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ORIGINAL RESEARCH ARTICLE

Deep learning-based cancer disease classification using Gene Expression Data

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ABSTRACT

Cancer disease caused a major death in worldwide. To prevent this, various cancer classification approaches are employed, which are mostly relied on clinical characteristics and histopathological characteristics. Deep learning-based classification models are very effective and accurate. As a result, this research established the Adam-based Deep Quantum Neural Network, which is the optimal deep learning-based cancer classification method. The information on gene expression is used to classify cancer. Using the Box-Cox transformation, which converts the data into a legible format, the data transformation procedure is carried out. Utilizing information gain, the features are chosen in order to choose the proper gene expression. Additionally, Deep QNN is used to classify cancer, and for better classification, which is trained via Adam optimization. The experimental result shows the developed model provide better classification result with respect to accuracy, true positive rate and true negative rate of 94.91%, 95.59% and 95.4%.

Keywords: cancer classification; Adam optimization; data transformation; deep learning; gene expression

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1. Introduction

The cancer disease causes a second major death in universe reported in World Health Organization (WHO)[1]. This issue motivates the investigators and various networks for reducing this risk. One of the ways to reduce the death caused by the cancer disease is premature detection and screening process[2]. Recently, deep learning (DL) approaches have been focused more attention in classification area. In medical field, the classification approaches rely on DL model, which acts as an important function for disease classification[3]. The DL approaches are mainly employed for resolving various complex issues[4,5]. The advantage of using DL approach is that, this method produced an outcome with best and optimal result[4,6]. The DL approaches in medical field is mainly employed for detecting the disease in early state in order to avoid the death of patients. An early detection of disease using DL method saves the life of patients[7]. Moreover, this method reduces the use of clinical equipment, cost and consume less time for classifying the disease. The DL method detects the disease at an early stage as well as this method has the ability to recognize the hidden problems exist within the entire part of body. The analysis of Gene Expression Data (GED) provides the pattern of various expression levels in all diseases. Some of the complex diseases, like diabetes, cancer and cardiovascular disease produce the severe cause of human health. Since, the various DL approaches have been employed for detecting the disease using genes with various biological

data[2].

DL methods have been widely employed in various applications, like machine translation, object detection, Natural Language Processing (NLP), speech and object recognition. The application of DL in various medical domains steadily improved the performance of disease recognition with maximum accuracy for various gene type applications. In gene data-based applications, the DL approaches are mainly employed. Recurrent Neural Network (RNN) is more familiar for handling the sequence of data, like Ribonucleic Acid (RNA) sequence and Deoxyribonucleic Acid (DNA) sequences. For GED, the diversified neural networks (NN) and feature extraction models are explored. Since, the disease with complex interactions of multiple genes are very difficult to predict with normal classification approaches. Thus, the prediction of disease affected genes is more important for recognizing the disease mechanism[8]. Moreover, the various deep learning approaches employed for the disease classification is Deep NN, Convolutional NN, RNN[2]. With the invention of DL approaches, various researchers are tried to develop numerous DL approaches for the treatment of several diseases. Various DL approaches employed for the assessment of GED demonstrates that DL approaches can provide better classification outcome.

This study's main goal is to construct and create a strategy for classifying cancer based on optimal DL-based data.

- Developed Adam-based Deep QNN: here, the Deep QNN model is employed to categorize the cancer disease using GED in which the weight of Deep QNN model is trained using Adam algorithm.

The following is how this research paper is organized. The literature overview of DL-based cancer classification is illustrated in Section 2, the suggested Adam-based Deep QNN is shown in Section 3, the results and analysis of cancer classification are shown in Section 4, and the conclusion of this paper is discussed in Section 5.

2. Motivation

Cancer disease causes the major death of several people in world wide. To avoid this, various researchers developed several classification approaches for predicting the cancer disease. However, the normal classification methods performed the incorrect outcome, which reduced the accuracy of classification. This encourages researchers to work in the deep learning-based categorization field.

