

Editorial

ISMB/ECCB 2007

This volume contains the papers accepted for presentation at the Fifteenth Conference on Intelligent Systems for Molecular Biology, which was held jointly with the Sixth European Conference on Computational Biology (ISMB/ECCB 2007; <http://www.iscb.org/ismbecb2007/>). The conference was held from 21–25 July 2007 at the Austria Center in Vienna, Austria. The conference united the annual meetings of the International Society for Computational Biology (ISCB) and of the European Computational Biology Community. The papers presented here are noteworthy for several reasons. First, for the second time, papers are open access and freely available to the worldwide community ahead of the conference and subsequently form an online only part of a regular issue of the journal *Bioinformatics*. Second, the review process was conducted even more rigorously than in previous years, as we describe below. We believe the scientific content to be outstanding. At the time of print, we expect the conference to become the largest scientific event in Computational Biology worldwide in the year 2007. This attests to the role of the conference and its organizing societies in furthering science in Computational Biology and fostering interdisciplinary scientific dialog on an international scale.

The call for papers resulted in 417 submissions in 11 different categories (Table 1). Area Chairs were recruited for each category and they in turn assigned reviewers for each paper. The Program Committee comprised over 300 reviewers who were assisted by a sizeable number of subreviewers. Aside from a few editorial rejects, all papers received at least two reviews; most were reviewed by three experts. During a 10-day period of internet discussion, the referees exchanged their views on controversial papers, based on the original reviews. After that period the area chairs decided on 51 ‘definite accepts’ and handed 40 more papers over to an inter-area discussion involving all area chairs and the program chair. That discussion was carried out over the internet and took two intensive phone conferences, lasted for 10 more days and yielded 15 more papers that were accepted for the conference. In total 66 papers have been included corresponding to an acceptance rate of 15.8%. The ratio is less than for typical submission to *Bioinformatics*, for three reasons. First, papers submitted to

ISMB/ECCB 2007 had to have the quality of a regular submission to *Bioinformatics*. In addition, they had to make for interesting talks and, finally, they had to be acceptable without major revision, because the timing of the paper selection process for the conference did not allow for a second round of reviewing.

Corresponding authors of submitted papers came from 42 countries, 194 papers were from North America, 140 from Europe and Israel, 69 from Asia, 5 from South America, 7 from Australia and 2 from Africa.

The contributed papers presented here comprise only one aspect of the scientific offerings of the conference, albeit a very important one. Ten invited keynotes were held by outstanding scientists in the field (Table 2), among them this year’s ISCB Award Winners Eran Segal (Overton Prize) and Temple Smith (ISCB Senior Scientist Accomplishment Award). Furthermore, the conference offered a Highlight Papers Track organized by Burkhard Rost featuring 65 talks on previously published high-quality work in computational biology, a PLoS Abstracts Track organized by Barbara Bryant, Phil Bourne and Steven Brenner with well over 30 talks on so far unpublished biology-oriented work in computational biology, and six ‘Special Sessions’ on relevant up-to-date topics (Table 3). Over 950 posters were selected to be presented in a Poster Session organized by Marco Punta. Reinhard Schneider organized an Industry Track with scientific presentations from industry and Shoba Ranganathan organized a Software Demonstrations Track. Before the conference, one Satellite Meeting and seven Special Interest Groups Meetings (SIGs) were held that were selected by Hershel Safer, Jill Mesirov and David Gilbert (Table 4), and there was a day of tutorials, featuring 14 tutorials selected by Janet Kelso and Fran Lewitter (Table 5).

We would like to thank the Area Chairs and reviewers for the quality they have brought to the conference, to Mario Albrecht for managing the paper selection process and coordinating the voluminous dialog with authors and reviewers, Andrei Voronkov for technical support with the EasyChair system which was used for managing the selection process, the team at Oxford University Press for proof-setting the papers, and Steven Leard for helping in many ways to get the proceedings out on time.

