Healthcare Analytics xxx (xxxx) xxx

Contents lists available at ScienceDirect

Healthcare Analytics

journal homepage: www.elsevier.com/locate/health

e-Health and artificial intelligence: Emerging trends, models, and applications

Artificial intelligence (AI) and machine learning (ML) have evolved remarkably in the past decade and are expected to develop further with the introduction of new algorithms. The increase in clinical data is also changing rapidly with the developments in sensors and the Internet of Things (IoT). Analyzing these increasing clinical data is essential and critical in healthcare management. The medical service industries are also looking for technological advancement and expansion of programming environments to achieve further advances through e-health, portable applications, and wearable gadgets. The guided system, AI, ML, and speedy information transmission have improved medical care and quality of life. AI of Things (AIoT) can also enhance and improve well-being.

This special issue aimed to gather innovative new approaches and proposals related to e-health models, applications, and emerging trends. This special issue has published five state-of-the-art articles among many submitted papers through a rigorous review.

The first article by Sutradhar et al. considers service quality improvement in e-health systems. The authors proposed the fruit fly optimization algorithm to achieve the near-best quality service. The best part of this article is that the proposed algorithm handles a considerable amount of medical data in an encrypted format. Still, when the user wants to access the data, it will be decrypted and available. In this article, the fruit fly optimization algorithm encrypts a large amount of medical data.

The second article by Shastry introduces a prediction method for Parkinson's disease. The author has gone through extensive literature reviews and proposed a novel algorithm. Even though much literature and proposals are available for the detection or prediction of Parkinson's disease, this proposed predictive algorithm has many innovative aspects. With multiple feature selection techniques, the author shows this algorithm outperforms several recently proposed methods.

In the third paper, Ghosh et al. propose a transfer learning-based AI system to classify breast cancer from histopathological images. Three different deep convolutional neural networks (DCNN) architectures, namely, the Visual Geometry Group-16 (VGG-16), Depthwise Separable Convolutions (Xception), and Dense Convolutional Network-201 (Densenet-201) have been used as the base model in this transfer learning method. After extracting the features from each test image using the three pre-trained base models, each test image was classified into benign or malignant classes. The proposed classification system is independent of the magnification factors of the images. The performance of the proposed breast cancer classification system has been evaluated on two widely used public datasets known as the Invasive Ductal Carcinoma (IDC) dataset and the BreaKHis dataset. The classification accuracies of 99.42% (IDC dataset) and 99.12% (BreaKHis dataset) have been obtained from the proposed system. The results demonstrate that the proposed breast cancer classification system outperforms the state-of-the-art methods in this research domain.

In the fourth paper, Hasan et al. develop an Alzheimer's disease image segmentation method. They explain that the neurological problems of these diseases can only be treated effectively when the structure and function of neurons are understood. The proposed algorithm is influenced by convolutional neural networks (CNNs) and graph attention networks (GATs) for segmenting biomedical images. The authors used the dataset composed of 606 microscopic images. Output of the proposed U-GAT algorithm, they obtained the highest accuracy of 86.5% and an F1 score of 0.719 compared to the CNN, U-Net, SegResNet, SegNet VGG16, and GAT benchmarking algorithms. We believe that the proposed method could help researchers in the biotech industry.

Baihaqi et al. in the fifth article, propose an exciting technique for predicting COVID-19 variants using a multivariate data-driven deep-learning model. Deep learning and long short-term memory (LSTM) have been used to predict disease progress with reasonable accuracy and minor errors. The authors show they obtained results by testing hidden sizes 25, 50, 75, and 100. The RNN model provided better results, with a minimum Mean Squared Error (MSE) value of 0.01 and a Root Mean Square Error (RMSE) value of 0.012 for B.1.427/B.1.429 variant with a hidden size of 100. Further testing layer sizes 2, 3, 4, and 5 shows in this model that the BiLSTM model provided better results, with a minimum MSE value of 0.01 and an RMSE of 0.01 for the B.1.427/B.1.429 variant with a hidden size of 100 and layer size of 2. This approach may open new predictive analytics opportunities in research on COVID-19 variants.

We extend our thanks to all authors and reviewers who contributed to the success of this special issue collection. We enjoyed working with Professor Dr. Madjid Tavana, Editor-in-Chief of the Healthcare Analytics Journal. Dr. Madjid extended his classical support and guidance to complete this special issue collection.

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https://doi.org/10.1016/j.health.2024.100354

Available online 28 June 2024