Fold Recognition by Predicted Model Quality, *J. Xu, L. Yu, M. Li (Univ of Waterloo)*
- 11.30–13.00 **Lunch Break**
- 13.00–14.00 **Protein Sorting** Auditorium (*chair: See-Kiong Ng, Inst for Infocomm Research*)
- no.116 A Novel Method for Protein Subcellular Localization: Combining Residue-couple Model and SVM, *J. Guo, Y. Lin and Z. Sun (Tsinghua Univ)*
- no.195 Detecting Residues in Targeting Peptides, *M. Boden, J. Hawkins (Univ of Queensland)*
- no.123 BLOMAP: An Encoding of Amino Acids which Improves Signal Peptide Cleavage Site Prediction, *S. Maetschke, M. Towsey, M. Boden (Univ of Queensland & Queensland Univ of Tech)*
- 14.00–14.40 **Sequence Alignment** Auditorium (*chair: Lusheng Wang, City Univ of Hong Kong*)
- no.192 Allowing Mismatches in Anchors for Whole Genome Alignment: Generation and Effectiveness, *S.M. Yiu, P.Y. Chan, T.-W. Lam, W.-K. Sung, H.F. Ting, P.W.H. Wong (Univ of Hong Kong, Natl Univ of Singapore, & Univ of Liverpool)*
- no.118 A Better Gap Penalty for Pairwise-SVM, *Hon Nian Chua, Wing-Kin Sung (Natl Univ of Singapore)*
- 14.40–15.40 **Tea Break & Poster Session 1** Multi-Purpose Hall
- 15.40–16.40 **Microarrays** Auditorium (*chair: Satoru Miyano, Univ of Tokyo*)
- no.162 Feature Dimension Reduction for Microarray Data Analysis Using Local Linear Embedding, *C. Shi, L. Chen (Nanyang Tech Univ)*
- no.246 PLS and SVD Based Penalized Logistic Regression for Cancer Classification Using Microarray Data, *L. Shen, E.C. Tan (Nanyang Tech Univ)*
- no.248 Genetic Algorithms and Silhouette Measures Applied to Microarray Data Classification, *T.-C. Lin, R.-S. Liu, S.-Y. Chen, C.-C. Liu, C.-Y. Chen (Yuan Ze Univ & Natl Central Univ)*

- 16.40–17.00 **PCR Primer** Auditorium (*chair: TBD*)
no.151 Improved Algorithms for Multiplex PCR Primer Set Selection with Amplification Length Constraints, *K.M Konwar, I.I. Mandoiu, A.C Russell, A. A. Shvartsman (Univ of Connecticut)*
- 19.00–21.30 **Conference Banquet**
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Wednesday, 19 January 2005

- 9.15–10.00 **Keynote 2** Auditorium (*chair: Phoebe Chen, Deakin Univ*)
Comparison of Core Promoters in *Fugu Rubripes* and Human, *Prof. Vladimir Bajic (Inst. for Infocomm Research)*
- 10.00–10.30 Tea Break Multi-Purpose Hall
- 10.30–11.30 **Motifs 1** Auditorium (*chair: Wing-Kin Sung, Natl Univ of Singapore*)
no.125 Exact Algorithms for Motif Search, *S. Rajasekaran, S. Balla, C.-H. Huang, V. Thapar, M. Gryk, M. Maciejewski, M. Schiller (Univ of Connecticut)*
no.126 Exact Algorithms for Planted Motif Challenge Problems, *S. Rajasekaran, S. Balla, C.-H. Huang (Univ of Connecticut)*
no.212 Voting Algorithms for Discovering Long Motifs, *F.Y.L. Chin, H.C.M. Leung (Univ of Hong Kong)*
- 11.30–13.00 **Lunch Break**
- 13.00–14.00 **Protein Structures 2** Auditorium (*chair: TBD*)
no.216 Profiles and Fuzzy K-Nearest Neighbor Algorithm for Protein Secondary Structure Prediction, *R. Bondugula, O. Duzlevski, D. Xu (Univ of Missouri-Columbia)*
no.111 Protein Folding Trajectory Analysis using Patterned Clusters, *J. Feng, L. Parida, R. Zhou (New York Univ & IBM T.J.Watson Research Center)*
no.147 The Use of Functional Domains to Improve Transmembrane Protein Topology Prediction, *E.W. Xu, D.G. Brown, P. Kearney (Univ of Calgary, Univ of Waterloo, & Caprion Pharmaceuticals)*
- 14.00–14.40 **Database Indexing and Querying** Auditorium (*chair: David Feng, Univ of Sydney*)
no.204 High Dimensional Indexing for Protein Structure Matching Using Bowties, *Z.H. Huang, X. Zhou, D. Song (Univ of Queensland)*
no.107 A Graph Database with Visual Queries for Genomics, *G. Butler, G. Wang, Y. Wang, L. Zou (Concordia Univ)*
- 14.40–15.40 **Tea Break & Poster Session 2** Multi-purpose Hall