2.1. Literature survey

Sevakula et al.[1] developed the DNN for classifying the cancer disease. Here, the stacked autoencoder was employed to train the weight of DNN algorithm. This method was consumed less execution time. Gao et al.[9] developed the DL-based approach for classifying the cancer with molecular subtype. Here, the cancer classification approach has several advantages, like better interpretability, platform independency, robustness and single sample prediction. Rubin et al.[10] proposed the deep learning-based classification method for performing the Label-free cancer cell classification using small training set. Here, the Generative Adversarial Networks (GAN) was employed to train the large quantity of unclassified data. Although, this method was achieved feasible and effective outcome. Joseph et al.[2] developed the DL method for performing the cancer classification with GED. In this model, the DL process categorized the various kinds of cancers using the gene data. The training and testing of GED were employed using CNN algorithm. Although, this method was classified the disease with complex data sets, but this method was not effective all time. Gupta et al.[11] analyze every study that examined how to apply artificial intelligence to improve gene selection for cancer diagnosis. Deep learning architectures are currently being used to assist doctors in identifying a variety of chronic diseases. These architectures have proven successful across a wide range of industries. Alharbi et al.[12] examine new developments in machine learning techniques for cancer classification utilizing gene expression analysis.

2.2. Challenges

The issues faced during the analysis of DL-based classification approaches are given below.

- The DL method for cancer classification was very effective with less execution time. Thus, the challenge lies on including more effective optimal network design and other feature ranking approaches for achieving the optimal classification. Moreover, the effectiveness of transfer learning approaches was low, which can be improved using other deep learning approaches[1].
- The effectiveness of cancer classification approach was low. Thus, the challenge lies on developing more effective algorithm for improving the interpretation of black box and achieving trustworthy predictions[2].
- The classification accuracy and computational efficiency of ML is poor since the irrelevant, redundant and the blaring genes in database, mostly with specified samples[13,14].
- The relevant gene selection is very challenging as the inappropriate genes exist in database imposes computational burden, unnecessary noises and reduces the accuracy[15].
- Cancer classification is a tedious approach since it is more historically relies on biological information rather than systematic as well as unbiased method for efficient identification of cancer sub types[14,16–18].

3. Proposed Adam-based Deep QNN

This part develops the Adam-based Deep QNN for cancer classification. The GED is used as an input in this instance and supplied into the data transformation stage utilizing the Box-Cox transformation to make the information legible. Following that, the information gain is used to complete the feature selection. Following that, Deep QNN is used to classify cancer, and for better classification, the weight of Deep QNN is trained via Adam optimization. **Figure 1** shows the block diagram of the Deep QNN created on the Adam platform.

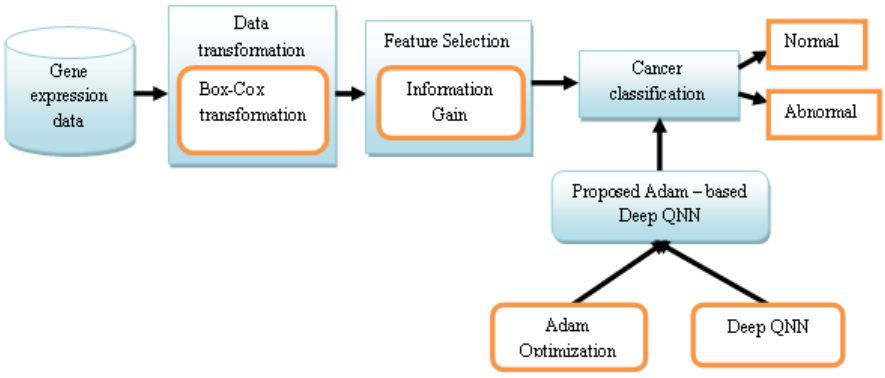

Figure 1. Block diagram of developed Adam-based Deep QNN.

