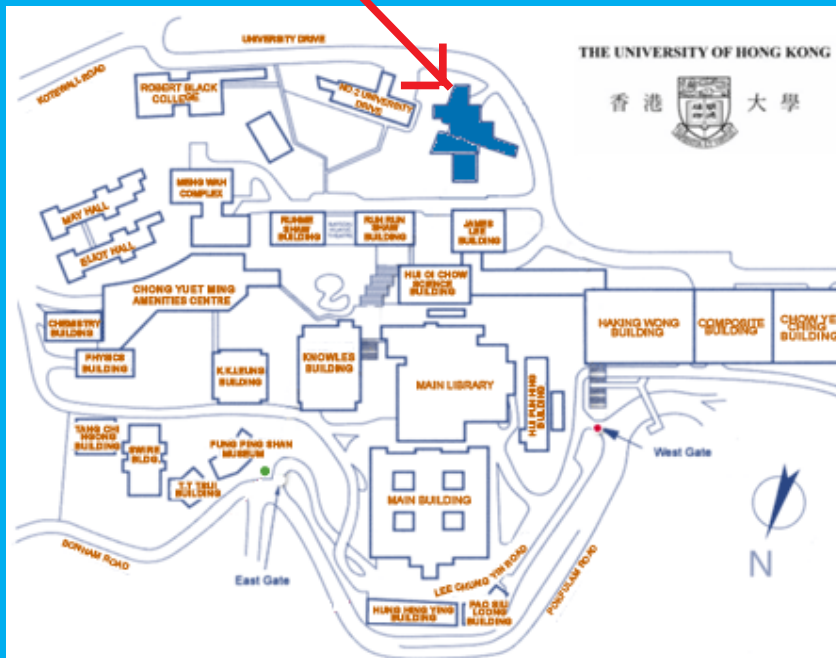




APBC 2007



CONFERENCE PROGRAM



APBC 2007

The Fifth Asia Pacific Bioinformatics Conference

Hong Kong, 14-17 January 2007



Hosted by



THE UNIVERSITY OF HONG KONG
DEPARTMENT OF
COMPUTER SCIENCE



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EXTRAS! EXTRAS!

PURCHASING EXTRA TICKETS OR PROCEEDINGS:

Each extra proceedings	US\$ 45	or HK\$ 360
Each extra lunch ticket	US\$ 10	or HK\$ 80
Each extra banquet ticket	US\$ 50	or HK\$ 400

Chairs and Committees

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Lusheng Wang, The City University of Hong Kong

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Other Useful Information

1) OTHER RESTAURANTS

On the main campus of The University of Hong Kong:

- Chong Yuet Ming Amenities Centre Restaurant
4/F, Chong Yuet Ming Amenities Centre
- Fong Shu Chuen Amenities Centre Restaurant
2/F, Swire Building
- Starbucks
G/F, Old Library Building
- Pacific Coffee
Global Lounge, Swire Hall

You can obtain more information at
<http://www.hku.hk/facilities/restaurants.html>
<http://www.hku.hk/osa/catering/catering.htm>

Off-campus: You can also find a lot of local restaurants and food shops in the Western district near The University of Hong Kong

2) INTERESTING PLACES TO VISIT (to name a few)

- Ocean Park: <http://www.oceanpark.com.hk>
- Hong Kong Wetland Park: <http://www.wetlandpark.com/>
- Hong Kong Disneyland: <http://park.hongkongdisneyland.com>
- Ngong Ping 360 Skyrail: <http://www.np360.com.hk>
- Giant Buddha/Po Lin Monastery at Lantau Island
- The Peak Tower, Hong Kong

You can obtain more information at <http://www.discoverhongkong.com/eng/index.jsp>

Welcome to APBC 2007 with Acknowledgments

Dear Attendees:

On behalf of the local organizing committee, The University of Hong Kong (HKU) and the City University of Hong Kong, I welcome you to Hong Kong. Apart from attending the conference, I do wish that you will have the chance to explore our really wonderful city in your spare time (see page 14 for some suggestions).

APBC 2007 will be action-packed, consisting of a one-day tutorial program (14 January 2007) followed by a three-day conference program (15-17 January 2007). This program booklet gives you the agenda for the three-day conference, as well as the schedule and topics for the three tutorials to be held on the 14th. On each of the three conference days, there will be a keynote in the morning and a poster session in the afternoon to complement the 11 or 12 20-minute paper presentations on each day. Other highlights include an **industrial talk** on Day 1, a **banquet talk** on Day 2, and a **Best Poster Award** to be presented at the close of the conference on Day 3.

Upon registration of attendance, you will receive the **proceedings** containing the 35 accepted papers and a **booklet of poster abstracts**. The meal tickets you receive will include one for the **Banquet** on Tuesday at the famous Jumbo Floating Restaurant in Aberdeen (see page 13).

Please note that **wireless Internet access** is available throughout most of the campus of The University of Hong Kong, the host of APBC 2007.

Finally, I would like to take this opportunity to thank the many people who have contributed to APBC 2007. Furthermore, without the generous support of the sponsors, this conference would not be possible, and so a special thanks should go to:

- **Lee Hysan Foundation** for their kind support in sponsoring a keynote speaker of our conference;
- **K.C. Wong Education Foundation** for their kind support in sponsoring a few Mainland scholars to attend this conference in Hong Kong; and
- **Hewlett-Packard** for their kind support in sponsoring the industrial talk on the first day of the conference (see Detailed Agenda of the Conference (Day 1)).

