Alexis Vandenbon (Institute of Medical Science, University of Tokyo)

After being held in Singapore last year, GIW stayed abroad this year for the second year in succession. The Nineteenth Conference on Genome Bioinformatics (GIW2008) was held in Australia for the first time, in Gold Coast, Queensland Australia, from Dec. 1st to 3rd. It was hosted by Bioinformatics Australia, and as such incorporated the annual Bioinformatics Australia conference. The Conference Chair was Mark Ragan (University of Queensland), and Program Committee Co-Chairs were Johnathan Arthur (University of Sydney) and See-Kiong Ng (Institute for Infocomm Research).

GIW2008 featured over 25 oral presentations, and more than 100 posters were presented. Here a short summary of the major themes is presented.

Gene expression starts with transcription and as usual the analysis of transcription and the transcriptome was one of the main subjects at this conference. In his keynote address, Sean Grimmond presented the results of RNA sequencing experiments in human and mouse which together with the second generation sequencing methods will give us a better idea of the complete transcriptome content. Lesley Collins presented an interesting application of Solexa sequencing in an organism that does not have sequenced genome. Tags from the plant Pachycladon enyssii were mapped to the nearest model reference genome, that of Arabidopsis thaliana, illustrating that the use of new high-throughput short-read sequencing techniques does not necessarily have to be restricted to model organisms. Ming Li discussed the ZOOM (“Zillions Of Oligos Mapped”) algorithm, an application of homology search fitted to the needs of the new sequencing methods.

Analysis of transcription however, cannot be complete without analysis of the processes that initiate transcription. A variety of topics in this field was covered, ranging from the discovery of potential cis-regulatory motifs (Patrick Ng), promoter sequence analysis using evolutionary conservation (Aaron Ingham), analysis of regulatory networks (Yixue Li), to promoter architecture modeling and prediction of gene expression (Alexis Vandenbon, Rui Yamaguchi).

It goes without saying that focus was not only on nucleotide sequences. Proteins, and in protein-protein interaction (PPI) analysis was also represented. Suk Hoon Junk and Guimei Liu both introduced approaches for decreasing false positive interactions in PPI networks. The former approach is based on structural interface data of protein domains, the later on the number of common neighbors of protein pairs. Other topics focusing on networks were presented by Lars Nielsen, who is working on the metabolic network in mouse, and Akira Ninagawa, who is working on link prediction in metabolic networks. It’s a small step from networks to graph theory. Zeyar Aung used a graph-based approach for detecting protein-ligand binding sites, and Yusuke Ishida worked on algorithms for enumerating tree-like chemical graphs.

The speed by which biological data is being generated keeps increasing, and our understanding of the genome and how its contents is being used has dramatically changed even in the last couple of years. Still, we are only scratching the surface of the tip of the iceberg, and John Mattick of the University of Queensland was there to remind us of the cold reality: for the past 50 years we have made serious errors in the interpretation of the way genetic information is used in complex eukaryotes. In the future too, the focus of biology is likely to shift more into the direction of noncoding RNA sequences and their role in various biological processes and phenomena.

In 2009 GIW will return to its home country, Japan. The 20th International Conference on Genome Informatics will be held in Yokohama from December 14 to 16.

Papers published in “Genome Informatics 2008” can be found at http://www.jsbi.org/modules/journal1/index.php/GI21.html