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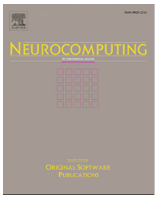

Editorial

# Guest editorial: Deep neural networks for precision medicine

Complex diseases are often classified into many subtypes that may require different treatment regiments. Precision medicine is an emerging approach for disease treatment and prevention that takes into account individual variability of patients. This approach assists medical doctors and technicians in accurate diagnosis, treatment, prevention and prognosis suitable for a particular disease, a specific patient or a group of patients. This is in contrast to traditional approaches in which treatment and prevention strategies are developed for large and heterogeneous populations of patients, with little attention to the differences among individuals.

Advances in high-throughput biotechnologies has resulted in creating massive “omics” datasets (e.g., genomics, proteomics, transcriptomics and metabolomics), medical imaging datasets, clinical datasets, electronic medical records, and others. These data is obtained from patients that have the same disease, and are often heterogeneous, providing unparalleled levels of insightful information that can be used to develop more accurate methods for precision medicine. Moreover, integration of these multi-modal data is seen as a feasible approach to improve accuracy of these methods. However, the development of accurate methods for precision medicine is very challenging, as it requires design of novel and sophisticated computational tools. Recently, deep neural networks have been shown to be very promising as the tools that offer several advantages in this context. They are capable to extracting useful end-to-end data and knowledge representations, benefitting from the availability of very large datasets. Deep neural networks integrate multiple network layers (e.g., convolution, pooling, flattening and fully connected) and/or network blocks (residual, dense, and others) to provide enhanced predictive performance when trained from big and multi-modal data. They have been applied to develop numerous tools for precision medicine that span multiple application areas including processing of omics data, image analysis, and text classification.

This Special Issue presents seven articles related to the analysis and prediction of precision medicine data that relies on deep neural networks. We expect that these articles promote more advanced studies in deep learning for precision medicine.

Magnetic resonance imaging (MRI) is widely used for understanding human brain mechanisms as well as for diagnosis and treatment of brain disorders. Compared with structure MRI (sMRI), functional MRI (fMRI) can capture both time and space resolving information. As such, this technique has gained a lot of attention for studying the brain disorders. Various deep learning models such as convolutional neural networks, recurrent neural network, or a combination of both, have been developed to learn from fMRI data for different tasks. In the review paper “Deep learning for brain disorder diagnosis based on fMRI images”, Yin et al. discussed the basics of deep learning methods and focused on its successful implementations for brain disorder diagnosis based on fMRI images. The review is expected to provide a high-level overview of brain disorder diagnosis with fMRI images from the perspective of deep learning applications.

Autism Spectrum Disorder (ASD) is a pervasive developmental disorder of the central nervous system, which is caused by the stimulation of various environmental and genetic factors. Diagnosing ASD is mainly relied on the patient’s behavioral symptoms, which could be very subjective. Recently, fMRI images have become a very important source of noninvasive data for diagnosing ASD. In the paper ”MAGE: automatic diagnosis of autism spectrum disorders using multi-atlas graph convolutional networks and ensemble learning”, Wang et al. proposed an automatic diagnostic method based on multi-atlas graph convolutional networks and ensemble learning for ASD based on brain fMRI data. Experimental results have shown that their proposed method is effective and promising for automatic diagnosis of ASD in clinical practices.

Besides MRI, Computed Tomography (CT) perfusion imaging is another popular pathological diagnostic tool, which can help the physicians to better interact with the organs of the human body. However, noise in MRI and CT images can degrade the performance of any task-specific methods. In the paper “Denoising of MR and CT images using cascaded multi-supervision convolutional neural networks with progressive training”, Song et al. proposed a cascaded multi-supervision convolutional neural network (CMSNet) for effective denoising, MRI and CT images, which consist of a multi-supervision network (MSNet) and a refinement network. The experimental results on clinic abdominal MR and CT images have shown that their proposed model achieves very high performance in terms of peak signal to noise ratio (PSNR) and global structure similarity index measurement (SSIM).

Immunotherapy has recently become a promising strategy for treatment of brain tumors. However, treatment response to immunotherapy can vary across patient groups. Imaging biomarkers are expected to offer a reliable way to predict this response prior to treatment in a non-invasive fashion. In the paper “Deep radiomic signature with immune cell markers predicts the survival of glioma patients”, Chaddad et al. used 3D-CNN to extract deep radiomic features (DRFs) from four MRI sequences (T1-weighted, T1-weighted post-contrast, T2-weighted and Fluid-Attenuated-Inversion-Recovery (FLAIR)) of brain images, and combined with the corresponding 22 immune cell markers of 151 patients with brain tumors to predict treatment response in patients with brain

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tumors. Their experimental results have demonstrated that DRFs extracted from MRI scans may be used effectively as a non-invasive biomarker for predicting treatment response in patients with brain tumors.

The International Classification of Diseases (ICD) is developed by the World Health Organization for systematically classifying diseases worldwide. ICD coding plays an important role in hospital statistics, prognosis, precision medicine and medical insurance reimbursement. In the paper "KAICD: A knowledge attention-based deep learning framework for automatic ICD coding", Wu et al. proposed a knowledge attention-based deep learning framework called KAICD for automatic ICD coding by making full use of the clinic notes and the ICD titles. Their experimental results have showed that KAICD can improve the accuracy of automatic ICD coding, compared to competing methods. The ablation experiments have showed that the features of clinical notes extracted by a multi-scale CNN play a key role in their model, while the features of ICD titles learned by attention-based Bi-GRU enhance the feature expression and improve the performance of the method.

Long non-coding RNAs (lncRNAs) have been found to play important roles in many physiological and pathological processes. The lncRNA-disease association prediction not only helps understanding of biological processes, but also provides new strategies for diagnosis, treatment, and prognosis of complex diseases. In the paper "GANLDA: Graph attention network for lncRNA-disease associations prediction", Lan et al. proposed an end-to-end computational model based on graph attention network (GANLDA) for predicting associations between lncRNAs and diseases. The results of computational experiments have showed that GANLDA outperforms other state-of-the-art methods in prediction of lncRNA-disease association. Furthermore, case studies have demonstrated that GANLDA is an effective method to infer potential lncRNA- disease associations.

DNA N6-methyladenine ($m^6A$) is the most prevalent epigenetic modification in prokaryotes and is related to the control of various DNA processes. In the paper "A convolutional neural network using dinucleotide one-hot encoder for DNA N6-methyladenine sites in the rice genome", Lv et al. developed a new protocol, iRicem6A-CNN, for identifying m6A sites in the rice genome with dinucleotide one-hot encoding to generate input tensors for predictions by convolutional neutral networks. Their analysis has showed that iRicem6A-CNN is capable of not only accurately predicting m6A-positive samples but also reducing the error rate of negative sample identification. Moreover, a user-friendly webserver for iRicem6A-CNN has been made available. Although their experiments were performed with human genome, the proposed model is expected to become a useful tool for computationally discerning m6A sites, which have been demonstrated to play an import role in human diseases.

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## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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