Enjoy the conference!

Francis Y.L. Chin
APBC 2007 Conference Chair

Agenda at a Glance - Tutorial/Conference

Venues: Reception – P4 Entrance Foyer, Graduate House, HKU
 Conference – Wang Gungwu Theatre, Graduate House, HKU
 Poster Sessions – P501, P503, Graduate House, HKU

PRE

January 14, 2007 (Sunday)

09:30 - 17:30 Tutorials - see separate Tutorial Schedule (facing page)
 18:00 - 20:00 Reception

DAY 1

January 15, 2007 (Monday)

08:30 - 17:00 Registration
 09:00 - 09:15 Opening Speech - Prof. P.K.H. Tam
 09:15 - 10:15 Keynote 1 - Prof. Jennifer A. Marshall Graves
 10:15 - 10:45 Tea Break
 10:45 - 12:05 Session 1 - Communities; Motifs
 12:05 - 13:30 Lunch Break (Union Restaurant, Composite Bldg, HKU)
 13:30 - 14:50 Session 2 - Biclustering and Microarray
 14:50 - 15:40 Tea Break/Poster Session 1 (Industrial talk: 15:00-15:35)
 15:40 - 17:00 Session 3 - Evolutionary Tree

DAY 2

January 16, 2007 (Tuesday)

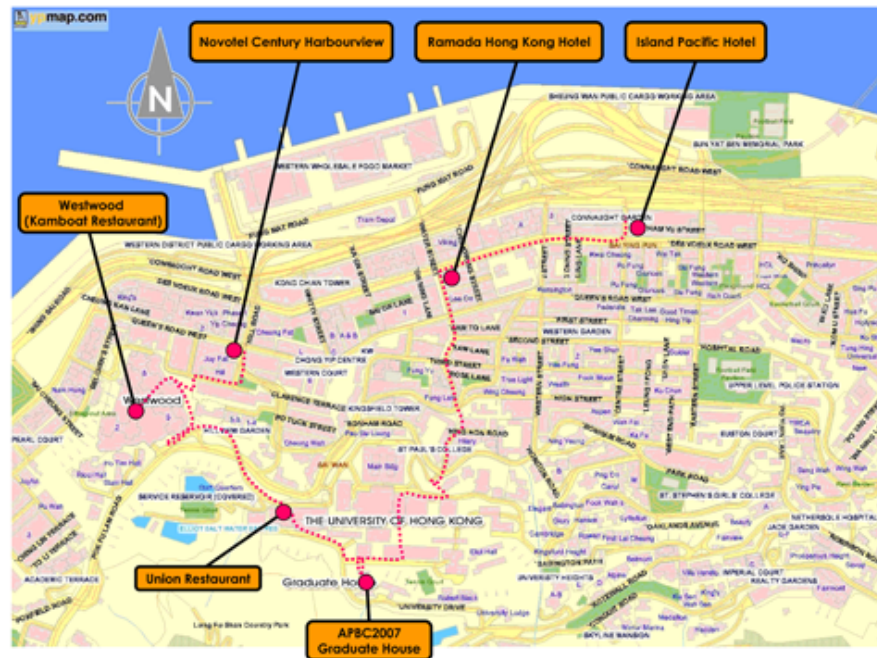
08:30 - 17:00 Registration
 09:00 - 10:00 Keynote 2 - Prof. Pavel Pevzner
 10:00 - 10:30 Tea Break
 10:30 - 11:50 Session 4 - Structure Prediction and Comparison
 11:50 - 14:00 Lunch Break (Kamboat Restaurant, WestWood Mall)
 14:00 - 15:00 Session 5 - Mapping and Disease
 15:00 - 15:40 Tea Break/Poster Session 2
 15:40 - 17:00 Session 6 - Genome Comparison
 18:30 - 21:30 Banquet (Jumbo Floating Restaurant, Talk: 19:15 - 19:45)

DAY 3

January 17, 2007 (Wednesday)

08:30 - 12:00 Registration
 09:00 - 10:00 Keynote 3 - Prof. Joe Nadeau
 10:00 - 10:30 Tea Break
 10:30 - 11:50 Session 7 - Biological Network
 11:50 - 13:30 Lunch Break (Joseph's Restaurant, Graduate House, HKU)
 13:30 - 14:50 Session 8 - MS; Protein-Protein Interaction
 14:50 - 15:30 Tea Break/Poster Session 3
 15:30 - 16:50 Session 9 - Alignment and Search
 16:50 - 17:00 Closing remark/promotion/presentation of Best Poster Award

Venue Maps and the Banquet (cont'd)



THE BANQUET

Our banquet will be at the famous **Jumbo Floating Restaurant** in Shum Wan, Aberdeen. The concept of the Jumbo Floating Restaurant is a restaurant on a boat that specializes in seafood. Since it originally opened in 1976 as the brainchild of the Macau gambling tycoon Dr. Stanley Ho, the Restaurant has received over 30 million visitors and is considered a must-see tourist attraction.

