

Editorial

ISMB/ECCB 2017 proceedings

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The 25th Annual Conference Intelligent Systems for Molecular Biology (ISMB), held jointly with the 16th annual European Conference on Computational Biology (ECCB), took place in Prague, Czech Republic, July 21–25, 2017 (<http://www.iscb.org/ismbeccb2017>). This special issue of Bioinformatics serves as the proceedings for this official conference of the International Society for Computational Biology (ISCB, <http://www.iscb.org/>).

The year 2017 was inaugural for a new program format introducing the ISCB Communities of Special Interest (COSIs) as scientific themes within the conference. The 12 COSIs presenting at ISMB/ECCB 2017 (Table 1) had previously organized the pre-conference Special Interest Group meetings. This year, the program

incorporated COSI sessions including proceedings, highlights (previously published research), and late-breaking research talks in addition to special sessions, workshop, posters and other scientific talks submitted directly to ISMB/ECCB.

ISMB/ECCB is the leading international forum in the field for presenting new methods and research results and for facilitating discussions at all levels of expertise. The 45 papers in this volume were selected from 279 original submissions, resulting in an acceptance rate of 16%. Submitted papers accumulated 3.2 reviews on average. The review process included 208 expert reviewers (with some reviewers working for more than one COSI) led by 42 Area Chairs (Table 1) to produce 899 reviews. The Area Chairs were appointed

Table 1. Thematic areas of ISMB/ECCB 2017. Areas have been defined as Communities of Special Interest (COSIs), except ‘Other Topics’

COSI/Area	Short name	Area chairs	No. of reviewers	No. of submissions	No. of accepted papers
3Dsig: Structural Bioinformatics and Computational Biophysics	3Dsig	Jianlin Cheng, Charlotte Deane, Rafael Najmanovich	30	18	4
Automated Function Prediction	Function	Simon Kasif	15	10	2
Bio-Ontologies	Bio-Ontologies	Michel Dumontier, Philippe Rocca-Serra, Karin Verspoor	27	9	2
Biological Data Visualization	BioVis	Alexander Lex, Michel Westenberg	5	2	0
Computational Modeling of Biological Systems	SysMod	Laurence Calzone, Andreas Dräger, Tomas Helikar, Jonathan Karr, Nicolas Le Novere, Julio Saez-Rodriguez	5	24	4
Computational RNA Biology	RNA	Rolf Backofen, Jerome Waldispühl	24	26	3
Critical Assessment of Massive Data Analysis	CAMDA	David P. Kreil	10	4	2
High-Throughput Sequencing Algorithms and Applications	HitSeq	Can Alkan, Valentina Boeva, Ana Conesa, Francisco De La Vega, Dirk Evers, Kjong Lehman, Gunnar Rätsch	91	55	8
Network Biology	NetBio	Alexander Pico, Natasa Przulj	34	39	6
Regulatory Genomics	RegGen	Finn Drablos, Jason Ernst, Saurabh Sinha, Lonnie Welch	45	31	5
Translational Medicine Informatics and Applications	TransMed	Bissan Al-Lazikani, Irina Balaur, Wei Gu, Winston Hide, Roland Krause, Mansoor Saqi, Venkata Satagopam	39	33	4
Variant Interpretation	VarI	Yana Bromberg, Emidio Capriotti, Hannah Carter	21	13	2
Other Topics	Other (no COSI)	Yana Bromberg, Niko Beerenwinkel	24	15	3
Total			370 (208 unique)	279	45

by the individual COSIs, and included a mix of experienced individuals intimately familiar with the field as well as with the review process.

Manuscripts submitted to the proceedings track were assigned to COSIs based on authors' suggestions and on the judgement of Area and Proceedings Chairs. An additional track was created to house all submissions unrelated to any of the existing COSI topics. The submissions in this 'Other Topics' area mostly addressed questions in microbiome analysis and evolutionary modeling. With the COSI-based structure, proceedings areas have become more community-driven and dynamic. We believe that going forward in this manner new emerging scientific themes can be detected quicker and represented better.

After initial screening, submissions were sent out to expert reviewers selected by the Area Chairs from the program committee. Each paper and its reviews were then discussed online among reviewers and Area Chairs. Finally, Area and Proceedings Chairs discussed the ranked papers to arrive at a subset of 46 papers, which were conditionally accepted. In continuation of the two-tier review process employed at ISMB 2016, Area Chairs, Proceedings Chairs and sometimes the corresponding reviewers inspected the revised papers again. All but one paper were re-submitted. These 45 revised papers were judged to have satisfactorily addressed the reviewers' comments and were finally accepted into the proceedings.

We would like to thank all authors of the 279 submissions for submitting their work. The excellent scientific quality of these papers is pivotal for the impact and the success of the conference. We believe that we have identified 45 outstanding pieces of bioinformatics research for the proceedings track. We note, however, that the review process was subject to some re-organization largely due to the new COSI-based conference format. It is, therefore, possible that excellent papers have not been fully recognized as such. Nevertheless, we know that submissions were evaluated fairly and diligently and hope that all authors have received useful feedback.

Like the conference itself, the review and selection process of the proceedings papers is a community effort. We would like to express our deep gratitude to all Area Chairs, members of the program committee, and external subreviewers for their outstanding efforts and rigorous focus on scientific quality. We would like to express deep gratitude to Steven Leard for all help with the review process—without his organizational support our work would not be possible. We would also like to thank the team at Oxford University Press for consistently handling this ISMB/ECCB special proceedings issue. Last, but certainly not least, we thank all members of the ISMB Steering Committee for their expert advice and support.

Conflict of Interest: none declared.