A Novel Classification of Multiple Sclerosis Using Quantum Convolution Neural Network

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ABSTRACT
Multiple Sclerosis (MS) is a neurological disorder that affects the central nervous system (CNS), including the brain, spinal cord, and optic nerve. The aim was to enhance the efficacy of a quantum machine-learning algorithm in identifying MS and categorizing its advancement by creating advanced techniques.Detecting MS lesions has become increasingly difficult owing to the imbalanced nature of the dataset, which contains a disproportionately small number of lesion pixels.Subsequently, a novel feature selection ensemble (FS-Ensemble) technique was implemented, which employed four distinct filtering methods for selecting features, utilizing various statistical techniques, including methods such as the chi-square test, information gain, Minimum Redundancy Maximum Relevance, and RelieF.Subsequently, an innovative classification approach utilizing a Quantum Convolutional Neural Network (QCNN)was applied to identify the most crucial features.The findings demonstrated the efficacy of MRI in examining MS lesions, with a study involving 30 patients with MS and 100 healthy brain MRI scans showing accurate predictions of disease progression.In the realm of MS identification, QCNN exhibited exceptional performance, achieving an accuracy of 87.7% and sensitivity of 87.0%.Other notable metrics included specificity of 88.5%, precision of 88.7%, and AUC of 0.8775.Furthermore, studies suggest that employing non-shared parameters and more sophisticated filter designs can significantly enhance QCNN's efficacy of QCNNs.These findings contribute to the development of powerful quantum classifiers for multicategory image classification challenges.

Introduction

Multiple sclerosis (MS) is a chronic autoimmune condition that affects the central nervous system (CNS), leading to the breakdown of myelin.This disease is primarily characterized by inflammation and degeneration of nerve cells.From a pathological perspective, MS is characterized by the development of sclerotic plaques or lesions, which are specific regions of myelin loss that predominantly affect the white matter of the CNS. The disorder presents in several forms, including relapsing-remitting MS (RRMS), primary progressive MS (PPMS), secondary progressive MS (SPMS), and progressive relapsing MS (PRMS) [1].

Over the past decade, machine learning (ML) techniques have made remarkable progress in neurological disease research. As data science methodologies, ML algorithms create predictive models capable of identifying patterns and relationships within datasets, with minimal human input [2].These algorithms can autonomously extract knowledge from the data they process. Thus far, the primary focus of ML applications in multiple sclerosis (MS) studies has been on several key areas. These include the categorization of patients into various stages of the disease, such as clinicall The text discusses different forms of multiple sclerosis, including clinically isolated syndrome (CIS), relapsing-remitting MS (RRMS), and secondary progressive MS (SPMS). It also mentions the use of machine learning techniques to aid in various aspects of managing multiple sclerosis.These applications encompass forecasting MS diagnoses, predicting the transition from clinically isolated syndrome to confirmed MS, estimating disability progression, and evaluating potential patient responses to therapies. The main objective of these tools is to support healthcare providers in determining the most appropriate treatment strategy [3]. A definitive diagnosis of multiple sclerosis (MS) cannot be made through a single clinical or laboratory test. Rather, the diagnostic process involves a combination of established clinical, imaging, and laboratory criteria [4]. Various blood serum markers have been investigated as potential indicators of MS [5].

Globally, MS is believed to affect approximately 2.8 million individuals, with a prevalence of 35.9 per 100,000 people [6]. A new MS case has been reported worldwide every five minutes [7].It primarily affects young adults, with a higher occurrence in women [8]. MS symptoms exhibit significant variability among patients, ranging from limb weakness and visual problems to dizziness, fatigue, and tingling sensations [9]. While the exact cause of MS remains unknown, studies indicate that environmental triggers may initiate the condition in individuals with a genetic predisposition [10].

Accurate diagnosis of MS is essential for initiating timely treatment because therapies that modify the disease can assist in symptom management and slow their advancement [11].Diagnosing MS requires identifying lesions in the central nervous system that are dispersed across both time and space, while ruling out all other possible causes. Several conditions share clinical and radiological features with MS [12]. Currently, no definitive laboratory tests exist for diagnosing this condition [13].Consequently, the 2017 McDonald diagnostic criteria for MS incorporate a blend of clinical evaluation, imaging studies, and laboratory results [14].

Currently, magnetic resonance imaging (MRI) is the most reliable technique for diagnosing MS [15], monitoring disease progression, and evaluating treatment efficacy in clinical trials [16]. Nevertheless, the process of interpreting MRI scans for MS diagnosis is labor-intensive, mentally taxing, and prone to human error.To improve the effectiveness of diagnosing multiple sclerosis (MS), scientists have employed machine learning (ML) and deep learning (DL) methods, which are subsets of artificial intelligence (AI) [17]. ML enables computers to acquire knowledge without explicit programming, whereas DL, a specialized form of ML, uses algorithms that allow software to train itself for particular tasks by exposing multilayered neural networks to extensive datasets.

