

**InCoB2013 Program Thursday, 19 Sept. 2013**

**9:30-18:30**

***Registration (The First Floor Foyer)***

Day 1	InCoB2013 Program		Friday, 20 Sept. 2013
8:00	<b>Registration (The First Floor Foyer)</b>		
Venue	Guoda Ballrooms A & B		
8:30	Welcome to InCoB2013 Conference Chair: Bairong Shen APBioNet President: Shoba Ranganathan		
9:00	Keynote 1: Yunping Zhu - Efficient labeled and label-free algorithms lay a solid foundation for quantitative proteomics. <i>Chair: Bairong Shen</i>		
9:45	Keynote 2: Wen-Hsiung Li - Assembling a genome using short sequencing reads <i>Chair: Shoba Ranganathan</i>		
10:30	Coffee Break		
11:00	Status and Future of InCoB2013 - Christian Schönbach		
11:30-12:30	Poster Session 1 (The Second Floor Foyer): odd number posters		
12:30	Lunch Break		
Venue	Guoda Ballroom A		Guoda Ballroom B
13:30 - 15:35	<b>1. Systems Biology</b> <i>Chair: Bairong Shen</i>	13:30 - 15:25	<b>2. Disease Informatics</b> <i>Chair: Christian Schönbach</i>
13:30	<b>Plenary lecture 1: Keith Dunker - An IDP-based Swiss-army-knife-like toolkit for signaling diversification</b>	13:30	<b>Plenary lecture 2: Jürgen Brosius - New parts of existing genes: a double-edged sword</b>
13:50	<b>1. Y López, A Patil and K Nakai. Identification of novel motif patterns to decipher the promoter architecture of co-expressed genes in <i>Arabidopsis thaliana</i>.</b>	13:50	<b>1. R Zhang, L Hao, L Wang, M Chen, W Li, M Esteban, J Yu, J Xiao and J Wu. Gene expression analysis of induced pluripotent stem cells from aneuploid chromosomal syndromes.</b>
14:05	<b>2. Haijun Gong. Analysis of intercellular signal transduction in the tumor microenvironment.</b>	14:05	<b>2. Y Xiang, J Zhang and K Huang. Mining Tissue-Tissue Gene Co-expression network for tumor microenvironment study and biomarker prediction.</b>
14:20	<b>3. K Yoshida, K Maeda, H Kusuhara and A Konagaya. Estimation of feasible solution space using Cluster Newton method: application to pharmacokinetic analysis of irinotecan with physiologically-based pharmacokinetic models.</b>	14:20	<b>3. Z Xiang, T Qin, Z Qin and Y He. A genome-wide MeSH-based literature mining system predicts implicit gene-to-gene relationships and networks.</b>
14:35	<b>4. P Chumnanpuen, I Nookaew and J Nielsen. Integrated analysis, transcriptome-lipidome, reveals the effects of INO-level (INO2 and INO4) on lipid metabolism in yeast.</b>	14:35	<b>4. Z Li, Y He, Q Liu, L Wong, CK Kwoh, H Nguyen and J Li. Structural analysis on mutation residues and interfacial water molecules for understanding genetic disease.</b>
14:50	<b>5. A Batagov, A Yarmishyn, P Jenjaroenpun, Y Nishida, I Kurochkin and JZ Tan. Role of genomic architecture in the expression dynamics of long noncoding RNAs during differentiation of human neuroblastoma cells.</b>	14:50	<b>5. Y Tang, J Chen, C Luo, A Kaipia and B Shen. Identification of novel microRNA regulatory pathways associated with heterogeneous prostate cancer.</b>
15:05	<b>A. I Tawornsamretkit, S Cheevadhanarak, D Waraho and A Meechai. Rational design for efficient linalool production in synthetic <i>Escherichia coli</i>. (10 min)</b>	15:05	<b>A. V Phav and A Konagaya. Comparison of computational approaches to estimate long-range chromatin interaction between human breast cancer candidate genes and estrogen receptor alpha proteins. (10 min)</b>
15:15	<b>B. Y-S Lo, S-H Huang, C-Y Lin, T-L Lee and J-M Yang. Infer human and zebrafish interactomes through structure protein protein interaction families. (10 min)</b>	15:15	<b>B. MP Grover, S Ballouz, KA Mohanasundaram, RA George, C Sherman, TM Crowley and M Wouters. Identification of novel therapeutics for complex diseases from genome-wide association data. (10 min)</b>
15:25	<b>C. S Sriganesh. Evolution and controllability of cancer networks: a Boolean perspective. (10 min)</b>		
15:35	Break		

