

InCoB/ISCB-Asia 2011 Conference Program Overview (as of Nov 19, 2011)

29-Nov-11 Tuesday		30-Nov-11 Wednesday		01-Dec-11 Thursday		02-Dec-11 Friday		
	7:30 AM	Registration and Poster Mounting (odd and even poster numbers)		8:00 AM	Registration		8:00 AM	Registration
	9:00 AM	Conference Opening		8:45 AM	Keynote 3		8:45 AM	Keynote 5
	9:30 AM	Keynote 1		9:45 AM	Sponsor Presentation		9:45 AM	Sponsor Presentations
	10:30 AM	Morning Break		10:15 AM	Morning Break		10:15 AM	Morning Break
	11:00 AM	Oral Presentations		10:45 AM	Oral Presentations		10:45 AM	Oral Presentations
	1:00 PM	Lunch Break	ISCB Open Meeting	12:45 PM	Lunch Break	APBioNet Open Meeting	12:45 PM	Lunch Break
	2:15 PM	Keynote 2		2:00 PM	Keynote 4		2:00 PM	Oral Presentations
	3:15 PM	Afternoon Break		3:00 PM	Afternoon Break		4:00 PM	Afternoon Break
	3:45 PM	Oral Presentations		3:30 PM	Oral Presentations		4:30 PM	Oral Presentations
	5:45 PM	Posters Session 1 (odd poster numbers)		5:30 PM	Poster Session 2 (even poster numbers) dismounting 6:15-6:30 PM		5:30 PM	Awards and Conference Closing
	6:30 PM	Official End of Day 1 Scientific Program		6:15 PM	Official End of Day 2 Scientific Program		6:00 PM	Official End of Conference
8:30 PM	Registration	6:40 PM	APBioNet/ISCB Reception	7:00 PM	Conference Dinner			

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Notes:

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30-Nov-11	WEDNESDAY		
8:00 AM	Ballroom	Function Rooms 3 and 4	Function Rooms 5 and 6
	Registration and Poster Mounting		
9:00 AM	<p>Opening remarks: Sheila NATHAN, Conference Chair, Welcome: Shoba RANGANATHAN, President APBioNet, Burkhard ROST, President ISCB Guest of Honour: The Hon Dato Seri Panglima Dr. Maximus Johnity ONGKILI, Minister MOSTI</p>		
9:30 AM	<p>Keynote 1 Chairs: Burkhard ROST and Paul HORTON</p> <p>Bench to Bedside: Changing Roles of Bioinformatics by Minoru KANEHISA (sponsored by ISCB)</p>		
10:30 AM	Morning Break		
11:00 AM	<p>1. ISCB Session (Invited Talks) Chair: Paul HORTON</p> <p>1.1. Ancient genomics and what it can tell us about modern humans by Janet Kelso (sponsored by Novocraft Technologies)</p>	<p>2. Databases and Software Tools I Chair: Vladimir BRUSIC</p> <p>2.1. ApicoAlign: an alignment and sequence search tool for apicomplexan proteins by J Ali, PU Devi and A Ranjan (BMC G)</p>	<p>3. Sequence Analysis and Evolution I Chair: Kenta NAKAI</p> <p>3.1. i-rDNA: Alignment-free algorithm for rapid in silico detection of ribosomal gene fragments from metagenomic sequence data sets by MH Mohammed, TS Ghosh, S Chadaram and S Mande (BMC G)</p>
11:30 AM	<p>1.2. Recent advancements in genome alignment by Martin Frith</p>	<p>2.2. UASIS: universal automatic SNP identification system by D Poo, S Cai, J Mah (BMC G)</p>	<p>3.2. Perfect Hamming code with a hash table for faster genome mapping by Y Takenaka, S Seno and H Matsuda (BMC G)</p>
12:00 PM	<p>1.3. Link clustering reveals biological contexts in signed molecular networks by Hsuan-Cheng Huang</p>	<p>2.3. INDUS - A composition based approach for rapid and accurate taxonomic classification of metagenomic sequences by MH Mohammed, TS Ghosh, RM Reddy, NK Singh, CVSK Reddy and S Mande (BMC G)</p>	<p>3.3. Prediction of dinucleotide-specific RNA-binding sites in proteins by M Fernandez, Y Kumagai, D Standley, A Sarai, K Mizuguchi and S Ahmad (BMC B)</p>
