DOI: 10.21917/ijsc.2026.0570

QUANTUM-INSPIRED EVOLUTIONARY MODEL FOR ACCURATE AND ROBUST BRAIN TUMOR SEGMENTATION

P.T. Kalaivaani and G. Prabakaran

Department of Electronics and Communication Engineering, Vivekanandha College of Engineering for Women, India

Abstract

Brain tumor segmentation has remained a critical task in medical image analysis, as accurate delineation has directly supported diagnosis, treatment planning, and clinical decision-making. Conventional deep learning approaches have achieved notable success; however, they have often struggled with limited robustness when facing heterogeneous tumor shapes, intensity variations, and imaging noise across multimodal MRI data. Existing segmentation frameworks have relied heavily on deterministic optimization strategies that have suffered from premature convergence and reduced generalization. These limitations have affected segmentation consistency, particularly in complex tumor boundaries and low-contrast regions, which have demanded adaptive and globally optimized solutions. This study has presented a quantum-inspired evolutionary framework that has integrated probabilistic quantum representation with an evolutionary optimization mechanism. The proposed framework has encoded segmentation candidates using quantum bits that have allowed superposition-based exploration of the solution space. An evolutionary update strategy has guided probability amplitudes toward optimal states, while a convolutional segmentation backbone has extracted hierarchical spatial features. A fitness-driven selection process has refined candidate solutions that have maximized region similarity and boundary accuracy. The training process has incorporated adaptive mutation and crossover operators that have preserved diversity and stability during convergence. Experimental evaluation demonstrates that the proposed method achieves superior performance on benchmark brain MRI datasets. The Dice similarity coefficient reaches 0.91–0.93 across modalities, while the Jaccard index ranges from 0.81–0.84. Sensitivity achieves up to 0.92, and specificity remains high at 0.90–0.94. Overall accuracy ranges between 0.89–0.94, surpassing conventional CNN-based and evolutionary baselines. Visual inspection confirms precise tumor boundary delineation, particularly in infiltrative regions, indicating enhanced robustness under noise and intensity variations.

Keywords:

Brain Tumor Segmentation, Quantum-Inspired Optimization, Evolutionary Algorithms, Medical Image Analysis, MRI

1. INTRODUCTION

Brain tumor segmentation has played a central role in neuroimaging, as accurate identification of tumor regions has supported diagnosis, therapy planning, and longitudinal assessment in clinical practice. Magnetic resonance imaging has remained the primary modality due to its superior soft tissue contrast and multi-parametric capability. Over the past decade, traditional image processing and machine learning methods have gradually been replaced by deep learning models that have demonstrated strong representational power for complex anatomical patterns [1–3]. These models have enabled automated segmentation pipelines that have reduced clinician workload and inter-observer variability. Nevertheless, the intrinsic heterogeneity of tumor appearance across patients and imaging protocols has continued to limit consistent performance, particularly in real-world clinical settings.

1.1 CHALLENGES

Despite significant progress, several challenges have persisted in brain tumor segmentation. Variations in tumor size, shape, and texture have complicated the learning process, while overlapping intensity distributions between healthy and pathological tissues have increased ambiguity during boundary delineation [4]. In addition, imaging noise, scanner-dependent artifacts, and class imbalance have further degraded segmentation robustness. Deep networks that have relied on gradient-based optimization have often converged to suboptimal solutions, especially when training data has been limited or highly imbalanced [5]. These challenges have highlighted the need for optimization strategies that have enhanced global search capability and adaptability.

1.2 PROBLEM STATEMENT

Current segmentation frameworks have primarily focused on architectural innovations, while the optimization process has received comparatively less attention. Deterministic training strategies have constrained the exploration of the solution space, which has resulted in sensitivity to initialization and local minima [6]. Moreover, evolutionary approaches that have been explored earlier have suffered from slow convergence and limited scalability when applied to high-dimensional medical images [7]. As a result, a gap has existed for a unified framework that has combined powerful feature extraction with robust, diversity-preserving optimization.

1.3 OBJECTIVES

The primary objective of this work has been to develop a robust brain tumor segmentation framework that has improved generalization and boundary accuracy across diverse MRI data. The study has aimed to integrate a quantum-inspired evolutionary optimization mechanism with a deep segmentation backbone that has efficiently captured spatial context. Another objective has been to enhance robustness under noise and intensity variations while maintaining computational feasibility.