Various researchers have examined the existing body of work on AI-based MS diagnosis. For example, [18] performed a thorough review of prior research that utilized DL methods for automated MS detection using MRI images. This review explores the most commonly employed preprocessing techniques and highlights the existing obstacles and potential avenues for future investigations.

Literature Survey

Researchers from diverse fields have endeavored to forecast Multiple Sclerosis (MS); however, there is still a demand for holistic predictive frameworks that can fully utilize all accessible information.This section provides an overview of the most commonly referenced MS investigations.Additionally, it briefly touches on studies involving imbalanced datasets in disease research, highlighting the fact that prior work has examined the connections between particular genes and illnesses.One such study [19] used random forest techniques to identify new genes linked to MS.

Research conducted by [20] employed a Support Vector Machine (SVM) to distinguish between individuals with relapsing-remitting MS (RRMS) and healthy controls. The investigation, which included 44 patients and 26 control subjects, focused on brain lesions and achieved a peak accuracy of 95%.This remarkable precision is believed to result from the substantially higher occurrence of lesions in MS patients than in healthy individuals, as well as potential microstructural alterations in apparently normal tissues.

Research conducted by [21] employed Support Vector Machines (SVMs) to perform binary classification of multiple sclerosis (MS) patients. This investigation aimed to categorize individuals based on three primary factors: illness duration, T2 lesion volume, and MS severity.Participants were divided into groups based on three distinct criteria.They were separated into short-term (< 5 years) and long-term (> 10 years) disease durations.The T2 lesion volume was categorized as either low (< 1 mL) or high (> 10 mL).MS severity was classified as either mild (Expanded Disability Status Scale (EDSS) score ≤ 3) or severe (EDSS score > 3). The classification accuracy rates achieved for these three parameters were 85, 83, and 77%, respectively.

[[22] introduced the voxel-wise displacement classifier (VDC), a classification method that utilizes Fisher's linear discriminant analysis, SVM, Random Forest (RF), and Adaboost, with displacement fields serving as features. This study included 29 relapse-emitting MS (RRMS), eight Secondary Progressive MS (SPMS), four CIS, and one Primary Progressive MS (PPMS) patients, as well as 36 healthy

controls.VDC consistently demonstrated superior performance compared to other techniques, achieving accuracy rates of up to 100%.

An alternative approach to diagnosing multiple sclerosis involves analyzing gene expression data. A previous study [23] constructed a classification model that identified genes based on their expression profiles.This approach was evaluated using a dataset comprising 44 samples, including 26 patients with MS and 18 control individuals with various neurological conditions.This study employed an analytical framework that integrated feature ranking algorithms with a support vector machine model, achieving an accuracy of 86% in identifying genes associated with multiple sclerosis.

A study by [24] investigated various supervised machine learning approaches by employing different feature vectors extracted from MRI scans to predict MS.The findings revealed that the selection of the feature vector had a more significant influence on predictive accuracy compared to the choice of the machine-learning algorithm.

A study described in [25] presented a method for detecting multiple sclerosis by combining clinical data with information on lesion volumes and metabolic features obtained from magnetic resonance imaging. The study utilized three classification methods: Linear Discriminant Analysis (LDA), support vector machine (SVMs), and Random Forest (RF). These findings indicate that metabolic characteristics play a crucial role in differentiating relapsing-remitting forms from primary progressive forms, while lesion extent is more useful in distinguishing relapsing-remitting from secondary progressive forms. Consequently, the integration of clinical information with magnetic resonance lesion measurements and metabolic profiles can enhance the precision of distinguishing between relapsing-remitting and progressive types.

Proposed Method

Figure 1 illustrates the process of MS detection using quantum machine-learning techniques.