12:30 PM	<p>1.4. Understanding nuclear protein trafficking with Bayesian networks by M Boden</p>	<p>2.4. Novel base triples in RNA structures revealed by graph theoretical searching methods by M Firdaus-Raih, AM Harrison, P Willett and P Artymiuk (BMC B)</p>	<p>3.4. In silico prediction of the granzyme B degradome by LJK Wee, L Ng, JC Tong and Esmond Ps Er (BMC G)</p>
1:00 PM	<p align="center">Lunch Break at Temptations ISCB Open Meeting 1:00-1:45 PM Poster Viewing (odd numbers)</p>		
2:15 PM	<p>Keynote 2 Chair: Shoba RANGANATHAN</p> <p>Biocuration: A cornerstone for research by Pascale GAUDET</p>		
3:15 PM	Afnoon Break		
3:45 PM	<p>4. Standards in Bioinformatics (Invited Talks) Chair: Shoba RANGANATHAN</p> <p>4.1. BioSharing and ISAcommons: cooperating procedures and standards in action by P Rocca-Serra, E Maguire, S-A Sansone</p>	<p>5. Databases and Software Tools II Chair: Habibah WAHAB</p> <p>5.1. DetoxiProt: an integrated database for detoxification proteins by Z Yang, Y Yu, L Yao, G Li, L Wang, Y Hu, H Wei, L Wang, R Hammami, R Razavi, Y Zhong and X Liang (BMC G)</p>	<p>6. Sequence Analysis and Evolution II Chair: Bruno GAETA</p> <p>6.1. Profiling ascidian promoters as the primordial type of vertebrate promoter by K Okamura, R Yamashita, N Takimoto, K Nishitsuji, Y Suzuki, T Kusakabe and K Nakai (BMC G)</p>
4:15 PM	<p>4.2. GigaScience - a journal's perspective on data standards and biocuration by Alexandra Basford</p>	<p>5.2. Liverome: a curated database of liver cancer-related gene signatures with self-contained context information by L Lee, K Wang, G Li, Z Xie, Y Wang, J Xu, S Sun, D Pocalyko, J Bhak, C Kim, KH Lee, YJ Jang, YI Yeom, HS Yoo and S Hwang (BMC G)</p>	<p>6.2. High similarity of phylogenetic profiles of rate-limiting enzymes with inhibitory relation in human, rat, mouse, budding yeast and E. coli by Z Min and H Qu (BMC G)</p>
4:45 PM	<p>4.3. Minimum Information about a Bioinformatics investigation (MIABi) by Tin Wee Tan</p>	<p>5.3. PTIGS-IdIt, an integrated web server for species identification by DNA sequences of the psbA-trnH intergenic region by C Liu, D Liang, T Gao, X Pang, J Song, H Yao, J Han, Z Liu, X Guan, K Jiang, H Li and S Chen (BMC B)</p>	<p>6.3. Interrogation of alternative splicing events in duplicated genes during evolution by TW Chen, TH Wu, WV Ng and WC Lin (BMC G)</p>
5:15 PM	<p>4.4. BioDBcore - a community-defined information specification for biological databases by Pascale Gaudet</p>	<p>5.4. fastapl and fastqpl, flexible tools for processing fasta and fastq format data by Paul Horton (Demo Short Talk)</p> <p>5.5. Extracting glycan motifs using a biochemically-weighted kernel by H Jiang, K Aoki-Kinoshita and WK Ching (Bioinformation)</p>	<p>6.4. Probing apicomplexan genomes by ultra-high-throughput sequencing by Arnab Pain (Invited Talk)</p> <p>6.5. Morphological and molecular identification of the metacestode parasitizing the liver of rodent hosts in bamboo growing areas of Mizoram, Northeast India by C Malsawmtluangi, P Prasad and V Tandon (Bioinformation)</p>
