InCoB2013 Program	Thursday, 19 Sept. 2013
9:00-17:30	*Registration (Foyer)*

8:00	Registration (Foyer)
Venue	**Ballrooms A & B**
9:00	Welcome to InCoB2013 Conference Chair: Bairong Shen APBioNet President: Shoba Ranganathan
9:30	**Keynote 1: Fuchu He - TBA** *Chair: Bairong Shen*
10:15	Plenary lecture 1: Keith Dunker - An IDP-based Swiss-army-knife-like toolkit for signaling diversification *Chair: Bairong Shen*
10:40	Break
11:00	**Keynote 2: Wen-Hsiung Li - Assembling a genome using short sequencing reads** *Chair: Shoba Ranganathan*
11:45	Plenary lecture 2: Luonan Chen - Early diagnosis on complex diseases by dynamical network biomarkers *Chair: Christian Schönbach*
12:10	**Status and Future of InCoB2013 - Christian Schönbach**
12:35	Lunch Break

Venue	Ballroom A		Ballroom B		Huashan Room		Xiangshan Room
13:30 - 15:40	*1. Systems Biology* *Chair: Bairong Shen*	13:30 - 15:40	*2. Disease Informatics* *Chair: Luonan Chen*	13:30 - 15:40	*3. Imaging and Emerging Bioinformatics Applications* *Chair: Tin Wee Tan*	13:30 - 15:30	*4. Immunoinformatics* *Chair: Vladimir Brusic*
13:30	**1.** Y López, A Patil and K Nakai. **Identification of novel motif patterns to decipher the promoter architecture of co-expressed genes in** *Arabidopsis thaliana* .	13:30	**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.**	13:30	**1.** D Laksameethanasan, R Zhen Tan, GW-L Toh and L-H Loo. **cellXpress: a fast and user-friendly software platform for profiling cellular phenotypes**	13:30	**1.** I-H Liu, Y-S Lo and J-M Yang. **Genome-wide structural modelling of TCR-pMHC interactions.**
13:50	**2.** Haijun Gong. **Analysis of intercellular signal transduction in the tumor microenvironment.**	13:50	**2.** Y Xiang, J Zhang and K Huang. **Mining Tissue-Tissue Gene Co-expression network for tumor microenvironment study and biomarker prediction.**	13:50	**2.** Y Wang, W Goh, L Wong and G Montana. **Random forests on Hadoop for genome-wide studies of multivariate neuroimaging phenotypes.**	13:50	**2.** L Guo, C Luo and S Zhu. **MHC2SKpan: A novel kernel based approach for pan specific MHC class II peptide binding prediction.**
14:10	**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.**	14:10	**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.**	14:10	**3.** P Charoenkwan, E Hwang, RW Cutler, H-C Lee, L-W Ko, H-L Huang and S-Y Ho. **HCS-Neurons: Identifying phenotypic changes in multi-neuron images upon drug treatments of high-content screening.**	14:10	**3.** K-C Huang, K-C Yang, H Lin, TT-H Tsao, W-K Lee, S-A Lee and C-Y Kao. **Analysis of schizophrenia and hepatocellular carcinoma genetic network with corresponding modularity and pathways: Novel insights to the immune system.**

