An Artificial Intelligence-Based Platform for Medical Diagnosis

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KEYWORDS

Artificial Intelligence; Back propagation; Classification; Convolutional Medical Diagnosis; Neural Networks; and Optimization

ABSTRACT

Medical diagnosis using artificial intelligence models uses methods of information collection via the Internet of Things (IoT) for the categorization of diseases. This may be attributed to a number different issues, such as inefficient auxiliary frameworks, high expenses associated with acquiring datasets, or difficulties encountered while constructing classifiers. The present paper analyses the recent developments in AI for medical diagnosis. The research uses a Deep Convolutional Neural Network (DCNN) to categorise medical conditions. In this paper, a model for categorising medical diagnosis has been introduced by making it easier for the network to adapt to new medical data. This article estimates the degree to which the classification falls into the right medical diagnosis category and separates the training sample into normal, critical, and suggestion samples using a dynamic threshold to solve the diagnostic issue. The recommended strategy categorises input to help the convolutional neural network learn more. This research modifies the convolutional neural network design to accommodate for input variety and data evolution temporal dynamics. This adjustment is made with the goal of achieving the five physiological data properties of bio signals (heart rate, blood pressure, EEG, ECG, and oxygen level). Because of the realised CNN optimisation algorithm model, the prediction effect has been increased, and the accuracy rate has been found to be 92.8% in medical diagnosis, which is a reasonably good performance in machine learning algorithms.

1. Introduction

Rapid advancements are being made in artificial intelligence-assisted diagnostic systems, but medical professionals will still be needed as limited people are familiar with artificial intelligence-assisted diagnostic tools at the moment [1]. Application development for artificial intelligence medical assistant diagnostic systems may be facilitated by gaining an understanding of how to facilitate the acceptance and utilisation of expert medical diagnosis by use of AI medical assistants. Artificial intelligence (AI) is being more widely applied in traditional sectors as the technology develops. Potential applications of artificial intelligence in healthcare include patient records, illness prevention, and medical diagnosis and treatment [2]. As a "smart medical assistant" based on AI principles, the artificial intelligence-assisted diagnostic system [3] might potentially help in the processes of diagnosis and decision-making, including localization of the affected region, screening for diseases, and the selection of an appropriate therapy. A well-trained AI-assisted system may be as competent as human professionals when it comes to making diagnoses. AI medical auxiliary diagnostic systems are still in the early stages of development, although progress is being made. The absence of standardised data and the immaturity of related technologies are an issue since they make it harder to put the system into place. The lives of patients rely on doctors making correct diagnosis. It is challenging for artificial intelligence medical auxiliary diagnostic systems to earn the confidence of medical professionals before they can be used in actual work with certainty [4, 5]. Doctors to accept and utilise an AI medical diagnostic system is a major challenge that has to be overcome to expand the field's use. AI-assisted diagnostics haven't advanced significantly [6]. User satisfaction with AI-based supplemental diagnostics is crucial [7-9].

In specifically, the following points sum up the technical contributions of the article. The physiology of bio signals data is presented and Deep Convolutional Neural Networks (DCNN) is used for these data collection methods to put to use. The accuracy of this the framework has been analysed in the results section. Next, error back propagation algorithm is detailed for the DCNN, both of which are critical to the success of the learning algorithm which is created on the basis of the complexity of medical diagnosis. It is important to improve the convolutional neural network's learning process and provided a framework for determining whether a sample is dangerous or not, taking into account the complexity of the medical diagnosis at hand. Finally, a convolutional neural network algorithm is trained on five distinct physiological characteristic data to predict medical interpretation for people with diseases. The experiment's efficacy is measured using three parameters: sensitivity, specificity, and accuracy. The accuracy rate of 92.8% is now achievable after employing CNN optimised algorithm model.

2. Literature Review

The process of making a medical diagnosis has been drastically altered by the advent of AI. Diseases may now be quickly and accurately diagnosed by medical experts thanks to the use of machine learning algorithms. A number of individuals remain sceptical about the efficacy of AI-based platforms used for medical diagnosis, and this has led to ongoing discussions regarding their usage. The ability to analyse patient data rapidly and deliver correct diagnoses in real time is a major benefit of AI-based medical diagnosis. As a result, doctors and nurses will have more time to focus on the most challenging patients. Rare or complicated disorders that are difficult for human physicians to diagnose may potentially benefit from AI-based diagnostic tools. However, there are several limitations to AI-based medical diagnostic systems. Some medical professionals worry that these diagnostic tools may provide false positives or overlook critical information about a patient's health. This is due to the fact that AI diagnostic systems are now limited in their ability to accurately diagnose patients since they can only analyse data patterns and ignore the patients' subjective accounts of their symptoms. The possibility of bias inside AI-based diagnostic systems is another important issue of concern. These systems may perpetuate mistakes or contribute to incorrect diagnoses since they are trained on data sets that may be insufficient or biassed itself. Using an AI-powered platform to make medical diagnoses might dramatically improve patient care. To avoid negatively impacting patient outcomes, however, this technology must be used with prudence and its accuracy, dependability, and bias must be constantly monitored and evaluated.