Thomas Lengauer, Conference Chair, ISMB/ECCB 2007
Burkhard Rost, Peter Schuster, Conference Co-Chairs, ISMB/ECCB 2007.

Table 1. ISMB/ECCB 2007 Program Areas, Area Chairs and Paper Distribution

Area	Area Chairs	Papers Received/Accepted
Sequence Analysis and Alignment	Des Higgins, Anders Gorm Pedersen	54/9
Evolution and Phylogeny	Manolo Gouy, Tandy Warnow	20/4
Comparative Genomics	Michal Linial, Manolis Kellis	20/3
Gene Regulation and Transcriptomics	Olga Troyanskaya, Zhaolei Zhang	58/12
Protein Structure	Nir Ben-Tal	47/6
Protein Function	Erik Sonnhammer	22/4
Protein Interactions and Molecular Networks	Joel Bader, Alfonso Valencia	43/7
Databases and Ontologies	Helen Parkinson, Robert Stevens	35/3
Text Mining	Christian Blaschke, Dietrich Rebholz-Schuhmann	29/3
Bioinformatics of Disease	Yanay Ofran, Predrag Radivojac	49/12
Other	Janice Glasgow, Rick Lathrop	40/3

Table 2. ISMB/ECCB 2007 Keynotes

Name	Affiliation	Title
Søren Brunak	Technical University of Denmark, Lyngby, Denmark	Understanding interactomes by data integration
Stephen K. Burley	SGX Pharmaceuticals, Inc., San Diego, CA, USA	Fragment-based discovery of BCR-ABL inhibitors for treatment of chronic myelogenous leukemia
Michael Eisen	University of California, Berkeley, CA, USA	Understanding and exploiting the evolution of the sequences that control gene expression
Anne-Claude Gavin John Mattick	European Molecular Biology Laboratory, Heidelberg, Germany University of Queensland, Brisbane, Australia	Interaction networks probed by mass spectrometry The majority of the genome of complex organisms is devoted to an RNA regulatory system that directs differentiation and development
Erin K. O'Shea	Harvard University, Cambridge, MA, USA	Dissecting transcriptional network structure and function
Renée Schroeder	University of Vienna, Austria	Genomic SELEX for the identification of novel non-coding RNAs independent of their expression level
Eran Segal	Computer Science and Applied Mathematics Department, Weizmann Institute of Sciences	Quantitative models for chromatin and transcription regulation
Temple F. Smith	Boston University, College of Engineering, Department of Biomedical Engineering, BioMolecular Engineering Research Center	Computational Biology: What is next?

Table 3. Special Sessions

Title	Organizer	Affiliation
Private fears in public places? Ethical and regulatory concerns regarding human genomics databases	David Gurwitz Barbara Praisack	Tel-Aviv University, Israel University of Vienna, Austria
Cheminformatics	Matthias Rarey	University of Hamburg, Germany
Genetic networks: Inferring pathways by combinatorial perturbation	Frederick "Fritz" Roth	Harvard Medical School, Cambridge, MA, USA
Computational epigenetics and chromatin regulation	Michael Q. Zhang	Cold Spring Harbor Laboratory, NY, USA
Computational Approaches to the Modern RNA World	Ivo Hofacker	University of Vienna, Austria
Dry work in a wet world: Improving methodology and access of computational methods in Systems Biology	Ewan Birney	European Bioinformatics Institute, Hinxton, UK