Venue	Ballroom A		Ballroom B		Huashan Room		Xiangshan Room
14:30	**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.**	14:30	**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.**	14:30	**4.** R Uttamatanin, P Yuvapoositanon, A Intarapanich, S Kaewkamnerd, R Phuksaritanon, A Assawamakin and S Tongsima. **METASEL: A Metaphase selection tool using Gaussian-based classification technique.**	14:30	**4.** M Pennisi, A-M Rajput, L Toldo and F Pappalardo. **Agent based modeling of Treg-Teff cross regulation in relapsing-remitting multiple sclerosis.**
14:50	**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.**	14:50	**5.** Y Tang, J Chen, C Luo, A Kaipia and B Shen. **Identification of novel microRNA regulatory pathways associated with heterogeneous prostate cancer.**	14:50	**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. **Simple re-instantiation of small databases using cloud computing.**	14:50	**5.** CTT Su, X Ouyang, J Zheng and C-K Kwoh. **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**
15:10	**A.** I Tawornsamretkit, S Cheevadhanarak, D Waraho and A Meechai. **Rational design for efficient linalool production in synthetic *Escherichia coli.* (10 min)**	15:10	**A.** G Kumar, E Breen and S Ranganathan. **Identification of ovarian cancer associated genes using an integrated approach in a Boolean framework. (10 min)**	15:10	**A.** Y-H Tseng, C-L Tsai, C-C Lin and J-Y Peng. **3D morphological analysis reveals mitochondrial biogenesis and quality control in cell cycle. (10 min)**	15:10	**6.** LR Olsen, UJ Kudahl, O Winther and V Brusic. **Literature classification for semi-automated updating of biological knowledgebases.**
15:20	**B.** F Liu and M Heiner. **Snoopy: A Colored Petri Net Tool for Modeling Multiscale Systems Biology. (10 min)**	15:20	**B.** 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)**	15:20	**B.** C Yan and Y Zhu. **Chemical compounds classification using graph methods. (10 min)**		
15:30	**C.** NN Nguyen, W Vongsangnak, B Shen and HW Leong. **Retrofitting function prediction methods to fill gaps in metabolic networks. (10 min)**	15:30	**C.** 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)**	15:30	**C.** S Ranganathan, J Khan, G Garg and M Baker. **Functional annotation of the human chromosome 7 "missing" proteins: a bioinformatics approach. (10 min)**		
15:40	Break						
16:00-17:00	*Poster Session 1 (Foyer): odd*						
17:00-18:00	*Reception Party* (Foyer)						
Day 1			InCoB2013 Program				**Friday, 20 Sept. 2013**

Day 2			InCoB2013 Program				Saturday, 21 Sept. 2013
8:00	*Registration (Foyer)*						
Venue	**Ballrooms A & B**						
9:00	**Keynote 3: Philip Payne - Translational Informatics: enabling knowledge-driven healthcare** *Chair: Bairong Shen*						
9:45	**Plenary lecture 3: Jürgen Brosius - New parts of existing genes: a double-edged sword** *Chair: Sissades Tongsima*						
10:10	**Plenary lecture 4: Xu Dong - Role of DNA methylation in cancers** *Chair: Shoba Ranganathan*						
10:35	Break						
11:00	**Keynote 4: Keynote 4: Manyuan Long - New genes as drivers of phenotypic evolution: The implication and challenge to translational medical studies** *Chair: Tin Wee Tan*						
11:45	**Plenary lecture 5: Paul Horton - Advances in predicting protein sub-cellular localization signals** *Chair: Kenta Nakai*						
12:10	**APBioNet 2013 Report & AGM - Shoba Ranganathan, Kenta Nakai, Christian Schönbach, Sissades Tongsima, Asif M Khan, Tin Wee Tan**						
12:35	Lunch Break						
Venue	**Ballroom A**		**Ballroom B**		**Huashan Room**		**Xiangshan Room**
13:30 - 15:40	*5. Pathways & Networks* *Chair: Kenta Nakai*	13:30 - 15:40	*6. Non-coding RNAs* *Chair: Jürgen Brosius*	13:30 - 15:40	*7. Proteins, motifs, ligands* *Chair: Paul Horton*	13:30 - 15:30	*8. Sequencing, Sequences, Evolution* *Chair: Manyuan Long*
13:30	**1.** D L-K Wong, X-L Li, M Wu, J Zheng and S-K Ng. **PLW: Probabilistic Local Walks for detecting protein complexes from protein interaction networks**	13:30	**1.** Xing Tang, Mei Hou, Yang Ding, Zhaohui Li, Lichen Ren and Ge Gao. **Systematically profiling and annotating long intergenic non-coding RNAs in human embryonic stem cell**	13:30	**1.** B Shashni, K Sharma, R Singh, K Sakharkar, S Dhillon, Y Nagasaki and M Sakharkar. **Coffee component Hydroxyl Hydroquinone (HHQ) as a putative ligand for PPAR gamma and implications in breast cancer.**	13:30	**1.** Chin Lui Goi, Peter Little and Chao Xie. **Cell-type and Transcription factor specific enrichment of transcriptional cofactor motifs in ENCODE ChIP-seq data**
13:50	**2.** J Li and Z Lu. **Pathway-based drug repositioning using causal inference**	13:50	**2.** Y Kremenska, V Nair, P Jenjaroenpun, M Kremenskoy, I Kurochkin and B Joseph. **Distinct features of RNA in exosomes produced by human breast cancer cell lines revealed by next-generation sequencing based approach.**	13:50	**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.**	13:50	**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.**
14:10	**3.** C Wu, J-MSchwartz and G Nenadic. **PathNER: a tool for systematic identification of biological pathway mentions in the literature**	14:10	**3.** D Kim, HH Shin, J-G Joung, SY Lee and JH Kim. **Intra-relation reconstruction from inter relation: miRNA to gene expression.**	14:10	**3.** PV Nguyen, S Srihari and HW Leong. **Identifying conserved protein complexes between species by constructing interolog networks.**	14:10	**3.** D Strbenac, N Armstrong and J Yang. **Detection and classification of peaks in 5' Cap RNA sequencing data.**