Medical information technology use increases as healthcare delivery improves [10]. Technology adoption behaviour theories have been used by several scholars to study adopter factors [11-13]. An adoption model was created using the theories of technology adoption and integration, including technology anxiety and resistance to change, to determine the most important factors affecting geriatric mobile health service acceptance [14]. This research examines how service features impact consumers' desire to utilise and uptake of mobile health technologies [15-17].

More data can be analysed, more links can be mined between different forms of data, and the model's influence can be increased with less effort utilising multi-modal data analysis [18]. The advantages of multi-modal data analysis [19] have led to its widespread adoption by researchers in the area of complementary diagnosis and decision-making. Research in the medical industry may be simplified into three categories based on the people's propensity to embrace new technology [21]. People who need care (patients), people who provide care (doctors, nurses, etc.), and the places where care is given (hospitals, clinics, etc.) make up the medical community. As more people make use of the system, the factors that affect its uptake are certain to change [22]. Experts in the field developed an evolutionary game model to examine the effects of different doctor and patient strategies when receiving medical care from specialists in tertiary hospitals via telemedicine [23]. Innovations in the AI have given the healthcare sector a new lease of life.

Artificial intelligence (AI) and deep learning are now two of the most talked-about methods for tackling difficult problems [9, 13]. These techniques have brought about a change in the emphasis placed on some aspects of medical examination, such as the detection of X-rays and the interpretation of electroencephalography (EEG) and electrocardiography (ECG) readings. The effectiveness of cutting-edge hacking findings, on the other hand, has been hampered by the restricted availability of databases as a result of issues in information gathering and marking [14]. Despite the fact that there have been some significant research on the topic of disease prediction employing need to be expanded upon [24-26]. The following are significant enhancements that we've made to the current corpus of study that we've conducted.

It has been proposed that a deep convolutional neural network (DCNN) with several layers be used in order to classify the diagnosis in three classes i.e. Critical, Normal and Recommendation. The Deep Convolutional Neural Network (DCNN) learns EEG, ECG, BP, HR and OL data. A database consisting of 60 patients was obtained from an online repository [27], and it was utilised in a study that was identical to it in order to evaluate the accuracy of the model.

3. The Physiological Data Assessment

The evaluation from qualified specialists, together with the use of hand-carried electronic sensors and polls, was utilised to collect data pertaining to vital indicators of the participants i.e. EEG, ECG, BP, HR and OL data. The time series features were recorded and saved using the microphone on the mobile device, and the quality of the tape recording was preserved by the use of sampling frequency and 192 kbps data rate. The following short-term properties of the sound signal obtained by the electronic sensors were computed [28] using the python package known as pyAudioAnalysis. Figure 1 shows the methodology for medical diagnosis.

4. Proposed Model for Medical Diagnosis

Deep convolutional neural networks (CNNs) used for deep learning rely heavily on activation maps. CNNs produce activation maps, which are representations of the features discovered in the input data, by filtering the input data. For a given output or classification, activation maps highlight the input regions that are crucial. In order to better understand CNN predictions, activation maps may be used to pinpoint regions of input that are responsible for a certain categorization. Let is assume that $a[i]$ denotes the activation map of the $i-th$ hidden neural network layer, also known as the feature map. Kernel and bias for the ith hidden layer are denoted by the variables $W[i]$ and $b[i]$, respectively. $x(i)$ represents the input data for the $i-th$ training example. Assuming that this hidden layer of the neural network is fully connected (FC), the notation $a[l]\ i$ is used to denote the ith entry of the activations in the layer l of the neural network. The height, breadth, and number of channels (depth) of a particular hidden neural network layer are denoted by the notations nH, nB, and nC, respectively. These notations can be used interchangeably. $nHprev$, $nBprev$, and $nCprev$ are the height, breadth, and channel count of the hidden layer preceding it.