3.1. Get the input data

Let us assume the database M with l number of GED, which is stated as,

$$B = \{M_1, M_2, ...M_d, ...M_l\} \quad (1)$$

where, B denotes the database, M indicates the GED, M_l signifies the total number of data, and M_d signifies the data available at d^{th} index, correspondingly. To perform the cancer classification process, the input data M_d is selected, and is send to the transformation phase in order to convert the data into readable format.

3.2. Data transformation using Box-Cox transformation

The input GED M_d is fed into the data transformation phase using Box-Cox transformation[19]. To improve the accuracy of the classification process, the Box-Cox transformation procedure converts the raw data into a comprehensible format. Power transformation is a key component of the Box-Cox transformation paradigm. This is done by employing the best parameters to transform the anomalous data into data that is

based on a normal distribution. Due to the efficient conversion of GED into variance stabilization, the Box-Cox transformation is essential. The expression for data transformation is specified by as follows.

$$M_T = \begin{cases} \dfrac{M_d^{(t)} - 1}{t} & ; t \neq 0 \\ \ln\left(M_d\right) & ; t = 0 \end{cases} \tag{2}$$

where, M_T be the transformed data, M_d be the input data, and t indicates the unmeasured parameter. This process needs the value of M_d should be greater than zero ($M_d > 0$). If this condition fulfills, then the data transformation process takes place. However, the value of t is evaluated with likelihood estimation model for transforming the information. Thus, the output obtained by the data transformation model is indicated as M_T, which is forwarded to the input of feature selection process.

3.3. Feature selection for cancer classification

The information gain (IG) is subjected to select the significant constraints from the transformed images. The feature selection process improved the classifier performance along with the reduced search space dimension. It also diminished the index size. After transforming the information, the process of selecting the appropriate features for effective classification is very important. Thus, the appropriate feature suitable for cancer classification is carried out using information gain[20]. Here, the transformed data M_T is fed to the input of feature selection phase. In this phase, the more relevant and appropriate features are selected using information gain. The advantage of feature selection process is less computational complexity and it achieves high accuracy. The initial data for Leukemia dataset is 71928 × 72. After feature selection, the number of data is 71028 × 68. The initial data for Colon dataset is 2062 × 62. After feature selection, the number of data is 2062 × 57.

Selection of relevant features using information gain

One of the important methods employed for the selection of appropriate feature is information gain[20]. The information theory is an idea behind the information gain. The expression for feature selection using information gain is given by as follows.

$$\begin{aligned} F(M_T) &= -\sum_{x=1}^{|\bar{C}|} P(\alpha_x) \log P(\alpha_x) + P(M_T) \\ &\sum_{x=1}^{|\bar{C}|} P(\alpha_x / M_T) \log P(\alpha_x / M_T) + P(\overline{M}_T) \times \sum_{x=1}^{|\bar{C}|} P(\alpha_x / M_T) \log P(\alpha_x / M_T) \end{aligned} \tag{3}$$

where, (α_x) represents the ith category, the probability of data transformation is given as, $P(M_T)$ and $P(\overline{M}_T)$, $F(M_T)$ specifies the selected features from M_T, M_T indicates the transformed data, $P(\alpha_X)$ represents the probability that feature X in M_T. Finally, the features selected using information gain is signified as F with dimension $[u \times v]$, which is given as the input to the Deep QNN.

3.4. Proposed Adam-based Deep QNN for cancer classification

The selected feature F is fed into an input to the Deep QNN[21] for classifying the cancer disease. The Deep QNN is the deep learning classifier, which is utilized for several engineering applications. Since it offers the best classification performance, the Deep QNN network is chosen for classifying the cancer disease. Deep QNN's capacity to generalize, its tolerance for noise, and its cost-effectiveness are its advantages.

