

# Preface

The 12<sup>th</sup> edition of the International Symposium on Bioinformatics Research and Applications (ISBRA 2016) was held during June 5–8, 2016, in Minsk, Belarus. The symposium provides a forum for the exchange of ideas and results among researchers, developers, and practitioners working on all aspects of bioinformatics and computational biology and their applications.

There were 77 submissions received in response to the call for papers. The Program Committee decided to accept 42 of them for publication in the proceedings and for oral presentation at the symposium: 22 for Track 1 (an extended abstract) and 20 for Track 2 (an abridged abstract). The technical program also featured invited keynote talks by five distinguished speakers: Dr. Teresa M. Przytycka from the National Institutes of Health discussed the network perspective on genetic variations, from model organisms to diseases; Prof. Ion Mandoiu from the University of Connecticut spoke on challenges and opportunities in single-cell genomics; Prof. Alexander Schoenhuth from Centrum Wiskunde and Informatica spoke on dealing with uncertainties in big genome data; Prof. Ilya Vakser from the University of Kansas discussed genome-wide structural modeling of protein–protein interactions; and Prof. Max Alekseyev from George Washington University spoke on multi-genome scaffold co-assembly based on the analysis of gene orders and genomic repeats.

We would like to thank the Program Committee members and external reviewers for volunteering their time to review and discuss symposium papers. Furthermore, we would like to extend special thanks to the steering and general chairs of the symposium for their leadership, and to the finance, publicity, local organization, and publication chairs for their hard work in making ISBRA 2016 a successful event. Last but not least, we would like to thank all authors for presenting their work at the symposium.

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