18th International Symposium on Bioinformatics Research and Applications (ISBRA 2022)

Zhipeng Cai[1], Pavel Skums[1], and Alexander Zelikovsky[1]

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 second part contains 9 papers.

In "SWsnn: A Novel Simulator for Spiking Neural Networks", authors present a fast simulator for spiking neural network based on a new Chinese processor, SW26010pro. The paper "HF-DDI: Predicting Drug-Drug Interaction Events Based on Multimodal Hybrid Fusion" proposes a hybrid fusion-based deep learning framework for drug-drug interaction event prediction using various biomedical information about drugs. The paper "Extracting Protein-Protein Interactions Affected by Mutations via Gaussian-enhanced Representation and Contrastive Learning" uses gaussian probability distribution to generate target entity representation based on BioBERT pre-trained model for extracting protein-protein interactions (PPI). The method proposed in "Protein Complex Identification Based on Heterogeneous Protein Information Network" combines Gene Ontology attribute information and PPI data to construct a heterogeneous PPI network, obtains the vector representation of protein nodes and identifies protein complexes. In "BLASTphylo—an Interactive Web Tool for Taxonomic and Phylogenetic Analysis of Genes", authors present a tool that intuitively and interactively visualizes the protein's occurrence in the taxonomy for different taxonomic ranks. The paper "Reconstruction of Viral Variants via Monte Carlo Clustering" applies minimum entropy and minimum Hamming distance Monte Carlo clustering methods to achieve more accurate reconstruction of intrahost viral populations. The paper "DAHNGC: A Graph Convolution Model for Drug-Disease Association Prediction by using Heterogeneous Network" proposes a method to automatically learn the distinctive information of drug and disease nodes and utilizes a bilinear decoder to identify potential drug-disease association. Authors of the paper "An Integration Framework of Secure Multiparty Computation and Deep Neural Network for Improving Drug-Drug Interaction Predictions" leverage the secret sharing technologies to incorporate the drug-related feature data from multiple institutions for predicting drug-drug interactions. The paper "The Reasoning Engine: An SMT-Based Framework for Reasoning About Discrete Biological Models" proposes a framework that utilizes an intermediate language for encoding partially specified discrete dynamical systems, which bridges the gap between domain specific languages and Satisfiability Modulo Theories problem solvers.

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[1] Department of Computer Science, Georgia State University, Atlanta, GA 30303, USA, {zcai, pskums, alexz}@gsu.edu

Address correspondence to:
Professor Alexander Zelikovsky
Department of Computer Science
Georgia State University
Atlanta, GA 30303
USA
E-mail: alexz@gsu.edu