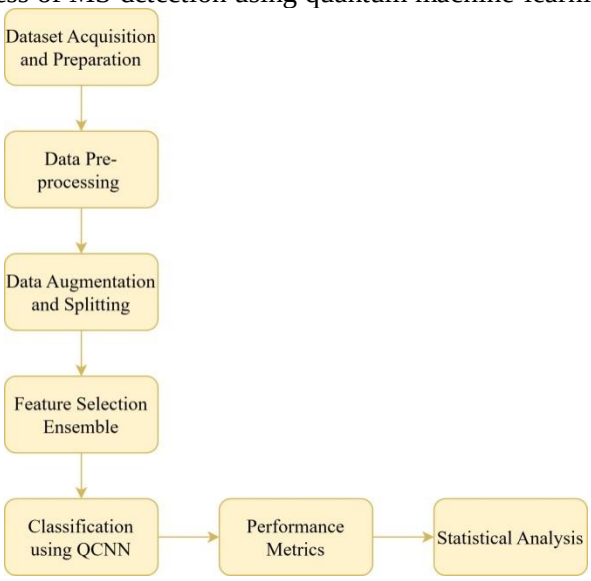

Figure 1: Overall Proposed Framework

Data Acquisition and Preparation

A set of 3D NIfTI images from 30 patients diagnosed with multiple sclerosis (MS) was assembled by the Laboratory of Imaging Technologies. For each patient, the dataset included four imaging modalities: T1-weighted, T2-weighted, T1-wks, and FLAIR. In total, the collection comprised 3766 brain MR image slices obtained from the 30 MS patients.The research also included 100 MRI scan slices from individuals without multiple sclerosis (MS) [18]. This study utilized a subset of brain MRI scans from an initial dataset. Within this collection, MS lesions were present in all but one MRI sample. The dimensions of each volume are 512 × 192 × 3 as Table 1.

Table 1: DEMOGRAPHIC CHARACTERISTICS OF DATASET

No. of Sujects	Age	Gender (F/M)	No. of Slices
30 (MS)	44.15 ± 19.5	23/7	3766
100 (Healthy)	-	-	100

Image Pre-processing

The processed images were further enhanced to achieve the best outcomes. After importing the image, we transformed the color channels from BGR to RGB (Figure 3). The RGB color model comprises of three fundamental hues: red, green, and blue.Images in RGB format are composed of discrete pixels, each with intensity values ranging from 0 to 255 pixels.To maintain uniformity and enhance the classification precision, all images in the input set were resized to a standard 224 × 224 pixel format (Figure 2). This adjustment was essential to mitigate the potential adverse effects of diverse image dimensions within the datasetTo facilitate testing, we created a comprehensive inventory of all test images by extracting class labels from the file names and compiling them into a single list. To address missing values, we computed the mean of these labels and utilized these average values as substitutes for any missing data point.

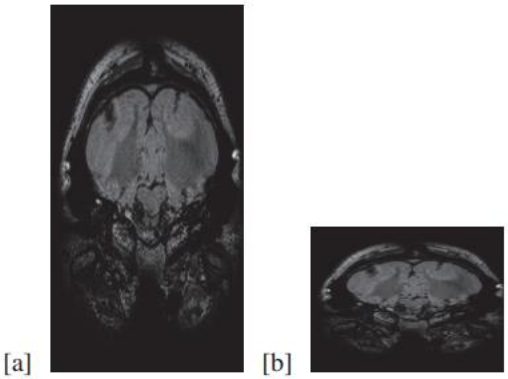

Figure 2: Image Resizing (a) Original Image (b) Resized Image

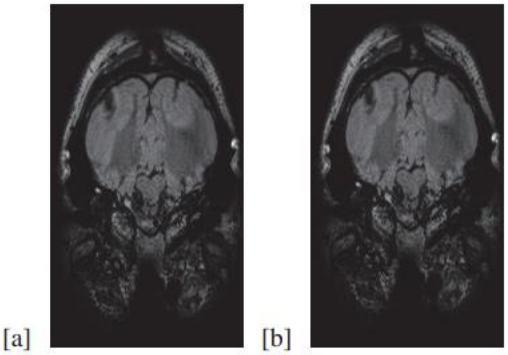

Figure 3: Color channel swapping (a) BGR (b) RGB

Data Augmentation

Under certain circumstances, acquiring high-quality data is challenging.The lack of dependable information can hinder and slow the model development process. Data Augmentation serves as a potential solution to this data deficiency. This method enhances model creation by producing significantly more data than initially accessible.As part of the pre-processing phase, Image Augmentation is utilized, particularly for datasets with limited size, and the training dataset is enhanced through a commonly employed Data Augmentation technique, image rotation. The method involved setting the angle θ to 15° (Figure 3). This process allowed the generation of nine additional images from each original image in the training set.As a result, the training set size increased nine-fold.

Data Splitting

This study utilized 3866 images for the analysis.Of these, 3013 were from patients with multiple sclerosis (MS) and 80 were from healthy individuals, which were used for training the model.The testing set consisted of 753 images from patients with MS and 20 healthy subjects as Table 2.

Table 2:NUMBER OF SLICES IN DATASETS

Dataset	Training Set	Test Set
MS	3013	753
Healthy	80	20

Feature Selection Ensemble

The objective was to determine which of the 11 datasets (including the comprehensive "All" dataset) was suitable for fall detection using machine learning methods and to identify the most important variables within each set. To accomplish this, a feature selection ensemble (FS-Ensemble) was developed. These ensembles have demonstrated their effectiveness in various research studies, and the primary goal of the FS-Ensemble is to eliminate irrelevant and noisy features, thereby enhancing the classification accuracy, as illustrated in Figure 4.