1.4 NOVELTY

The novelty of this research has resided in the integration of quantum-inspired probabilistic representation with evolutionary learning for medical image segmentation. Unlike conventional evolutionary algorithms, the proposed framework has modeled candidate solutions using quantum bits that have enabled superposition-based exploration. This design has balanced exploration and exploitation more effectively during training, which has differentiated it from existing CNN-only and hybrid approaches.

1.5 CONTRIBUTIONS

The main contributions of this work have been twofold. First, a quantum-inspired evolutionary segmentation framework has been proposed that has improved optimization stability and segmentation robustness. Second, comprehensive experimental analysis has validated the effectiveness of the proposed approach across standard evaluation metrics, demonstrating consistent improvements over existing methods.

2. RELATED WORKS

Early research in brain tumor segmentation has relied on classical image processing techniques such as thresholding, region growing, and clustering. These methods have exploited handcrafted features that have captured intensity and texture cues; however, their performance has remained limited under complex tumor morphologies and imaging noise [8]. To address these limitations, machine learning classifiers such as support vector machines and random forests have been introduced. These approaches have improved discrimination capability but have depended heavily on feature engineering and expert knowledge.

The emergence of deep learning has significantly transformed the segmentation landscape. Convolutional neural networks have demonstrated superior capability in learning hierarchical features directly from raw MRI data. Architectures such as fully convolutional networks and encoder–decoder models have enabled end-to-end segmentation that has reduced manual intervention [9]. Variants with skip connections and multi-scale fusion have further enhanced spatial detail preservation. Despite these advances, CNN-based models have remained sensitive to data scarcity and have required extensive tuning.

To overcome generalization issues, several studies have incorporated attention mechanisms and multi-modal fusion strategies. These methods have emphasized salient tumor regions and have leveraged complementary information across MRI modalities. Although performance has improved, such models have introduced additional complexity and computational overhead, which has limited their practical deployment [10]. Furthermore, optimization has continued to rely on gradient descent, which has constrained global exploration.

Evolutionary algorithms have been explored as an alternative optimization paradigm in medical imaging. Genetic algorithms and particle swarm optimization have been applied to feature selection, parameter tuning, and segmentation refinement. These methods have offered global search capability but have often suffered from slow convergence and instability when dealing with large-scale image data [11]. Hybrid models that have combined evolutionary strategies with neural networks have attempted to mitigate these issues, yet scalability has remained a concern.

Quantum-inspired evolutionary algorithms have emerged as a promising extension of classical evolutionary computation. By modeling individuals using probability amplitudes, these algorithms have maintained population diversity more effectively and have accelerated convergence in complex optimization problems. Previous studies have applied quantum-inspired methods to pattern recognition and optimization tasks, reporting improved search efficiency [12]. However, their application to medical image segmentation has remained limited and underexplored.

Recent works have attempted to integrate advanced optimization techniques with deep learning for segmentation tasks. Some approaches have introduced reinforcement learning and meta-heuristic tuning to adapt network parameters dynamically. While these methods have shown potential, they have increased training complexity and have required extensive computational resources [13]-[16]. Moreover, robustness under noisy and heterogeneous medical data has not been consistently addressed.

3. PROPOSED METHOD

The proposed method has presented a quantum-inspired evolutionary framework for robust brain tumor segmentation. This framework has combined a deep convolutional segmentation backbone with a quantum-inspired evolutionary optimizer that has guided network parameter tuning and candidate solution refinement. The approach has leveraged quantum bit-based probabilistic encoding to maintain solution diversity, while evolutionary operators such as adaptive mutation and crossover have explored the solution space effectively. The integration of a fitness-driven selection mechanism has ensured that candidate solutions have been refined toward optimal tumor delineation. Overall, the proposed method has improved segmentation accuracy, boundary delineation, and robustness under heterogeneous MRI data.

1) Initialize population with quantum bit representation for segmentation candidates.
2) Encode each candidate solution into a probabilistic superposition state.
3) Pass MRI images through a convolutional segmentation backbone to extract hierarchical features.
4) Evaluate fitness of each candidate using Dice similarity coefficient and boundary accuracy metrics.
5) Apply quantum-inspired evolutionary operators:
    a) Adaptive mutation to modify probability amplitudes
    b) Crossover to combine promising candidates
    c) Update quantum probability amplitudes based on fitness-driven selection.
    d) Repeat steps 3–6 until convergence or maximum iterations are reached.
    e) Decode the optimal candidate solution to obtain final segmentation mask.

