Editorial

This special issue hosts the proceedings of the joint 21st annual meeting of Intelligent Systems for Molecular Biology (ISMB) and 12th European Conference on Computational Biology (ECCB), which will take place in Berlin, Germany, between July 21 and 23, 2013 (http://www.iscb.org/ismbeccb2013). This official conference of the International Society for Computational Biology (http://www.iscb.org/), preceded by 11 Special Interest Group (SIG) meetings of 1 or 2 days, two satellite meetings, a Student Council Symposium, Junior Principal Investigators Symposium and two half-day tutorials during July 19–20, 2013, is likely to be the largest annual gathering in the field.

The 40 articles in this volume were selected from 233 submissions divided into 13 research areas, led by 26 area chairs. The chairs selected their area's program committee and oversaw the reviewing process. The chairs included a blend of individuals with experience from previous years and newcomers. Twelve submissions for which area chairs were in conflict were reviewed within 'Applied Bioinformatics' headed jointly by the two area chairs and the proceedings chair; four were accepted. Areas, co-chairs and acceptance data are listed in Table 1.

A two-tire review procedure was used, which is different from previous years. Of the total submissions, 89 were accepted to round two, including some with conflicting opinions. Of these, 85 were submitted to the second round. The final decision was made based on the revised submissions, taking into consideration the authors response to the reviewer reports, as well as reviewer reports on the revisions. Only 40 articles could be accommodated in the proceedings, forcing us to turn down 35, many of which were of high quality. I was hoping that the authors of most of these would be granted the opportunity to submit revised manuscripts to *Bioinformatics*, where they could be evaluated while their review history is considered. Unfortunately this opportunity was granted only to 11 manuscripts; I hope that if submitted, these will be readily accepted. More importantly, I would like to extend my apology to the authors of the remaining 24 who went through highly demanding and painful review process. I am hopeful that the authors of these manuscripts found the reviewer comments helpful.

The division into areas was somewhat different this year. Two new areas were defined: 'Metabolic Networks' and 'RNA Bioinformatics' and chairs and reviewers with suitable expertise recruited. 'Databases and Ontologies' and 'Text Mining' were merged into a single area.

All in all 368 members of the bioinformatics community provided reviews. Most articles were assigned to three reviewers and some to four or more. There was significant discussion of the merits of the articles first between referees and the area chairs, and then between area chairs and the proceedings chair. The review also included two conference calls with the area chairs.

Table 1. Areas, co-chairs and acceptance data

Topic area	Chairs	Submissions	Accepted to round two	Submitted to round two	Accepted to proceedings	Granted the opportunity to redirect to *Bioinformatics*
Applied bioinformatics and conflicts management	Nir Ben-Tal, Thomas Lengauer and Ora Schueler-Furman	18	11	10	4	3
Bioimaging and data visualization	Sean O'Donoghue and Carolina Wählby	11	7	7	4	1
Databases and ontologies and text mining	Alex Bateman and Hagit Shatkay	13	4	4	2	0
Disease models and epidemiology	Simon Kasif	12	1	1	1	0
Evolution and comparative genomics	Tal Pupko and Tandy Warnow	13	4	4	0	0
Gene regulation and transcriptomics	Alexander Hartemink and Zohar Yakhini	42	14	11	5	3
Mass spectrometry and proteomics	Rob Russell and Olga Vitek	8	3	3	1	0
Metabolic networks	Bonnie Berger and Jason Papin	8	6	6	3	0
Population genomics	Eleazar Eskin and Russell Schwartz	8	5	5	3	1
Protein interactions and molecular networks	Roded Sharan and Mona Singh	32	7	7	5	0
Protein structure and function	Lenore Cowen and Jie Liang	30	10	10	4	0
RNA bioinformatics	Ivo Hofacker and Hanah Margalit	6	5	5	3	1
Sequence analysis	Serafim Batzoglou and Cenk Sahinalp	32	12	12	5	2
Total	26	233	89	85	40	11

I am hopeful that the revised review process, which resembles that of journal articles, helped us to correctly choose the most suitable articles for the proceedings, but there is no guarantee.

I thank the area chairs and reviewers for their hard work in maintaining a professional review process; it has been harder and longer this year. I thank Steven Leard's team for extensive technical support with the EasyChair submission and reviewing system; the team at Oxford University Press for type-setting the articles; Conference Chairs Burkhard Rost, Anna Tramontano and Martin Vingron, as well as the ISMB 2013 Steering Committee, for their valuable input; and Steven Leard for helping us oversee the process. Special thanks to Mona Singh for her valuable notes from 2010 and to Bonnie Berger for many good advices at critical moments.

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