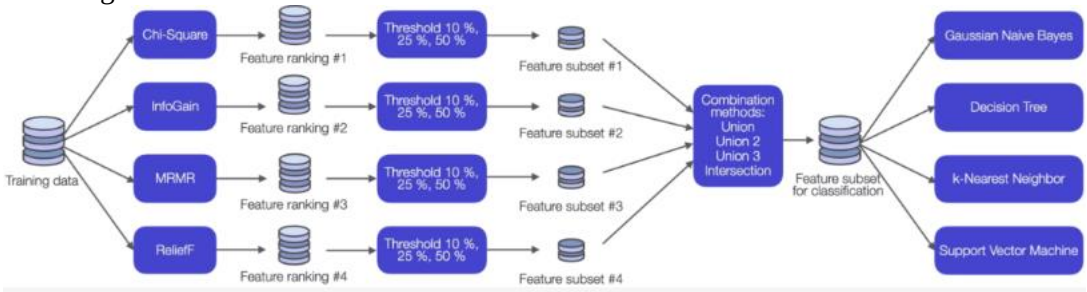

Figure 4: The feature selection ensemble and classification techniques

The diversity of metrics used by individual filter methods to evaluate feature importance contributes to the overall effectiveness of an ensemble [50]. To capitalize on this, we incorporated four filter techniques: chi-square test (chi-square), information gain (InfoGain), Minimum Redundancy Maximum Relevance (MRMR), and RelieF.These methods employ a range of approaches, including statistical, information-theoretic, mutual information, and distance-based metrics, making them ideal candidates for integration into ensemble systems.The research concentrated on filter-based feature selection methods owing to their autonomy from classification models, in contrast to wrapper and embedded approaches.This independence of filter techniques reduces the risk of overfitting and produces results with broader applicability than wrapper methods.The investigators used MATLAB R2021b to implement the Chi-Square, MRMR, and RelieF filter techniques. Furthermore, they employed WEKA 3.8 to execute the InfoGain filter method.

Each of the four filter methods produces a prioritized list of features.A cutoff point was then established to select a subset of features for each filter method (filter subsets).Subsequently, a combination technique is employed to merge the four filter subsets.Previous research has demonstrated that this approach yields superior results compared to the first application of a combination method, followed by a threshold method.

Based on research conducted by Seijo-Pardo et al., this study examined three distinct thresholds and four different combination techniques.Thresholds were established at 50%, 25%, and 10%, which determined the number of features within each filter subset.Four combination approaches were employed to consolidate these subsets.

- Union: The final subset included features that appeared in at least one of the filter subsets.
- Union 2: A feature was selected in the final subset if it was in at least two filter subsets.
- Union 3: A feature was selected in the final subset if it was in at least three filter subsets.
- Intersection: A feature was selected in the final subset if this feature was in all filter subsets.

Each process generates a final subset encompassing all the input features utilized in the classification models.The combining methods were executed using Python version 3.8.8.

QCNN based Classification

A QCNN circuit, consisting of several key elements, is crucial at this point.The process was initiated by setting up a four-qubit quantum device using PennyLane's standard qubit simulator, as shown in Figure 5.A vital part of this setup involves configuring parameter θ to π/2.This setup affected the CRZ (Controlled-Rotation-Z) and CRX (Controlled-Rotation-X) gates.The quantum circuit employed an RX (rotating X) gate on each qubit.This specific gate induces rotation of the qubit around the X-axis on the Bloch sphere.

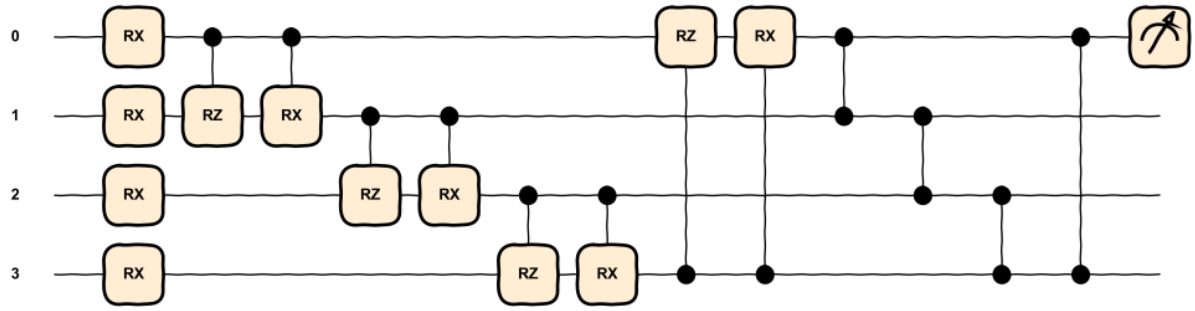

Figure 5: QCNN circuit

To calculate the rotation angle, the pixel value is multiplied by π. This calculation can be mathematically represented as:

$$|\psi'| = \otimes_{i=0}^{3} R_X(\phi_i \pi)|\psi| \qquad (1)$$

With

$$R_X(\phi_i \pi) = \begin{pmatrix} cos\phi_i \pi/2 & -\frac{isin\phi_i \pi}{2} \\ -isin\phi_i\left(\frac{\pi}{2}\right) & cos\phi_i \pi/2 \end{pmatrix} \qquad (2)$$

In this context, ϕi represents the elements of the array containing the pixel values that are input into the quantum circuit. The quantum system's starting configuration is denoted by $|\psi = |0\rangle \otimes 4$. The circuit is then enhanced by the addition of controlled rotation gates, specifically CRZ and CRX gates, which are implemented between the initial and final qubits as well as between each set of neighboring qubits.

The measurement phase marked the final step of the process.In this stage, the expectation value of the initial qubit for the Pauli-Z operator is determined. This involves conducting multiple measurements and computing their average outcome, which can be expressed mathematically as

$$M = |\phi''''|Z|\phi''''| \qquad (8)$$

The state denoted as |ϕ'' '' represents the outcome following the application of CZ gates.This result demonstrates the quantum characteristics of the operation by expressing the output of the quantum convolution process on a 2 × 2 patch as an intricate function dependent on the values of the pixels.

Optimization routine

The algorithm used in the optimization process iteratively adjusts the parameters of the ansatz circuit, which consists of tunable quantum-gate rotation angles. For QCNNs, the optimizer refines the parameter vector θ to ensure the predicted output matches the desired outcome.The goal of the optimization process is to minimize the loss function L(θ) with respect to the parameter vector θ. Similar to conventional neural network models, QCNNs can utilize common loss functions, such as the mean squared error and

cross-entropy.This step was crucial for enhancing the effectiveness of the model.The research utilizes a multi-category cross-entropy loss function, which can be mathematically represented as

$$L(\vec{\theta}) = \frac{1}{N}\sum_{j=1}^{N}\sum_{c=1}^{C}[y_{jc} f(p_{i=c})] \qquad (9)$$

In this scenario, N indicates the batch size and C represents the total category count.Variable yjc is a binary class indicator that can be either zero or one.The expression pi=c represents the probability of observing eigenstates |i> associated with category c. The measurement results are processed through the application of function f (·), which establishes a connection between the outcome and class label yjc. Similar to conventional neural networks, Quantum Convolutional Neural Networks (QCNNs) employ gradient-based optimization methods to adjust their parameters. In this context, we employed the Adam optimizer for the parameter updates.Specifically, parameter vector θ is modified according to the following procedure:

$$g_t = \frac{1}{N}\nabla_\theta L(\vec{\theta}_{t-1}) \qquad (10)$$

$$m_t = \beta_1 m_{t-1} + (1-\beta_1) g_t \qquad (11)$$

$$v_t = (\beta_2 v_{t-1} + 1 - \beta_2) g_t^2 \qquad (12)$$

$$\theta_t = \theta_{t-1} - \frac{\eta}{\sqrt{v_t}+\varepsilon} m_t \qquad (13)$$

In this equation, N represents the batch size, η denotes the learning rate, and β1, β2, and ε are the hyperparameters.

CNN Training

In this method, quantum-processed image data were utilized to train the CNN.The model structure incorporated several layers, each with a distinct purpose.The first layer, a Conv2D layer, utilized 32 filters with a 3 × 3 kernel size and ReLU activation. This initial layer is tasked with identifying fundamental features within the input image, such as edges and corners. Following this, a MaxPooling2D layer with a 2×2 pool size is implemented.This process aids in achieving translation invariance and reduces computational demands by decreasing the spatial dimensions of the input through selecting the highest value within each 2×2 region. To detect more complex features from the output of the preceding layer, an additional Conv2D layer was employed, utilizing 64 filters and ReLU activation.A second MaxPooling2D layer further diminished the spatial dimensions of the input.The flattened layer converts the 2D output into a 1D array, enabling processing by dense layers.A dense layer with 128 units and ReLU activation then identifies high-level features and learns to represent the input in 128-dimensional space.To prevent overfitting, a dropout layer with a 0.5 rate randomly deactivates half of the input units during the training process, and a second dense layer, featuring four units and softmax activation, subsequently generates the likelihood of the input image belonging to each of the four categories.This comprehensive architecture enables the traditional CNN to effectively learn from quantum-processed information.

