

APBC 2015 Program Schedule

General Information for speakers

- For keynote speakers, the presentation time is 40 min plus 10 min discussion.
- For oral presenters, the presentation time is 25 min plus 5 min discussion.

General Information for poster presenters

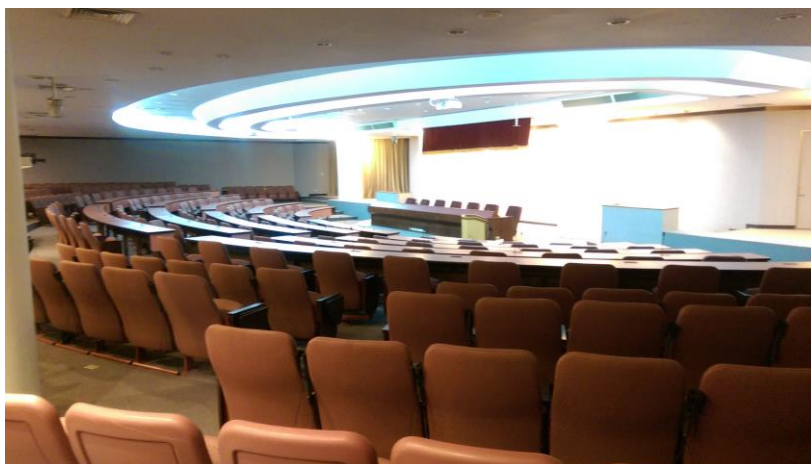
- All posters will be set up between 08:00 AM-09:10 AM on the first day (21 Jan.).
- The poster sessions will run for a total of three days. During the three days, the poster presenters should attend full three day and participants are free to ask questions.
 - Our poster board is 90cm x 150cm (Portrait).

Venue

Microelectronics and Information Systems Research Center



International Conference Hall



January 21, 2015 (Wednesday)

1st Floor, Microelectronics and Information Systems Research Center, National Chiao Tung University

Time	Event		
8:30 – 9:20	Registration and Poster Setup		
9:20 – 9:30	Opening Messages		
9:30 – 10:20	<p align="center">Keynote 1 <i>Neuroinformatics of the Fly Brain</i> Ann-Shyn Chiang, National Tsing Hua University, <i>Taiwan</i> Session Moderator: Ping-Chiang Lyu International Conference Hall</p>		
10:20 – 10:35	Taking Group Photo		
10:35 – 10:50	Coffee Break		
10:50 – 12:20	<p align="center">Session 1: Regulatory Genomics</p> <p align="center">Moderator: Ka-Lok NG (Asia University)</p> <p align="center">International Conference Hall</p>	<p align="center">Session 2: Systems Biology</p> <p align="center">Moderator: Bin Liu (Harbin Institute of Technology Shenzhen Graduate School)</p> <p align="center">Conference Room 4</p>	<p align="center">Session 3: CNV- and SNP-associated Applications</p> <p align="center">Moderator: Laxmi Parida (IBM T.J. Watson Research Center)</p> <p align="center">Conference Room 1</p>
12:20 – 13:10	Lunch		
13:10 – 14:20	Poster Session		
14:20 – 14:40	<p align="center">Workshop: <i>How to Publish with Genomics, Proteomics & Bioinformatics</i> Jialei Xie, Editor of Genomics, Proteomics and Bioinformatics (GPB) Beijing Institute of Genomics, Chinese Academy of Sciences, <i>China</i> International Conference Hall</p>		
14:40 – 15:00	Coffee Break		
15:00 – 17:30	<p align="center">Session 4: Next-Generation Sequencing Data Analysis</p> <p align="center">Moderator: Jui-Hung Hung (National Chiao Tung University)</p> <p align="center">International Conference Hall</p>	<p align="center">Session 5: Biological Data Clustering and Classification</p> <p align="center">Moderator: Li-Ching Wu (National Central University)</p> <p align="center">Conference Room 4</p>	<p align="center">Session 6: Algorithms & Data Mining</p> <p align="center">Moderator: Shanfeng Zhu (Fudan University)</p> <p align="center">Conference Room 1</p>

Session 1: Regulatory Genomics (10:50 – 12:20)

- 10:50 – 11:20 Kai-Yao Huang, ViralmiR: Identification of Viral microRNA Precursor Based on Sequence and Structure Information.
- 11:20 – 11:50 Ka-Lok NG, Transcription Factor and microRNA-Regulated Network Motifs for Cancer and Signal Transduction Networks.
- 11:50 – 12:20 Sheng-Da Hsu, Integrated Analyses to Reconstruct microRNA-Mediated Regulatory Networks in Mouse Liver Using High-Throughput Profiling.