The University of Hong Kong is located on the west side of Hong Kong Island and Aberdeen is located to the west of HKU. Aberdeen was known as a fishing village in the old days. The bus will drop us off at the pier and we will be taking a short ferry ride to the Restaurant.

One of the highlights will be a very interesting **talk during dinner** given by Prof. K.Y. Yuen of the Department of Microbiology in The University of Hong Kong.

Separate tickets can be purchased for the Banquet. Enjoy!

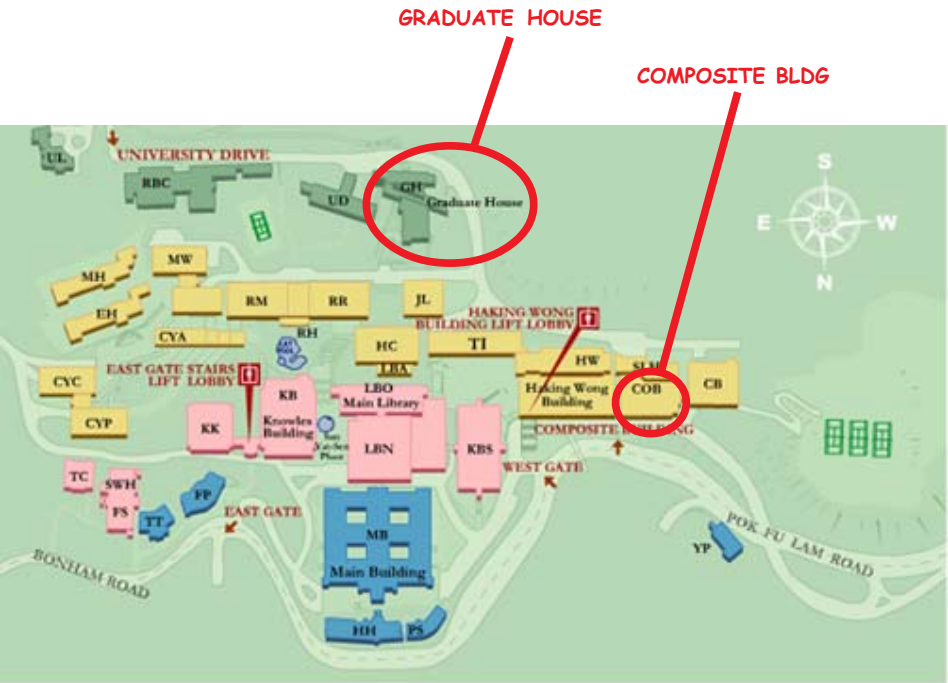


Venue Maps and the Banquet

Please find a **HKU Campus Map** below, with the following shown:

- **Graduate House** - this is the site of the tutorials, reception, conference and lunch on Day 3;
- **Composite Building (COB)** - this is where Union Restaurant (lunch on Day 1) is located.

Lunch on Day 2 and the banquet are off-campus.



Places identified on the map on the facing page:

- The three recommended hotels: (1) **Novotel Century Harbourview**; (2) **Ramada Hong Kong Hotel**; and (3) **Island Pacific Hotel**;
- **Union Restaurant** in the Composite Building (COB), HKU - lunch on Day 1;
- **Kamboat Restaurant** in WestWood Mall - lunch on Day 2;
- Joseph's Restaurant in **Graduate House**, HKU - lunch on Day 3.

Transportation Provided by APBC 2007

(A) Bus to **Graduate House** (conference site) from hotels on 15-17 Jan.

Pick-up Location	Pick-up Time	
	15 Jan 2006	16-17 Jan 2006
Island Pacific Hotel Hong Kong	7:45 am	8:15 am
Ramada Hong Kong Hotel (at Chiu Kwong Street)	7:47 am	8:17 am
Novotel Century Harbourview	7:50 am	8:20 am

(B) Bus to and from **Jumbo Floating Restaurant** (banquet) on 16 Jan.

Pick-up Location	16 Jan 2006
Graduate House, HKU (to Restaurant)	5:30 pm
Jumbo Floating Restaurant, Aberdeen (returning to the three hotels)	9:30 pm

Tutorial Schedule and Topics

Venue: P503, Graduate House, HKU
 Time: : January 14, 2007 (Sunday)

- 09:30 - 11:30 Tutorial 1 - Prof. Limsoon Wong, National University of Singapore
Guilt by Association: A Tutorial on Protein Function Inference
- 11:30 - 12:30 Lunch
- 12:30 - 14:30 Tutorial 2 - Prof. Zhen Zhang, Johns Hopkins University School of Medicine
Clinical Proteomics and Biomaker Discovery: Usage and Abuse of Bioinformatics Tools
- 14:30- 15:00 Break
- 15:00 - 17:00 Tutorial 3 - Prof. Daniel H. Huson, Tübingen University
Introduction to Phylogenetic Networks

* Separate information on tutorials available.

