Editorial

The Fifth Georgia Tech—Oak Ridge National Laboratory International Conference in Bioinformatics: in silico Biology, Computational Genomics and Evolutionary Biology

The 2005 bioinformatics conference continues the tradition of four previous international bioinformatics meetings organized by Georgia Tech and held in Atlanta in 1997, 1999, 2001 and 2003. This time Georgia Tech is joined by the Oak Ridge National Laboratory as a co-organizer of the meeting. Previous co-organizers have included the University of Georgia and the Emory University. The conference continues to keep medium size format, with around 200 participants, which allows presentations to take place in succession rather than by dividing them between concurrent sessions. The choice of the format, the bi-annual schedule and the permanent location (Atlanta) make this conference distinct from other larger forums such as ISMB and RECOMB. On the other hand the conference could be compared with the Gordon conferences which have a similar size, but perhaps are less intensive and longer. Scheduling the conference near a weekend has also been a traditional feature aiming to create less conflict with the busy teaching schedule of university faculty. Note that the smaller the conference the easier to keep on the academic side and prevent it from sliding into a commercial venture (through the years we have kept the registration fees as low as possible). Since 2003 the conference site has been located in the brand new Georgia Tech Conference Center and Hotel opened in the Midtown area as an extension of Georgia Tech campus, near the Atlanta Arts Center and the city’s historic area.

The Georgia Tech meetings have consistently featured presentations of research accomplishments by leading experts in the field, both senior and junior. Participants from more than 15 countries around the globe have attended the previous conferences. The conference is now well established as a major academic forum for high level science presentations, discussions and exchange of ideas. The focus of the 2005 conference has been on searching for the direction in which computational genomics research would further advance the established field of evolutionary biology. This year we have again invited rising junior scientists to deliver keynote lectures on the discoveries made in silico, with many of these advances driven by the explosive growth of genomic and proteomic data. Natalia Komarova (University of California at Irvine, Irvine, CA, USA) described how mathematical insights can be combined with experimental studies to improve our understanding of cancer biology. Her topics included stem cells and tissue architecture, geometric constraints in cancer dynamics and drug resistance in cancer. Naama Barkai (Weizmann Institute of Science, Rehovot, Israel) discussed new methods that are able to reveal the genetic basis underlying the evolution of gene expression and its contribution to phenotypic diversity using both genomic information and DNA expression data. In particular, the analysis she described allows reconstruction of the evolution of the yeast transcriptional network through the evolution of motif usage. These results bring new insights into the genetic mechanisms underlying the large-scale evolution of transcriptional networks. Michael Lynch (Indiana University, Bloomington, IN, USA) talked about recent contributions that advance the understanding of mechanisms that are responsible for the origin of the fundamental features of the eukaryotic genome, such as eukaryotic gene structure. With the hypothesis that much of the eukaryotic genomic complexity initially evolved as a passive indirect response to reduced population size it is very challenging to learn how the complex intron-splicing machinery, the spliceosome, evolved and diversified among various phylogenetic lineages. Still it is possible to estimate the rate of intron gain and loss in various lineages.

The most frequent word in the titles of 17 plenary lectures was ‘evolution’. Philip Bourne considered evolution at the protein structure level and presented a tree of life based on fold usage; John Logsdon described methods for efficiently identifying phylogenetically informative genes from large genomic datasets and Jeffrey Lawrence suggested new methods of genomic analysis to infer directions of bacterial gene transfer. Three speakers—Alex Kondrashov, Boris Shakhnovich and Jeffrey Thorne—talked about various aspects of inferring natural selection by sequence comparison and modeling sequence evolution. John McDonald focused on the evolution of LTR retrotransposons. Other speakers gave account of their latest results in machine learning in biochemistry (Pierre Baldi), gene prediction (Volker Brendel) and genome annotation (Dmitrij Frishman), RNA structure analysis (Andrew Ellington), protein interaction networks (Eric Deeds) and distribution and information content of human SNPs (Sorin Istrail). King Jordan and Eugene Koonin described advances in the emerging field of evolutionary systems biology. The comparative genomics paradigm was extended to the comparative study of gene expression data uncovering important features of evolution of co-expressed genes and their networks (King Jordan), while various characteristics of genes and their protein products (reflecting their phylogenetic distribution and cell system interactions) have been integrated into a few unifying measures (Eugene Koonin). Seven contributed papers presented in Atlanta appear in this special Bioinformatics issue.

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