5:45 PM	Poster Viewing (odd numbers)		
6:30 PM	Official End of Conference Day 1 Scientific Program		
6:40 PM	APBioNet · ISCB Reception at Stage Lounge		

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01-Dec-11	THURSDAY		
8:00 AM	Ballroom	Function Rooms 3 and 4	Function Rooms 5 and 6
	Registration		
8:45 AM	Keynote 3 Chair: Rofina Yasmin Binti OTHMAN Sequencing, Sequencing, and Sequencing by Jun WANG		
9:45 AM	Sponsor Presentation Chair: Rofina Yasmin Binti OTHMAN Interactive Analysis of Human Genetic Variation by Stephen Rudd, Malaysian Genomics Resource Centre Berhad (MGRC)		
10:15 AM	Morning Break		
10:45 AM	7. Gene Expression Analysis Chair: Arnab PAIN	8. Proteins: Structures, Mutations and Interactions I Chair: Burkhard ROST	9. RNomics and NGS analysis I Chair: Christian SCHÖNBACH
	7.1. Comprehensive evaluation of matrix factorization methods for the analysis of DNA microarray gene expression data by MH Kim, HJ Seo, JG Joung and JH Kim (BMC B)	8.1. Assessing the utility of gene co-expression stability in combination with correlation in the analysis of protein-protein interaction networks by A Patil, K Nakai and K Kinoshita (BMC G)	9.1. In silico secretome analysis approach for next generation sequencing transcriptomic data by G Garg and S Ranganathan (BMC G)
11:15 AM	7.2. Extracting Regulatory Modules from Gene Expression Data by Sequential Pattern Mining by M Kim, H Shin, TS Chung, JG Joung and JH Kim (BMC G)	8.2. Functional characterization of protein domains common to animal viruses and their hosts by A Kinjo, Y Kumagai, H Dinh, O Takeuchi and D Standley (BMC G)	9.2. Identification of nucleotide patterns enriched in secreted RNAs as putative cis-acting elements targeting them to exosome nano-vesicles by A Batagov, V Kuznetsov and I Kurochkin (BMC G)
11:45 AM	7.3. Building gene expression profile classifiers with a simple and efficient reject option in R by A Benso, S Di Carlo, G Politano, A Savino and H Hafeezurrehman (BMC B)	8.3. A multi-species comparative structural bioinformatics analysis of inherited mutations in beta-D-Mannosidase reveals a genotype-phenotype correlation by T Hyunh, J Khan and S Ranganathan (BMC G)	9.3. Expression profile of small RNAs in Acacia mangium secondary xylem tissue with contrasting lignin content - a potential regulatory sequence in monolignol biosynthetic pathway by SS Ong and R Wickneswari (BMC G)
12:15 PM	7.4. Comparison of methods for identifying differentially expressed genes across multiple conditions from microarray data by Y Tan and Y Liu (Bioinformatics)	8.4. Comparative analysis and assessment of M. tuberculosis H37Rv protein-protein interaction datasets by H Zhou and L Wong (BMC G)	9.4. Prediction of RNA-binding amino acids from protein and RNA sequences by S Choi and K Han (BMC B)
12:45 PM	Lunch Break at Temptations APBioNet Open Meeting 12:30-1:15 PM Poster Viewing (even numbers)		
2:00 PM	Keynote 4 Chair: Janet KELSO Why Biologists should care about Wikipedia by Alex BATEMAN (sponsored by Universiti Sains Malaysia)		
3:00 PM	Afternoon Break		
3:30 PM	10. RNomics & NGS analysis II Chair: Hideo MATSUDA	11. Drug Design and Discovery Chair: Martti TAMMI	12. Proteins: Structures, Mutations and Interactions II Chair: Akira KINJO