4.1 Deep Convolutional Neural Networks (DCNN)

Deep CNNs generate feature maps that mirror input image features. CNNs have convolutional, pooling, and fully connected layers. CNN convolutional layers filter data to highlight found characteristics. The feature map is calculated by sliding the filter across the input and adding element-wise products. A convolutional layer's output feature map is a matrix of filter activations at input locations. The value of each feature map element provides the filter's response to a tiny portion of the input. Thus, filters identify visual properties like borders, corners, and colours. Before being fed into fully connected layers for classification or regression, convolutional layer feature maps are downsampled by pooling layers. CNN output feature maps help visualise learnt information and understand how the network predicts. Visualisation and activation maps may reveal crucial input areas that match output attributes.

DCNNs are nonlinear functions that translate the input characteristics of diseases. These functions are used to diagnose patient conditions. In the forward pass, input features undergo three convolutional operations, a dense layer, and an output softmax layer. A single convolution operation on the input shape or data yields the following feature map dimensions:

$$nH = \left\lfloor \frac{nHprev - f + 3 \times pad}{stride} \right\rfloor + 1$$

$$nB = \left\lfloor \frac{nBprev - f + 3 \times pad}{stride} \right\rfloor + 1$$

$$nC = Number\ of\ filters\ used$$

nC denotes count of filters, also known as kernel maps, that were used in the convolution process for layer. Backpropagation was used in order to train the layer parameters known as $W[i]$ and $b[i]$.

4.2 The Network Structure

CNN has several versions. AlexNet, VGGNet, GoogleNet, and ResNet are CNN models developed from the widespread use of convolutional neural networks. All models have the same input, entirely connected, fully convolutional, pooling, and output layers. Each convolutional layer has several identical convolution kernels and is connected immediately after the input or pooling layer. Insert the image in the input or pooling layer with the same size and convolution kernel to extract it. The convolution kernel retrieves abstract and diverse features than the neural network's first convolutional layer. Every neural network's convolutional operator is visualised. Best value: 3x3 convolution kernel. Matrix multiplications begin at the upper left corner of the 5x5 input graphic. Then, the kernel's intricate structure may travel left-to-right or right-to-bottom on the surface. Grid sliding causes convolution as the stride is 1. The current layer's non-linear activation convolution kernel matches the feature map's to analyse the picture and learn its hidden non-linear properties more effectively. The whole of the procedure for processing images via the convolutional layer, it is possible to demonstrate in using $a[i] = f\left[\lim_{n\to\infty}\sum_{l=1}^{k} W(i,l-1)b(i,l-1)\right]$. Among them, $a[i]$ denotes the activation map function, while $x(j,l)$ stands for input the representation. l denotes the layer of the network. The pooling layer maps picture-retrieved features on feature maps. This reduces aircraft range. This makes lowering network parameters simpler and lessens the network's susceptibility to image rotation, scaling, and other distortions.

The two-dimensional feature that was acquired is converted by the network map into a vector that is just one dimension and then sends it to the layer that is completely linked. The framework of the completely interconnected layer is analogous to the neural network's hidden layer in its classic form network, and the approach of completely linked nodes is put into operation between layers. This layer's primary purpose is to put the information that was learned information that is distinctive and the fulfilment of the role of medical diagnosis. For the most part, the output layer is used in the medical diagnosis work with the purpose of obtaining the opportunity for the input picture to be split into multiple categories, with the most plausible category serving as the one to focus on medical diagnosis outcome. The number of layers and categories matches the number of neurons. The second medical diagnosis may simply customise the number of neurons impacted to one, allowing the network output to be $y[i] = Activation\_Function\left(\prod_{i=1}^{k} B[i].x[i-1] + C[i]\right)$. Sigmoid/ReLU or Tanh activation function transformation yields the network's output value, y, in the interval (0, 1). During this, $y[i]$ will indicate the chance that the image is from the provided category and the class of fortunate results. If y is larger than 0.5, the input image is positive; otherwise, it is negative.

4.3 Minimizing Cross-Entropy Loss

Cross-entropy loss function reduces output error in deep convolutional neural networks (CNNs). The cross-entropy loss function evaluates predicted probabilities. The cross-entropy loss function helps classification jobs that produce a vector of probabilities for each class. Deep CNNs' final layer cross-entropy loss function compares projected probabilities to input data labels. CNNs adjust model parameters to reduce output error by minimising cross-entropy function. Backpropagation reduces loss by modifying weights using loss gradients. CNN classification relies on cross-entropy loss function minimization. It enhances network prediction. Cross-entropy loss function reduces overfitting and enhances deep CNN generalisation.