Detailed Agenda of the Conference (Day 1)

- Day 1: Monday, January 15, 2007**
Venue: Wang Gungwu Theatre, Graduate House, HKU
- 08:30 - 17:00 Registration
 09:00 - 09:15 **Opening Speech** - Prof. P.K.H. Tam, Pro-VC, HKU
- 09:15 - 10:15 **Keynote 1** - Prof. Jennifer Marshall Graves, Australian National Univ. Exploring Genomes of Distantly Related Mammals (Chair: Prof. David Sankoff)
- 10:15 - 10:45 Tea Break
 10:45 - 12:05 **Session 1 - Communities; Motifs** (Chair: Prof. Hong Yan)
1. Metagenome Analysis using Megan
by Daniel Huson, Alexander Auch, Ji Qi, Stephan Schuster
 2. Algorithmic Approaches to Selecting Control Clones in DNA Array Hybridization Experiments
by Qi Fu, Elizabeth Bent, James Borneman, Marek Chrobak, Neal Young
 3. Subtle Motif Discovery for Detection of DNA Regulatory Sites
by Matteo Comin, Laxmi Parida
 4. An Effective Promoter Detection Method using the Adaboost Algorithm
by Xudong Xie, Shuanhu Wu, Kin-Man Lam, Hong Yan
- 12:05 - 13:30 Lunch Break (Union Restaurant, Composite Bldg, HKU)
 13:30 - 14:50 **Session 2 - Biclustering and Microarray** (Chair: Prof. Michael Zhang)
5. A New Strategy of Geometrical Biclustering for Microarray Data Analysis
by Hongya Zhao, Alan W. C. Liew, Hong Yan
 6. Using Formal Concept Analysis for Microarray Data Comparison
by Vicky Choi, Yang Huang, Vy Lam, Dustin Potter, Reinhard Laubenbacher, Karen Duca
 7. An Efficient Biclustering Algorithm for Finding Genes with Similar Patterns in Time-series Expression Data
by Sara Madeira, Arlindo Oliveira
 8. Selecting Genes with Dissimilar Discrimination Strength for Sample Class Prediction
by Zhipeng Cai, Randy Goebel, Mohammad Salavatipour, Yi Shi, Lizhe Xu, Guohui Lin
- 14:50 - 15:40 Tea Break/**Poster Session 1** (P501, P503) - see list on facing page
- 15:00 -15:35 **Industrial Talk** - sponsored by Hewlett-Packard
- 15:40 - 17:00 **Session 3 - Evolutionary Tree** (Chair: Prof. Gavin Huttley)
9. Computing the All-Pairs Quartet Distance on a Set of Evolutionary Trees
by Martin Stissing, Thomas Mailund, Christian N. S. Pedersen, Gerth S. Brodal, Rolf Fagerberg

Detailed Agenda of the Conference (Day 3)

Poster Session - Posters (Day 3)

