

The 4th Asia-Pacific Bioinformatics Conference

Program Overview, 12–16 February 2006

Sunday, 12 February 2006

14.30–20.30 **Registration** Main entry of the activity center

18.30–20.30 **Reception** The Plato Hall

Monday, 13 February 2006

8.30–16.30 **Registration** Main entry of the activity center

9.00–9.15 **Opening Session** The Alexander Hall

9.15–10.00 **Keynote 1** The Alexander Hall (*chair: Tao Jiang, Univ of California - Riverside*)

Whole Genome Optical Mapping. *Prof. Michael Waterman (Univ of Southern California)*

10.00–10.30 **Tea Break** Lobby

10.30–11.30 **Algorithm** The Alexander Hall (*chair: Michael Waterman, Univ of Southern California*)

1. Property-dependent Analysis of Aligned Proteins from Two or More Populations, *Steinar Thorvaldsen, Elinor Ytterstad, Tor Fla*
2. Alignscope : A Visual Mining Tool for Gene Team Finding with Whole Genome Alignment, *Hee-Jeong Jin, Hye-Jung Kim, Jeong-Hyeon Choi, Hwan-Gue Cho*
3. A Randomized Algorithm for Learning Mahalanobis Metrics: Application to Classification and Regression of Biological Data, *Christopher Langmead*

11.30–13.00 **Lunch Break** (The Alexander Hall) & **Poster Session 1** (The Plato Hall)

13.00 – 14.00 **Structure classification and prediction** The Alexander Hall (*chair: Chris Langmead, Carnegie Mellon Univ*)

1. Predicting Ranked SCOP Domains by Mining Associations of Visual Contents in Distance Matrices, *Pin-Hao Chi, Chi-Ren Shyu*
2. A New Neural Network for Beta-turn Prediction: The Effect of Site-specific Amino Acid Preference, *Zhong-ru Xie, Ming-jing Hwang*
3. A Knowledge-Based Approach to Protein Local Structure Prediction, *Ching-Tai Chen, Hsin-Nan Lin, Kuen-Pin Wu, Ting-Yi Sung, Wen-Lian Hsu*

14.00–15.00 **Microarray data analysis** The Alexander Hall (*chair: Ping-Chiang Lyu, Nat'l Tsing-Hua Univ*)

1. Microarray Missing Value Imputation by Iterated Local Least Squares, *Zhipeng Cai, Maysam Heydari, Guohui Lin*
2. A generalized output-coding scheme with SVM for multiclass microarray classification, *Li Shen, Eng Chong Tan*
3. Gene Expression Data Clustering Based on Local Similarity Combination, *De Pan, Fei Wang, Jiankui Guo*

15.00–16.00 **Tea Break** (Lobby) & **Poster Session 1** (The Plato Hall)

16.00–17.00 **Genome rearrangement** The Alexander Hall (*chair: Kun-Mao Chao, Nat'l Taiwan Univ*)

1. RECOMP: A Parsimony-based Method for Detecting Recombination, *Derek Ruths, Luay Nakhleh*
2. Accuracy of four heuristics for the full sibship reconstruction problem in the presence of genotype error, *Dmitry Kononov*
3. A Recursive Method for Solving Haplotype Frequencies in Multiple Loci Linkage Analysis, *Michael Ng*

19.00–21.00 **Conference Banquet**

Tuesday, 14 February 2006

8.30–16.30 **Registration** Lobby (information desk)

9.15–10.00 **Keynote 2** The Alexander Hall (*chair: Phoebe Chen, Deakin Univ*)

Automating the Search for Lateral Gene Transfer. *Prof. Mark Ragan (Univ. of Queensland)*

10.00–10.30 **Tea Break** Lobby

10.30–11.30 **Phylogenetics** The Alexander Hall (*chair: Mark Ragan, Univ. of Queensland*)

1. Resolving gene tree and species tree problem by phylogenetic mining, *Xiaoxu Han*
2. Techniques for assessing phylogenetic branch support, *Derek Ruths, Luay Nakhleh*
3. A More Accurate and Efficient Whole Genome Phylogeny, *P.Y. Chan, T.W. Lam, Siu-Ming Yiu*