Performance Metrics

Several performance metrics were calculated to evaluate the predictive capabilities of the compared classifiers.These include the confusion matrix (CM), accuracy, sensitivity, specificity, logistic loss (log loss), cross-entropy loss, and area under the curve (AUC) metrics.

Results and Discussion

This study compared the effectiveness of the newly developed QCNN model against four traditional machine-learning approaches.This study utilized the most significant features extracted from 74 genes associated with multiple sclerosis (MS) etiology as input data to predict an individual's likelihood of developing the disease.

Evaluation metrics

Evaluating trial outcomes involves utilizing various performance measures, including accuracy, sensitivity, specificity, precision, false predictive value, positive predictive value, and the F1 score.The measures were constructed using four categories: true positive (TP), true negative (TN), false positive

(FP), and false negative (FN).TPs represent the correctly identified positive pixels.FNs are positive pixels that are mistakenly undetected.TNs are negative pixels that are correctly recognized.FPs are negative pixels that are incorrectly classified as positive pixels.

A confusion matrix is constructed using the test dataset to evaluate the performance of the proposed model. This matrix displays the actual class information in rows and the predicted class information in columns. The matrix yielded four key outcomes: TP, TN, FP, and FN.

Accuracy: Accuracy is expressed as the proportion of correctly classified pixels relative to the total number of pixels in an image..

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (14)$$

$$Precision = \frac{TP}{TP+FP} \quad (15)$$

$$Sensitivity/recall = \frac{TP}{FN+TP} \quad (16)$$

$$specificity = \frac{TN}{FP+TN} \quad (17)$$

This study thoroughly examined the application of a specific QCNN for classifying MS images, with the aim of developing a more sophisticated model suitable for diagnostic medicine.The performance metrics from our results highlight the model's exceptional precision and feasibility for commercial and practical implementations.

Over the course of 20 epochs, the accuracy and loss of the model were evaluated for both the training and validation datasets.As illustrated in Fig. 6(a), the continuous decline in loss indicates the effective error-reduction capability of the model.The QCNN model demonstrates successful learning from the training data and exhibits good generalization to unfamiliar data, as evidenced by the consistent decrease in both training and validation losses.This trend clearly indicates the ability of the model to avoid overfitting, which is a significant challenge often encountered in deep learning models used for medical image analysis.

The effectiveness of the model in accurately identifying MS was further evidenced by the consistent increase in precision, as shown in Fig. 6(b).Considering the intricate and variable nature of the medical imaging data, a high level of accuracy was achieved. In particular, the peak validation accuracy of 99.67%is exceptionally noteworthy, which suggests that the QCNN can detect intricate patterns and characteristics in images, which are crucial for accurate diagnosis.However, it is worth noting that changes in image complexity and dataset diversity may affect performance.

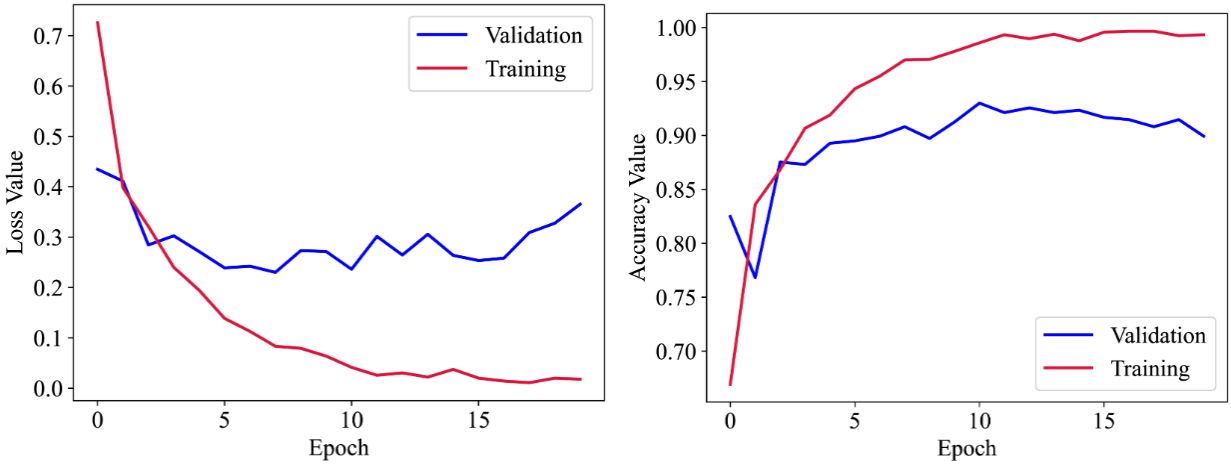

Figure 6: Training and validation performance plots: (a) loss and (b) accuracy.

