

# The 18<sup>th</sup> International Conference on Genome Informatics (GIW2007)

3<sup>rd</sup> – 5<sup>th</sup> December 2007

Auditorium, Matrix, Biopolis,  
Singapore

## Conference Programme

## Preface

Genome Informatics Workshop (GIW) is the longest running international bioinformatics conference, which has provided unique opportunities that bridge theory and experiments, academia and industry, and East and West. The scope includes all work that is ultimately devoted to the computational understanding of biological systems on a molecular basis and the aims are to present recent results of both theoretical and practical research, to show new applications, to demonstrate systems, and to indicate directions of future research.

GIW was traditionally held in Japan. For 2007, it is the first time that GIW is held outside of Japan. The School of Computing and the Bioinformatics Programme at the National University of Singapore are honoured to jointly host GIW 2007. We are delighted to give you a warm welcome to Singapore.

The programme for GIW2007 is described in the following pages. In essence, it comprises 5 keynote talks, 16 technical talks from the accepted papers, 9 oral presentations selected from over 100 poster submissions, and 5 poster viewing sessions. We hope the inclusion of oral presentations from selected posters will increase the interaction between the more computing oriented and the more biology oriented members of the bioinformatics community.

Enjoy!

Limsoon Wong  
Conference Chair, GIW2007

Ps., immediately before GIW2007 will be the 6<sup>th</sup> Association of Asian Societies for Bioinformatics Symposium (AASBi2007) on 2<sup>nd</sup> December. Immediately after GIW2007 will be the 2<sup>nd</sup> International Symposium on Languages for Biology and Medicine on 6<sup>th</sup>-7<sup>th</sup> December. All three symposia are co-located at Biopolis. Delegates to GIW2007 are cordially welcome at both AASBi2007 and LBM2007 at no extra registration charge.

## GIW2007 Programme

@ Auditorium, Matrix Building, Biopolis, Singapore

### Day 1: Monday, 3 December 2007

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09.00-09.15	<b>Opening address</b>
09.15-10.15 Session chair: <b>Limsoon Wong</b>	<b>Keynote I:</b>  <b>The P53 Pathway</b> Sir David Lane, <i>IMCB, Singapore</i>
10.15-10.45	<b>Tea Break</b>
10.45-11.45 Session chair: <b>Seiya Imoto</b> 10.45-11.15	<b>Oral Presentation Session 1:</b>  <b>Computational Analysis and Modeling of Genome-scale Avidity Distribution of TFBS in ChIP-PET Experiments</b> V. Kuznetsov, Y. Orlov, C. L. Wei and Y. Ruan
11.15-11.45	<b>Predicting B Cell Epitope Residues with Network Topology Based Amino Acid Indices</b> J. Huang, W. Honda and M. Kanehisa
11.45-12.15 Session chair: <b>Seiya Imoto</b> 11.45-12.00	<b>Poster Oral Presentation Session 1:</b>  <b>Structural Difference with Temperature in Prokaryotic Metabolic Networks and a Hypothesis of Its Origin</b> K. Takemoto, J.C. Nacher and T. Akutsu
12.00-12.15	<b>Sensitivity Analysis of Acetone-Butanol-Ethanol (ABE) Fermentation by Kinetic Model</b> H. Shinto, Y. Tashiro, G. Kobayashi, T. Sekiguchi, T. Hanai, Y. Kuriya, M. Okamoto and K. Sonomoto
12.15-14.00	<b>Lunch</b>
13.00-14.00	<b>Poster Viewing Session 1 (Odd Numbers)</b>
14.00-15.00 Session chair: <b>See-Kiong Ng</b>	<b>Keynote II:</b>  <b>Computational Dissection of Mamalian Regulation Networks</b> Michael Zhang, <i>CSHL, USA</i>