11.30–13.00 **Lunch Break** (The Alexander Hall) & **Poster Session 2** (The Plato Hall)

13.00–14.00 **Gene variation and mutation** The Alexander Hall (*chair: Hsueh-Feng Juan, Nat'l Taiwan Univ*)

1. Discriminative Detection of Cis-Acting Regulatory Variation from Location Data, *Yuji Kawada, Yasubumi Sakakibara*
2. Trends in codon and amino acid usage in human pathogen *Tropheryma whipplei*, the only known actinobacteria with reduced genome, *Sabyasachi Das, Sandip Paul, Chitra Dutta*
3. Consequences of mutation, selection and physico-chemical properties of encoded proteins on synonymous codon usage in adenoviruses, *Sandip Paul, Sabyasachi Das, Chitra Dutta*

14.00–14.40 **Database** The Alexander Hall (*chair: Wen-Lian Hsu, Academia Sinica*)

1. Analyzing inconsistency toward enhancing integration of biological molecular databases, *Phoebe Chen, Qingfeng Chen*
2. ONBIRES: ONtology-based BIological Relation Extraction System, *Minlie Huang, Xiaoyan Zhu, Shilin Ding, Hao Yu, Ming Li*

14.40–15.40 **Tea Break** (Lobby) & **Poster Session 2** (The Plato Hall)

15.40–16.40 **Structure analysis** The Alexander Hall (*chair: Ming-Jing Hwang, Academia Sinica*)

1. Disentangling the Role of Tetranucleotide in the Sequence-Dependence of DNA Conformation: A Molecular Dynamics Approach, *Marcos J. Arauzo-Bravo, Satoshi Fujii, Hidetoshi Kono, Akinori Sarai*
2. Characterization of Multi-Charge Mass Spectra for Peptide Sequencing, *Ket Fah Chong, Kang Ning, Hon Wai Leong*
3. Structure Based Chemical Shift Prediction Using Random Forests Non-Linear Regression, *Christopher Langmead, K Arun*

16.40–17.15 **Invited Talk** The Alexander Hall (*chair: Limsoon Wong, Institute for Infocomm Research*)

Advances in transcriptome analysis. *Shoba Ranganathan (McQuarrie Univ)*

Wednesday, 15 February 2006

8.30–16.30 **Registration** Lobby (information desk)

9.15–10.00 **Keynote 3** The Alexander Hall (*chair: Ueng-Cheng Yang, Nat'l Yang-Ming Univ*)

On the Inference of Regulatory Elements, Circuits and Modules. *Wen-Hsiung Li (Academia Sinica & U. of Chicago)*

10.00–10.30 **Tea Break** Lobby

10.30–11.30 **Systems biology and gene network (I)** The Alexander Hall (*chair: Hoong-Chien Lee, Nat'l Central Univ*)

1. Inference of gene regulatory networks from microarray data: a fuzzy logic approach, *Ma Chi Hung, Chan Chun Chung*
2. System identification and robustness analysis of the circadian regulatory network via microarray data

- in *arabidopsis thaliana*, *Bor-Sen Chen*
3. On the Complexity of Finding Control Strategies for Boolean Networks, *Tatsuya Akutsu, Morihiro Hayashida, Wai-Ki Ching, Michael Ng*

11.30–13.00 **Lunch Break** (The Alexander Hall) & **Poster Session 3** (The Plato Hall)

13.00–14.00 **Systems biology and gene network (II)** The Alexander Hall (*chair: Christian Schoenbach, RIKEN*)

1. Identification of Over-represented Combinations of Transcription Factor Binding Sites in Sets of Co-expressed Genes, *Shao-shan Huang, Debra Fulton, David Arenillas, Paul Perco, Shannan Ho Sui, James Mortimer, Wyeth Wasserman*
2. Characterization of the existence of galled-tree networks, *Jan Manuch, Xiaohong Zhao, Ladislav Stacho, Arvind Gupta*
3. Semi-Supervised Threshold Queries on Pharmacogenomics Time Sequences, *Johannes Assfalg, Hans-Peter Kriegel, Peer Kroeger, Peter Kunath, A. Pryakhin, & Matthias Renz,*

