

17th International Symposium on Bioinformatics Research and Applications (ISBRA 2021)

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This special issue includes a selection of papers presented at the 17th International Symposium on Bioinformatics Research and Applications (ISBRA 2021) which was held in Shenzhen, China on November 26-28, 2021. 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 2021, 135 abstracts were submitted in response to the call for papers, out of which 51 extended abstracts appeared in the ISBRA proceedings published as volume 13064 of Springer Verlag's Lecture Notes in Bioinformatics series. Authors of 7 papers were invited to submit extended versions of their abstracts to this special issue.

In “A transfer learning-based classification model for particle pruning cryo-electron microscopy”, authors train and optimize parameters of convolutional neural network for particle pruning cryo-electron microscopy. The paper “Semi-Supervised Cell Detection with Reliable Pseudo-Labels” propose to generate pseudo-labels for unlabeled pathological images and for training which significantly improves detection of cancer cells. In the paper “SuccSPred2.0: a Two-step Model to Predict Succinylation Sites Based on Multi-feature Fusion and Selection Algorithm”, a novel method is developed to predict sites of protein succinylation post-translational modification using dimensionality reduction and maximal information coefficient feature selection. The paper “Detecting and Classifying Nuclei Using Multi-scale Fully Convolutional Network” proposes a novel multi-scale fully convolution network, with dilated convolution for fine-grained nuclei classification and localization in histology images. In “SGFNNs: Signed Graph Filtering-based Neural Networks for Predicting Drug-Drug Interactions”, authors divide the signed graph into two unsigned subgraphs which captures both commonality and difference of drug pairs and use them for the signed graph filtering-based neural networks. The authors of “Dimensionality Reduction of Single-cell RNA-seq Data by Combining Entropy and Denoising AutoEncoder” present a single cell clustering approach based on essential gene selection, maximizing the distribution similarity between input and reconstructed data, and denoising. The paper “Determining significant correlation between pairs of extant characters in a small parsimony framework” identifies pairs of discrete characters that are significantly correlated across all most parsimonious reconstructions, given a set of species on these characters, and an evolutionary tree.

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