

Wong Lim Soon

From: Wong Lim Soon [limsoon@nus.edu.sg]
Sent: Tuesday, April 16, 2013 2:25 PM
To: David Hsu Xu Ye (SoC); Wynne Hsu (SoC); leeml@comp.nus.edu.sg; leonghw@comp.nus.edu.sg; Ooi Beng Chin (SoC); ksung@comp.nus.edu.sg; Tan Kian Lee (SoC); thiagu@comp.nus.edu.sg; atung@comp.nus.edu.sg; liugm@comp.nus.edu.sg; chongket@comp.nus.edu.sg; tanhuiyi@comp.nus.edu.sg; melvin@comp.nus.edu.sg; yenan@comp.nus.edu.sg; srigsri@comp.nus.edu.sg; Nguyen Nam Ninh; Nguyen Phi Vu; suchee@comp.nus.edu.sg; ben.gyori@gmail.com; xxqqxiao@gmail.com; Sucheendra Kumar Palaniappan; th.chiang@gmail.com; Won Kok Sung; Bai Haoyu; kevinl@comp.nus.edu.sg; zhouhufeng@gmail.com; iamwym@gmail.com; zhanghao@comp.nus.edu.sg; misias@mimuw.edu.pl; g0600212@nus.edu.sg; Yong Chern Han; jin-jing@comp.nus.edu.sg; yusufif@comp.nus.edu.sg; Fan Mengyuan; hoang@comp.nus.edu.sg; zhizhuo@comp.nus.edu.sg; Lim Jing Quan; Wang Jianxing; drcyber@gmail.com
Cc: wongls@comp.nus.edu.sg
Subject: CBL Update - Jan - April 2013

Dear CBL Members,

1/

Looks like we have many visitors passing by... here are two talks they are giving tomorrow. The first is an exposition on SWATH-MS, the latest hot innovation in proteomic mass spectrometry.

[CS Seminar: A robust, fast and reproducible proteomic solution to convert human tissue into a digital data set for targeted data analysis](#)

Guo Tiannan, ETH Zurich

17 April 2013 @ 1pm in SR 8 (Level 2, COM1 Building)

[CS Seminar: Accurate Genome-Wide Survival Analysis of Somatic Mutations](#)

Fabio Vandin, Brown University

17 April 2013 @ 2.30pm in Video Conference Room (Level 2, COM1 Building)

2/

A dozen papers from the lab have been published since our last update (in December). These are:

Wilson Wen Bin Goh, Mengyuan Fan, Hong Sang Low, Marek Sergot, Limsoon Wong. **Enhancing the utility of Proteomics Signature Profiling (PSP) with Pathway Derived Subnets (PDSs), performance analysis and specialised ontologies.** *BMC Genomics*, 14:35, February 2013.

Jesper Jansson, Chuanqi Shen, Wing-Kin Sung. **An Optimal Algorithm for Building the Majority Rule Consensus Tree.** *Proceedings of 17th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, pages 88--99, April 2013.

Jingjing Jin, Jun Liu, Huan Wang, Limsoon Wong, Nam-Hai Chua. **PLncDB: Plant Long noncoding RNA Database.** *Bioinformatics*, 29(8):1068--1071, April 2013.

N. Nagarajan, D. Bertrand, A. M. Hillmer, Z. J. Zang, F. Yao, P. E. Jacques, A. S. Teo, I. Cutcutache, Z. Zhang, W. H. Lee, Y. Y. Sia, S. Gao, P. N. Ariyaratne, A. Ho, X. Y. Woo, L. Veeravali, C. K. Ong, N. Deng, K. V. Desai, C. C. Khor, M. L. Hibberd, A. Shahab, J. Rao, M. Wu, M. Teh, F. Zhu, S. Y. Chin, B. Pang, J. B. So, G. Bourque, R. Soong, W. K. Sung, B. T. Teh, S. Rozen, X. Ruan, K. G. Yeoh, P. B. Tan, Y. Ruan. **Whole-genome reconstruction and mutational signatures in gastric cancer.** *Genome Biology*, 13(12):R115, December 2012.

E. A. Simoes, C. Patel, W. K. Sung, C. W. Lee, K. H. Loh, M. Lucero, H. Nohynek, G. Nai, P. L. Thien, C. W. Koh, Y. S. Chan, J. Ma, S. Maurer-Stroh, P. Carosone-Link, M. L. Hibberd, C. W. Wong; IVAC Consortium. **Pathogen chip for respiratory tract infections**. *J Clin Microbiol*, 51(3):945--953, March 2013.

