

## Editorial

### ISMB/ECCB 2015

This special issue of *Bioinformatics* serves as the proceedings of the joint 23rd annual meeting of Intelligent Systems for Molecular Biology (ISMB) and 14th European Conference on Computational Biology (ECCB), which took place in Dublin, Ireland, July 10–14, 2015 (<http://www.iscb.org/ismbecb2015>). ISMB/ECCB 2015, the official conference of the International Society for Computational Biology (ISCB, <http://www.iscb.org/>), was accompanied by nine Special Interest Group meetings of 1 or 2 days each, and two satellite meetings. Since its inception, ISMB/ECCB has been the largest international conference in computational biology and bioinformatics. It is the leading forum in the field for presenting new research results, disseminating methods and techniques, and facilitating discussions among leading researchers, practitioners, and students in the field. The 42 papers in this volume were selected from 241 original submissions divided into 13 research areas, collectively led by 25 Area Chairs. For each area, the Area Chairs selected an expert program committee for their subdiscipline and oversaw the reviewing process for that area. By design, the Area Chairs included a mix of experienced individuals reappointed from previous years and experts newly recruited to ensure broad technical expertise and to promote inclusivity of various elements of the research community. In total, the review process involved the 25 Area Chairs, 378 program committee members, and an additional

175 external reviewers recruited as sub-reviewers by program committee members. Table 1 provides a summary of the areas, area chairs and a review summary by area. The conference used a two-tier review system—a continuation and refinement of a process that begun with ISMB/ECCB 2013 in an effort to better ensure thorough and fair reviewing. Under the revised process, each of the 241 submissions was first reviewed by at least three expert referees, with a subset receiving between four and six reviews, as needed. Consensus on each paper was reached through online discussion among reviewers and Area Chairs. Among the 241 submissions, 27 were conditionally accepted for publication directly from the first round review. A subset of 29 papers was viewed as potentially publishable subject to revision and re-review of the manuscripts. Of the 27 papers that were resubmitted, 15 were judged to have addressed the concerns of the reviewers and were accepted for the conference proceedings, resulting in a total of 42 acceptances and an overall acceptance rate of  $42/241 = 17.4\%$ . We believe that this two-tier system, which is more reflective of typical multi-round journal review procedures, provided a means of ensuring that only the highest quality original work was accepted within the tight timing constraints imposed by the conference scheduling. We thank all authors for submitting their work. These proceedings would simply not be possible without the scientific ingenuity of the

**Table 1.** ISMB/ECCB 2015 review summary by area.

Topic area	Chairs	Submissions	Accepted round 1	Invited for round 2	Accepted in round 2	Approved for proceedings
Applied Bioinformatics	Thomas Lengauer and Christophe Dessimoz	30	1	6	3	4
Bioimaging and Data Visualization	Robert Murphy	12	1	2	1	2
Databases, Ontologies and Text Mining	Hagit Shatkay and Helen Parkinson	11	1	1	1	2
Disease Models and Epidemiology	Simon Kasif and Alice McHardy	21	3	3	3	6
Evolution and Comparative Genomics	Bernard Moret and Louxin Zhang	12	2	0	0	2
Gene Regulation and Transcriptomics	Uwe Ohler and Zohar Yakhini	30	2	4	2	4
Mass Spectrometry and Proteomics	Olga Vitek and Knut Reinert	11	2	0	0	2
Metabolic Networks	Bonnie Berger and Hidde de Jong	5	2	0	0	2
Population Genomics	Russell Schwartz and Jennifer Listgarten	22	3	2	1	4
Protein Interactions and Molecular Networks	Natasa Przulj and Igor Jurisica	29	2	5	3	5
Protein Structure and Function	Torsten Schwede and Anna Tramontano	22	3	2	1	4
RNA Bioinformatics	Jerome Waldispuhl and Hanah Margalit	6	0	1	0	0
Sequence Analysis	Michael Brudno and Siu-Ming Yiu	30	5	3	0	5
		241	27	29	15	42

contributors of all the papers. We recognize that the process is not perfect, and some outstanding work might have been rejected despite our best efforts. Nonetheless, we are hopeful that all authors received helpful feedback on their work and that most believed their submissions were judged fairly and diligently. In total, the two-tier review process involved 896 individual reviews. We are immensely grateful to the Area Chairs, the members of the program committee and the external subreviewers for their outstanding efforts in conducting a thorough review process in just 3 months. Their contribution is at the core of the scientific quality of the conference. We also thank Steven Leard for his continuing support with the review process; the team at Oxford University Press for preparing this special proceedings volume and the Conference Chairs, Janet Kelso and Alex Bateman, the Theme Chairs and other members of the ISMB

Steering Committee for their advice and supervision. We are also grateful to Russell Schwartz, Proceedings Chair of ISMB 2014, for sharing his experience and various helpful documents on the review process.

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