

Editorial

This special issue contains the papers accepted for presentation at the 2009 ISMB/ECCB Conference (<http://www.iscb.org/ismbecb2009/>); the joint conference of 'Intelligent Systems for Molecular Biology' and 'European Conference on Computational Biology' to be held in Stockholm, Sweden from June 27 to July 2, 2009.

The papers contained in this volume are a selection of the 242 papers submitted to the conference. The papers were submitted to 11 distinct areas, with two co-chairs for most areas, who selected their area committees and oversaw the reviewing process. Several of the area chairs were new, and this year 'Population Genomics' was added to the 10 areas that made up the ISMB Conference in 2008. The areas, co-chairs and submission/acceptance information are listed in the following table.

The area chairs were responsible for selecting the members of the Program Committee that consisted of more than 300 reviewers, assisted by a sizeable number of sub-reviewers.

Most papers received three reviews and several received four or more reports. There was an intense discussion between referees and the area chairs. In a first round of evaluation, during a long phone discussion of area chairs, 37 papers were selected for acceptance, with another 16 papers selected to undergo a further evaluation by a broad range of area chairs; from those 16 papers, another 9 were accepted for the conference after a second phone discussion.

For all the papers where the referee comments might have confused the authors, particularly for rejected papers, additional comments were added by the area chairs. In total, 46 papers were accepted (formally, conditionally accepted pending revision).

After acceptance notices were sent, the authors had 2 weeks to modify their papers, incorporating suggestions from the reviews and responding to reviewers comments. These modified papers and the authors' responses were examined during the next week to spot any additional problems and to check how each paper was modified in response to the reviewers comments. Any modified paper that did not incorporate reviewers suggestions or defend that omission in the author's explanation could have been rejected at this point. We are happy to say that all 46 conditionally accepted papers were finally accepted for the conference.

The final acceptance rate was 19%, a bit higher than in previous years, reflecting a lower number of submissions this year (242 submissions compared with 287 submissions, and 17.1% acceptance rate in 2008; 15.8% acceptance rate in 2007). The corresponding authors of submitted papers came from 29 countries, including 450 from North America, 271 from Europe and Israel, 164 from Asia and Australia and 14 from South America.

We would like to thank the area chairs and reviewers for their efforts, dedication and quality of their professional work; all authors of submitted papers; Alfonso Valencia for sharing his experience from ISMB08; Andrei Voronkov for technical support with the EasyChair system; the team at Oxford University Press for typesetting the papers; the Conference Chairs, Gene Myers and Marie-France Sagot for their continuous support; and Steven Leard for helping us to deal with the all kinds of issues.

Dan Gusfield (ISMB/ECCB Proceedings Chair)

Anna Tramontano (ISMB/ECCB Proceedings Co-Chair)

No.	Areas	Co-chairs	No. of submitted papers	No. of accepted papers
1	Sequence analysis and alignment	Esko Ukkonen and Lior Pachter	35	8
2	Evolution and phylogeny	Jens Lagergren and Junhyong Kim	12	2
3	Comparative genomics	Roderic Guigo and David Sankoff	6	2
4	Protein structure and function	Nir Ben-Tal and Ora Schueler-Furman	28	6
5	Gene regulation and transcriptomics	Olga Troyanskaya and Zhaolei Zhang	30	5
6	Protein interactions and molecular networks	Joel Bader and Nir Friedman	30	4
7	Databases and ontologies	Alex Bateman	14	3
8	Text mining	Alfonso Valencia and Lynette Hirschman	11	0
9	Bioinformatics of disease	Igor Jurisica and Yanay Ofran	25	5
10	Other Bioinformatics Applications	Richard H. Lathrop and Larry Hunter	31	5
11	Population genomics	Andrew Clark and Eleazar Eskin	16	6