The confusion matrix in Figure 7 offers additional insight into the effectiveness of the model, particularly regarding its accuracy for each class.The model's precision is evident in its perfect classification of cases involving "pituitary tumors ".Distinguishing between glioma and meningioma classification can be challenging, highlighting areas that require further enhancement.These misclassifications may stem from shared imaging characteristics among different tumor types, suggesting the need for more advanced feature extraction techniques or additional training data to improve the differentiation.

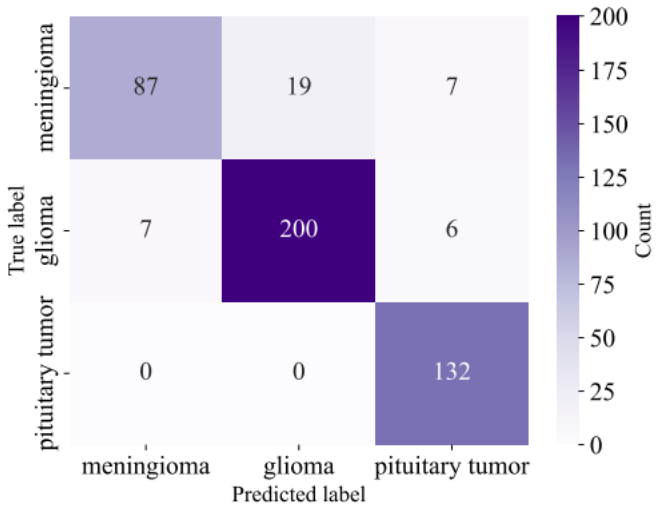

Figure 7: Confusion matrix displaying class-wise performance.

ROC

When conducting identification and classification tasks, the Receiver Operating Characteristic (ROC) curve serves as an essential metric, as illustrated in Figure 8. Evaluation of the specificity and sensitivity of the proposed method is crucial for determining its efficacy.Sensitivity can be calculated using TP and FN values, while specificity is derived from the TN and FP ratios, as shown that ROC curve.When the ROC curve approaches the upper left corner, it displays true positive (TP) and false positive (FP) rates. This suggests that the proposed method may effectively categorize tumor types in magnetic resonance imaging (MRI) scan images.

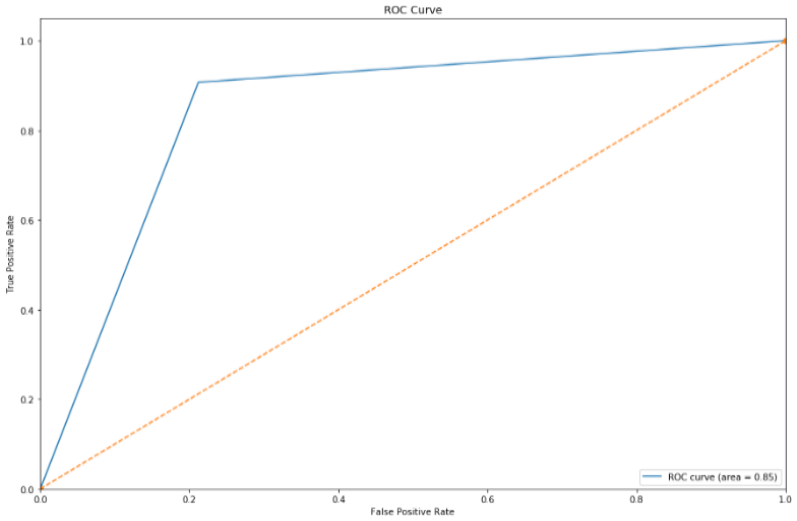

Figure 8: ROC curve of the proposed model

Feature Selection

Figure 9 displays the feature importance results provided by the FS-Ensemble.