14.00–15.00 **Motif analysis** The Alexander Hall (*chair: Francis Chin, Hong-Kong Univ*)

1. An efficient algorithm for string motif discovery, *Francis Chin, Henry Leung*
2. EDAM An Efficient Clique Discovery Algorithm with Frequency Transformation for Finding Motifs, *Guoren Wang, Yifei Ma*
3. A novel approach for structured consensus motif inference under specificity and quorum constraints, *Christine Sinoquet*

15.00–16.00 **Tea Break** (Lobby) & **Poster Session 3** (The Plato Hall)

16.00–17.00 **Analysis of biological molecules** The Alexander Hall (*chair: Shoba Ranganathan McQuarrie Univ*)

1. SVM-based Identification of microRNA precursors, *Liang Huai Yang, Wynne Hsu, Mong Li Lee, Limsoon Wong*
2. Genome-wide computational analysis of small nuclear RNA genes of *Oryza sativa* (Indica and Japonica), *M. Shashikanth, A. Snehalatharani, Sk. Mubarak, K. Ulaganathan*
3. Protein Subcellular Localization Prediction with wolf PSORT, *Horton Paul, Keun-Joon Park, Takeshi Obayashi, Kenta Nakai*

17.00–17.15 **Closing Session** The Alexander Hall

Closing Remarks by General Co-chair, *Dr. Wen-Hsiung Li (Academia Sinica & U. of Chicago)*

Closing Remarks by PC Co-chair, *Dr. Ueng-Cheng Yang (National Yang-Ming Univ)*

Thursday, 16 February 2006

8.30–17.30 **Registration** Classroom I & II (map will be available on the information desk)

9.00–12.00 **Classroom I at NTU**

Biostatistical and Bioinformatics Approaches in High Dimensional Data Derived from High Throughput Assays: A Consumer Guide

Prof. Yu Shyr (Vanderbilt University, USA)

9.00–12.00 **Classroom II at NTU**

Systems biology

Prof. Hsuan-Cheng Huang (National Yang-Ming University, Taiwan, R.O.C.)

13.30–16.30 **Classroom I at NTU**

Matrix visualization and information mining

Dr. Han-Ming Wu & Prof. Chun-Houh Chen (Institute of Statistical Science, Academia Sinica, Taiwan, R.O.C.)

13.30–16.30 **Classroom II at NTU**

Gene Ontology Browsing Utility

Dr. Wen-Dar Lin & Prof. Jan-Ming Ho (Institute of Information Science, Academia Sinica, Taiwan, R.O.C.)

Poster session

Poster should be posted before 9:00, presented during the afternoon tea break, and taken off before 17:15.

Session 1 (No. 1-28): Feb. 13

Session 2 (No. 29-56): Feb. 14

Session 3 (No. 57-80): Feb. 15

Paper ID	Paper title	Authors
P001	Qualiseq: quality genomic sequence retrieval	Tz-chao Lin, Kuo-his Lee, Yan-hau Chen, Ming-fang Tsai, Adam Yao
P002	D-space: distributed sequence pattern capture engine	Hasegawa A, Konagaya A
P003	Metadata extraction from biological experimental data	Badr Al-Daihani, Alex Gray, Peter Kille
P004	Polymerase chain reaction amplification and molecular characterization of <i>Pasteurella multocida</i> species gene from cultural lysates of vaccine strain of Nepal	Banshi Sharma
P005	Global analysis of micro-RNA target gene expression reveals the potential roles of micro-RNA in maintaining tissue identity.	Zhenbao Yu, Zhaofeng Jian, Shi-Hsiang Shen, Enrico Purisima, Edwin Wang
P006	Enhanced structure prediction of gene products containing class III adenylate cyclases	C.S. Reddy, A. Manonmani, M. Babu and R. Sowdhamini
P007	Discovery and characterization of novel transcription binding motifs in the promoters of primate eosinophil RNases	Chang HT, Chang YS, Chou WY, Pai TW, Chou WY, Lee YH, Chang MDT
P008	Detection of peroxisomal protein candidates using motif search, co-expression and promoter content	Marlis Herberth and Christian Schönbach
P009	Identification of genomic regions that are potentially involved in low-copy repeat mediated chromosome deletion/duplication	Chun-Ming Chen, Shaw-Jenq Tsai, Ko-Fan Chen, Hsiang-Han Chan, H.Sunny Sun
P010	Hypoxia-regulated gene network and cell migration	Ko-Fan Chen, H. Sunny Sun, and Shaw-Jenq Tsai
P011	Lidaeus: a virtual screening program for drug discovery	Kan D, Taylor P, Walkinshaw MD
P012	Identify disease associated genes by literature mining	Hsin-Ta Wu, Jung-Hsien Chiang, Ueng-Cheng Yang
P013	Kernel pls-svm for microarray cancer classification	Shen L, Tan EC
P014	A fuzzy expert system for the inference of antidepressants based on gene polymorphisms	Eugene Lin and Yuchi Hwang
P015	Comparative Modeling and Receptor based pharmacophore model development for pfemp1 protein of <i>Plasmodium falciparum</i>	Niveditha M, Sowmiya D, Ragul G
P016	Comparative genome analysis of the cytophaga-flavobacteria-bacteroides (cfb) group species	Xie G, Brettin TS

