
Editorial

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Biographical notes: Deepak Gupta is an Assistant Professor in the Department of Computer Science and Engineering of Motilal Nehru National Institute of Technology Allahabad, Prayagraj, India. Previously he has worked in the Department of Computer Science and Engineering of National Institute of Technology Arunachal Pradesh. He received his PhD in Computer Science and Engineering from the Jawaharlal Nehru University, New Delhi, India. His research interests include support vector machines, ELM, RVFL, KRR, and other machine-learning techniques. He has published over 75 referred journal and conference papers of international repute.

Jian Cao is currently a Tenured Professor with the Department of Computer Science and Engineering, Shanghai Jiao Tong University. He is also the Director of research institute of network computing and service computing. His research interests include intelligent data analytics, service computing, collaborative computing and software engineering. Besides national and provincial government research grants, his research is also supported by many industry partners. He has published more than 300 research papers in prestigious journals and conferences. He has won ten ministerial or provincial level scientific and technological achievements rewards. Currently, he is a distinguished member of CCF.

Elham Bagheri is a Post-doctoral Fellow at the Vector Institute in Toronto working with Yalda Mohsenzadeh. She completed her Doctoral degree at the Nanyang Technological University in Singapore. Her research within AI is broad and interdisciplinary, with a particular emphasis on machine learning techniques for healthcare. Presently, her work revolves around deep learning techniques, image memorability research, computer vision, and crafting AI-driven biomedical solutions using images, signals, and hospital data. Please visit her Google Scholar page for her list of publications. She welcomes potential collaborations and invites anyone interested to connect with her.

Mukesh Prasad is a Senior Lecturer at the School of Computer Science in the Faculty of Engineering and IT at UTS who has made substantial contributions to the fields of machine learning, artificial intelligence and the internet of things. His research interests include also big data, computer vision, brain computer interface, and evolutionary computation. He is working also in the evolving and increasingly important field of image processing, data analytics and edge computing, which promise to pave the way for the evolution of new applications and services in the areas of healthcare, biomedical, agriculture, smart cities, education, marketing and finance. His research has appeared in numerous prestigious journals, including *IEEE/ACM Transactions*, and at conferences, and he has written more than 120 research papers.

1 Introduction

Healthcare and biomedical sciences have become data-intensive fields, with a strong need for sophisticated data mining methods to extract knowledge from the available information. For example, data analysis methods are applied to biomedical datasets, namely DNA microarray data or Next Gen sequencing data to predict treatment outcomes of paediatric acute lymphoblastic leukaemia patients. Moreover, clustering methods are routinely used to investigate the interpretation of the correlated genes associated with cellular and biological functions.

Biomedical data contains several challenges in data analysis, including high dimensionality, class imbalance, and low numbers of samples. Although the current research in this field has shown promising results, several research issues need to be explored as follows. There is a need to explore feature selection methods to select stable sets of genes to improve predictive performance along with interpretation. There is also a need to explore big data in biomedical and healthcare research. An increasing flood of data characterises human health care and biomedical research. Healthcare data are available in different formats, including numeric, textual reports, signals, and images, and the data are available from different sources. An interesting aspect is to integrate different data sources in the data analysis process which requires exploiting the existing domain knowledge from available sources. The data sources can be ontologies, annotation repositories, and domain experts' reports.

This special issue intends to prompt the current research progress on machine learning, artificial intelligence, and data analysis for biomedical and healthcare applications. Special attention has been devoted to handling feature selection, class imbalance, and data fusion in biomedical and healthcare applications. To achieve the goal of this special issue, the guest editors have comprehensively evaluated the originality, technical novelties, presentation quality, and relevance of all the submitted papers.

Through a rigorous and careful review process, six high-quality papers have been selected for publication. Overall, these six papers provide emerging computational intelligence techniques for biomedical data and imaging. A brief summary of each paper is introduced below.

Classification of brain haemorrhage is a challenging task and needs to be solved to help advance medical treatment. Recently, it has been observed that efficient deep-learning architectures have been developed to detect such bleeding accurately. The proposed system includes two different transfer learning strategies to train and fine-tune ImageNet pre-trained state-of-the-art architecture such as VGG 16, Inception V3, and DenseNet121. The evaluation metrics have been calculated based on the performance analysis of the employed networks. Experimental results show that the modified fine-tuned Inception V3 performs well and achieves the highest test accuracy.