(i) Structure of deep QNN

The quantum perceptron and its quantum equivalent, which are used in conventional ML algorithms, are the smallest constituents of the QNN in this Deep QNN design. The quantum perceptron is the arbitrary unitary

operator, which contains the input and output qubits, such as i and j qubits. Here, the perceptron is exposed to $i+j$ input qubits and the output qubits relies on the parameter $\left(2^{i+j}\right)^2-1$. The input is varied in the unknown mixed state χ_{in}, and the output qubits in the fiducial product state $|0...0\rangle_{out}$. The perceptron's processed on the input qubit i and one output qubit, as they become $(i+1)$-qubit unitaries. QNN is the quantum circuit with quantum perceptron's structured into the hidden layer J of qubits, operating on a starting state χ_{in} of the qubit inputs, and attained a mixed state χ_{out} for the output qubits regarding the Equation given below,

$$\chi_{out}=tr_{in,hid}\left(D\left(\chi_{in}\otimes|0...0\rangle_{hid,out}\langle 0...0|\right)D^{+}\right) \tag{4}$$

where, $D=d^{out}d^{K}d^{K-1}...d^{1}$ is the quantum circuit, d^{K} signifies the layer unitaries, and these layer unitaries comprised of a quantum perceptron product processing on the qubits in the layers $K-1$ and K. Here, the list of operations is selected as the perceptron, which are the arbitrary operators. In QNN, the output of the network is demonstrated as the sequence of fully positive layer-to-layer transition maps σ^{k}.

$$\chi_{out}=\sigma^{out}\left(\sigma^{K}\left(...\sigma^{2}\left(\sigma^{1}\left(\chi^{in}\right)\right)...\right)\right) \tag{5}$$

$$\chi^{k}\left(U^{k-1}\right)\equiv tr_{k-1}\left(\prod_{n=c_k}^{1}d_n^{k}\left(U^{k-1}\otimes|0...0\rangle_k\langle 0...0|\right)\prod_{n=1}^{c_k}d_n^{k+}\right) \tag{6}$$

where, d_n^{k} indicates the n^{th} perceptron working on $k-1$ and k layers, c_k indicates the total perceptron's processing on $k-1$ and k layers. The expression for the quantum perceptron as the controlled unitary is deliberated as,

$$d=\sum_{v}|v\rangle\langle v|\otimes d(v) \tag{7}$$

where, $\langle v|$ denotes the input space basis, the parameterized unitaries are depicted as $d(v)$. By substituting Equation (7) into Equation (5), the resulting Equation is deliberated as,

$$\chi_{out}=\sum_{v}\langle v|\chi_{in}|v\rangle d(v)|0\rangle\langle 0|d(v)^{+} \tag{8}$$

Equation (8) denotes that the state of the output, which is the outcome of a measure-and-prepare.

The Deep QNN architecture is shown in **Figure 2**. Thus, the proposed Deep QNN classified into cancerous, and non-cancerous, respectively.

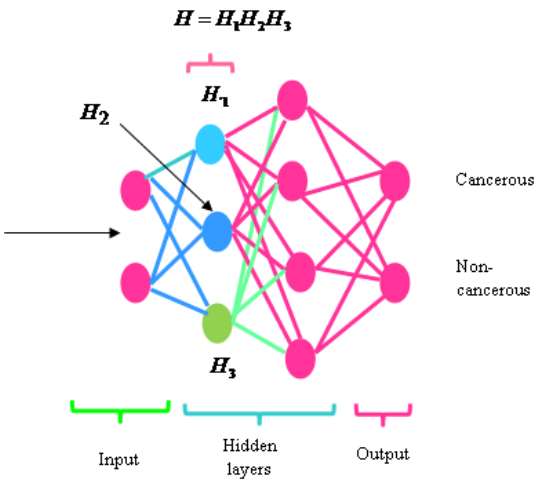

Figure 2. Architecture of Deep QNN.