	10.1. HabiSign: A novel approach for comparison of metagenomes and rapid identification of habitat-specific sequences by TS Ghosh, MH Mohammed, H Rajasingh, S Chadaram and S Mande (BMC B)	11.1. In silico modification of suberoylanilide hydroxamic acid (SAHA) as potential inhibitor for Class II Histone Deacetylase (HDAC) Homo sapiens by USF Tambunan, B Nindyapati and AA Parikesit (BMC B)	12.1. Revealing the functionality of hypothetical protein KPN00728 from Klebsiella pneumoniae MGH78578: molecular dynamics simulation approaches by SB Choi, NM Yahaya and HA Wahab (BMC B)
4:00 PM	10.2. Analysis of 16S rRNA environmental sequences using MEGAN by S Mitra, M Stärk and D Huson (BMC G)	11.2. Non-nucleosidic inhibition of Herpes simplex virus DNA polymerase: mechanistic insights into the anti-herpetic mode of action of herbal drug withaferin-A by A Grover, V Agrawal, A Shandilya, V Bisaria and D Sundar (BMC B)	12.2. Investigation and identification of protein γ-glutamyl carboxylation sites by TY Lee, SA Chen, TC Lu, NA Bretaña and TH Cheng (BMC B)
4:30 PM	10.3. Effective gene collection from the metatranscriptome of marine microorganisms by A Ogura, M Lin, Y Shigenobu, A Fujiwara, K Ikeo and S Nagai (BMC G)	11.3. Structure-based and ligand-based virtual screening of novel methyltransferase inhibitors of the dengue virus by LS Ven, MBA Rahman and B Tejo (BMC B)	12.3. Exploiting heterogeneous features to improve in-silico prediction of peptide status – amyloidogenic or non-amyloidogenic by SSK Nair, NVS Reddy and KS Hareesha (BMC B)
5:00 PM	10.4. MysiRNA-Designer: a Workflow for Efficient siRNA Design by M Mysara, JM Garibaldi and M Elhefnawi (Demo Short Talk)	11.4. In silico approach to screen compounds active against parasitic nematodes of major socio-economic importance by V Khanna and S Ranganathan (BMC B)	12.4. Descriptor-based computational analysis reveals a novel classification scheme for feruloyl esterase enzyme families by DBRKG Udata, I Kouskoumvekaki, L Olsson and G Panagiotou (Demo Short Talk)
	10.5. Computational annotation of tertiary motifs in RNA crystallographic structures by AS Devan and MF Raih (Poster Short Talk)		12.5. Structure-based design of cytokine agonists and antagonists by PJ Artymiuk, IR Wilkinson, SL Pradhananga, JR Sayers and RJ Ross (invited talk)
5:30 PM	Poster Session 2 (even numbers)		
6:15 PM	Poster Dismounting and Official End of Conference Day 2 Scientific Program		
7:00 PM	Conference Dinner at Saloma Restaurant and Bistro (sponsored by ISCB and APBioNet)		

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02-Dec-11 Friday			
8:00 AM	Ballroom	Function Rooms 3 and 4	Function Rooms 5 and 6
		Registration	
8:45 AM	Keynote 5 Chair: Peter J ARTYMIUK Interacting with Protein Interactions by Arthur OLSON (sponsored by Universiti Sains Malaysia)		
9:45 AM	Sponsor Presentations Chair: Peter J ARTYMIUK 1. BaseSpace: Illumina's next-generation sequencing cloud-computing for biologists by Siew-Fen Lye, Illumina Inc. and Malaysia ScienceVision (M) Sdn Bhd 2. Highly-accurate data intensive applications in next-generation DNA sequencing by Zayed Albertyn, Novocraft Technologies 3. High-Performance Computing in the Life Sciences by Nicholas Low, Silicon Graphics (M) Sdn Bhd and Karisma Electronic System Sdn Bhd		