Session 2: Systems Biology (10:50 – 12:20)

- 10:50 – 11:20 Fengzhu Sun, Network Tuned Multiple Rank Aggregation and Applications to Gene Ranking.
- 11:20 – 11:50 Jie Zheng, Computational Cell Fate Modelling for Discovery of Rewiring in Apoptotic Network for Enhanced Cancer Drug Sensitivity.
- 11:50 – 12:20 Hyundoo Jeong, Accurate Multiple Network Alignment Through Context-Sensitive Random Walk.

Session 3: CNV- and SNP-associated Applications (10:50 – 12:20)

- 10:50 – 11:20 Takahiro Mimori, Estimating Copy Numbers of Alleles from Population-Scale High-Throughput Sequencing Data.
- 11:20 – 11:50 Xin Chen, LGH: a Fast and Accurate Algorithm for Single Individual Haplotyping Based on a Two-Locus Linkage Graph.
- 11:50 – 12:20 Laxmi Parida, Data-Driven Encoding for Genetic Trait Prediction.

Session 4: Next-Generation Sequencing Data Analysis (15:00 – 17:30)

- 15:00 – 15:30 Michiaki Hamada, A Semi-Supervised Learning Approach for RNA Secondary Structure Prediction.
- 15:30 – 16:00 Chiung-Chih Hsiao, An Intelligent and Efficient Paired-End Adapter-Trimming Algorithm and Its Implementation in the Cloud.
- 16:00 – 16:30 Wei Li, Accurate Inference of Isoforms from Multiple Sample RNA-Seq Data.
- 16:30 – 17:00 Hong Sun, IAOfseq: Inferring Abundance of Overlapping Genes Using RNA-Seq Data.
- 17:00 – 17:30 Yang Bai, IRcall and IRclassifier: Two Methods for Flexible Detection of Intron Retention Events from RNA-Seq Data.

Session 5: Biological Data Clustering and Classification (15:00 – 17:30)

- 15:00 – 15:30 Junjie Li, Genome-Wide Association Data Classification and SNPs Selection Using Two-Stage Quality-Based Random Forests.
- 15:30 – 16:00 Huidong Chen, DPNuc: Identifying Nucleosome Positions Based on the Dirichlet Process Mixture Model.
- 16:00 – 16:30 Hung-Ming Lai, A New Vision of Evaluating Gene Expression Signatures.
- 16:30 – 17:00 Jiyun Zhou, Identifying DNA-binding Proteins by Combining Support Vector Machine and PSSM Distance Transformation.
- 17:00 – 17:30 Naoki Nariai, HLA-VBSeq: accurate HLA Typing at Full Resolution from Whole-genome Sequencing Data.

Session 6: Algorithms & Data Mining (15:00 – 17:30)

- 15:00 – 15:30 Jinyan Li, Laplacian, Normalization and Random Walk on Heterogeneous Networks for Disease-gene Prioritization.
- 15:30 – 16:00 Xiaojing Xie, CoGI: Towards Compressing Genomes as an Image.
- 16:00 – 16:30 Kazuki Ichikawa, A Linear Time algorithm for Detecting Long Genomic Regions Enriched with a Specific Combination of Epigenetic States.
- 16:30 – 17:00 Tsukasa Fukunaga, GroupTracker: Video Tracking System for Multiple Animals Under Severe Occlusion.
- 17:00 – 17:30 Kengo Sato, A Machine Learning Based approach to de Novo Sequencing of Glycans from Tandem Mass Spectrometry Spectrum.