The cross-entropy loss function ($Loss_{CE}$) can be written as, $Loss_{CE} = -\frac{1}{n-1}\prod_{i=1}^{k-1}\ln(y(i-1).T_{i-1}^{T})$. Among them, n denotes the total number of samples that were taken. The standard loss function samples may be used to calculate the error in each result, and their weights match. However, only network-critical signals are employed during network training. These samples are prone to medical investigation errors, therefore the network is needed more for samples that are true but not correct. The understanding of many examples of medical investigation, mistakes in medical research, as well as examples of research those are proper but not great degree of accuracy during the course of training need improvement. In most cases, the threshold for medical investigation is established at 0.5, and 0 and 1 represent the goal values for the negative and positive kinds, respectively. In the event that the sample's actual output value is less than 0.5, then it is considered to be of the negative type. There is a possibility of a negative sample over the course of the training. Despite the fact that it might be right its actual output value, might be getting closer to a medical diagnosis threshold of 0.5 as opposed to the desired value of 0.

4.4 Classification of Medical Diagnosis: The Three Classes

In order to determine which samples need more thorough examination and separate them. Nevertheless, picking the right level for the threshold is quite critical. The distribution of the samples in the graph is directly influenced by its value similar to this category. If the value of the threshold is set to be too high, it's possible that none of the samples will pass deemed to be harmful samples; if the value of the threshold is set to be too low, samples may not even be examined. These are the circumstances, prevent the network from concentrating on samples of low quality and consultation with a doctor, which is the same thing as an everyday techniques for training a network. The determination of the threshold is a difficult and intricate process.

In an effort to combat the issue of how difficult it is to get threshold in the condense of medical study, concluded that a dynamic threshold $(\mathcal{T})$was developed in order to permit samples of the same sort that can undergo dynamic division. The shape that the dynamic takes is written as, $\mathcal{T} = \left|\frac{1}{k-1}\left|\sum_{i=0}^{k-1} y[i]\right| - T_{i-1}\right|^{-1}$. If the results of the medical investigation confirm the sample if lower than the dynamic threshold $\mathcal{T}$, one might say that the sample is below the dynamic threshold have a low level of confidence, which means that the sample might be harmful sample. The dynamic threshold $\mathcal{T}$ is calculated during network training regularly and is readjusted according to the constantly changing mean of the actual outcome of the sample, which makes up the value of the sample's classification of potentially hazardous samples with less risky ones in comparable examples that are more malleable and realistic. The split in opinion of samples that are comparable may be represented in a more straight forward manner. In the a second round of medical diagnosis, the distribution of samples expressing the diagnosis category as

$$Diagnosis_i = \left\{ \begin{matrix} Critical, & T_{i-1}.(y[i] - \mathcal{T}) > 0 \\ Normal, & T_{i-1}.(y[i] - \mathcal{T}) \leq 0 \\ Recommendation, & x[i] \rightarrow y[i] \end{matrix} \right\}$$

The presence of the ith potentially critical diagnosed sample in the critical class indicates that the actual output of it, denoted by $y[i]$, is higher than the mean value of the actual output of each and every sample belonging to the negative class. The fact that the $j - th$ normal sample is in the negative class indicates that its real j is a smaller value than the output value $y[j]$.

4.6 The Optimisation Framework

In order to improve the network's ability to learn about potentially harmful samples, this research suggests increasing the influence of by using a combination of potentially hazardous samples that have been uploaded to the network weight update by properly a rise in the error rate and loss function. The value of the abnormal samples is equivalent to the category that they fall within. In the learning algorithm that was devised, the difficulty of progression of the learning algorithm that takes into account the complexity of the medical investigation based on the results of a medical diagnosis.

After training, the probability distribution of the network is continuously subject to change as well as the possibility of the output probability distribution being adjusted to be essentially consistent with the likelihood that was predicted of them. Not until the distribution has been samples that are difficult to categorise continue to move closer and closer to the change in the probability distribution according to the group that they belong to is deeper and more significant. Since this is the case, it is essential to various samples should be handled differently depending on their classification.

Due to the observed singularity of the activation function; specifically in the ReLU activation function, it is often easy to create a network topology with few nodes, which serves as a reminder that additional focus is needed for the network's settings to extract information from training samples.

The technology that underpins the internet of things, especially in the case of samples that are difficult to classify. The BP algorithm is a standard learning method for convolutional neural networks. It modifies the network's weights and thresholds so that they are more accurately reflective of the accuracy of the training set. BP processes all dataset samples. When computing the error, the training set is treated in the same way every time, which does not assist with learning from examples that are difficult to classify. Therefore, it is suggested to use learning strategy for convolutional neural networks that takes into consideration the difficulty of categorising data in order to boost the impact of these samples on the network parameter adjustment. Convolutional neural networks use a multi-layer feedforward network to understand the visual and aural data that they receive as input. Noise is filtered out and features are selected via convolutional neural networks.