- 15.40–16.40 **Bacteria and Viruses** Auditorium (*chair: Vladimir Brusic, Inst for Infocomm Research*)
- no.130 Bacterial Population Assay via K-Mer Analysis, *D. Papamichail, S.S. skiena, D. van der Lelie, S.R. McCorkle (SUNY Stony Brook & Brookhaven Natl Lab)*
- no.180 A Database to Aid Probe Design for Virus Identification, *F.-M. Lin, H.-D. Huang, Y.-C. Chang, P.-L. Chan, J.-T. Horng, M.-T. Ko (Natl Central Univ, Natl Chiao-Tung Univ, & Academia Sinica)*
- no.209 A Support Vector Machine Approach for Prediction of T Cell Epitopes, *L. Huang, Y. Dai (Univ of Illinois at Chicago)*
- 16.40–17.15 **Invited Talk** Auditorium (*chair: Limsoon Wong, Inst for Infocomm Research*)
Trends in Bioinformatics Research and Singapore's Role, *Dr. Santosh K. Mishra (Bioinformatics Inst of Singapore)*
- 19.30–10.00 **Dinner for PC Members, Keynote and Invited Speakers**
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Thursday, 20 January 2005

- 9.15–10.00 **Keynote 3** Auditorium (*chair: Santosh K. Mishra, Bioinformatics Inst of Singapore*)
Protein Informatics Towards Integration of Data Grid and Computing Grid, *Haruki Nakamura (Osaka University)*
- 10.00–10.30 **Tea Break** Multi-Purpose Hall
- 10.30–11.30 **Systems Biology** Auditorium (*chair: TBD*)
- no.196 Cells In Silico (CIS): A Biomedical Simulation Framework Based on Markov Random Field, *K.-H. Liang (Univ of Nottingham)*
- no.201 Toward Discovering Disease-Specific Gene Networks from Online Literature, *Z. Zhang, S. Tang, S.-K. Ng (Inst. for Infocomm Research)*
- no.203 A New Regulatory Interaction Suggested by Simulations for Circadian Genetic Control Mechanism in Mammals, *H. Matsuno, S.-I. Inouye, Y. Okitsu, Y. Fujii, S. Miyano (Yamaguchi Univ & Univ of Tokyo)*
- 11.30–13.00 **Lunch Break**

