Preface
Special Issue: 15th International Symposium on Bioinformatics Research and Applications (ISBRA 2019)

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THIS SPECIAL ISSUE INCLUDES a selection of articles presented at the *15th International Symposium on Bioinformatics Research and Applications (ISBRA 2019)*, which was held in Barcelona, Spain, on June 3–6, 2019. 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 2019, 95 extended abstracts were submitted in response to the call for articles, out of which 22 extended abstracts appeared in the ISBRA 2019 proceedings published as volume 11,490 of Springer Verlag's Lecture Notes in Bioinformatics series. Authors of 10 articles were invited to submit extended versions of their abstracts to this special issue. In addition, authors of three articles accepted for a short oral presentation at ISBRA 2019 were also invited to submit full articles to this special issue.

The first two articles are devoted to Boolean models in cells. ''A Robustness Analysis of Dynamic Boolean Models of Cellular Circuits'' studies the robustness of such models using stochastic simulation and integer linear programming and ''Revision of Boolean Models of Regulatory Networks Using Stable State Observations'' finds the set of minimum repairs to make a model consistent with the experimental observations.

Three articles are devoted to evolutionary models. ''Sorting by Genome Rearrangements on both Gene Order and Intergenic Sizes'' give constant-factor approximation algorithms for estimation of evolutionary distance between genomes when various genome rearrangements and indels are allowed. ''Computing a Consensus Phylogeny via Leaf Removal'' efficiently finds an exact and heuristic consensus phylogenetic tree for a given set of trees. ''Evolutionary Switches Structural Transitions via Coarse Grained Models'' proposes a fast method for systematic and extensive exploration of the multistable proteins transition pathways. The article ''Maximum Stacking Base Pairs: Hardness and Approximation by Nonlinear LP-Rounding'' deals with problem RNA secondary structure prediction based on maximization of number of base pairs with parallel and adjacent partners.

Two articles offer speedup for time-consuming bioinformatics problems. ''A Consensus Framework of Distributed Multiple-Tilt Reconstruction in Electron Tomography'' gives a $5.4\times$ speedup and $7\times$ memory reduction compared with the raw multitilt reconstruction in electron tomography. ''Iterative Spaced Seed Hashing: Closing the Gap Between Spaced Seed Hashing and k-mer Hashing'' can compute the hashing values of spaced seeds with a speedup of $6.2\times$ compared with state-of-the-art.

Three articles apply AI methods to classification problems. ''Explainable Deep Learning for Augmentation of sRNA Expression Profiles'' reliably generates tissue and sex annotations for human tissues and cell lines from small RNA-seq expression data. ''Comparative Study Using Neural Networks for 16S Ribosomal Gene Classification'' proposes three different deep learning architectures to classify bacteria at a family, genus, and species. ''PeakPass: Automating ChIP-Seq Blacklist Creation'' improves ChIP-Seq data quality by efficiently classifying regions that frequently produce artifacts and noise in ChIP-Seq experiments.

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The article ''Combining Graph Transformations and Semigroups for Isotopic Labeling Design'' proposes a graph transformation approach for biochemical systems in which individual atoms of molecules can be traced automatically within chemical reaction networks. The article ''Toward a Dynamic Threshold for Quality-Score Distortion in Reference-Based Alignment'' offers a method for lossy distortion of the quality scores to substantially reduce the sequencing read data files while avoiding any impact on read alignment.

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