Venue	Ballroom A		Ballroom B		Huashan Room		Xiangshan Room
14:30	**4.** M Lee, K Park and D Kim. **Interaction network among functional drug groups.**	14:30	**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. **Co-modulated behavior and effects of differentially expressed miRNA in colorectal cancer.**	14:30	**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.**	14:30	**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).**
14:50	**5.** AW-Ti Chiang and M-J Hwang. **A computational pipeline for identifying kinetic motifs to aid in the design and improvement of synthetic gene circuits.**	14:50	**5.** Y-J Na and JH Kim. **Understanding cooperativity of microRNAs via microRNA association networks.**	14:50	**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.**	14:50	**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 & matK) with a Bayesian relaxed clock implying phylogeographic inference in continuous space.**
15:10	**6.** PB. Madhamshettiwar, SR Maetschke, MJ. Davis and Mark A. Ragan. **RMaNI: Regulatory Module Network Inference Framework.**	15:10	**6.** J-K Rhee, S-Y Shin and B-T Zhang. **Construction of microRNA functional families by a mixture model of position weight matrices.**	15:10	**6.** Afiahayati, K Sato and Y Sakakibara. **An extended genovo metagenomic assembler by incorporating paired-end information.**	15:10	**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.**
15:30	**A.** W Yan, M un, G Hu, J Zhou, J Chen, B Chen and B Shen. **Characterization of protein structure and evolution with amino acid network.** (10 min)	15:30	**A.** I Kurochkin and A Batagov. **Exosomes secreted by human cells transport largely mRNA fragments that are enriched in the 3'-untranslated regions.** (10 min)	15:30	**A.** 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)		
16:00	Break						
16:00-17:00	*Poster Session 2 with refreshments and snacks (Foyer): even number posters*						
18:00-20:30	*Conference Dinner*						

Day 3	InCoB2013 Program	Sunday, 22 Sept. 2013
8:00	*Registration (Foyer)*	
Venue	**Ballrooms A & B**	
9:00	**Keynote 4: Kazuyuki Aihara - Mathematical modeling and its application to personalized medicine for prostate cancer** *Chair: Jinn-Moon Yang*	
9:45	**Plenary lecture 6: Zhao Zhongming - A personalized mutation network approachfor detecting putative cancer genes from next-generation sequencing data** *Chair: Chen Luonan*	
10:10	**Bioinformatics education session** *Chair: Shoba Ranganathan*	
10:35	Coffee break	
11:00	**Plenary lecture 7: Kun Huang - Beyond co-expression: integrating nonlinear correlation with Boolean relationships for biological network inference** *Chair: Ge Gao*	
11:25	**Plenary lecture 8: Ruiqiang Li - Bioinformatics development for next-generation sequencing data analysis** *Chair: Bairong Shen*	
11:50	**Closing session - Bairong Shen, Shoba Ranganathan, Kenta Nakai, Christian Schönbach** *- Best paper awards and Poster prizes* *- APBioNet awards* *- Announcement of InCoB2014*	