P017	Metabolic control analysis for enhanced lycopene production in <i>Escherichia coli</i>	Woo HW, Lee SY
P018	Metafluxnet: platform for metabolic flux analysis of in silico genome-scale models	Woo HM, Lee D-Y, Choi HS, Kim TY, Yun H, Lee SY
P019	Determination of conserved genes based on the ortholog network	Hijiri Maeno, Misako Arai, Yoko Shinbo, MD. Altaf-Ul-Amin, Ken Kurokawa, Naotake Ogasawara AND Shigehiko Kanaya
P020	Phenotype microarray analysis of <i>Escherichia coli</i> K-12 : in silico approach	Hiroaki Gobara, Baba Tomoya, Md. Altaf-Ul-Amin1, Masanori Arita, Kurokawa Ken, Shigehiko Kanaya, Hirotada Mori
P021	Detection of regulons based on integration of gene expression profiles and promoter searches	H Kobayashi, J Akitomi, N Fujii, H Maeno, K Yamakura, MAU Amin, K Kurokawa, K Kobayashi, N Ogasawara and S Kanaya
P022	Sphsom: a toolkit for visualize intrinsic structure in high dimensional data space	Hirokazu Nishio, Md. Altaf-Ul Amin, Ken Kurokawa, Shigehiko Kanaya
P023	Development of a new ab initio gene prediction system to reduce false positives	Hisataka Numa, Takeshi Itoh
P024	A modeling and simulation framework for in silico metabolic flux analysis	Hongseok Yun, Sang Yup Lee
P025	Identification of RNA-binding protein residues using machine learning approaches	Jia-Je Li, Hsueh-Fen Juan, I-Fang Chung, Hsuan-Cheng Huang
P026	Topological characteristics of protein interaction network and roles of essential genes in <i>E. coli</i> K-12	Yih-Chii Hwang, Chen-Ching Lin, Hsueh-Fen Juan, Hirotada Mori, Hsuan-Cheng Huang
P027	Elucidating the essentiality of essential genes in <i>E. coli</i> K-12	Yue-Yang Bow, Jen-Yun Chang1, Hsueh-Fen Juan, Hirotada Mori, Hsuan-Cheng Huang
P028	Bsip – a web server for systems-biology structure identification program development	Chern-Han Ou, Chih-Chin Chang, Hung-Ching Hsia, Feng-Sheng Wang, Hsueh-Fen Juan, Hsuan-Cheng Huang
P029	Bioinformatics approach to study the correlation between gene expression profiles and protein-protein interactions using matrices	Nancy Lin, Shyh-Horng Chiou, Hsueh-Fen Juan, Hsuan-Cheng Huang
P030	Prediction of protein secondary structures by neural networks with combined information	Hui-Huang Hsu and Jian-Tsang Chang
P031	Automated prediction of bacterial replication origin (apbro)	I Hsuan Lin, Kuan-Bei Chen, Yu-Hsuan Lin, Chuan-Hsiung Chang
P032	Discovery of genes involved in DNA repair using phylogenetic profiles to compare genomes	Kristin Robertsen and Torbjorn Rognes
P033	Gene Interactions in a social setting: Identification of relevant gene groups in genomic data	Jochen Brumm, Elizabeth Conibear1, Jenny Bryan, Wyeth Wasserman
P034	Sequence and structure analysis of avian influenza A hemagglutinin	Hsu, JW, Chan, CH, Kao, CY