- 13.00–14.00 **Motifs 2** Auditorium (*chair: TBD*)
- no.188 A Highly Scalable Algorithm for the Extraction of Cis-Regulatory Regions, *A.M. Carvalho, A.T. Freitas, A.L. Oliveira, M.-F. Sagot (IST/INESC-ID & Univ Claude Bernard)*
- no.138 Modeling 5' Regions OF Histone Genes Using Bayesian Networks, *R. Chowdhary, R.A. Ali, V.B. Bajic (Inst. for Infocomm Research & Natl Univ of Singapore)*
- no.142 Unique Peptide Prediction of RNase Family Sequences Based on Reinforced Merging Algorithms, *H.-T. Chang, T.-C. Fan, M.D.-T. Chang, T.-W. Pai, B.-H. Su, P.-C. Wu (Natl Tsing Hua Univ & Natl Taiwan Ocean Univ)*
- 14.00–15.00 **Proteomics** Auditorium (*chair: Tak-Wah Lam, Univ of Hong Kong*)
- no.120 PRIMA: Peptide Robust Identification from MS/MS Spectra, *J. Liu, B. Ma, M. Li (Univ of Waterloo & Univ of Western Ontario)*
- no.184 SVM-RFE Peak Selection for Cancer Classification with Mass Spectrometry Data, *K. Duan, J. Rajapakse (Nanyang Tech Univ)*
- no.241 Hybrid Registration for Two-Dimensional Gel Protein Images, *X. Wang, D.D. Feng (Univ of Sydney & Hong Kong Polytechnic Univ)*
- 15.00–16.00 **Tea Break & Poster Session 3** Multi-Purpose Hall
- 16.00–17.00 **Evolution** Auditorium (*chair: TBD*)
- no.128 Faster Solution to the Maximum Quartet Consistency Problem with Constraint Programming, *G. Wu, G. Lin, J.-H. You, X. Wu (Univ of Alberta)*
- no.173 Inferring Phylogenetic Relationships Avoiding Forbidden Rooted Triplets, *Y.-J. He, T. Huynh, J. Jansson, W.-K. Sung (Natl Univ of Singapore)*
- no.186 An $O(n^2)$ Algorithm for Signed Translocation Problem, *L. Wang, D. Zhu, X. Liu, S. Ma (City Univ of Hong Kong & Shandong Univ)*
- 17.00–17.15 **Closing Session** Auditorium
- Closing Remarks by General Chair, *Prof. Ming Li (Univ of Waterloo)*
- Closing Remarks by PC Co-Chair, *A/Prof. Phoebe Chen (Deakin Univ)*
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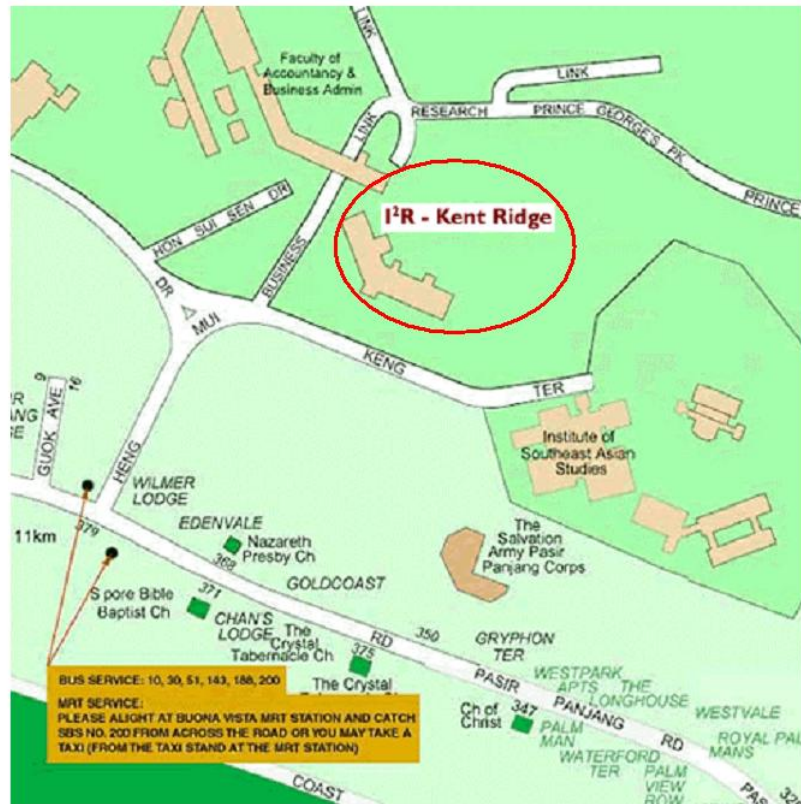
Friday, 21 January 2005

- 9.15–12.00 **SIG Meetings**
- Please contact Dr. Vladimir Brusic, vladimir@i2r.a-star.edu.sg, if you wish to organize a SIG meeting.*
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Venue Information

Institute for Infocomm Research (I²R)
21 Heng Mui Keng Terrace, Singapore 119613
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It is located within the campus of the National University of Singapore. The URL for a map of I²R is <http://www.i2r.a-star.edu.sg/files/phatfile/I2Rmap.gif>.



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