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15.00-15.30	<b>Tea Break</b>
15.30-16.30 Session chair: <b>Sang Yup Lee</b> 15.30-16.00	<b>Oral Presentation Session 2:</b>  <b>An Accurate and Efficient Algorithm for Peptide and PTM Identification by Tandem Mass Spectrometry</b> K. Ning, H. K. Ng and H. W. Leong
16.00-16.30	<b>Detection of Monosaccharide Types From Coordinates</b> M. Arita and T. Tokimatus
16.30-17.00 Session chair: <b>Sang Yup Lee</b> 16.30-16.45	<b>Poster Oral Presentation 2:</b>  <b>In Silico Model Predicts the Existence of Novel Pathways in Activating Transcription Factor AP-1 in TNF-alpha Signaling</b> K. Hayashi, M. Helmy, H. A. Magdi, M. Tomita, M. Tsuchiya and K. Selvarajoo
16.45-17.00	<b>Mining Protein Networks with Maximal Quasi-bicliques</b> K. Sim, H. Li, J. Li and V. Gopalkrishnan
17.00-18.30	<b>Poster Viewing Session 2 (Even Numbers)</b>
19.00-21.30	<b>Conference Banquet and Award Ceremony</b> Venue: Guild Hall, Kent Ridge Guild House, NUS

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## Day 2: Tuesday, 4 December 2007

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09.00-10.00 Session chair: <b>Satoru Miyano</b>	<b>Keynote III:</b>  <b>Regulation of Gene Expression by Small Non-Coding RNAs</b> Hanah Margalit, <i>Hebrew University of Jerusalem, Israel</i>
10.00-10.30	<b>Tea Break</b>
10.30-12.00 Session chair: <b>Mark Ragan</b> 10.30-11.00	<b>Oral Presentation Session 3:</b>  <b>Weighted Lasso in Graphical Gaussian Modeling for Large Gene Network Estimation Based on Microarray Data</b> T. Shimamura, S. Imoto, R. Yamaguchi and S. Miyano
11.00-11.30	<b>GO based Tissue Specific Functions of Mouse using</b>

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	<b>Countable Gene Expression Profiles</b> Y. Takenaka, A. Matsumoto and H. Matsuda
11.30-12.00	<b>Functional Centrality: Detecting lethality of proteins in protein interaction networks</b> K. L. Tew, X. Li and S.-H. Tan
12.00-12.30 Session chair: Mark Ragan 12.00-12.15	<b>Poster Oral Presentation Session 3:</b>  <b>Local Singular Value Decomposition to Identify Recurrent Expression Amplicons from Massive Gene Expression Data</b> R. K. M. Karuturi, D. S. Bangarusamy, E. T. Liu and L.D. Miller
12.15-12.30	<b>Sequential Logic Model Deciphers Dynamic Interactions of Genes Regulation Mechanism</b> K. Sasidharan, V. Piras, Z. X. Yeo, M. Tomita, K. Selvarajoo and M. Tsuchiya
12.30-1400	<b>Lunch</b>
13.00-14.00	<b>Poster Viewing Session 3 (Even Numbers)</b>
14.00-15.00 Session chair: Hiroshi Mamitsuka	<b>Keynote IV:</b>  <b>Mapping the Transcriptional Network in Stem Cells Regulated by REST</b> Lawrence W. Stanton, <i>GIS, Singapore</i>
15.00-15.30	<b>Tea Break</b>
15.30-17.00 Session chair: Vladimir Bajic 15.30-16.00	<b>Oral Presentation Session 4:</b>  <b>A Conservative Parametric Approach to Motif Significance Analysis</b> U. Keich and P. Ng
16.00-16.30	<b>The In Silico Prediction of Promoters in Bacterial Genomes</b> M. Towsey, J. Hogan, S. Mathews and P. Timms
16.30-17.00	<b>Recognition of Polyadenylation Sites from Arabidopsis Genomic Sequences</b> C. H. Koh and L. Wong
17.00-17.30 Session chair:	<b>Poster Oral Presentation 4:</b>

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Vladimir Bajic 17.00-17.15	<b>varDB: a sequence database of protein families involved in antigenic variation in pathogens</b> N. Hayes, D. Diez, M. Kanehisa, M. Wahlgren, C. E. Wheelock and S. Goto
17.15-17.30	<b>An Alignment Method Based on Compound Similarity to Analysis of Metabolic Pathway Duplications</b> Y. Tohsato and Y. Nishimura
17.30-18.30	<b>Poster Viewing Session 2 (Odd Numbers)</b>
19.00-21.30	<b>PC Dinner</b> Venue: Minjiang @ One North, 5 Rochester Park

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### Day 3: Wednesday, 5 December 2007