P035	Evolutionary approach to identifying domain subtypes	Tajul-Arifin, K and Mattick, JS
P036	Parameter optimization technique using the rsm and parameter space visualization for cardiac myocyte model	Koji Sakai, Koji Koyamada, Yukiko Yamashita, Nobuaki Sarai, Keiichi Asakura, Akinori Noma
P037	Development of a prototype system for the inference of genetic networks based on genetic programming	Kouji Tanaka, Yutaka Akiyama, Hayato Yamana
P038	Constrained multiple structure feature alignment (cmsfa) for unique peptide identification	Bo-Han Su, Tun-Wen Pai, Wen-Shyong Tzou
P039	Log linear algorithm for syntenic distance	Dunnett LJ, Litow B
P040	Inter-test agreement of pathway discovery of five statistical methods commonly used in the analysis of DNA microarrays	Liu XX, Loh M, Dong P, Mondry A
P041	Diagnostic performance of five statistical methods commonly used in the analysis of DNA microarrays	Loh M, Liu XX, Dong P, Mondry A
P042	Data envelopment analysis approach applied to gene expression data	Masako Hoshino, Hiroshige Inazumi
P043	A pipeline for analysis of published abstracts for information on protein-protein inter-relations	Ling, MHT, Nicholas, KR, Lefèvre, C
P044	Structural analysis, discrimination of α -barrel membrane proteins and prediction of their membrane spanning segments	M. Michael Gromiha, Shandar Ahmad and Makiko Suwa
P045	Gene classification for Arabidopsis thaliana based on expression profiles utilized by 1000 genechip	Munehide Itoyama, Hirokazu Kobayashi, Md. Altaf-Ul-Amin, Ken Kurokawa, Shigehiko Kanaya
P046	Bootstrap confidence levels for full sibship reconstruction	Bajema N, Konovalov DA, Litow B
P047	Leucine-rich repeat (Lrr) variants in proteins associated with human diseases	Norio Matsushima, Purevjav Enkhbayar, Mitsuru Osaki
P048	Structural features of α -helices in proteins revealed by new helix fitting method	Purevjav Enkhbayar, Mitsuru Osaki, Norio Matsushima
P049	Spip – sh2 domain-protein interaction predictor	Rajasekaran M., Suresh Kumar R
P050	Genomic organization of highly conserved non-coding sequences is similar in metazoan genomes	Ho Sui SJ, Sandelin A, Lenhard B, Wasserman WW
P051	Pspml: physiological simulation protocol markup language	Shimayoshi T, Amano A, Matsuda T
P052	Bioinformatic discovery of microRNAs and their target genes from human ESTs and introns	Sung-Chou Li, Wen-Chang Lin
P053	Comparative and in silico metabolic engineering to drive anaerobic fermentative flux to succinic acid in Escherichia coli	Tae Yong KIM, Dong-Yup LEE, Sang Jun LEE, and Sang Yup LEE
P054	Nebir – an nlp-enabled biomedical information retrieval system	Tsai TH, Wu CW, Hung HC, He D, Sung TY, Hsu WL
P055	A knowledge-based natural language query method for search on human genetic mutation	Wei Qu, David Feng
P056	Improved pairwise alignment of proteins in the twilight zone using local structure predictions	Yao-ming Huang and Christopher Bystroff