January 22, 2015 (Thursday)

1st Floor, Microelectronics and Information Systems Research Center, National Chiao Tung University

Time	Event	
9:00 – 9:30	Registration and Poster Setup	
9:30 – 10:20	<p align="center">Keynote 2 <i>Cancer Big Data Challenges with Supercomputers</i> Satoru Miyano, The University of Tokyo, <i>Japan</i> Session Moderator: Phoebe Chen International Conference Hall</p>	
10:20 – 10:40	Coffee Break	
10:40 – 12:10	<p align="center">Session 7: Functional Genomics Moderator: Wen-Chi Chang (National Cheng Kung University) International Conference Hall</p>	<p align="center">Session 8: Clinical Case Study Moderator: H.Sunny Sun (National Cheng Kung University) Conference Room 4</p>
12:10 – 13:10	Lunch	
13:10 – 14:40	Poster Session	
14:40 – 15:00	Coffee Break	
15:00 – 17:00	<p align="center">Session 9: Genomics and Metagenomics Moderator: Tzu-Hao Chang (Taipei Medical University) International Conference Hall</p>	<p align="center">Session 10: Development and Evolution Moderator: Yeong-Shin Lin (National Chiao Tung University) Conference Room 4</p>
18:00 – 21:30	Banquet	

Session 7: Functional Genomics (10:40 – 12:10)

- 10:40 – 11:10 Chia-Hung Chien, EXPath: a Database of Comparative Expression Analysis Inferring Metabolic Pathways for Plants.
- 11:10 – 11:40 Mengmeng Wu, Pinpointing Disease Genes Through Phenomic and Genomic Data Fusion.
- 11:40 – 12:10 Hsing-Jen Sun, Discovering Monotonic Stemness Marker Genes from Time-Series Stem Cell Microarray Data.

Session 8: Clinical Case Study (10:40 – 12:10)

- 10:40 – 11:10 Guan-Mau Huang, An Interpretable Rule-Based Diagnostic Classification of Diabetic Nephropathy Among Type 2 Diabetes Patients.
- 11:10 – 11:40 Hyun-Hwan Jeong, Investigating the Utility of Clinical Outcome-Guided Mutual Information Network in Network-based Cox Regression.
- 11:40 – 12:10 Renhua Song, Connecting Rules from Paired miRNA and mRNA Expression Data Sets of HCV Patients to Detect Both Inverse and Positive Regulatory Relationships.

Session 9: Genomics and Metagenomics (15:00 – 17:00)

- 15:00 – 15:30 Sergey Aganezov, Scaffold Assembly Based on Genome Rearrangement Analysis.
- 15:30 – 16:00 Yi Li, MixClone: a Mixture Model for Inferring Tumor Subclonal Populations.
- 16:00 – 16:30 Tomohiro Yasuda, Inferring the Global Structure of Chromosomes from Structural Variations.
- 16:30 – 17:00 H. Sunny Sun, Characterization and Distribution of Repetitive Elements in Association of Genes in the Human Genome.

Session 10: Development and Evolution (15:00 – 17:00)

- 15:00 – 15:30 Martin Middendorf, Cophylogenetic Reconciliation with ILP.
- 15:30 – 16:00 Jijun Tang, A Cooperative Co-evolutionary Genetic Algorithm for Tree Scoring and Ancestral Genome Inference.
- 16:00 – 16:30 Benjamin Drinkwater, A Time and Space Complexity Reduction for Coevolutionary Analysis of trees Generated Under Both a Yule and Uniform Model.
- 16:30 – 17:00 Jade Cheng, Ancestral Population Genomics Using Coalescence Hidden Markov Models and Heuristic optimisation Algorithms.