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09.00-10.00 Session chair: Limsoon Wong	<b>Keynote V:</b>  <b>Discovering Biomolecular Mechanisms with Protein Sequence Studies</b> Frank Eisenhaber, <i>BII, Singapore</i>
10.00-10.30	<b>Tea Break</b>
10.30-12.00 Session chair: Christian Schoenbach 10.30-11.00	<b>Oral Presentation Session 5:</b>  <b>Comparative Pair-wise Domain-Combinations for Screening the Clade Specific Domain-architectures in Metazoan Genomes</b> S. Kawashima, T. Kawashima, N. Putnam, D. Rokhsar, H. Wada and M. Kanehisa
11.00-11.30	<b>The Comparative Genomics of Protein Interactions</b> J. M. Peregrin-Alvarez and C. Ouzounis
11.30-12.00	<b>Linear-Time Reconstruction of Zero-Recombinant Mendelian Inheritance on Pedigrees without Mating Loops</b> L. Liu and T. Jiang
12.00-12.30 Session chair: Christian Schoenbach	<b>Poster Oral Presentation Session 5:</b>

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12.00-12.15	<b>Comprehensive Analysis of Domain-Domain Interactions Using In Vitro Virus</b> R. Saito, Y. Ozawa, S. Fujimori, M. Matsui, S. Ushiyama, H. Kashima, H. Yanagawa, E. Miyamoto-Sato and M. Tomita
12.15-14.00	<b>Lunch</b>
13.00-14.00	<b>Poster Viewing Session 5 (All Numbers)</b>
14.00-15.30 Session chair: <b>Wing-Kin Sung</b>	<b>Oral Presentation Session 6:</b>
14.00-14.30	<b>FragQA: Predicting Local Fragment Quality of a Sequence-Structure Alignment</b> X. Gao, D. Bu, S. C. Li, J. Xu and M. Li
14.30-15.00	<b>Mining Super-Secondary Structure Motifs from 3D Protein Structures: A Sequence Order Independent Approach</b> Z. Aung and J. Li
15.00-15.30	<b>Computed Protonation Properties: Unique Capabilities for Protein Functional Site Prediction</b> L. F. Murga, Y. Wei and M. J. Ondrechen
15.30-16.00	<b>Closing Ceremony</b>

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## Brief Information on Keynote Speakers



**Dr Frank Eisenhaber**, Director at Bioinformatics Institute, A\*STAR, since August 2007. He was previously head of the bioinformatics research group at the Institute of Molecular Pathology in Vienna. He has made a number of significant discoveries, including the discovery of the very first set of enzymes involved in the transformation of a “lightly packed” (euchromatic) complex of DNA and protein to a “tightly packed” (heterochromatic) form. His team has also developed a series of sequence-based prediction tools, and the accuracy of their tools for predicting protein post-translation modifications is still unmatched in the world today.



**Professor Sir David Lane** was until recently Executive Director of A\*STAR's Institute of Molecular and Cell Biology. He is one of the scientists credited with the landmark discovery of cancer gene p53. For his contributions to cancer research, the Queen of England knighted Professor Lane on 24th October 2000. He is also the founder of Cyclacel Ltd. Cyclacel's lead drug candidate, CYC202, is the only orally available CDK inhibitor drug candidate currently in Phase II clinical trials on patients with blood or lung cancer



**Professor Hanah Margalit** is head of the computational molecular biology lab and head of the graduate program in genomics and bioinformatics at the Hebrew University of Jerusalem. Her research topics are: noncoding RNAs, protein-protein interactions, integrative analysis of cellular networks, and gene expression regulation.



**Dr. Lawrence Stanton** is Deputy Director (Research Affairs) at the Genome Institute of Singapore, A\*STAR. Prior to coming to Singapore, he was Director of Functional Genomics at Geron Corp. His lab is currently active in research on transcriptional control of embryonic stem cells and in cancer stem cells.