apbc071 Local Optima Resistant Gibbs Sampling Methods for Motif Discovery Realized by an Improved Annealing <i>K Shida</i>	apbc097 Suggestion of Method for Inference of Genetic Network Using cDNA Microarray Gene Expression Data <i>Hye Young Kim, Jin Il Han, Yong Sung Lee, Jin Hyuk Kim</i>
apbc072 A Novel Approach For Anterior Chamber Angle Analysis - Anterior Chamber Angle Detection with Edge Measurement and Identification Algorithm (ACADEMIA) <i>CYL Cheung, CKS Leung, CKF Yiu, CP Pang, DSC Lam</i>	apbc098 Investigation of Information Flow through Genetic Network from Large Gene Expression Data <i>Min Jung Kim, Bo Kyung Kim, Yong Sung Lee, Jin Hyuk Kim</i>
apbc073 Over-Representation Pattern of SNPs in the Genome of Restless Legs Syndrome Samples <i>MX Li, L JIANG, YQ Song, SL Ho, P Sham</i>	apbc099 In Silico Reconstruction and Comparison of Flavour-Forming Pathways in Lactic Acid Bacteria <i>MJ Liu, RJ Siezen</i>
apbc074 Molecular Phylogeny of the Genus <i>Ceropegia</i> <i>S Surveswaran, M Sun, H Corke</i>	apbc100 Molecular Clocks in Virus Evolution: Is Synonymous Clock Homogenous in a Genome? <i>Tsan-Yuk Lam, Chung-Chau Hon, Zhenggang Wang, Frederick CC Leung</i>
apbc076 Development and Improvement of a Prototype System for the Inference of Genetic Networks Based on Genetic Programming <i>Kouji Tanaka, Yutaka Akiyama, Hayato Yamana</i>	apbc101 Investigating Epistasis in Degenerative Disc Disease <i>PYP Kao, D Chan, KMC Cheung, KSE Cheah, PC Sham, YQ Song</i>
apbc077 A Genetic Algorithm for Consensus RNA Secondary Structure Prediction Based on Base-Pairing Probability Matrices <i>A Taneda</i>	apbc102 Gene and Protein Expression Profiles of the Intervertebral Disc: In Health and Disease <i>Anita FY Yee, Mauro Alini, Ian Melhado, Kathryn SE Cheah, Kenneth MC Cheung, Danny Chan</i>
apbc078 Characterisation of Two Evolutionary and Functional Distinct Subpopulations of Genes with Promoter CpG Island <i>SM Tang, YZ Zhao, RJ Epstein</i>	apbc103 Evolutionary Insights into the Ecology of Coronaviruses <i>D Vijaykrishna, GJD Smith, H Chen, Y Guan</i>
apbc081 Genomic Investigation of Primary Open Angle Glaucoma <i>TK Ng, CP Pang</i>	apbc104 The Anti-Angiogenic Signaling Network of rAAV-HGFK1 <i>Wing Sze Leung, Zan Shen, Siu Ming Yiu, Hsiang Fu Kung, Marie CM Lin</i>
apbc083 Two Novel Missense Mutations of Crystalline Genes Caused Autosomal Dominant Congenital Cataract <i>LY Zhang, POS Tam, DSP Fan, CKS Leung, DSC Lam, CP Pang</i>	apbc105 Genomic Analysis of Early Response Induced by Hepatitis B Virus Infection in Human Hepatoma Hepad38 Cells <i>William Ka-Chun Cheung, Ming-Liang He, Hsiang-Fu Kung, Marie CM Lin</i>
apbc084 Genome-Wide Study Reveals the Signaling Pathways Modulated By Gold-1a Treatment in Hepatocellular Carcinoma <i>Gloria Hoi-Yee Li, Ching Tung Lum, Raymond Wai-Yin Sun, Samuel Sai-Ming Ng, David K Smith, Siu Ming Yiu, Chi-Ming Che, Marie CM Lin</i>	apbc107 Specificity Prediction of PDZ Domain Using Kernel Based Machine Learning <i>Jinho Kim, Jaeseong Yang, Jongkyung Kim, Seungjin Choi, Sanguk Kim</i>
apbc088 Distribution of Highly Conserved Non-Coding Elements (HCNEs) in <i>Danio Rerio</i> <i>Xianjun Dong, Altuna Akalin, Boris Lenhard</i>	apbc108 Assessing Limitations of Gene Regulatory Network Inference Methods <i>JWK Ho, MA Charleston</i>
apbc089 A Guided Sampling Algorithm for Identifying Network Motifs in a Transcription Regulatory Network <i>Raymond Wan, Nelson Hayes, Susumu Goto, Hiroshi Mamitsuka</i>	apbc109 The Challenges and Strategies for Computational Mass Spectrometry <i>Ruixiang Sun</i>
apbc091 Experiments on Fitting Protein Chains to Lattices <i>Dallas Thomas, Jan Maouch, Daya Gaur</i>	apbc110 Study of S and Z allele frequencies of Alpha I-Aniltrypsin in healthy subjects in Iranian population <i>Bahman GH Goudarzi, Abbas S Lotfi, Abbas Zare M Seyed A Mesbah-Namin, Roya Bagherian</i>
apbc092 Using Position Specific Scoring Matrices to Improve the Prediction Performance of Protein Subnuclear Localization <i>Guan-Hau Chen, Yu-Yen Ou, Su-An Chen</i>	apbc111 Bioinformatics Analysis and Identification of non-Synonymous SNPs in Candidate Genes for Ascites <i>Limei Han, MAM Groenen</i>
apbc095 Analysis of Alternative Splicing in Plant Genomes Based on Clustering of Full-Length cDNAs <i>SK Chang, YT Chao, RS Liu, SY Chen</i>	apbc112 PyCOGENT: A Comprehensive Toolkit For Comparative Genomic Data Analysis <i>P Maxwell, R Knight, J Widman, M Wakefield, S Smit, B Easton, Z Liu, R Sammut, C Lozupone, M Hamady, S Wilson, JG Caporaso, A Birmingham, GA Huttley</i>
apbc096 Reduction of Noise in Microarray Gene Expression Data Originated from the Microarray Scanner <i>Jungeun Yang, Hye Young Kim, Jin Hyuk Kim, Yong Sung Lee</i>	

Detailed Agenda of the Conference (Day 3)

Day 3: Wednesday, January 17, 2007
Venue: Wang Gungwu Theatre, Graduate House, HKU

08:30 - 12:00 Registration
 09:00 - 10:00 **Keynote 3** - Prof. Joe Nadeau, Case Western Reserve University
 Bugs, Guts and Fat - a Systems Approach to the Metabolic
 'Axis of Evil'
 (Chair: Prof. David Sankoff)

10:00 - 10:30 Tea Break
 10:30 - 11:50 **Session 7 - Biological Network** (Chair: Prof. Alfonso Valencia)

- 24. Inferring Gene Regulatory Networks by Machine Learning Methods
by Jochen Supper, Holger Fröhlich, Christian Spieth, Andreas Dräger, Andreas Zell
- 25. A Novel Clustering Method for Analysis of Biological Networks Using Maximal Components of Graphs
by Morihiro Hayashida, Tatsuya Akutsu, Hiroshi Nagamochi
- 26. Gene Regulatory Network Inference via Regression Based Topological Refinement
by Jochen Supper, Holger Fröhlich, Andreas Zell
- 27. Algorithm Engineering for Color-Coding to Facilitate Signaling Pathway Detection
by Falk Hüffner, Sebastian Wernicke, Thomas Zichner

11:50 - 13:30 Lunch Break (Joseph's Restaurant, Graduate House, HKU)

13:30 - 14:50 **Session 8 - MS; Protein-Protein Interaction**
 (Chair: Prof. Jenn-Kang Hwang)

