

Editorial

ISMB 2006

This volume contains the papers accepted for presentation at the 2006 Intelligent Systems for Molecular Biology conference (ISMB 2006; www.iscb.org/ismb2006) held in Fortaleza, Brazil from August 6–10, 2006. The conference is the annual meeting of the International Society for Computational Biology (ISCB). The papers presented here are noteworthy for several reasons. First, papers are open access and freely available to the worldwide community ahead of the conference and subsequently form an on-line only issue of the journal *Bioinformatics*. Second, the review process was conducted slightly differently to previous years. Finally, and most importantly, we believe that the scientific content to be outstanding. This indicates both the strength of the field and a desire to present the best work in an important part of the world for the first time, making a truly international meeting and ISCB a truly international society.

The call for papers resulted in 404 submissions in one of thirteen different categories (Table 1). Area Chairs were recruited for each category and they in turn assigned reviewers for each paper. All papers received two or three reviews. Based on the reviews Area Chairs made recommendations on the papers to be presented. The final program was then decided by the Program Chairs based on these recommendations and the need to provide a balanced program. As a result 67 papers are included making for an acceptance rate of 16.6%.

A total of 347 papers had authors from a single country, 52 from 2 countries, 4 from 3 countries and 1 from 4 countries, respectively. Of the 347 papers from one country, 180 were from North America, 90 were from Europe and Israel, 49 from Asia, 16 from South America, 11 from Australia and 1 from Africa.

The papers accepted (Table 1) were organized slightly differently from previous years, with a category for Human Health added. This resulted in 20 submissions indicating strong interest from the community. Conversely, molecular and supramolecular dynamics was added and only resulted in 5 submissions.

Table 1. ISMB 2006 Program Areas, Program Chairs and Paper Distribution

Area	Area Chairs	Papers Received/Accepted
Comparative Genomics	Koonin, Eugene	25/4
Databases & Data Integration	Claverie, Jean-Michel	31/3
Evolution and Phylogeny	Kanehisa, Minoru	21/3
Human Health	Apweiler, Rolf	20/3
Molecular and Supramolecular Dynamics	Gouy, Manolo	5/1
Ontologies	Warnow, Tandy	8/2
Proteomics	Ofran, Yanay	38/6
Sequence Analysis	Radivojac, Predrag	59/10
Structural Bioinformatics	Kann, Maricel	51/8
Systems Biology	Punta, Marco	55/11
Text Mining & Information Extraction	Murray, Diana	33/6
Transcriptomics	Shakhnovich, Eugene	42/7
Miscellaneous	Kumar, Anand	16/3
	Stevens, Robert	
	Parkinson, Helen	
	Zhang, Zhaolei	
	Troyanskaya, Olga	
	Grishin, Nick	
	Brunak, Soren	
	Thornton, Janet	
	Russell, Rob	
	Bader, Joel	
	Sander, Chris	
	Valencia, Alfonso	
	Rzhetsky, Andrey	
	Margalit, Hanah	
	Zhang, Michael	
	Bourne, Philip	

Other areas remained approximately proportional to 2005 submissions.

We would like to thank the Area Chairs and reviewers for the quality they have brought to the conference, to Richard van de Stadt for support with Cyberchair in managing the selection

process and Steven Leard for following up with many of the loose ends needed to produce the volume in a timely manner.

Philip E. Bourne and Soren Brunak, Program Chairs
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