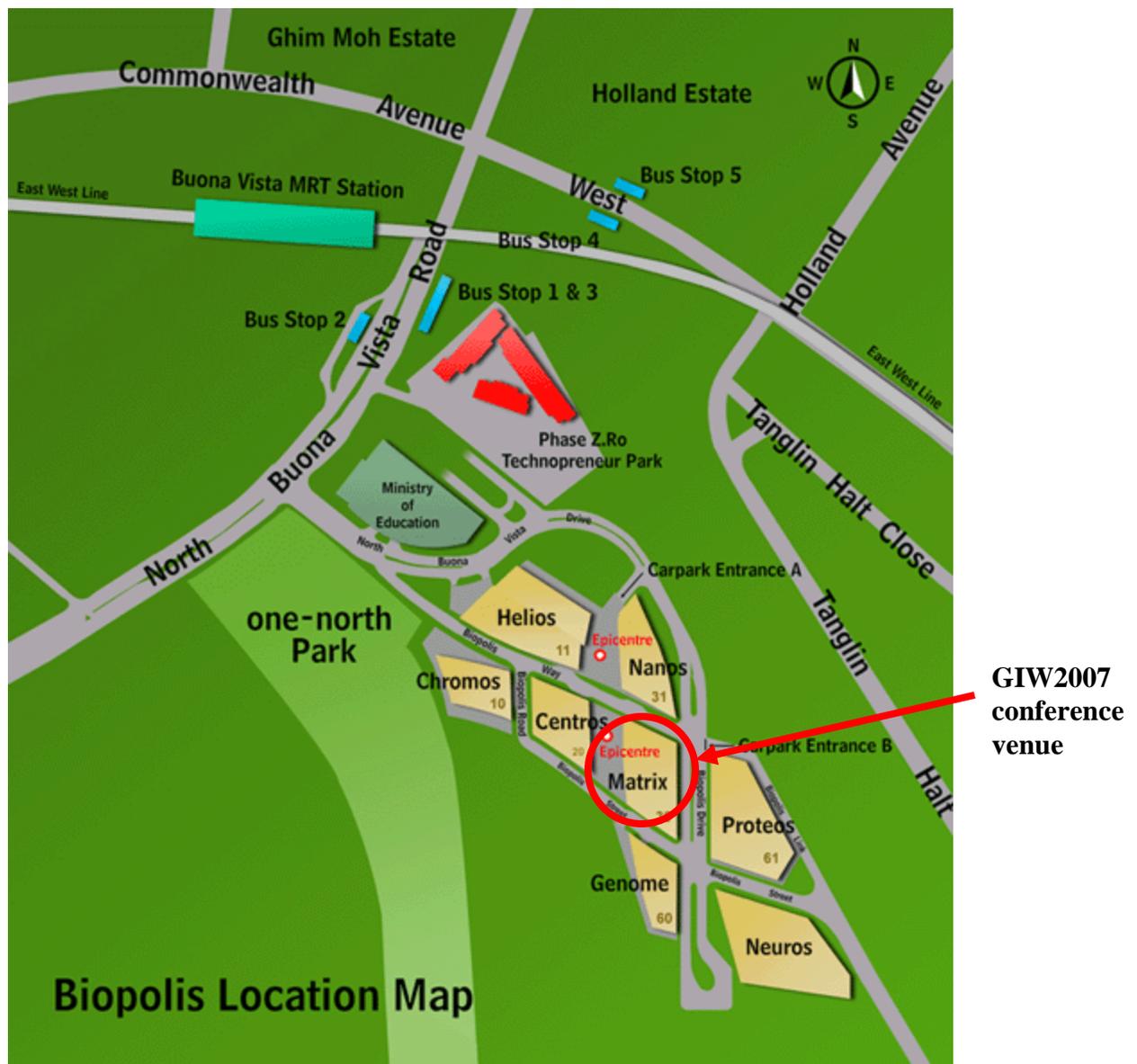
**Professor Michael Zhang** works in the Cold Spring Harbor Lab. He is well recognized for his contributions to mathematical and computational methods that can be combined with advanced experimental technologies to identify (1) functional genetic elements within molecular sequences and (2) pathways that control and regulate gene expression. The notable computational tools from his group include MZEF, Core\_Promoter, CpG\_Promoter, JTEF, and FirstEF.

## Venue and Location

GIW2007 will be held in the Auditorium at [Matrix, Biopolis, Singapore](#) during Monday 3<sup>rd</sup> – Wednesday 5<sup>th</sup> December 2007.

**Address of Biopolis:** Matrix, 30 Biopolis Street, Singapore 138671

**Getting to Biopolis: By MRT:** Alight at Buona Vista MRT station and walk 8 minutes; or take the free Biopolis Shuttle Bus service. **By Taxi:** Instruct driver to take you to “Biopolis” or to “MOE” (MOE = Ministry of Education, about 2 minutes walk to Biopolis).



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