- 28. De Novo Peptide Sequencing for Mass Spectra Based on Multi-Charge Strong Tags
by Kang Ning, Ket Fah Chong, Hon Wai Leong
- 29. Complexities and Algorithms for Glycan Structure Sequencing using Tandem Mass Spectrometry
by Baozhen Shan, Bin Ma, Kaizhong Zhang, Gilles Lajoie
- 30. Semi-supervised Pattern Learning for Extracting Relations from Bioscience Texts
by Shilin Ding, Minlie Huang, Xiaoyan Zhu
- 31. Flow Model of the Protein-protein Interaction Network for Finding Credible Interactions
by Masanori Arita, Kiyoshi Asai, Kinya Okada

14:50 - 15:30 Tea Break/**Poster Session 3** (P501, P503) - see list on facing page

15:30 - 16:50 **Session 9 - Alignment and Search** (Chair: Prof. Jinyan Li)

- 32. All Hits All The Time: Parameter Free Calculation of Seed Sensitivity
by Denise Mak, Gary Benson
- 33. Fast Structural Similarity Search Based on Topology String Matching
by Sung Hee Park, David Gilbert, Keun Ho Ryu
- 34. Simple and Fast Alignment of Metabolic Pathways by Exploiting Local Dissimilarity
by Sebastian Wernicke, Florian Rasche
- 35. Combining N-grams and Alignment in G-protein Coupling Specificity Prediction
by Betty Yee Man Cheng, Jaime Carbonell

16:50 - 17:00 Closing remark/promotion/presentation of **Best Poster Award**

Detailed Agenda of the Conference (Day 1)

- 10. Computing the Quartet Distance Between Evolutionary Trees of Bounded Degree
by Martin Stissing, Christian N. S. Pedersen, Thomas Mailund, Gerth S. Brodal, Rolf Fagerberg
- 11. A Global Maximum Likelihood Super-Quartet Phylogeny Method
by Penghao Wang, BingBing Zhou, Monther Tarawneh, Daniel Chu, Albert Zomaya
- 12. A Randomized Algorithm for Comparing Sets of Phylogenetic Trees
by Seung-Jin Sul, Tiffani Williams

Poster Session - Posters (Day 1)

apbc002 Studying the Genetic Diversity in Tetraploid Cotton Cultivars (<i>Gossypium Hirsutum</i>) by Using Cytogenetic and RAPD Characteristics <i>Masoud Sheidai, Zahra Hawaii Shahriari</i>	apbc017 Multi-Class Combination of Microarray Data: From Data Preprocessing to Functional Aspects <i>YY Leung, CQ Chang, YS Hung</i>
apbc005 Bioengineering: A DNA Encoding Technology with Bioinformatics Analysis to Application of Linear Mechanics Systems <i>Quan-Fang Wang</i>	apbc018 Dynamical and Structural Studies of Amyloid Formation: A Discrete Molecular Dynamics Simulation Perspective <i>Chiu Fan Lee, James Loken</i>
apbc006 SideChain and Backbone Ordering in Homopolymers <i>Yanjie Wei, Walter Nadler, Ulrich HE Hansmann</i>	apbc020 Sat DNA Analyzer, The First Computing Solution for Satellite-DNA Evolutionary Analysis <i>R Navajas-Pérez, M Ruiz Rejon, MA Garrido Ramos, JL Aznarte, C Rubio Escudero</i>
apbc007 Discovering Progressive High-Order Patterns in Biosequences <i>David K. Y. Chiu, Thomas W.H. Lui</i>	apbc021 Differential Evolutionary Conservation of Motif Modes in the Yeast Protein Interaction Network <i>Wei-Po Lee, Tun-Wen Pai, Wen-Shyang Tzou</i>
apbc008 Surface Accessibility Of Post-Translational Modifications and Protein-Protein Interactivity <i>CNI Pang, A Hayen, MR Wilkins</i>	apbc022 Motifcombinator: A Web Tool to Search for Combinations of Cis-Regulatory Motifs <i>M Kato, T Tsunoda</i>
apbc009 Structural and Functional Characteristics of the Promoter Regions of the Genes on Human Chromosome 22 <i>Guang Bin Liu</i>	apbc023 Nonparametric Tests of Association of Multiple Genes with Qualitative and Quantitative Phenotypes Based on Data-Adaptive U-Statistics <i>Zhi Wei, Mingyao Li, Hongzhe Li</i>
apbc010 BayesMD: Flexible Biological Modelling for Motif Discovery <i>Ole Winther, Man-Hung Eric Tang, Anders Krogh</i>	apbc026 Novel Tag SNP Selection Strategy That Incorporates Functional Information and Genotyping Assay Failure Rates <i>JSH Kwan, PC Sham</i>
apbc012 Characterization and Prediction of the Antioxidant Response Elements <i>AY Chou, PJ Sudmant, WW Wasserman</i>	apbc027 Genome-Scale Prediction of Protein Subcellular Location in Gram-Positive Bacteria <i>M Zhou, J Boekhorst, C Francke, RJ Slezén</i>
apbc013 DP-Bind: Sequence-Based Application of Multiple Machine Learning Methods to Predict DNA-Binding Sites in DNA-Binding Proteins <i>IB Kuznetsov, Z Gou, S Hwang</i>	apbc028 Combining Structure Mining and Text Mining for Functional Annotation of Proteins <i>K Au-Yeung, D Reibholz-Schuhmann, K Henrick, TJ Oldfield</i>
apbc014 Prediction of Human Mitochondrial Proteins Using SVM and Neural Network <i>Zhong Huang</i>	apbc030 Mapping of Genetic Modifier of Congenital Heart Defects in Type IIa Procollagen Deficient Mice <i>PLF Tang, KSE Cheah, P Sham, YQ Song</i>
apbc015 Phenotypic-Specific Gene Module Discovery Using a Diagnostic Tree and caBIG(tm) VISDA <i>Yilan Zhu, Zuyi Wang, Yuanjian Feng, Jianhua Xuan, David J. Miller, Eric P Hoffman, Yue Wang</i>	
apbc016 Confirmation of the Existence of CRISPRs in Microbial Genomes by BLAST <i>MCJ Ma, SK Ng, H Xue</i>	