10:15 AM	Morning Break		
10:45 AM	13: Systems Biology: Networks, Pathways and Imaging I Chair: Reinhard SCHNEIDER 13.1. Parameter Estimation Web Service Tailored for Data-Rich Biochemical Pathways by TH Nim, MV Clément, JK White and L Tucker-Kellogg (Poster Short Talk) 13.2. Grid Layout algorithm for biochemical networks using approximate pattern matching by K Inoue, S Shimozono and H Kurata (Poster Short Talk)	14: Disease Informatics I Chair: Ueng-Cheng YANG 14.1. A study of deregulated miRNA targets in hepatocellular carcinoma identifies novel insights into oncogenesis and drug targets by M Elhefnawi, S Zada, G Abdelrahman and M Amer (Poster Short Talk) 14.2. A pipeline for MS data - an application towards liver cancer by WWB Goh (Poster Short Talk)	15: 4th BCII Joint Session I Chair: Filippo CASTIGLIONE 4 th BCII opening remarks: F Castiglione, Chair; V Brusica, President IIMMS; C Schönbach, APBioNet Vice President (Conferences) 15.1. The design of optimal therapeutic small interfering RNA molecules targeting diverse strains of influenza A virus by M Elhefnawi, R Siam, N Hassan, M Kamar, A Remoli, I El-Azab, O Alaidy, G Marsili and M Sgarbanti (Late-breaking Short Talk)
11:15 AM	13.3. Network-based functional enrichment by C Poirel, C Owens and TM Murali (BMC B)	14.3. Construction and analysis of protein-protein interaction networks for schizophrenia, bipolar disorder, and major depression by SA Lee, TTH Tsao, KC Yang, H Lin, YL Kuo, CH Hsu, WK Lee, KC Huang and CY Kao (BMC B)	15.2. Immunoinformatics analysis of H5N1 proteome for designing an epitope-derived vaccine and predicting the prevalence of pre-existing cellular-mediated immunity toward bird flu virus in Indonesian population by M Gustiananda (Immunome Res)
11:45 AM	13.4. Stability of building gene regulatory networks with sparse autoregressive models by J Rajapakse and P Mundra (BMC B)	14.4. Genetic copy number variants in myocardial infarction patients with hyperlipidemia by WC Shia, FR Hsu, TH Ku, YM Tsao, Chien-Hsun Hsia, YM Chang, CH Huang, YC Chung, SL Hsu and KW Liang (BMC G)	15.3. Does difference exist between epitope and non-epitope residues? by J Sun, T Xu, S Wang, G Li, D Wu and Z Cao (Immunome Res)
12:15 PM	13.5. Near-membrane ensemble elongation in the proline-rich LRP6 intracellular domain may explain the mysterious initiation of the Wnt signaling pathway by C Liu, M Yao and C Hogue (BMC B)	14.5. Prioritizing disease candidate genes by a gene interconnectedness-based approach by CL Hsu, YH Huang, CT Hsu and UC Yang (BMC G)	15.4. A systematically improved high quality genome and transcriptome of the human blood fluke Schistosoma mansoni by A Protasio, JJ Tsai and M Berriman (Poster Short Talk) 15.5. Interaction of ganoderic acid on HIV related target: molecular docking studies by R Akbar and WK Yam (Bioinformatics)
12:45 PM	Lunch Break at Temptations		