The automated extraction of features paired with the process of learning medical diagnosis is mostly based on the convolution kernel with shared weights. This helps to more accurately depict the underlying relationship between the data and makes it possible to conduct extensive analysis.

2. Result and Discussion

In order to use the strategy that was recommended, the data set is divided into three sections: a training set, a test set, and a validation set in the proportions 8:1:1, respectively. The performance results for the testing, training, and validation data are provided in Table 1-1 through Table 1-3, respectively, under the titles "Critical," "Normal," and "Recommendation." Table 1-1 shows the results of the testing. Table 1-3 shows the training. Table 1-3 shows the validation data. The neural network will gain information with the help of the training set, the accuracy of the network's predictions will be assessed with the help of the test set, and the configuration of the validation set will hopefully prevent CNN over-fitting by means of its use. As can be seen in Figure 2-4, which illustrates the accuracy curves between the training set, the test set, and the validation set, each and every one of the training samples was utilised as input to CNN. The number of epochs at which these inputs were used can be seen in the figure.

In order to evaluate how well the strategy works, the model looks at how the performance of the proposed approach shifts depending on the activation functions and choose Sigmoid, tanh, and ReLU, specifically. Both the tanh function and the Sigmoid function are examples of functions that get saturated during their application; the tanh function is the deformation of the Sigmoid function. Figure 5 indicates that the Sigmoid tanh ReLU acquires an accuracy rate that does not go over the threshold of 87%, even if the accuracy rates of the two components, Sigmoid and tanh, do not go above this level. This is the case despite the fact that the Sigmoid and tanh accuracy rates do not go above this level. When compared to the other two saturated activation functions, for example, the use of ReLU leads in an improvement in the overall accuracy of the approach to around 88% of the time. This improvement was brought about as a direct consequence of an increase in the accuracy of the method.

During the process of training the model, eliminate a portion of the training data, and then utilise the data that is still available after processing it as a test set. This helps to limit the influence that the training data has on the validity of the model that is built, which is a significant benefit. During the training of the network, one phase that is of the utmost importance is the one in which the weights of the model are first set. However, having appropriate values might speed up convergence and increase the possibility of finding an optimal solution. If the starting parameters are not acceptable, training may take longer, and there may be difficulties with the way gradients are propagated. In this article, the performance of the model is evaluated by applying four different strategies to the process of initialising the parameters. Figure 6 is an illustration of the degree of accuracy achieved by the categorization of the three distinct groups.

Following the completion of the traversal of the data contained inside a batch, the gradient of each parameter is computed in order to update the gradient, and the procedure is then repeated until all batches have been processed. Figure 6 presents a comparison of the accuracy of the model optimisation approach under a variety of different batch sizes. When the batch size is too small, the level of accuracy is poor because there is an excessive amount of unpredictability and there is not enough training depth. This may be seen. Within reasonable bounds, the precision of the findings will increase proportionally with the size of the batch. However, if a given threshold is crossed, the number of repeats required to run the whole dataset decreases, which ultimately leads to a slower rate of parameter adjustment. As can be seen in figure 6, the model with a batch size of 51 is the one that achieves the highest level of accuracy.

The DCNN optimisation algorithm model is the one that this research recommends using since it achieves an average accuracy of 92.8%, which is a better accuracy than any of the other two approaches can achieve. Because of this, the CNN optimisation algorithm structure that was proposed in this research has offered superior results in the prediction of proper medical diagnosis after some modification and adjustment of physiological data. This was accomplished by analysing the data in a way that took into account the findings of the study. The results of the experimental simulation demonstrate that convolutional neural networks are superior to classic neural networks in terms of their performance in the area of medical diagnostics.

3. Conclusion and future scope

A training strategy that is based on the complexity of medical diagnosis is offered in this study as a way to improve the performance of convolutional neural networks when it comes to medical diagnosis. The new learning method lays a greater emphasis on the potentially essential samples in each category when the network is being trained, and it indicates that these samples should also affect the network's parameter modifications. This takes place while the network is being trained. The performance of the convolutional neural network degrades if it commits an error when processing crucial samples associated with a low level of medical inquiry confidence. This is done in order to assist the network in better understanding the critical samples. The findings of the simulation show that the algorithm model that was described in this research provides an accurate comparison.