Sriganesh Srihari, Hon Wai Leong. **A Survey of Computational Methods for Protein Complex Prediction from Protein Interaction Networks**. *Journal of Bioinformatics and Computational Biology*, 11(2):1230002, April 2013.

Hugo Willy, Wing-Kin Sung, See-Kiong Ng. **Discovering interacting domains and motifs in protein-protein interactions**. *Data Mining for Systems Biology*, edited by Hiroshi Mamitsuka, Charles DeLisi, and Kanehisa Minoru, chapter 2, pages 9--20, January 2013.

M. T. Weirauch, A. Cote, R. Norel, M. Annala, Y. Zhao, T. R. Riley, J. Saez-Rodriguez, T. Cokelaer, A. Vedenko, S. Talukder; DREAM5 Consortium, P. Agius, A. Arvey, P. Bucher, C. G. Callan Jr, C. W. Chang, C. Y. Chen, Y. S. Chen, Y. W. Chu, J. Grau, I. Grosse, V. Jagannathan, J. Keilwagen, S. M. Kielbasa, J. B. Kinney, H. Klein, M. B. Kursa, H. Lähdesmäki, K. Laurila, C. Lei, C. Leslie, C. Linhart, A. Murugan, A. Mysickova, W. S. Noble, M. Nykter, Y. Orenstein, S. Posch, J. Ruan, W. R. Rudnicki, C. D. Schmid, R. Shamir, W. K. Sung, M. Vingron, Z. Zhang, H. J. Bussemaker, Q. D. Morris, M. L. Bulyk, G. Stolovitzky, T. R. Hughes. **Evaluation of methods for modeling transcription factor sequence specificity**. *Nature Biotechnology*, 31(2):126--134, January 2013.

Z. Zhang, C. W. Chang, W. Hugo, E. Cheung, W. K. Sung. **Simultaneously learning DNA motif along with its position and sequence rank preferences through expectation maximization algorithm**. *Journal of Computational Biology*, 20(3):237--248, March 2013.

Zhizhuo Zhang, Guoliang Li, Kim-Chuan Toh, Wing-Kin Sung. **Inference of Spatial Organizations of Chromosomes Using Semi-definite Embedding Approach and Hi-C Data**. *Proceedings of 17th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, pages 317--332, April 2013.

Liang Zhao, Steven C. H. Hoi, Limsoon Wong, Tobias Hamp, Jinyan Li. **Structural and functional analysis of multi-interface domains**. *PLoS ONE*, 7(12):e50821, December 2012.

Hufeng Zhou, Jingjing Jin, Limsoon Wong. **Progress in computational studies of host-pathogen interactions**. *Journal of Bioinformatics and Computational Biology*, 11(2):1230001, April 2013.

3/

The following invited talk was given:

Limsoon Wong. **Large-scale bio and medical data mining**. Invited talk at UTS AAI Big Data Summer School, Sydney, Australia, 10 April 2013.

4/

The following events were hosted:

CS Seminar: Accurate Genome-Wide Survival Analysis of Somatic Mutations
Fabio Vandin, Brown University
17 April 2013 @ 2.30pm in Video Conference Room

CS Seminar: A robust, fast and reproducible proteomic solution to convert human tissue into a digital data set for targeted data analysis
Guo Tiannan, ETH Zurich

17 April 2013 @ 1pm in SR 8

CS Seminar: On the relation of gene function and organization in normal and cancer cells

Ron Shamir, Tel Aviv University

12 April 2013 @ 2pm in SR2

CS Seminar: Whole-Genome Sequencing and Chromosome Contacts in Human Genome

Yuriy Orlov, Institute of Cytology and Genetics SB RAS, Novosibirsk

12 April 2013 @ 11am in SR @ LT19

CS Seminar: Modular and scalable bioinformatics approaches to agricultural and biomedical research and development

Matthew Bellgard, Centre for Comparative Genomics, Murdoch University

20 March 2013 @ 11am in MR1

Korea-Singapore Workshop on Bioinformatics and NLP

18 February 2103 @ 9am - 5pm in MR1 (COM1) and EC (COM2)

Regards,

Limsoon