12:30	Lunch Break		
16:00 - 17:55	<b>3. Imaging and Emerging Bioinformatics Applications</b> <i>Chair: Tin Wee Tan</i>	16:00 - 17:55	<b>4. Immunoinformatics</b> <i>Chair: Vladimir Brusic</i>
16:00	<b>Plenary lecture 3: Kun Huang - Beyond co-expression: integrating nonlinear correlation with Boolean relationships for biological network inference</b>	16:00	<b>Plenary lecture 4: Luonan Chen - Early diagnosis on complex diseases by dynamical network biomarkers</b>
16:20	1. D Laksameethanasan, R Zhen Tan, GW-L Toh and L-H Loo. <b>cellXpress: a fast and user-friendly software platform for profiling cellular phenotypes</b>	16:20	1. I-H Liu, Y-S Lo and J-M Yang. <b>Genome-wide structural modelling of TCR-pMHC interactions.</b>
16:35	2. Y Wang, W Goh, L Wong and G Montana. <b>Random forests on Hadoop for genome-wide studies of multivariate neuroimaging phenotypes.</b>	16:35	2. L Guo, C Luo and S Zhu. <b>MHC2SKpan: A novel kernel based approach for pan specific MHC class II peptide binding prediction.</b>
16:50	3. P Charoenkwan, E Hwang, RW Cutler, H-C Lee, L-W Ko, H-L Huang and S-Y Ho. <b>HCS-Neurons: Identifying phenotypic changes in multi-neuron images upon drug treatments of high-content screening.</b>	16:50	3. K-C Huang, K-C Yang, H Lin, TT-H Tsao, W-K Lee, S-A Lee and C-Y Kao. <b>Analysis of schizophrenia and hepatocellular carcinoma genetic network with corresponding modularity and pathways: Novel insights to the immune system.</b>
17:05	4. R Uttamatin, P Yuvapootanon, A Intarapanich, S Kaewkamnerd, R Phuksaritanon, A Assawamakin and S Tongsima. <b>METASEL: A Metaphase selection tool using Gaussian-based classification technique.</b>	17:05	4. M Pennisi, A-M Rajput, L Toldo and F Pappalardo. <b>Agent based modeling of Treg-Teff cross regulation in relapsing-remitting multiple sclerosis.</b>
17:20	5. TW Tan, C Xie, M De Silva, K Siong Lim, CPK Patro, SJ Lim, KR Govindarajan, JC Tong, KH Choo, S Ranganathan and AM Khan. <b>Simple re-instantiation of small databases using cloud computing.</b>	17:20	5. CTT Su, X Ouyang, J Zheng and C-K Kwoh. <b>Structural analysis of the novel influenza A (H7N9) viral Neuraminidase interactions with the current approved neuraminidase inhibitors Oseltamivir, Zanamivir, and Peramivir in the presence of mutation R289K</b>
17:35	A. Y-H Tseng, C-L Tsai, C-C Lin and J-Y Peng. <b>3D morphological analysis reveals mitochondrial biogenesis and quality control in cell cycle. (10 min)</b>	17:35	6. LR Olsen, UJ Kudahl, O Winther and V Brusic. <b>Literature classification for semi-automated updating of biological knowledgebases.</b>
17:45	B. C Yan and Y Zhu. <b>Chemical compounds classification using graph methods. (10 min)</b>		
18:00-18:30	<b>Reception Party</b>		
Day 1	<b>InCoB2013 Program</b>		<b>Friday, 20 Sept. 2013</b>