The liver is a key organ in the human body that aids in the digestion of food, the elimination of toxins, and the storage of energy. Patients with liver disorders are on the rise all over the world. However, because the disorder's symptoms are unclear, it is difficult to diagnose it, which raises the disease's death rate. The study introduces novel fuzzy twin models for liver disease classification. In the first model, the membership is calculated based on the quadratic function called fuzzy twin kernel ridge regression-quadratic (FTKRR-Q). In the second model, we have calculated the fuzzy membership based on the centroid and named the model as fuzzy twin kernel ridge regression-centroid (FTKRR-C). For our research, the BUPA or liver disease dataset has been used from the UCI machine learning repository. Experimental results are compared with the twin support vector machine, kernel ridge regression classifier and twin kernel ridge regression classifier. The accuracy, sensitivity, F1-score, and Mathew's correlation coefficient are used to evaluate the suggested model's performance. Experiments are also carried out on some real-world benchmark datasets. The results reveal the applicability of the proposed models.

Anomaly detection is a crucial step in any diagnostic procedure. With the advent of continuous monitoring devices, it is inevitable to use technological assistance for the same. Many methods, including autoencoders, have been proposed for anomaly detection in time series ECG data. The attention mechanism dynamically highlights the relevant portion of the input data and provides the decoder with the information from every encoder hidden state in its temporal vicinity. This work proposes a performance enhancement of autoencoders in identifying an ECG anomaly with the help of attention. A comparison of different autoencoder models, LSTM and hybrid, with and without attention to detect an anomaly, is proposed in this work. The comparison of the different models in terms of precision, recall, F1-score, false-positive rate (FPR), false-negative rate (FNR) and area under the ROC curve (AUC) are specified. The obtained results indicate that attention helps to enhance the autoencoder's performance.

We analyse the most obvious distributed writing in Facial emotion recognition conveyed throughout the last decade in this paper. This paper assesses the analysis of the work done as such far and tries to assess each based on a set of composite parameters. Also, under the equivalent, bearing is looking for future work based on new specialisation regions and identifying research gaps. There is a project underway to determine the optimum procedure that could be employed to meet all of the established constraints. Furthermore, a heading is expected for work ahead on new stronghold locations below the same. The magnitude of such labour cannot be undervalued,

especially for the injured and the more prepared, where outer appearance may continue to play an important role in conveying thoughts in a robotic manner. Furthermore, there are numerous other beneficial applications that cover a wide variety of our daily lives.

Most of the diseases are diagnosed from the image data like CT scans, MRIs, and X-rays. Gene data carries vital information related to the diseases that needs to be analysed for diagnosis. Both the logics are combined and a flexible deep ensemble learning-based model is proposed for the classification of images generated from one-dimensional data. Earlier works in the detection of brain tumours and epileptic seizures have been developed either directly providing one-dimensional data or images to the classification model, whereas the proposed method utilises the effectiveness of two-dimensional convolutional neural networks to analyse one-dimensional data like gene expressions and EEG signals after effective conversion to images. The data conversion is performed using three data reduction techniques, i.e., locally linearly embedding, multi-dimensional scaling, and t-distributed stochastic neighbour embedding with convex hull algorithm to wrap all the data points. Multilayer perceptron is used for second-stage training. The proposed method is verified using brain tumour gene data collected from the Genomic Data Commons (GDC) data portal and the EEG data for epileptic seizures detection provided by the University of Bonn (UoB dataset) and provided 97.38% and 97.33% accuracies respectively.

The deadly respiratory disease corona virus-2 (COVID-19) which was declared a pandemic by the World Health Organization (WHO) has resulted in over a million death around the world within less than a year. With the rapid spread of the virus, the currently adopted COVID-19 test by the WHO is the reverse transcription polymerase chain reaction (RT-PCR) test, which is expensive, time-consuming and not accessed by underdeveloped countries. Computed tomography (CT) scan images that were used in profiling suspected COVID-19 patients can serve as an alternative to the RT-PCR test method. In this study, two different pre-trained deep learning models ResNet-50 and ResNet-101 were trained to classify positive COVID-19 scan images. The best model which was trained on the augmented CT scan images achieved an accuracy of 98.3%, a sensitivity of 0.984, specificity of 0.983.