

## Editorial

# ISMB/ECCB 2019 Proceedings

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The biennial joint meeting of ISMB (27th Annual Conference on Intelligent Systems for Molecular Biology) and ECCB (18th European Conference on Computational Biology) was held in Basel, Switzerland, July 21–25, 2019. ISMB is the flagship conference of the International Society for Computational Biology and the world's premier forum for dissemination of scientific research in computational biology and its intersection with other areas. ECCB is similarly a top venue in the field, with a long tradition of publishing and presenting world-class research. This special issue serves as the Proceedings of ISMB/ECCB 2019.

Following a successful model with a centralized manuscript review and acceptance process, this year's conference organization provided the community with a unified submission interface for high-quality papers in the field of computational biology. The review process across 10 scientific areas was supervised by the Senior Program Committee (SPC), consisting of the Proceedings Chairs and Area Chairs (AC). About a third of the ACs were nominated by the Communities of Special Interests (COSIs), reflecting the desire of the ISMB/ECCB 2019 Steering Committee to involve COSIs in conference organization and the review process. Overall, the SPC consisted of 21 individuals; see [Table 1](#).

The scope of the conference includes theoretical papers, algorithms and statistical methods that allow for important novel

biological insights and broadly defined intellectual contributions. We invited submission of papers in nine general scientific areas, organized by the relevant biological problems ([Table 1](#)). The 10th area of General Computational Biology was created to accommodate innovation outside of specified fields. The papers submitted to this area were largely in Text Mining, Mass Spectrometry and Visualization subfields, indicating community interest in these areas. All papers submitted to all areas were expected to present methodological and scientific contributions to the specific areas of submission. Abstracts, previously published papers, position papers, perspectives and reviews are not eligible for submission to the ISMB/ECCB Proceedings track.

In total, 366 papers were submitted—a 10.6% increase over ISMB 2018. Of these, 363 papers were sent to review, receiving 1303 reviews from 388 Program Committee members. This constitutes an average of 3.6 reviews per submission. Three submissions had two completed reviews, 175 had three, 157 had four, 24 had five and four submissions had six completed reviews. The conditional acceptance information was provided to the authors a month after the submission deadline and final acceptance conveyed in another month. Overall, 69 manuscripts were accepted for a final acceptance rate of 18.9%. The distribution of papers reviewed in different areas is shown in [Table 1](#).

**Table 1.** Thematic areas of ISMB/ECCB 2019

Area	Area chairs	Submissions	Accepted papers	Acceptance rate (%)
Studies of Phenotypes and Clinical Applications	Sara Mostafavi, Venkata Satagopam	80	13	16.3
Comparative and Functional Genomics	Can Alkan, Carl Kingsford	65	13	20.0
Bioinformatics Education	Anne Rosenwald	2	1	50.0
Genomic Variation Analysis	Martin Kircher, Sriram Sankararaman	25	3	12.0
Bioinformatics of Microbes and Microbiomes	Curtis Huttenhower, Yuzhen Ye	19	3	15.8
Population Genomics and Molecular Evolution	Christophe Dessimoz, Dannie Durand	15	6	40.0
Macromolecular Sequence, Structure and Function	Lenore Cowen, Jérôme Waldispühl	59	13	22.0
Systems Biology and Networks	Sushmita Roy, Roded Sharan	60	10	16.7
Genome Privacy and Security	Haixu Tang	4	1	25.0
General Computational Biology	Olga Vitek, Daisuke Kihara	34	6	17.6

*Note:* The table lists the ACs for each theme, the number of reviewed papers, the number of accepted papers, and the acceptance rate for each area. A special area of General Computational Biology was created for papers not fitting in any of the predefined areas.

**Table 2.** Distribution of ISMB/ECCB 2019 Proceedings papers to COSIs

COSI	Number of papers
MLCSB	12
HiTSeq	9
Evolution	8
RegSys	7
TransMed	6
CompMS	4
RNA	4
Function	3
Microbiome	3
3DSIG	2
VarI	2
BioVis	2
CAMDA	2
NetBio	2
Bio-Ontologies	1
Education	1
No COSI	3

As was the case in 2018, the authors had the opportunity to request that their accepted manuscripts be presented in one of the COSI sessions. The most requests were made for MLCSB (64),

followed by NetBio (39), Evolution (37), RegSys (37), TransMed (34), HiTSeq (33), Function (30), Microbiome (18), VarI (16), RNA (15), Text Mining (11), BioVis (10), Bio-Ontologies (7), CAMDA (4), Education (2) and CompMS (2). A further 35% of the submitted manuscripts made no specific COSI session request. Final assignments to COSI sessions were made by the Proceedings Chairs on the basis of the author and COSI requests. Three papers were assigned to the General Computational Biology session for presentation. The distribution of accepted papers to COSIs is shown in [Table 2](#).

We thank the ISMB/ECCB 2019 Steering Committee for their support and guidance. Special thanks go to the SPC and reviewers for their fantastic work dedicated to maintaining the high-quality standards of ISMB/ECCB in a compressed time frame. We are particularly grateful to Steven Leard, Diane Kovats and Pat Rodenburg for world-class organizational support. We would also like to thank the COSIs for nominating the ACs and the COSI contacts for their help in identifying reviewers and incorporating accepted papers into their programs. Finally, we thank the community for their interest and engagement in this conference—ISMB/ECCB 2019 belongs to you! With this, we invite you to read the Proceedings of ISMB/ECCB 2019. See you next year in Montreal, Canada, for ISMB 2020.

*Conflict of Interest:* none declared.