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Preface

Special Issue: 16th International Symposium on Bioinformatics Research and Applications (ISBRA 2020)

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This special issue includes a selection of articles presented at the 16th International Symposium on Bioinformatics Research and Applications (ISBRA 2020) which was held in Moscow, Russia, on December 1–4, 2020. ISBRA 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.

In 2020, 131 abstracts were submitted in response to the call for articles, out of which 23 extended abstracts and 18 short abstracts appeared in the ISBRA proceedings published as volume 12,304 of Springer Verlag's *Lecture Notes in Bioinformatics* series. Authors of 15 articles were invited to submit extended versions of their abstracts to this two-part special issue. The second part contains the following seven articles.

In the article ''Quantitative Analysis of the Dynamics of Maternal Gradients in the early *Drosophila* Embryo,'' authors substantiate the role of active transport in the redistribution of the bcd mRNA by analyzing dynamic models of experimental data. The authors of ''Taming the Duplication-Loss-Coalescence Model with Integer Linear Programming'' apply integer linear programming (ILP) to constrained versions of the duplication-loss-coalescence (DLC) model to find accurate evolutionary histories for large gene families.

In ''SVLR: Genome Structural Variant Detection Using Long Read Sequencing Data,'' the authors propose a novel method to detect three new kinds of structural variants: block replacements, block interchanges, and translocations long sequencing reads. The article ''Fast and Accurate Algorithms for Mapping and Aligning Long Reads'' proposes new k-mer-based mapping and aligning methods for nanopore and single molecular real-time sequencing (SMRT) reads that significantly improve state-of-the-art methods both in quality and runtime.

In ''IsoDA: Isoform-Disease Association Prediction by Multi-omics Data Fusion,'' a multiinstance learning-inspired computational approach is proposed to fuse genomic and transcriptomics data for isoform–disease association prediction. The authors of ''SC1: A Tool for Interactive Web-Based Single Cell RNA-Seq Data Analysis'' present a web-based interactive scRNA-seq data analysis pipeline providing a novel method for informative gene selection as well as methods for cell clustering, differential expression analysis, gene enrichment, visualization, and cell cycle analysis.

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Finally, the article ‘‘Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data’’ proposes a methodology for a simultaneous expectation-maximization–based estimation of enzyme expression, pathway activity level, and enzyme participation level in each pathway, and shows that the majority of pathways strongly correlate with environmental parameters.

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