Future AI-based medical diagnostic platforms will need further research, development, and optimisation to improve accuracy, reliability, and accessibility. AI-based diagnostic systems need large, diverse datasets to improve accuracy and reliability. Healthcare providers and academics must combine resources and data to create such databases. AI-based medical diagnostics systems use machine learning algorithms to improve diagnosis accuracy. Algorithms require more machine learning and AI research. By giving doctors rapid access to patient data and medical histories, AI-based diagnostic tools and EHRs will increase diagnosis accuracy and timeliness. As with any new technology, AI-based diagnostic systems create privacy and security concerns. Further research is needed to ease these concerns and encourage ethical technology usage. AI-based diagnostic technologies may benefit rural areas with inadequate medical care. Future research must concentrate on low-cost, scalable methods to improve healthcare outcomes in these places.

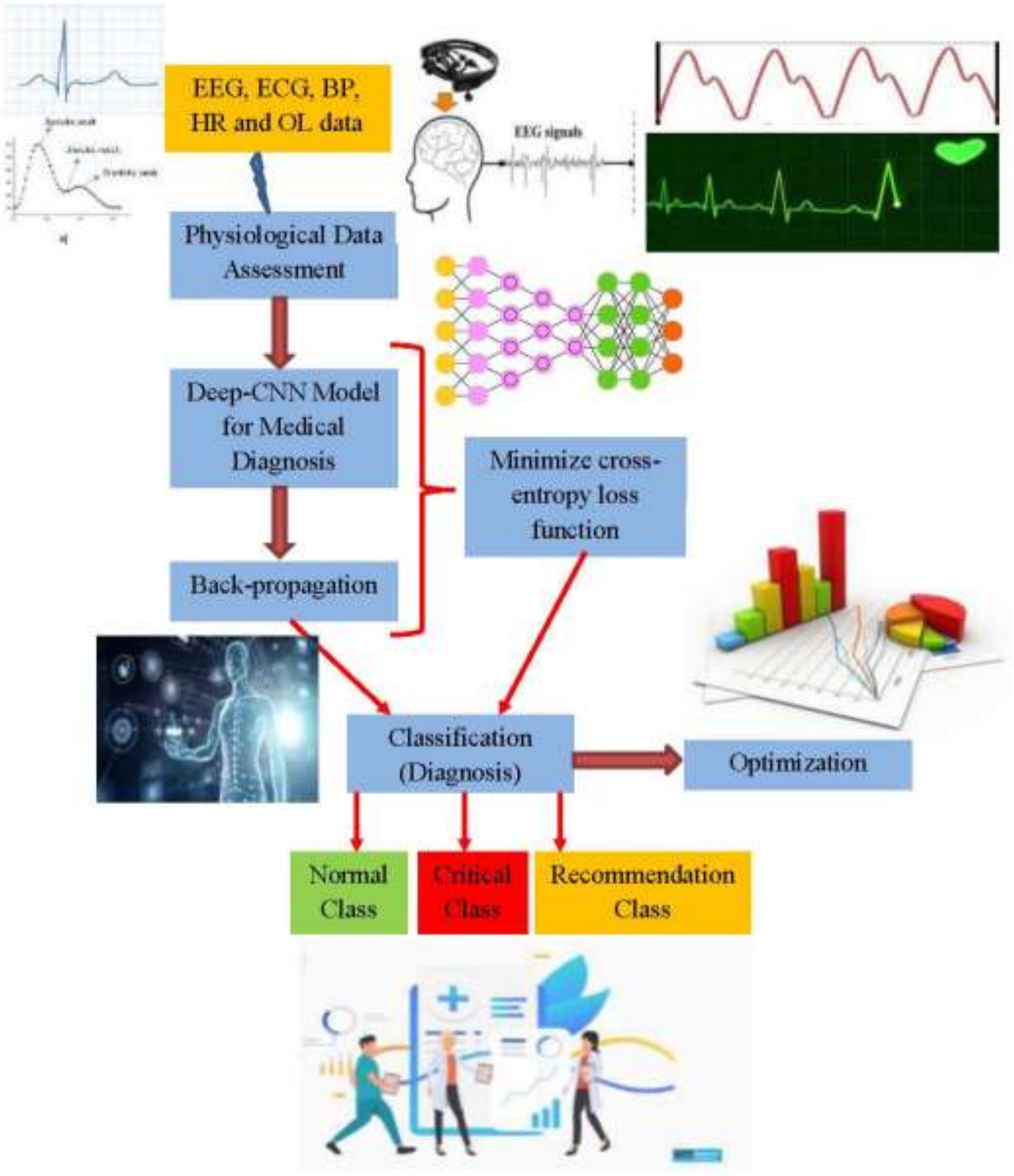

Figure 1: Block diagram of the methodology for medical diagnosis

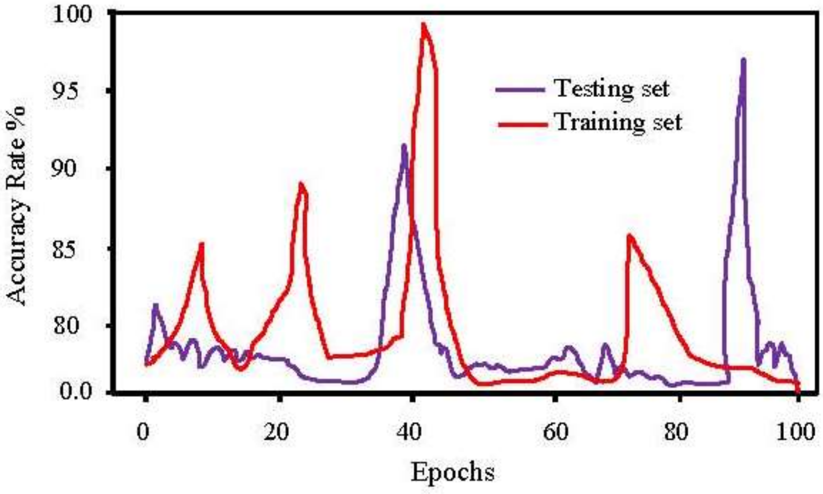

Figure 2: Accuracy rate of test and training data

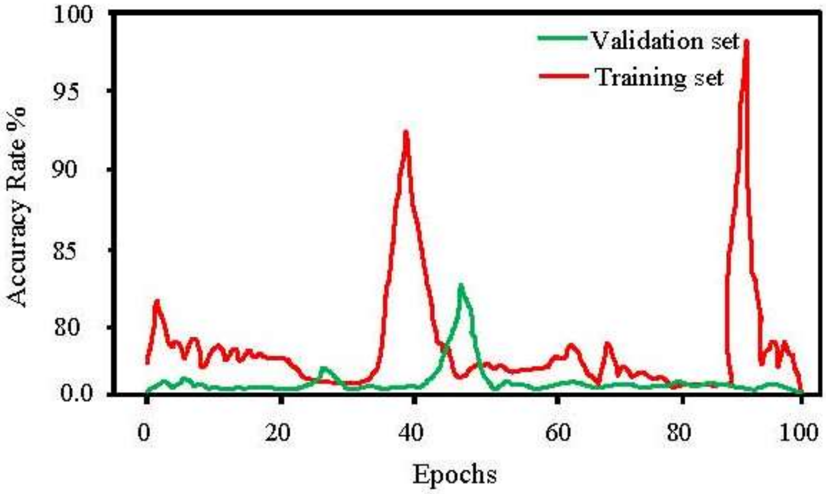

Figure 3: Accuracy rate of validation and training data