P057	Search tool for relationship between metabolites and species	Yoko Shinbo, Yukiko Nakamura, Hiroko Asahi, Md.Altaf-Ul-Amin, Ken Kurokawa, Hirokazu Kobayashi, Masayoshi Wada, Shunichi Sakaguchi, Kazuaki Natsuhara, Toshiaki Tokimatsu, Masanori Arita and Shigehiko Kanaya
P058	Dynamic sensitivity analysis of complex biochemical oscillation networks using a modified collocation method	Ming-Laing Chen and Feng-Sheng Wang
P059	Inference of genetic networks using evolutionary multi-objective optimization approach	Pang-Kai Liu and Feng-Sheng Wang
P060	Learning genic interaction using markov model	Chia-Wei Wu, Tzong-Han Tsai, Cheng-Pu Sun, Wen-Lian Hsu
P061	Scaling behavior of maximal repeat distributions in genome sequences	Wang J.D., Liu Hsiang-Chuan, Ng Ka-Lok
P062	Topological stability of the protein-protein interaction networks	Huang Chien-Hung, Tsai J.F., Fang Jywe-Fei, Ng Ka-Lok
P063	Large scale prediction of domain-domain interactions from protein-protein interactions	Lee Jeng-ru, Liu Hsiang-Chuan, Tsai J.F, Ng Ka-Lok
P064	V-mitosnp: visualization of mitochondrial snp	Gu D-L, Cheng Y-H, Yang C-H, Chang P-L, Chuang L-Y, Chang H-W
P065	Motif constituents in the yeast protein interaction network discovered through the asymmetric functional annotation	Wei-Yao Chou, Tun-Wen Pai, Wei-Yuan Chang, Wen-Shyong Tzou
P066	Apply genetic algorithms and neural networks to seldi proteomic data for prostate cancer detection	Lin TC, Liu RS, Chen SY, Hwang JI, Chao YT
P067	Fly-DPI, database of protein interactomes for Drosophila melanogaster: A framework of experimental and putative interactions	Chung-Yen Lin, Chi-Shiang Cho, Chia-Ling Chen, Fan-Kai Lin, Chieh-Hua Lin, Pao-Yang Chen, Shu-Hwa Chen, Chen-Zen Lo and Chao A. Hsiung
P068	MOLAS : microarray on line analysis system, a web platform for massive data management and analysis	Chung-Yen Lin, Wei-Chen Chen, Yueng-Shiang Huang, and, Chao A. Hsiung
P069	Potential electrophysiologic interactions between ik(atp) activation and ikr blockade in patients with ischemic heart disease: a simulation study	Chang HD, Wu SN, Wu JS, Sung RJ
P070	Gene structure assembly through analysis of large-scale ESTs	Fang-Rong Hsu, Jiun-Tang You, and W. C. Shia
P071	Non-arbitrary judgment algorithm for periodicity of time series data	Tominaga D, Horton P
P072	Primerz: a web-based primer design tool for exons and promoters of a gene	Kuo-Hsi Lee, Ming-Fang Tsail, Adam Yao
P073	Correlation among gene density, recombination rate and te distribution in rice genome	Ya-Ting Chao, Yao-Cheng Lin, Hui-Ling Cheng, Ru-Sheng Liu, Shu-Yuan Chen, Hsing, Yue-le Caroline

P074	Affyrmation: A SNP affirmation and visualization tool for Affymetrix DNA chip	Yan-Hau Chen, Ming-Fang Tsai, Adam Yao
P075	Identifying the functions of genes by a computational approach: Rosetta stone method used to discover genes involved in DNA repair	Inger Solberg and Torbjorn Rognes
P076	Transformation and optimization of pyruvate branches in metabolic pathways of Lactococcus lactis	Hui- Hsin Yu, I-Fang Chung, Feng-Sheng Wang
P077	Evolution of hepatitis B virus in an acute hepatitis B patient co-infected with genotypes B and C	Bing-Fang Chen, Chun-Jen Liu, Guey-Mei Jow, Pei-Jer Chen, Jia-Horng Kao, and Ding-Shinn Chen
P078	An analysis of H5N1 influenza a virus hemagglutinin	Chen YJ , Chu HT
P079	Group feature extraction from multiple indexing sequence alignment	Wei-Yao Chou, Tun-Wen Pai, Wei-Yuan Chang, Wen-Shyong Tzou
P080	Representation of alternative transcript diversity in the human tissue kallikrein gene family using splicing graphs	Durgaprasad Bollina, Shoba Ranganathan