Adam algorithm for training Deep QNN

The output of Deep QNN network χ_{out} is trained using Adam algorithm. The Deep QNN training is

performed using Adams technique that assists to train best weights of classifier for classifying cancer. Adam algorithm[22] is a first-order stochastic gradient-based optimization where the evaluation is done using fitness function. Moreover, this method achieved the less computational complexity and consumes less memory for storage. This approach successfully addresses the issue of non-stationary targets and the persistence of noisy gradients. In this case, the updated parameter magnitudes are invariant, and the step size is determined by a hyperparameter that uses sparse gradients. Additionally, the Adams works well for step-size annealing. The steps of Adam are given as:

Step 1: Initialization

Initialize the parameters, like $\hat{w}_d$ and $\hat{s}_d$, where, $\hat{w}_d$ represents corrected bias of first moment estimate and $\hat{s}_d$ depicts the corrected bias of second moment estimate.

Step 2: Discovery of error

In order to choose the best weight for the Deep QNN, the bias error is estimated. The error function in this context is what produces the overall best answer. The global best solution is chosen to be the minimization error function. The error minimization function is expressed as,

$$e = \frac{1}{l}\sum_{d=1}^{l}\left(K_d - \chi_{out}\right)^2 \tag{9}$$

where, l signifies total data, χ_{out} symbolize output produced from Deep QNN classifier, K_d indicates expected value.

Step 3: Discovery of updated bias

The Adam algorithm is used to increase convergence and produce the best categorization outcome. This method generates smooth variation with efficient calculation and less memory usage. As per Adam[22], the bias is expressed as,

$$\delta_d = \delta_{d-1} - \frac{\lambda \hat{w}_d}{\sqrt{\hat{s}_d + \phi}} \tag{10}$$

where, λ indicates the step size, $\hat{w}_d$ denoted the corrected bias, $\hat{s}_d$ represents the bias corrected second moment estimate, ϕ depicts constant, δ_{d-1} signifies parameter at prior time instant $(d-1)$. The corrected bias of first order moment is expressed as,

$$\hat{w}_d = \frac{w_d}{(1-\mu_1^d)} \tag{11}$$

$$\hat{w}_d = \mu_1 w_{d-1} + (1-\mu_1)Q_d^1 \tag{12}$$

The corrected bias of second order moment is indicated by,

$$\hat{s}_d = \frac{s_d}{(1-\mu_2^d)} \tag{13}$$

$$\hat{s}_d = \mu_2 s_{d-1} + (1-\mu_2)R_d^2 \tag{14}$$

where, μ_1 and μ_2 represents the exponential decay rates and s_{d-1} indicates the bias corrected second moment estimate at prior time instant $(d-1)$. The value of R_d is given by,

$$R_d = \Omega_\delta \, loss\,(\delta_{d-1}) \tag{15}$$

Step 4: Determination of best solution

Using error value, the best solution is obtained, and the best solution is used for classifying cancer.

Step 5: Termination

Optimal weights are generated continuously until the maximum number of iterations is reached. **Figure 3** shows the Pesudo code of developed Adam-based Deep QNN.

Input : $\hat{w}_d$: corrected bias of first moment estimate and $\hat{s}_d$: corrected bias of second moment estimate
Output: Resultant parameters
Initialize λ step size
Initialize $\mu_1, \mu_2 \in [0,1)$:Exponential rate decay
Initialize first moment vector
Initialize second moment vector
Initialize time step
While δ_d not converged do
$d \leftarrow d+1$
Acquire gradients
Renew first biased moment estimate using equation (12)
Renew second biased moment estimate using equation (14)
Predict corrected bias first moment estimate
Predict corrected bias second moment estimate
Update parameters
End while
Return δ_d

Figure 3. Pseudo code of Adams algorithm.

Thus, the proposed Adam-based Deep QNN categories the data as either cancerous or non-cancerous data.

4. Results and discussion

This section presents the findings and analysis of the developed model for classifying cancer.