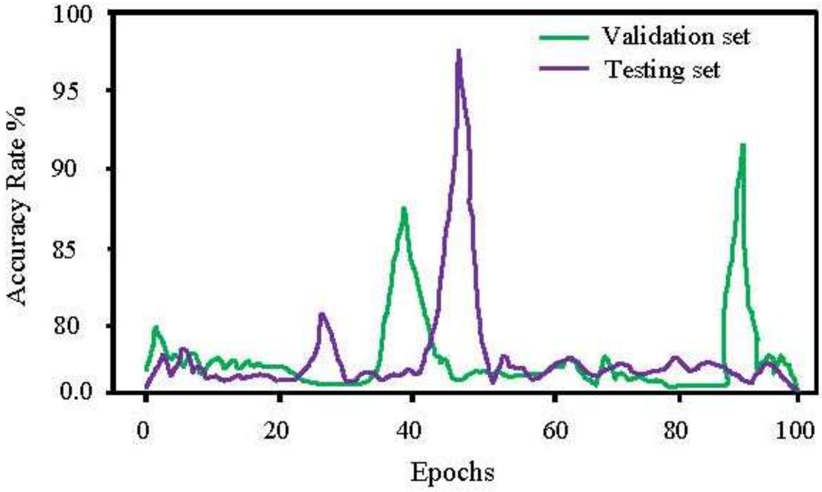

Figure 4: Accuracy rate of validation and testing data

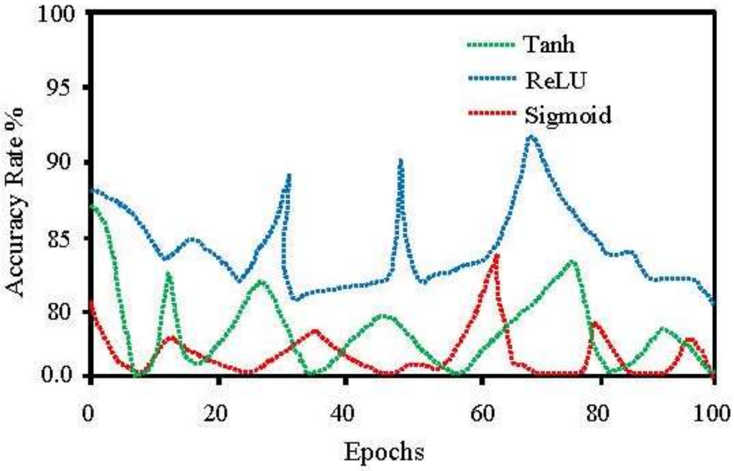

Figure 5: Accuracy rate for different activation functions (Tanh, ReLU and Sigmoid)

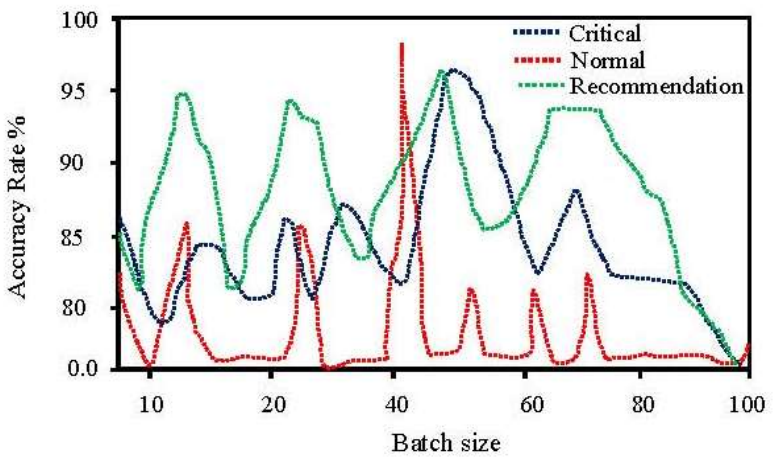

Figure 6: Accuracy rate for three classes (‘Normal’, ‘Critical’ and ‘Recommendation’)

Table 1: Performance results for the testing data under the ‘Critical’, ‘Normal’ and ‘Recommendation’ class

	Before optimization			After optimization		
Sigmoid	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	92.56	91.89	91.02	94.45	93.77	92.88
Specificity	94.23	90.34	92.12	96.15	92.18	94
Accuracy	91.23	91.45	90.17	93.09	93.32	92.01
Tanh	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	91.45	90.79	89.93	93.32	92.64	91.77
Specificity	93.10	89.26	91.01	95.00	91.07	92.87
Accuracy	90.14	90.35	89.09	91.97	92.20	90.91
ReLu	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	89.22	89.44	88.19	91.04	91.27	89.99
Specificity	91.05	87.29	89.01	92.91	89.07	90.83
Accuracy	90.52	89.87	89.02	92.37	91.71	90.84

Table 2: Performance results for the training data under the ‘Critical’, ‘Normal’ and ‘Recommendation’ class

	Before optimization			After optimization		
Sigmoid	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	92.18	92.41	91.11	94.06	94.30	92.97