Table 4. ISMB/ECCB 2007 SIGs and Satellite Meetings

Title	Organizer	Affiliation
Alternative Splicing AS-SIG	Shoba Ranganathan Dirk Holste Eduardo Eyra Andrea Barta	Macquarie University, Sydney, Australia University of Vienna, Austria Pompeu Fabra University, Barcelona, Spain University of Vienna, Austria
Bioinformatics Open Source Conference (BOSC)	Darin London	Duke University, Durham, NC, USA
Bioinformatics Open Source Conference	David London	Duke University
BioLINK SIG	Christian Blaschke Lynette Hirschman Hagit Shatkay Alfonso Valencia	Bioalma, Madrid, Spain MITRE Corp., Bedford, MA, USA Queen's University, Kingston, Ontario, Canada Spanish National Cancer Research Center, Madrid, Spain
Bio-Ontologies SIG	Phillip Lord Robert Stevens Robin McEntire Susanna-Assunta Sansone	Newcastle University, UK University of Manchester, UK GlaxoSmithKline, Uxbridge, UK European Bioinformatics Institute, Hinxton, UK
BioPathways	Vincent Danos Joanne Luciano Eric Neumann Aviv Regev Vincent Schachter	University Paris-Diderot, France Harvard Medical School, Boston, MA, USA Teranode Corp., Boston, MA, USA The Broad Institute, Cambridge, MA, USA Genoscope, Evry, France
Joint AFP-Biosapiens SIG	Iddo Friedberg Christine Orengo Adam Godzik	University of California, San Diego, CA, USA University College London, UK University of California, San Diego, CA, USA
Microbe-SIG: Comparative Genomics, Evolution and Regulation in Microbes	Adam Arkin Eric Alm Inna Dubchak	Lawrence Berkeley Laboratory, CA, USA Massachusetts Institute of Technology, Cambridge, MA, USA Lawrence Berkeley Laboratory, CA, USA
3D-SIG: Structural Bioinformatics and Computational Biophysics Meeting (Satellite Meeting)	John Moulton Rafael Najmanovich Ilan Samish Melissa Landon	University of Maryland, College Park, MD, USA European Bioinformatics Institute, Hinxton, UK University of Pennsylvania, Philadelphia, PA, USA Boston University, MA, USA

Table 5. ISMB/ECCB 2007 Tutorials

Title	Organizer	Affiliation
Comparative analysis of protein structures: Principles, tools, and applications for establishing evolutionary relationship and predicting function	Raza Mazumder Sona Vasudevan	Georgetown University, Washington DC, USA
Workflow Approaches to Transcriptomics Analysis	Katy Wolstencroft Georgina Moulton	University of Manchester, UK
Ontologies for Biomedicine – How to make and use them	Barry Smith Nigam Shah	University at Buffalo, USA
Exploring computational biology with a massively parallel high performance computing environment	Kirk Jordan Srinivas Aluru	IBM T.J. Watson Research Center, Yorktown Heights, NY, USA Iowa State University, Ames, IA, USA
Genomes, browsers and databases: Tools for integrative sequence and annotation data from multiple genomes	Peter Schattner	University of California, Santa Cruz, CA, USA
Implementing phylogenetic workflows for comparative genomics using BioPerl	Jason Stajich Albert Vilella	University of California, Berkeley, CA, USA European Bioinformatics Institute, Hinxton, UK
Genomic data fusion for gene prioritization and function prediction	Yves Moreau	University of Leuven, Belgium
Gene and protein networks	Debra Goldberg Todd Gibson	University of Colorado, Boulder, CO, USA University of Colorado, Aurora, CO, USA
Automatic text analysis based on Web Services	Dietrich Rebholz-Schuhmann	European Bioinformatics Institute, Hinxton, UK
Reverse engineering mammalian transcriptional regulatory circuits	Pavel Sumazin Andrea Califano Andrei D. Smith Michael Q. Zhang	Columbia University, New York, NY, USA Cold Spring Harbor Laboratory, NY, USA
Systems Biology of host-pathogen interactions and microbial communities	Christian Forst	Los Alamos National Labs, Santa Fe, NM, USA
Comprehensive analysis of Affymetrix exon expression data using BioConductor	Crispin Miller Michal Okoniewski	University of Manchester, UK
Introduction to phylogenetic networks An introduction to bioinformatics for glycomics research	Daniel Huson Kiyoko Aoki-Kinoshita Claus-Wilhelm von der Lieth	University of Tübingen, Germany Soka University, Hachioji, Japan German Cancer Research Center, Heidelberg, Germany