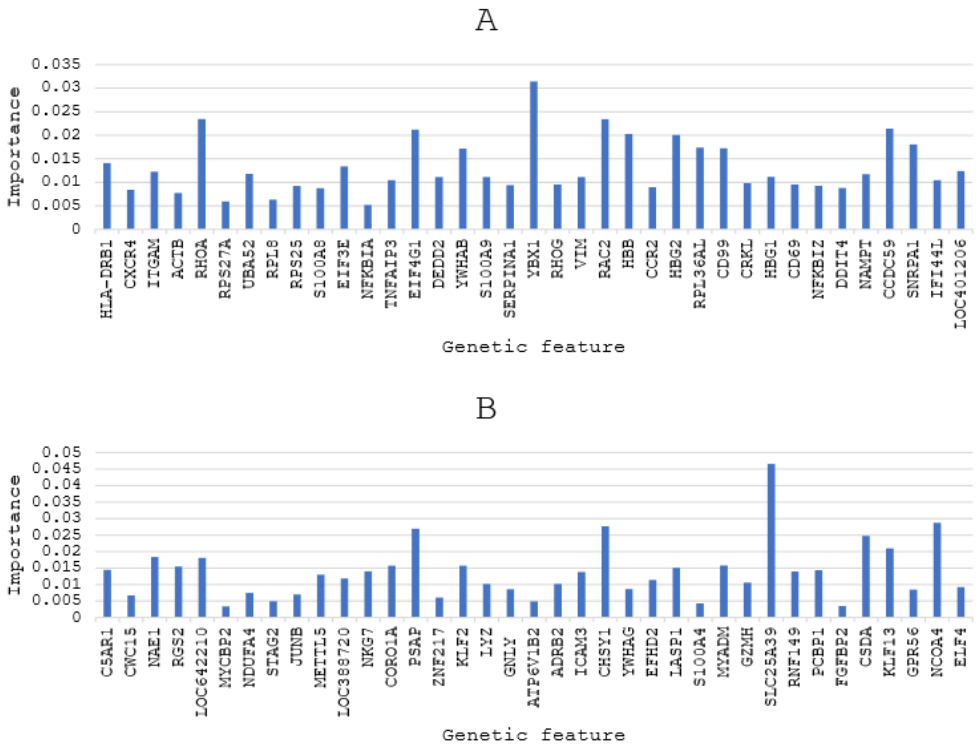

Figure 9: Feature importance and this graph presents the 74 genes divided into two blocks: (A) first part; (B) second part.

Classification

In our research, we explored various methods for identifying MS lesions on MRI scans, in addition to developing our own approach.Upon completing the implementation of our technique, we conducted a comparative analysis of its accuracy with the other methods we studied.Table 3 presents a summary of different studies on MS lesion detection using MRIs, showing their respective accuracy levels.

Table 3: THE OBTAINED RESULTS FROM DIFFERENT TOP RANK STRATEGIES

Method	Sensitivity	Specificity	Accuracy
[14]	69%	73%	72%
[15]	72%	89%	75%
[16]	84%	95%	95%
Proposed	98%	97%	99.65%

The table's findings indicate that our methodology is effective, as it exhibits greater precision than the techniques outlined in the cited research.

In addition to QCNN, we employed two other methods for MS lesion detection: VGG19 and Resnet50, both of which are CNN-based techniques. Among these three approaches, Resnet50 proves to be the quickest but least accurate, requiring an average of 244 s per epoch.VGG19, on the other hand, was the slowest method with moderate accuracy, taking approximately 490 s per epoch.Although QCNN was not the fastest, it yielded the highest accuracy of the three, with an average processing time of 390 s per epoch.Table 4 presents the detection results obtained using different approaches.

Table 4: THE OBTAINED RESULTS FROM DIFFERENT STRATEGIES OF CNN

Method	Sensitivity	Specificity	Accuracy
ResNet50	100%	95.45%	79.92%
VGG19	100%	97.54%	95.96%
Proposed (QCNN)	100%	99%	99.14%

Conclusion

This study demonstrated that a Quantum Machine Learning approach can accurately and efficiently identify MS lesions from MRI scans and determine disease progression.A smaller dataset can be effectively analyzed by training a model on an extensive dataset.To enhance accuracy, it also incorporated a dataset of MRI scans from healthy individuals to expedite the automated identification and categorization of Multiple Sclerosis.The system utilizes fluid-attenuated inversion recovery (FLAIR) MRI scans to enhance efficiency and reduce the overall processing time.Additionally, a novel feature selection ensemble was implemented in this method, and a Quantum Convolutional Neural Network was employed for the final step of MS lesion classification.The classifier processes the labeled segmentation features to categorize the MRI images.The proposed model demonstrated an impressive accuracy rate of 99.65%.Compared with state-of-the-art methods, the proposed model exhibits superior performance, delivering optimal results in terms of Sensitivity, Specificity, and Accuracy.In addition, the ROC, loss, and accuracy of the proposed hybrid model were evaluated against existing approaches.objectives include enhancing accuracy while reducing processing time. utilized a more extensive dataset to develop a robust system that delivers high efficiency and precision with minimal execution time.Furthermore, the system was redesigned to make it more computationally efficient.The computational efficiency of the system could enable its deployment in compact devices such as smartphones and tablets.In contemporary society, people increasingly rely on portable gadgets owing to their improved convenience and mobility.This strategy is expected to substantially enhance the value of this study.These findings indicate that the suggested model can effectively and accurately identify MS lesions and evaluate their advancement.

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