

Editorial

Special Issue: Deep Learning and Neuro-Evolution Methods in Biomedicine and Bioinformatics

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Emerging technologies in biomedicine and bioinformatics are generating an increasing amount of complex and heterogeneous data. To tackle the growing complexity associated with emerging and future life science challenges, bioinformatics, and computational biology researchers need to explore, develop, and apply novel computational concepts, methods, tools, and systems.

Recent years have seen the rise of deep learning (DL). Thanks to the advances in terms of hardware, algorithms, and availability of data, DL has been used successfully to address complex problems that would have been impossible to address a few decades ago. Nonetheless, the revolution brought by DL techniques is just in its early infancy, with new contributions and new ideas constantly being proposed and published.

A related approach comes from the field of neuro-evolution, the use of evolutionary algorithms to optimize DL architectures. Neuro-evolution has the potential to achieve better performance with respect to DL-based models, considering that it can optimize the whole architecture, its hyperparameters, and the learning algorithm.

This editorial summarizes the research papers published in the context of the Special Issue (SI) “Deep Learning and Neuro-Evolution Methods in Biomedicine and Bioinformatics”. This Special Issue was led by Mauro Castelli from Universidade NOVA de Lisboa (Portugal). This SI aimed at collecting original research articles that focus on the development and application of new DL architectures for addressing complex problems in the fields of biomedicine and bioinformatics. Five contributions have been received and published in the SI.

In the first contribution “Classification of Photoplethysmographic Signal Quality with Deep Convolution Neural Networks for Accurate Measurement of Cardiac Stroke Volume” [1], the authors propose the use of two-dimensional deep convolution neural networks (DCNN) to classify the quality of photoplethysmographic (PPG) signals when the PPG pulse is used to measure cardiac stroke volume (SV) by impedance cardiography. In particular, an image derived from a PPG pulse and its differential pulse is used as the input to the two DCNN models. The experimental results, obtained by analyzing 3135 PPG pulses, suggest that the proposed DCNN may be applied for the classification of PPG quality and help improve the SV measurement in impedance cardiography.

The second paper, “How Deeply to Fine-Tune a Convolutional Neural Network: A Case Study Using a Histopathology Dataset” [2], deals with a relevant problem related to the fine-tuning of convolutional neural networks (CNNs) in the medical domain. In more detail, while CNNs can improve the image classification domain by eliminating the need to manually select which features to use to classify images, training CNNs from scratch requires very large annotated datasets that are scarce in the medical field. Transfer learning of CNN weights from another large non-medical dataset can help overcome the problem of medical image scarcity. The main questions when using transfer learning are how deeply to fine-tune the network and what difference in generalization that will make. In this study, the authors considered two histopathology datasets and three state-of-the-art architectures to systematically study the effect of block-wise fine-tuning of CNN. Results show that fine-tuning the entire network is not always the best option; especially for shallow networks,



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alternatively fine-tuning the top blocks can save both time and computational power and produce more robust classifiers.

In the third contribution, “A Hybrid End-to-End Approach Integrating Conditional Random Fields into CNNs for Prostate Cancer Detection on MRI” [3], the authors develop a DL architecture for the task of classifying clinically significant prostate cancer (PCa) on non-contrast-enhanced MR images. In particular, they propose the use of Conditional Random Fields as a Recurrent Neural Network (CRF-RNN) to enhance the classification performance of XmasNet, a CNN architecture specifically tailored to the PROSTATEx17 Challenge. The devised approach builds a hybrid end-to-end trainable network, CRF-XmasNet, composed of an initial CNN component performing feature extraction and a CRF-based probabilistic graphical model component for structured prediction, without the need for two separate training procedures. Experimental results show the suitability of this method in terms of classification accuracy and training time, even though the high variability of the observed results must be reduced before transferring the resulting architecture to a clinical environment.

In the fourth contribution, “A Neuronal Morphology Classification Approach Based on Locally Cumulative Connected Deep Neural Networks” [4], Lin and co-authors present a neuronal morphology classification approach based on locally cumulative connected deep neural networks, where 43 geometric features were extracted from two different neuron datasets and applied to classify types of neurons. Subsequently, the effects of different hyperparameters (including mini-batch size, number of intermediate layers, and number of building blocks) on the performance of neuron classification are analyzed. The experimental results showed that the proposed approach is effective for solving complex neuronal morphology classification problems.

Finally, in the fifth contribution, “Performance Evaluation of a Proposed Machine Learning Model for Chronic Disease Datasets Using an Integrated Attribute Evaluator and an Improved Decision Tree Classifier” [5], the authors propose, focusing on chronic diseases, a comparative analysis of the impact of wrapper and filter selection methods on classification performance. The considered filter methods include the Correlation Feature Selection (CFS) method, the Information Gain (IG) method, and the Chi-Square (CS) method. The wrapper methods that have been considered include the Best First Search (BFS) method, the Linear Forward Selection (LFS) method, and the Greedy Step Wise Search (GSS) method. A Decision Tree algorithm has been used as a classifier for this analysis. Based on the experimental results, the authors propose a new hybrid Attribute Evaluator method that effectively integrates enhanced K-Means clustering with the CFS filter method and the BFS wrapper method.

The SI published interesting contributions in the area of DL and neuro-evolution. However, additional efforts and contributions are necessary to further explore these methods and to achieve state-of-the-art performance in the bioinformatics and biomedicine fields.

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