

Editorial

This special issue contains the papers accepted for presentation at the 18th Annual International Conference on Intelligent Systems for Molecular Biology, an official conference of the International Society for Computational Biology (ISCB; <http://www.iscb.org>). ISMB 2010 (<http://www.iscb.org/ismb2010/>) will be held in Boston, MA, USA from July 11 through July 13, 2010.

The 48 papers contained in this volume are a selection of the 235 papers submitted to the conference. The papers were assigned to 11 distinct areas. Two co-chairs led each topic area by selecting their area's program committee and overseeing the reviewing process. Many of the area chairs were new compared to 2009, and 'Bioimaging' was added as a completely new area in 2010. The areas, co-chairs and acceptance information are listed in the Table 1.

Most papers received three reviews and several received four or more. There was significant discussion of the merits of the papers between referees and the area chairs. Initial decisions to accept papers were made during a comprehensive phone discussion with the area chairs, and several papers underwent a further evaluation by additional area chairs before acceptance decisions were finalized. We appreciate that in several cases reviewers' opinions might have changed with additional input or further clarifications from the authors; because the ISMB 2010 timeline did not allow for a second round of reviews, however, only papers where referees suggested minor revisions could be accepted.

For several papers where the referee comments might have been unclear to the authors, the area chairs added additional comments

and explanations. In total, 48 papers were conditionally accepted, pending revision. After acceptance notices were sent, the authors had 2 weeks to modify their papers according to the suggestions made by the reviewers and to respond to reviewers' comments. Modified papers and the authors' responses were re-examined during the next week to ensure that each paper was modified appropriately in response to the reviewers' comments. We were pleased that all 48 conditionally accepted papers were finally accepted for the conference.

The final acceptance rate was 20%, which is similar to last year's acceptance rate of 19%. The authors of submitted papers came from 34 countries, including 418 from North America, 199 from Europe, 138 from Asia (excluding Israel), 22 from Israel, 16 from Oceania, 5 from Africa and 1 from South America. The authors of accepted papers came from 14 countries, with 27 corresponding authors from North America, 13 from Europe, 5 from Asia (excluding Israel) and 3 from Israel.

We would like to thank the area chairs and reviewers for their all of their hard work; all authors of submitted papers; Andrei Voronkov for extensive technical support with the EasyChair submission and reviewing system, including making last minute changes to the system; Dan Gusfield and Alfonso Valencia for sharing their experiences from previous years; the team at Oxford University Press for type-setting the papers; the Conference Chairs Olga Troyanskaya, Jill Mesirov and Michal Linial, as well as the ISMB 2010 Steering Committee, for their valuable input; and Steven Leard for helping us oversee the process.

Mona Singh (ISMB Proceedings Chair)

Joel S. Bader (ISMB Proceedings Co-Chair)

Table 1. Areas, co-chairs and acceptance information

Topic areas	Area co-chairs	No. of submitted papers	No. of accepted papers
Bioimaging	Robert F. Murphy and Gene Myers	23	8
Databases and Ontologies	Alex Bateman and Suzanna E. Lewis	23	3
Disease Models and Epidemiology	Thomas Lengauer and Yves Moreau	15	2
Evolution and Comparative Genomics	Dannie Durand and Teresa Przytycka	11	4
Gene Regulation and Transcriptomics	Hanah Margalit and Eric P. Xing	32	3
Population Genomics	Eleazar Eskin and Eran Halperin	20	6
Protein Interactions and Molecular Networks	Roded Sharan and Alfonso Valencia	28	4
Protein Structure and Function	Nir Ben-Tal and Bonnie Berger	34	7
Sequence Analysis	Michael Brudno and S. Cenik Sahinalp	31	7
Text Mining	Andrey Rzhetsky and Hagit Shatkay	7	2
Other Bioinformatics Applications	Barbara Bryant and Philip E. Bourne	11	2