Editorial

This special issue of Bioinformatics serves as the proceedings of the 22nd annual meeting of Intelligent Systems for Molecular Biology (ISMB), which took place in Boston, MA, July 11–15, 2014 (http://www.iscb.org/ismbeccb2014). The official conference of the International Society for Computational Biology (http://www.iscb.org/), ISMB, was accompanied by 12 Special Interest Group meetings of one or two days each, two satellite meetings, a High School Teachers Workshop and two half-day tutorials. Since its inception, ISMB has grown to be the largest international conference in computational biology and bioinformatics. It is expected to be the premiere 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 37 papers in this volume were selected from 191 submissions divided into 13 research areas, collectively led by 24 Area Chairs. Each area's chair or chairs selected an expert program committee for their subdiscipline and oversaw the reviewing process for that area. Program committee members themselves could optionally recruit subreviewers to assist in their reviews. 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 promote inclusivity of various elements of the research community. In total, the review process involved the 24 Area Chairs, 322 program committee members and an additional 131 external reviewers recruited as subreviewers by program committee members. Table 1 provides a summary of the areas, their chairs and the review process by area.

The conference used a two-tier review system, a continuation and refinement of a process begun with ISMB 2013 in an effort to better ensure thorough and fair reviewing. Under the revised process, each of the 191 submissions was first reviewed by at least three expert referees, with a subset receiving between four and eight reviews, as needed. These formal reviews were frequently supplemented by online discussion among reviewers and Area Chairs to resolve points of dispute and reach a consensus on each paper. Among the 191 submissions, 29 were conditionally accepted for publication directly from the first round review based on an assessment of the reviewers that the paper was clearly above par for the conference. A subset of 16 papers were viewed as potentially in the top tier but raised significant questions the reviewers felt might be resolved by the authors in a response. The authors of these 16 papers were invited to submit revisions and responses to the round one criticisms for a second round review by the area chairs and other members of the program committee as needed. Nine of these 16 papers were judged to have addressed the concerns of the reviewers and were conditionally accepted for the conference proceedings, making a total of 38 conditional acceptances. In total, the two-tier review process involved 665 individual reviews. One conditionally accepted paper was subsequently withdrawn based on problems arising post-review, while the remaining 37 were approved for the final conference proceedings and presentation. We believe this two-tier system, more reflective of typical multi-round journal review procedures, provided a fairer process for ensuring only the highest quality original work was accepted within the tight timing constraints imposed by the conference scheduling. We recognize

Table 1. Areas, cochairs and acceptance data

Topic area	Chairs	Submissions	Accepted in round 1	Invited for round 2	Accepted in round 2	Approved for proceedings
Applied Bioinformatics	Lenore Cowen and Thomas Lengauer	18	3	1	1	4
Bioimaging and Data Visualization	Robert Murphy	3	1	0	0	1
Databases, Ontologies and Text Mining	Alex Bateman and Hagit Shatkay	12	1	1	0	1
Disease Models and Epidemiology	David Heckerman and Simon Kasif	11	2	0	0	2
Evolution and Comparative Genomics	Bernard Moret and Tandy Warnow	11	2	1	0	2
Gene Regulation and Transcriptomics	Alexander Hartemink and Zohar Yakhini	31	5	2	1	6
Mass Spectrometry and Proteomics	Bill Noble and Olga Vitek	8	2	0	0	2
Metabolic Networks	Jason Papin	8	1	2	1	2
Population Genomics	Eran Halperin and Itsik Pe'er	21	3	2	1	4
Protein Interactions and Molecular Networks	Trey Ideker and Mona Singh	21	2	3	3	4
Protein Structure and Function	Jie Liang and Jinbo Xu	13	2	1	0	2
RNA Bioinformatics	Ivo Hofacker and Jerome Waldispuhl	7	2	0	0	2
Sequence Analysis	Michael Brudno and Cenk Sahinalp	27	3	3	2	5
Total		191	29	16	9	37

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 expertly, if not always correctly.

We are 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 under tight time constraints. 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; Conference Chairs Bonnie Berger and Janet Kelso; and the other members of the ISMB Steering Committee, including Burkhard Rost, Diane Kovats, Paul Horton and Reinhard Schneider, for their advice and supervision. We are also grateful to Nir Ben-Tal, the proceedings chair of ISMB 2013, for sharing his experience and various helpful documents on the review process.

Serafim Batzoglou[1] and Russell Schwartz[2]
[1]Computer Science Department, Stanford University and
[2]Department of Biological Sciences and Lane Center for Computational Biology, Carnegie Mellon University