

Preface

On behalf of the Program Committee, we would like to welcome you to the proceedings of the 13th edition of the International Symposium on Bioinformatics Research and Applications (ISBRA 2017), held in Honolulu, Hawaii, May 29 to June 2, 2017. 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. This year we received 118 submissions in response to the call for extended abstracts. The Program Committee decided to accept 27 of them for full publication in the proceedings and oral presentation at the symposium. We also accepted 24 of them for oral presentation and short abstract publication in the proceedings. Furthermore, we also received 18 submissions in response to the call for short abstracts.

The technical program invited keynote talks by Prof. Michael Q. Zhang from The University of Texas at Dallas and Tsinghua University. Prof. Zhang reviewed the history of computational genome regulation and then introduced some new biochemical (BL-Hi-C), biophysical (super-resolution imaging), and bioinformatics (MICC, 3CPET, FIND) technology developments that may be used for studying 3D genomes and disease markers in the near future.

We would like to thank the Program Committee members and the additional reviewers for volunteering their time to review and discuss symposium papers. We would like to extend special thanks to the steering and general chairs of the symposium for their leadership, and to the finance, publicity, workshops, local organization, and publications chairs for their hard work in making ISBRA 2017 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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