January 23, 2015 (Friday)

1st Floor, Microelectronics and Information Systems Research Center, National Chiao Tung University

Time	Event		
9:00 – 9:30	Registration and Poster Setup		
9:30 – 10:20	<p style="text-align: center;">Keynote 3 <i>Whole Genome Sequencing of Six Dog Breeds from Continuous Altitudes Reveals Adaption to High-Altitude Hypox</i> Li Yixue, Chinese Academy of Sciences, <i>China</i> Session Moderator: Hsien-Da Huang International Conference Hall</p>		
10:20 – 10:40	Coffee Break		
10:40 – 12:10	<p style="text-align: center;">Session 11: Protein Structure, Folding and Interaction (Part I) Moderator: Tzong-Yi Lee (Yuan Ze University) International Conference Hall</p>	<p style="text-align: center;">Session 12: Protein Function and Mutation (Part I) Moderator: Shinn-Ying Ho (National Chiao Tung University) Conference Room 4</p>	<p style="text-align: center;">Session 13: Biomedical Text Mining Moderator: Wenlian Hsu (Academia Sinica) Conference Room 1</p>
12:10 – 13:10	<i>Lunch</i>		
13:10 – 14:40	Poster Session		
14:40 – 16:10	<p style="text-align: center;">Session 14: Protein Structure, Folding and Interaction (Part II) Moderator: Tzong-Yi Lee (Yuan Ze University) International Conference Hall</p>	<p style="text-align: center;">Session 15: Protein Function and Mutation (Part II) Moderator: Jinyan Li (University of Technology Sydney) Conference Room 4</p>	
16:10 – 16:30	Coffee Break		
16:30 – 17:00	<p style="text-align: center;">Presenting Best Paper/Best Student Paper/Best Poster Awards Close Messages International Conference Hall</p>		

Session 11: Protein Structure, Folding and Interaction (Part I) (10:40 – 12:10)

- 10:40 – 11:10 Tsun-Tsao Huang, On the Packing Density of the Unbound Protein-Protein Interaction Interface and Its Implications in Dynamics.
- 11:10 – 11:40 Chun-Chi Liu, IIIDB: A Database for Isoform-Isoform Interactions and Isoform Network Modules.
- 11:40 – 12:10 Qingyao Wu, Protein Functional Properties Prediction in Sparsely-Label PPI Networks Through Regularized Non-Negative Matrix Factorization.

Session 12: Protein Function and Mutation (Part I) (10:40 – 12:10)

- 10:40 – 11:10 Jaspreet Kaur Dhanjal, Mechanistic Analysis Elucidating the Relationship Between Lys96 Mutation in Mycobacterium Tuberculosis Pyrazinamidase Enzyme and Pyrazinamide Susceptibility.
- 11:10 – 11:40 Guoxian Yu, Integrating Multiple Networks for Protein Function Prediction.
- 11:40 – 12:10 Shinn-Ying Ho, SCMPSP: Prediction and Characterization of Photosynthetic Proteins Based on a Scoring Card Method.

Session 13: Biomedical Text Mining (10:40 – 12:10)

- 10:40 – 11:10 Yijia Zhang, Integrating Experimental and Literature Protein-Protein Interaction Data for Protein Complex Prediction.
- 11:10 – 11:40 Liang Cheng, Using Semantic association to Extend and Infer Literature-oriented Relativity Between Terms.
- 11:40 – 12:10 Shanfeng Zhu, BMExpert: Mining MEDLINE for Finding Experts in Biomedical Domains Based on Language Model.

Session 14: Protein Structure, Folding and Interaction (Part II) (14:40 – 16:10)

- 14:40 – 15:10 Van-Nui Nguyen, Characterization and Identification of Lysine Ubiquitination with Substrate Site Specificities.
- 15:10 – 15:40 Caihua Wang, Predicting Target-Ligand Interactions Using Protein Ligand-Binding Site and Ligand Substructures.
- 15:40 – 16:10 Likun Wang, cisPath: an R/Bioconductor Package for Cloud Users for Visualization and Management of Functional Protein interaction Networks.

Session 15: Protein Function and Mutation (Part II) (14:40 – 16:10)

- 14:40 – 15:10 Can Zhao, BagReg: Protein Inference Through Machine Learning.
- 15:10 – 15:40 Takehiro Shimoda, Protein-Protein Docking on Hardware Accelerators: Comparison of GPU and MIC Architectures.
- 15:40 – 16:10 Xiaoning Qian, Tumor Stratification by a Novel Graph-regularized Bi-clique Finding Algorithm.