Specificity	93.53	92.85	91.97	95.44	94.75	93.85
Accuracy	87.39	87.59	86.39	89.13	89.34	88.12
Tanh	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	92.14	88.33	90.07	94.01	90.13	91.91
Specificity	89.20	89.42	88.17	91.02	91.25	89.96
Accuracy	97.19	93.18	95.01	99.17	95.07	96.95
ReLu	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	90.50	89.85	89.00	92.35	91.69	90.82

Specificity	90.98	87.31	88.99	92.80	89.05	90.77
Accuracy	90.47	89.83	88.99	92.27	91.62	90.77

Table 3: Performance results for the validation data under the 'Critical', 'Normal' and 'Recommendation' class

	Before optimization			After optimization		
Sigmoid	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	94.49	93.81	92.92	96.42	95.73	94.82
Specificity	96.20	92.23	94.04	98.16	94.10	95.96
Accuracy	93.13	93.36	92.05	95.03	95.27	93.93
Tanh	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	89.58	88.93	88.09	91.41	90.75	89.89
Specificity	91.20	87.43	89.15	93.05	89.21	90.97
Accuracy	88.29	88.51	87.27	90.09	90.32	89.05
ReLu	Class Critical	Class Normal	Class Recommendation	Class Critical	Class Normal	Class Recommendation
Sensitivity	88.29	88.49	87.28	90.05	90.26	89.02
Specificity	90.05	86.42	88.08	91.85	88.14	89.84
Accuracy	89.54	88.91	88.09	91.33	90.69	89.85

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