18th International Symposium on Bioinformatics Research and Applications (ISBRA 2021)

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This special issue includes a selection of papers presented at the 18th International Symposium on Bioinformatics Research and Applications (ISBRA 2022) which was held at the University of Haifa, Israel on November 14-17, 2022. 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 2022, 72 abstracts were submitted in response to the call for papers, out of which 30 extended abstracts appeared in the ISBRA proceedings published as volume 13760 of Springer Verlag's Lecture Notes in Bioinformatics series. Authors of 19 papers were invited to submit extended versions of their abstracts to this 2-part special issue. The first part contains 9 papers.

In “A Clonal Evolution Simulator for Planning Somatic Evolution Studies”, authors present a simulator of a wide range of clonal lineages, variant classes, and sequencing technology choices, intended to provide a platform for effective study design in somatic lineage analysis. The paper “ARGLRR: A Sparse Low-rank Representation Single-cell RNA-sequencing Data Clustering Method Combined with a New Graph Regularization” proposes a practical sparse subspace clustering method to identify cell types. The paper “Reversal and Transposition Distance on Unbalanced Genomes using Intergenic Information” studies the intergenic transposition distance on unbalanced genomes, which also considers insertions and deletions as non-conservative rearrangements in the set of possible rearrangements. The paper “A Gene Correlation Measurement Method for Spatial Transcriptome Data Based on Partitioning and Distribution” proposes to calculate the joint probability density of Gaussian distributions of the gene pair (X, Y) to exclude outliers. In “Multi-View Enhanced Tensor Nuclear Norm and Local Constraint Model for cancer clustering and feature gene selection”, authors improve the flexibility of the tensor nuclear norm and introduce the anisotropic spatial-temporal total variation regularization. The papers “Multi-Granularity Label Prediction Model for Automatic ICD Coding in Clinical Text” and “Automatic ICD coding via Note-Code Interaction Network with Denoising Mechanism” propose code prediction for the International Classification of Disease using learning models, which explicitly train multiple classifiers for different code levels and introduce a denoising mechanism to reduce the influence of noise, respectively. The paper “Identification of Disease-Associated MiRNAs via Locality-Constrained Linear Coding-Based Ensemble Learning” ensembles multi-source biological information and introduces the hypergraph-regular term to establish complex relationships between samples. Authors of the paper “A Graph Representation Approach Based on Light Gradient Boosting Machine for Predicting Drug-Disease Associations” propose a machine learning approach for Drug-Disease Association prediction based on a new heterogeneous network of proteins and feature extraction from network topology and biological knowledge prospectibes.

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