4.1. Experimental setup

The experimentation of developed model is completed in MATLAB tool.

4.2. Dataset description

The experimentation of developed cancer classification method is analyzed using Leukemia dataset[23] and Colon dataset[24].

Leukemia dataset: The Leukemia dataset comprises GED of 72 patients. The leukemia dataset has 7128 genes, which is kept in the matrix of dimension is 7128 × 72 (10 MB) with column representing the class labels.

Colon dataset: The colon dataset includes 40 colon tumor samples with 6500 genes, along with 22 samples of normal colon tissue.

4.3. Comparison methods

The performance improvement of developed Adam-based Deep QNN is analyzed by comparing the developed method with existing approaches, namely Probabilistic Principal Component Analysis + Deep Belief Network (PPCA + DBN)[25,26], Deep RNN[27], Bhattacharya + GOA-DBN and Fractional ASO-based Deep RNN.

4.3.1. Assessment of cancer classification using Leukemia dataset

Based on performance criteria, **Table 1** compares the developed Adam-based Deep QNN for cancer classification with the Leukemia dataset. When the percentage of training data is 80, the created model's highest accuracy, highest TPR, and highest TNR values are 94.91%, 95.59%, and 95.40%, respectively.

Table 1. Comparative assessment using Leukemia dataset.

Training data	PPCA + DBN	Deep RNN	Bhattacharya + GOA-DBN	Fractional ASO-based Deep RNN	Developed Adam-based Deep QNN
Accuracy					
40	84.45	86.13	89.30	89.54	91.95
50	85.59	86.67	90.89	91.13	92.99
60	87.61	89.79	91.46	91.69	93.68
70	90.26	91.80	92.02	92.26	94.25
80	92.27	92.50	92.59	92.83	94.91
TPR					
40	83.48	83.56	88.77	89.05	91.67
50	84.00	84.09	91.39	91.68	93.56
60	84.53	87.03	91.96	92.25	94.20
70	86.40	92.18	92.53	92.82	94.93
80	92.65	93.01	93.10	93.39	95.59
TNR					
40	88.64	90.73	90.82	91.11	93.00
50	89.20	91.30	91.39	91.68	93.67
60	89.76	91.87	91.96	92.25	94.25
70	91.67	92.44	92.53	92.82	94.79
80	92.91	93.01	93.10	93.39	95.40

4.3.2. Assessment of cancer classification using Colon dataset

Table 2 compares the performance of created Adam-based Deep QNNs for cancer classification using different training datasets and evaluation measures. The created Adam-based Deep QNN attained an accuracy of 94.81% for the percentage of training data equal to 80. The Adam-based Deep QNN was built with a 95.44% TPR. The Adam-based Deep QNN was built with a 95.39% TNR.

Table 2. Comparative assessment using Colon dataset.

Training data	PPCA + DBN	Deep RNN	Bhattacharya + GOA-DBN	Fractional ASO-based Deep RNN	Developed Adam-based Deep QNN
Accuracy					
40	84.57	90.01	90.35	90.37	92.19
50	85.63	90.58	90.94	91.18	93.06
60	89.72	91.41	91.51	91.74	93.68
70	90.58	91.98	92.07	92.31	94.19
80	91.50	92.54	92.64	92.88	94.81
TPR					
40	83.56	90.29	90.67	90.92	92.77
50	84.09	90.86	91.49	91.77	93.73
60	88.64	91.96	92.06	92.34	94.33
70	89.82	92.53	92.63	92.91	94.82
80	91.10	93.10	93.20	93.48	95.44
TNR					
40	88.72	90.82	90.92	91.20	93.08
50	89.29	91.39	91.49	91.77	93.91
60	91.87	91.96	92.06	92.34	94.31
70	92.44	92.53	92.63	92.91	94.84
80	93.01	93.10	93.20	93.48	95.39

4.4. Analysis of AUC-ROC curve

Figure 4 shows the analysis of AUC-ROC curve for Leukemia dataset. When TPR is 0.5, the values obtained by the PPCA + DBN, Deep RNN, Bhattacharya + GOA-DBN, Fractional ASO-based Deep RNN and the developed Adam-based Deep QNN is 0.852, 0.862, 0.876, 0.885, and 0.894.