Day 2	InCoB2013 Program		Saturday, 21 Sept. 2013
8:00	<i>Registration (The First Floor Foyer)</i>		
Venue	Guoda Ballrooms A & B		
9:00	<b>Keynote 3: Philip Payne - Translational Informatics: enabling knowledge-driven healthcare</b> <i>Chair: Bairong Shen</i>		
9:45	<b>Keynote 4: Manyuan Long - New genes as drivers of phenotypic evolution: The implication and challenge to translational medical studies</b> <i>Chair: Tin Wee Tan</i>		
10:30	Coffee Break		
11:00	<b>APBioNet 2013 Report &amp; AGM - Shoba Ranganathan, Kenta Nakai, Christian Schönbach, Sissades Tongsima,</b>		
11:30	<b>Poster Session 2 (The Second Floor Foyer): even number posters</b>		
12:30	Lunch Break		
Venue	Guoda Ballroom A		Guoda Ballroom B
13:30 - 15:30	<b>5. Pathways &amp; Networks</b> <i>Chair: Kenta Nakai</i>	13:30 - 15:30	<b>6. Non-coding RNAs</b> <i>Chair: Christian Schönbach</i>
13:30	<b>Plenary lecture 5: Paul Horton - Advances in predicting protein sub-cellular localization signals</b>	13:30	<b>Plenary lecture 2: Xu Dong - Role of DNA methylation in cancers</b>
13:50	1. D L-K Wong, X-L Li, M Wu, J Zheng and S-K Ng. <b>PLW: Probabilistic Local Walks for detecting protein complexes from protein interaction networks</b>	13:50	1. Xing Tang, Mei Hou, Yang Ding, Zhaohui Li, Lichen Ren and Ge Gao. <b>Systematically profiling and annotating long intergenic non-coding RNAs in human embryonic stem cell</b>
14:05	2. J Li and Z Lu. <b>Pathway-based drug repositioning using causal inference</b>	14:05	2. Y Kremenska, V Nair, P Jenjaroenpun, M Kremenskoy, I Kurochkin and B Joseph. <b>Distinct features of RNA in exosomes produced by human breast cancer cell lines revealed by next-generation sequencing based approach.</b>
14:20	3. C Wu, J-MSchwartz and G Nenadic. <b>PathNER: a tool for systematic identification of biological pathway mentions in the literature</b>	14:20	3. D Kim, HH Shin, J-G Joung, SY Lee and JH Kim. <b>Intra-relation reconstruction from inter relation: miRNA to gene expression.</b>
14:35	4. M Lee, K Park and D Kim. <b>Interaction network among functional drug groups.</b>	14:35	4. K-W Tsai, W-S Chen, T-W Chen, T-H Yang, L-Y Hu, H-W Pan, S-C Li, M-R Ho, S-Y Yu, Y-T Tu, W-C Lin, TT Wu, C-W Shu and PF Liu. <b>Co-modulated behavior and effects of differentially expressed miRNA in colorectal cancer.</b>
14:50	5. AW-Ti Chiang and M-J Hwang. <b>A computational pipeline for identifying kinetic motifs to aid in the design and improvement of synthetic gene circuits.</b>	14:50	5. Y-J Na and JH Kim. <b>Understanding cooperativity of microRNAs via microRNA association networks.</b>
15:05	6. PB. Madhamshettiwar, SR Maetschke, MJ. Davis and Mark A. Ragan. <b>RMaNI: Regulatory Module Network Inference Framework.</b>	15:05	6. J-K Rhee, S-Y Shin and B-T Zhang. <b>Construction of microRNA functional families by a mixture model of position weight matrices.</b>
15:20	A. W Yan, M un, G Hu, J Zhou, J Chen, B Chen and B Shen. <b>Characterization of protein structure and evolution with amino acid network. (10 min)</b>	15:20	A. I Kurochkin and A Batagov. <b>Exosomes secreted by human cells transport largely mRNA fragments that are enriched in the 3'-untranslated regions. (10 min)</b>
15:30	Coffee Break		
16:00 - 17:30	<b>7. Proteins, motifs, ligands</b> <i>Chair: Shoba Ranganathan</i>	16:00 - 17:30	<b>8. Sequencing, Sequences, Evolution</b> <i>Chair: Asif Khan</i>
16:00	1. B Shashni, K Sharma, R Singh, K Sakharkar, S Dhillon, Y Nagasaki and M Sakharkar. <b>Coffee component Hydroxyl Hydroquinone (HHQ) as a putative ligand for PPAR gamma and implications in breast cancer.</b>	16:00	1. Chin Lui Goi, Peter Little and Chao Xie. <b>Cell-type and Transcription factor specific enrichment of transcriptional cofactor motifs in ENCODE CHIP-seq data</b>