Detailed Agenda of the Conference (Day 2)

Day 2: Tuesday, January 16, 2007

Venue: Wang Gungwu Theatre, Graduate House, HKU

- 08:30 - 17:00 Registration
 09:00 - 10:00 **Keynote 2** - Prof. Pavel Pevzner, Univ. of California, San Diego
 Positive Identification via Spectral Networks Analysis
 (Chair: Dr. Lusheng Wang)
- 10:00 - 10:30 Tea Break
 10:30 - 11:50 **Session 4** - Structure Prediction and Comparison
 (Chair: Prof. Gavin Huttley)
13. Protein Structure-Structure Alignment with Discrete Frechet Distance
 by Minghui Jiang, Ying Xu, Binhai Zhu
 14. Deriving Protein Structure Topology from the Helix Skeleton in Low Resolution Density Map using Rosetta
 by Yonggang Lu, Jing He, Charlie Strauss
 15. Fitting Protein Chains to Cubic Lattice is NP-Complete
 by Jan Manuch, Daya Gaur
 16. Inferring a Chemical Structure from a Feature Vector Based on Frequency of Labeled Paths and Small Fragments
 by Tatsuya Akutsu, Daiji Fukagawa
- 11:50 - 14:00 Lunch Break (Kamboat Restaurant, WestWood Mall)
 14:00 - 15:00 **Session 5 - Mapping and Disease** (Chair: Prof. Concettina Guerra)
17. Exact and Heuristic Approaches for Identifying Disease-Associated SNP Motifs
 by Gaofeng Huang, Peter Jeavons
 18. Genotype-Based Case-Control Analysis, Violation of Hardy-Weinberg Equilibrium, and Phase Diagrams
 by Young Ju Suh, Wentian Li
 19. A Probabilistic Method to Identify Compensatory Substitutions for Pathogenic Mutations
 by Brett Easton, Peter Maxwell, Alexander Isaev, Gavin Huttley
- 15:00 - 15:40 Tea Break/Poster Session 2 (P501, P503) - see list on facing page
 15:40 - 17:00 **Session 6 - Genome Comparison** (Chair: Prof. Laxmi Parida)
20. Exploring Genome Rearrangements using Virtual Hybridization
 by Mahdi Belcaid, Anne Bergeron, Annie Chateau, Cedric Chauve, Yannick Gingras, Guilaine Poisson, Marc Vendette
 21. Two Plus Two Does not Equal Three: Statistical Tests for Multiple Genome Comparison
 by Narayanan Raghupathy, Rose Hoberman, Dannie Durand
 22. The Distance Between Randomly Constructed Genomes
 by Wei Xu
 23. Computing the Breakpoint Distance between Partially Ordered Genomes
 by Zheng Fu, Tao Jiang
- 18:30 - 21:30 Banquet (Jumbo Floating Restaurant, Dinner talk: 19:15 - 19:45)

Detailed Agenda of the Conference (Day 2)

Poster Session - Posters (Day 2)