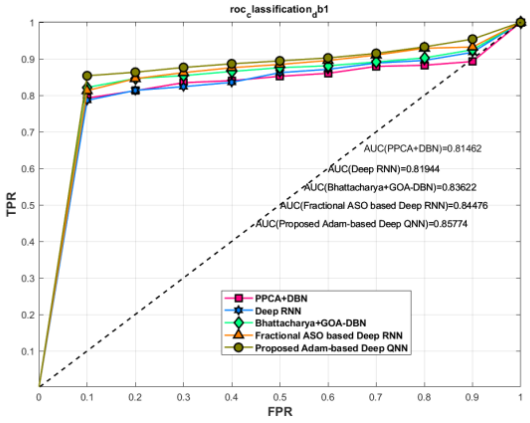

Figure 4. AUC-ROC curve for Leukemia dataset.

The analysis of AUC-ROC curve for Colon dataset is displayed in **Figure 5**. When TPR is 0.8, the values obtained by the PPCA + DBN is 0.885, Deep RNN is 0.869, Bhattacharya + GOA-DBN is 0.888, Fractional ASO-based Deep RNN is 0.907 and the developed Adam-based Deep QNN is 0.933.

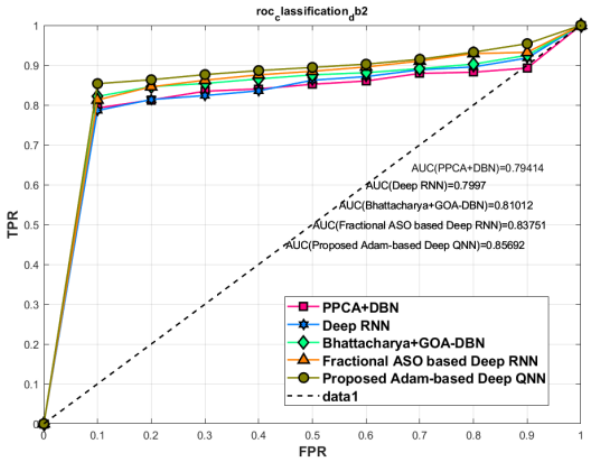

Figure 5. AUC-ROC curve for Colon dataset.

5. Conclusion

In this paper, the Adam-based Deep QNN network is developed to classify the cancer disease using GED. Initially, the GED is gathered from Leukemia and Colon database. The collected information is fed to the data transformation module using Box-Cox transformation for transforming the GED as understandable format. Then, the relevant features are takeout from the transformed data using information gain in order to achieve the better classification. The feature extraction process is performed for extracting the relevant features suitable for further classification. After that, the extracted features are fed to the classification module for classifying the cancer disease, which is carried out using Deep QNN. Then, the weight of Deep QNN is trained using Adam optimization algorithm to get the optimal classified outcome. The experimental result provided that the developed Adam-based Deep QNN method provided better classification performance than the existing approaches-based accuracy, TPR and TNR of 94.91%, 95.59% and 95.4% using GED. This research is more

helpful in various medical applications. The developed Adam-based Deep QNN model for cancer disease classification process can be further extended with other effective DL algorithms.

Author contributions

Conceptualization, JDR and KV; methodology, DM; software, KV; validation, JDR, KV and DM; formal analysis, JDR; investigation, JDR; resources, KV; data curation, KV; writing—original draft preparation, JDR; writing—review and editing, DM; visualization, JDR; supervision, JDR; project administration, KV. All authors have read and agreed to the published version of the manuscript.

Conflict of interest

The authors declare no conflict of interest.

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