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Editorial

ISMB 2016 Proceedings

This special issue of *Bioinformatics* serves as the proceedings of the 24th annual conference Intelligent Systems for Molecular Biology (ISMB), which took place in Orlando, Florida, July 8–12, 2016 (http://www.iscb.org/ismb2016). ISMB 2016, the official conference of the International Society for Computational Biology (ISCB, http://www.iscb.org/), was accompanied by 11 Special Interest Group meetings of 1 or 2 days each, and two satellite meetings. Since its inception, ISMB 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 188 original submissions divided into 5 Themes and 11 associated Areas, collectively led by 10 Theme Chairs and 22 Area Chairs (Tables 1 and 2). For each area, the Area Chairs selected an expert program committee for their sub-discipline and oversaw the reviewing process for that area in coordination with the corresponding Theme Chairs. By design, the Theme and Area Chairs included a mix of experienced individuals re-appointed 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 10 Theme Chairs, the 22 Area Chairs, 331 program committee members and an additional 129 external reviewers recruited as sub-reviewers by program committee members. Table 2 provides a summary of the areas, Area Chairs and a summary of the reviews by area. The conference used a slightly streamlined 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 188 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, Area Chairs and Theme Chairs. Among the 188 submissions, 42 were accepted for publication conditionally on revisions properly addressing the comments of the reviewers. All revised versions were

Table 1. Complete list of Themes, Theme Chairs, and Areas associated with each Theme

Theme	Theme Chairs	Areas associated with the Theme
Data	Alex Bateman, Bonnie Berger	Applied Bioinformatics, Bioimaging, Databases, Ontologies and Text Mining
Diseases	Yana Bromberg, Yves Moreau	Disease Models and Epidemiology
Genes	Russell Schwartz, Jean-Philippe Vert	Evolution and Comparative Genomics/Proteomics, Gene/Protein Sequence Analysis, Gene Regulation, RNA Bioinformatics
Proteins	Ioannis Xenarios, David Jones	Evolution and Comparative Genomics/Proteomics, Gene/Protein Sequence Analysis, Protein Interactions and Molecular Networks, Protein Structure and Function
Systems	Niko Beerenwinkel, Donna Slonim	Protein Interactions and Molecular Networks, Population Genomics

Table 2. Complete list of Areas, Area Chairs, and submission statistics

Area	Area Chairs	Submissions	Invited for round 2	Approved for preceedings
Applied Bioinformatics	Stefano Lonard, Florian Markowetz	19	5	5
Bioimaging	Charless Fowlkes, Robert Murphy	4	2	2
Databases, Ontologies and Text Mining	Zhiyong Lu, Hagit Shatkay	12	2	2
Disease Models and Epidemiology	Trey Ideker, Maricel Kann	20	3	3
Evolution and Comparative Genomics/Proteomics	Mathieu Blanchette, Bernard Moret	12	0	0
Gene/Protein Sequence Analysis	Uwe Ohler, S. Cenk Sahinalp	34	6	6
Gene Regulation	Knut Reinert, Siu Ming Yiu	23	7	7
Population Genomics	Jennifer Listgarten, Oliver Stegle	7	2	2
Protein Interactions and Molecular Networks	Hidde de Jong, Natasa Przulj	29	6	6
Protein Structure and Function	Jianlin Cheng, Lenore Cowen	19	5	5
RNA Bioinformatics	Rolf Backofen, Jerome Waldispuhl	9	4	4
		188	42	42

inspected by the corresponding Theme Chairs and Area Chairs, sometimes relying on additional assessments provided by the original reviewers. All 42 submissions were judged to have properly addressed the concerns of the reviewers and were accepted for the conference proceedings, resulting in an overall acceptance rate of $42/188 = 22.3\%$. We believe that this two-tier system, which is more reflective of typical multiround 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 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 believe their submissions were judged fairly and diligently. In total, the two-tier review process involved 687 individual reviews. We are deeply grateful to the Theme Chairs and 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 all the other members of the ISMB Steering Committee for their expert advice and supervision.

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