2:00 PM	16: Systems Biology: Networks, Pathways and Imaging II Chair: Daniele SANTONI 16.1. Cell cycle phase classification in 3D in vivo microscopy of Drosophila embryogenesis by T Du, W Puah and M Wasser (BMC B)	17: Disease Informatics II Chair: Igor V KUROCHKIN 17.1. Finding consistent disease subnetworks across datasets by D Soh, D Dong, Y Guo and L Wong (BMC B)	18: 4th BCII Joint Session II Chair: Filippo CASTIGLIONE 18.1. FLAViDB: A data mining system for knowledge discovery in flaviviruses with direct applications in immunology and vaccinology by L Olsen, GL Zhang, E Reinherz and V Brusica (Immunome Res)
2:30 PM	16.2. Correlation of cell membrane dynamics and cell motility by M Veronika, R Welsch, A Ng, P Matsudaira and J Rajapakse (BMC B; will be presented by P Mundra)	17.2. Sorting permutations by cut-circularize-linearize-and-paste operations by KH Huang, KT Chen, CL Lu (BMC G)	18.2. Genotyping of Mumps viruses based on SH gene: Development of a server using alignment-free and alignment-based methods by P Kolekar, M Kale and U Kulkarni-Kale (Immunome Res)
3:00 PM	16.3. A quantitative analysis of monochromaticity in genetic interaction networks by CH Hsu, TY Wang, CY Kao and KC Chen (BMC B)	17.3. A robust tool for discriminative analysis and feature selection in paired samples impacts the identification of the genes essential for reprogramming lung tissue to adenocarcinoma by SH Toh, P Prathipati, E Motakis, PS Yanamandra, CK Kwok and V Kuznetsov (BMC G)	18.3. Scanning influenza sequences for PB1-F2 encoding RNA segments by D Deluca, D Keskin, GL Zhang, E Reinherz and V Brusica (BMC B)
3:30 PM	16.4. Assessments of predictive models for chlorophyll-a concentration at tropical water bodies by S Malek, SMS Ahmad, Sarinder KKS, P Millow and A Salleh (BMC B)	17.4. Drug Response Phenotype Standardization and SNP-phenotype Reliability Score by J Yoon, J Kim and JH Kim (Poster Short Talk) 17.5. Gentrepid: a web server for candidate disease gene prediction by S Ballouz, J Liu, R George, NP Bains, A Liu, M Oti, B Gaeta, D Fatkin and M Wouters (Demo Short Talk)	18.4. Whole proteome phylogeny of family Flaviviridae using alignment-free approach by P. Kolekar, M Kale and U Kulkarni-Kale (Poster Short Talk) 18.5. Potential "antibiotics" from flowering plants - a unique database by R Swaminathan, I Purushothaman, S Kothandan and TM Mohan (Demo Short Talk)
4:00 PM	Afternoon Break		
4:30 PM	19: BioCloud/Grid Computing for Sharing Bioinformatics Resources Chairs: Tin Wee TAN and Asif M KHAN 19.1. BioDB100 - the 100 bioinformatics database initiative for building exemplar databases with standards-compliance to BioDBcore and MIABi by AM Khan, JC Tong, M De Silva, KS Lim, S Napis, S Ranganathan and TW Tan		
4:45 PM	19.2. An extensible cloud-based platform for building reinstantiable BioDB100 databases by TW Tan, M De Silva, KS Lim, C Xie, CPK Patro, SJ Lim, KR Govindarajan, JC Tong, KH Choo, Bernett TK Lee, JM Khan, J Gaikwad, S Ranganathan and AM Khan		
5:00 PM	19.3. Biruni Grid: moving towards HPC on demand by S Napis, MF Sjaugi and MZ Yusof		
5:20 PM	19.4. Parallelising life science supercomputing applications at the A*STAR computational resource centre by C Xie, NH Hiew, M De Silva, KS Lim, TW Tan		
5:30 PM	Closing Ceremony Best Paper and Poster Awards APBioNet Awards Hello Bangkok: InCoB 2012		
6:00 PM	Official End of Scientific Program and InCoB/ISCB-Asia 2011 Conference		