apbc031	MIBDQC, A Knowledge Base Implemented Using the Entity-Attribute-Value Model for Quality Control of Botanical Drug Products <i>Charlie Chang Liu, Kei Cheung, Tommy Yungchi Cheng, Allan Sik-Yin Lau, Paul Kwong-Hang Tam</i>	apbc050	Detection of Transcription Units Based on Integration of Non-Targeted Analyses <i>Hirokazu Kobayashi, Joe Akitomi, Nobuyuki Fujii, Md Altaf-Ul-Amin, Ken Kurokawa, Kazuo Kobayashi, Naotaka Ogasawara, Shigehiko Kanaya</i>
apbc032	iCartiGD: The Integrated Cartilage Gene Database <i>Ming Yiu Yeung, David K. Smith, Matthew S.Y. Chan, Brian C. Wong, Kenneth M.C. Cheung, Kathryn S.E. Cheah, Pak Sham, Danny Chan, You-Qiang Song</i>	apbc051	Developing Algorithm for Visualizing Orthologous Gene Clusters Having Common Domains <i>Misako Arai, Yoko Shinbo, Md Altaf-Ul-Amin, Shigehiko Kanaya, Ken Kurokawa</i>
apbc034	A Predictive Model for Macrophage-Specific Genomic Regulatory Regions <i>Ying Sheng, Boris Lenhard</i>	apbc052	Identification of Molecular Chaperones and Glycolytic Enzymes Involved in Enhanced Production of Recombinant Antibody: Proteomic Studies <i>K Lee, HT Lee, H Im, DH Kim, DJ Oh</i>
apbc035	Splitstree4 - A Program for Computing and Exploring Phylogenetic Networks & Trees <i>Daniel H Huson</i>	apbc053	Applications of Domain-Domain Interaction in Pathways Study <i>Hsueh-Chuan Liu, Chien-Hung Huang, JF Tsai, Ka-Lok Ng</i>
apbc036	Genome Halving with an Outgroup <i>Chunfang Zheng, Qian Zhu</i>	apbc054	Predicting Putative Human miRNA Precursor Candidates Associated with Promoter Regions and CpG Islands <i>Ming-Cheng Tsai, Ka-Lok Ng</i>
apbc037	Relative Roles of PAK4 Kinase Activity and PAK4-Integrin Binding for Promotion of Cell Motility <i>Zhilun Li, Hongquan Zhang, John Lock, Steffen Teller, Yajuan Liu, Staffan Strömblad</i>	apbc055	Protein Hierarchical Selection: An Information Portal for Multiple Protein Structural Alignment <i>Tun-Wen Pai, Jian-Ming Chen, Bo-Han Su, Margaret Dah-Tsyr Chang, Hao-Teng Chang, Wei-I Chou</i>
apbc038	Global Topological Properties of the Integral Membrane Protein Interactome in Yeast <i>Kelvin Xi Zhang, BF Francis Ouellette</i>	apbc056	Linkage Analysis on Familial Early-Onset Degenerative Disc Disease (DDD) <i>Daniel WH Ho, Kenneth MC Cheung, Danny Chan, Jaro Karpainen, SP Yip, Jurg Ott, Keith DK Luk, John CY Leong, Kathryn SE Cheah, Pak Sham, You-Qiang Song</i>
apbc039	Predicting Protein-Protein Interactions Using Fuzzy Inference Approach <i>Xuejian Xiong, Kevin Breitkreuz, Mike Tyers</i>	apbc059	Identification of Regulatory Gene Module Composite by Latent Variable Modeling and nICA <i>Ting Gong, Yitan Zhu, Jianhua Xuan, Huai Li, Chen Wang, Robert Clarke, Eric P Hoffman, Yue Wang</i>
apbc040	Large-Scale Comparative Genomic Analyses of Cytoplasmic Membrane Transport Systems in Prokaryotes <i>Qinghu Ren, Kaixi Chen, Ian T Paulsen</i>	apbc060	Modelling the Distribution of Gene Expressions Using Stable Distributions <i>Salas-Gonzalez D, Kuruoglu E, Ruiz DP</i>
apbc043	A Projection and Search Algorithm for the Bicluster Problem <i>Feng Liu, Xiaowen Liu, Hui Fan, Qingsong Xie</i>	apbc061	Computational Prediction of Cis-Regulatory Modules in Human Genome <i>KL Mok, FYL Chin, DK Smith, PC Sham, KSE Cheah</i>
apbc044	Gene-Gene Interactions for Asthma and Plasma Total IgE Concentration in Chinese Children by Using Multifactor-Dimensionality Reduction (MDR) Method <i>IHS Chan, TF Leung, NLS Tang, CY Li, YM Sung, GWK Wong, CK Wong, CWK Lam</i>	apbc063	Low-Resolution Structural Genomics by Structure Prediction and Filtering of Decoys Using Sparse Experimental Data <i>JM Bujnicki, MJ Gajda, J Kosinski, A Obarska, M Feder, AA Chmiel, S Pawlak, IA Cymerman, KJ Skowronek</i>
apbc045	Osmotic Stress Response Gene Mining System in Plant Genomes <i>Yong Li, Yanming Zhu, Dianjing Guo</i>	apbc066	Mapping the Myopia Genes <i>CY Lam, CP Pang</i>
apbc046	Genome Strategy for Recognition Sites of Restriction Enzymes <i>Ken Yamakura, Yoko Shinbo, Md Altaf-Ul-Amin, Ken Kurokawa, Shigehiko Kanaya</i>	apbc069	Identification and Characterization of Novel Transcription Factor Binding Motif in the Promoter of Human Ribonuclease <i>Hsiu-Yiu Wang, Tun-Wen Pai, Hao-Teng Chang, Yuan-Hon Lee, Yen-Shin Chang, Tan-chi Fan, Shu-Chuan Lin, Margaret Dah-Tsyr Chang</i>
apbc047	Experimental Design for Time-Series Microarray Analysis <i>Hiroki Takahashi, Ryosuke Ito, Taku Oshima, Naotake Ogasawara, Md Altaf-Ul-Amin, Shigehiko Kanaya, Ken Kurokawa</i>	apbc070	Computational Drug Repositioning and Side Effect Prediction for Kinase Inhibitors <i>YY Li, J An, SJM Jones</i>
apbc048	Integrated Analyses of Genechip Data in Arabidopsis <i>Thalana Masayoshi Wada, Munehide Itoyama, Md Altaf-Ul-Amin, Yukio Nakagawa, Ken Kurokawa, Shigehiko Kanaya</i>		
apbc049	Species-Metabolite Database (KNAPSAcK): Elucidating Diversity of Flavonoids <i>Shun-ichi Sakaguchi, Yoko Shinbo, Yukiko Nakamura, Md Altaf-Ul-Amin, Ken Kurokawa, Toshiaki, Tokimatsu, Masahiro Arita, Kimito Funatsu, Shigehiko Kanaya</i>		