Venue	Guoda Ballroom A		Guoda Ballroom B
16:15	<b>2. M-G Su and TY Lee. Incorporating substrate sequence motifs and spatial amino acid composition to identify kinase-specific phosphorylation sites on protein three-dimensional structures.</b>	16:15	<b>2. S Mitra, K Foerster-Fromme, A Damms-Machado, T Scheurenbrand, S Biskup, DH. Huson and SC. Bischoff. Analysis of the intestinal microbiota using SOLiD 16SrRNA gene sequencing and SOLiD shotgun sequencing.</b>
16:30	<b>3. PV Nguyen, S Srihari and HW Leong. Identifying conserved protein complexes between species by constructing interolog networks.</b>	16:30	<b>3. D Strbenac, N Armstrong and J Yang. Detection and classification of peaks in 5' Cap RNA sequencing data.</b>
16:45	<b>4. K-Y Huang, C-T Lu, NA Bretaña, TY Lee and T-H Chang. ViralPhos: incorporating a recursively statistical method to predict phosphorylation sites on virus proteins.</b>	16:45	<b>4. D Biswal, S Ghatani, J Shylla, R Sahu, N Mullapudi, A Bhattacharya and V Tandon. An integrated pipeline for next-generation sequencing and annotation of the complete mitochondrial genome of the giant intestinal fluke, Fasciolopsis buski (Lankester, 1857) Looss, 1899 (Digenea: Fasciolidae).</b>
17:00	<b>5. Liang Jiang, Hua-Zhang Zhu, Yin-Zhen Xu, Yan Zhang, Jia-Zuan Ni and Qiong Liu. Comparative selenoproteome analysis reveals a reduced utilization of selenium in parasitic platyhelminthes.</b>	17:00	<b>5. D Biswal, J Valrie and P Tandon. Age estimation for the genus Cymbidium (Orchidaceae: Epidendroideae) with implementation of fossil data calibration using molecular markers (ITS2 &amp; matK) with a Bayesian relaxed clock implying phylogeographic inference in continuous space.</b>
17:15	<b>6. Afiahayati, K Sato and Y Sakakibara. An extended genovo metagenomic assembler by incorporating paired-end information.</b>	17:15	<b>6. J Choi, K-T Kim, JJeon and Y-H Lee. Fungal plant cell wall-degrading enzyme database: a platform for comparative and evolutionary genomics in fungi and oomycetes.</b>
18:00-20:30	<i>Conference Dinner</i>		
Day 2	InCoB2013 Program		Saturday, 21 Sept. 2013

Day 3		InCoB2013 Program	Sunday, 22 Sept. 2013
8:00	<b>Registration (The First Floor Foyer)</b>		
Venue	Guoda Ballrooms A & B		
9:00	<b>Keynote 5: Kazuyuki Aihara - Mathematical modeling and its application to personalized medicine for prostate cancer</b> <b>Chair: Jinn-Moon Yang</b>		
9:45	<b>Plenary lecture 7: Zhao Zhongming - A personalized mutation network approach for detecting putative cancer genes from next-generation sequencing data</b>		
10:10	<b>Bioinformatics education session</b> <b>Chair: Shoba Ranganathan</b>		
10:45	Coffee break		
11:15	<b>Plenary lecture 8: Ruiqiang Li - Bioinformatics development for next-generation sequencing data analysis</b>		
11:40	<b>Closing session - Bairong Shen, Shoba Ranganathan, Kenta Nakai, Christian Schönbach</b> - <i>Best Paper and Poster awards</i> - <i>APBioNet awards</i> - <i>Announcement of InCoB2014</i>		