Algorithm: Quantum-Inspired Evolutionary Brain Tumor Segmentation

Input: MRI dataset D, Max Iterations T, Population Size N

Output: Segmentation mask S_opt

1. Initialize population P with N candidates using quantum bits
2. For each candidate p in P:
    Encode p in quantum superposition state
3. For t = 1 to T do:
    For each candidate p in P:

Extract features F_p using convolutional segmentation backbone

Compute fitness f_p = α * Dice(F_p, GT) + β * Boundary(F_p, GT)

Select top candidates based on fitness

Apply quantum-inspired mutation and crossover

Update quantum probability amplitudes for each candidate

4. End For

5. Decode the best candidate p_best to obtain final segmentation mask S_opt

6. Return S_opt

In this step, the segmentation candidates have been encoded as quantum bits (qubits), each representing a probabilistic state of a potential solution. The qubit representation allows each candidate to simultaneously encode multiple potential solutions, which enhances the exploration of the solution space.

The Qubit State Representation is represented by:

$$|\psi\rangle = \alpha|0\rangle + \beta|1\rangle$$

where,

$$|\alpha_i|^2 + |\beta_i|^2 = 1$$

$|\psi\rangle$ represents the i^{th} candidate, and α_i and β_i are probability amplitudes for the 0 and 1 states respectively.

Table.1. Qubit Initialization

Candidate	α (Amplitude 0)	β (Amplitude 1)
P1	0.6	0.8
P2	0.7	0.7
P3	0.5	0.9

This table illustrates how each candidate has been initialized with distinct probability amplitudes to allow diverse exploration.

The MRI images have been passed through a convolutional segmentation network, which has extracted hierarchical spatial features. This backbone has captured local and global contextual information essential for tumor delineation.

The Feature Map Computation

$$F^{(l)} = \sigma\left(W^{(l)} * F^{(l-1)} + b^{(l)}\right)$$

where $F^{(l)}$ represents the feature map at layer l, $W^{(l)}$ and $b^{(l)}$ are convolution weights and biases, $*$ denotes convolution, and σ is the activation function.

Table.2. Feature Map Values

Layer	Feature Map Size	Activation Values
Conv1	128x128x32	0.12, 0.45, 0.78
Conv2	64x64x64	0.23, 0.56, 0.81
Conv3	32x32x128	0.31, 0.67, 0.92

The feature maps show the hierarchical extraction that has enhanced the distinction between tumor and healthy tissue.

3.1 FITNESS EVALUATION

Each candidate solution has been evaluated using a fitness function that has combined region similarity and boundary precision. The Dice coefficient has quantified volumetric overlap, while boundary accuracy has captured edge alignment with ground truth.

The Fitness Function is estimated as:

$$f_p = \alpha \cdot \frac{2|S_p \cap GT|}{|S_p| + |GT|} + \beta \cdot \frac{|\partial S_p \cap \partial GT|}{|\partial GT|}$$

where S_p is the candidate segmentation, GT is the ground truth, and ∂ denotes the boundary. α and β are weighting factors.

Table.3. Fitness Evaluation

Candidate	Dice Coefficient	Boundary Accuracy	Fitness Score
P1	0.82	0.79	0.805
P2	0.78	0.81	0.795
P3	0.85	0.76	0.805

The table indicates how candidates have been evaluated for selection in the evolutionary process.

4. QUANTUM-INSPIRED EVOLUTIONARY OPERATORS

Adaptive mutation has modified qubit probability amplitudes based on fitness, allowing candidates to explore new regions of the solution space. Crossover has combined promising candidates to generate offspring with enhanced diversity.

The Quantum Amplitude Update is referred to as:

$$\begin{bmatrix} \alpha_i' \\ \beta_i' \end{bmatrix} = \begin{bmatrix} \cos(\theta_i) & -\sin(\theta_i) \\ \sin(\theta_i) & \cos(\theta_i) \end{bmatrix} \begin{bmatrix} \alpha_i \\ \beta_i \end{bmatrix}$$

where θ_i is the rotation angle determined adaptively from candidate fitness.

Table 4: Amplitude Update

Candidate	α (Old)	β (Old)	α (Updated)	β (Updated)
P1	0.6	0.8	0.62	0.78
P2	0.7	0.7	0.72	0.68
P3	0.5	0.9	0.53	0.88

This update ensures that high-fitness candidates are more likely to guide the evolution process.

Candidates have been selected based on fitness-driven probability. The quantum-inspired mechanism has allowed multiple candidates to maintain diversity while converging toward optimal segmentation.

The Probability-Based Selection

$$P(S_i) = \frac{f_i}{\sum_{j=1}^{N} f_j}$$

where $P(S_i)$ is the selection probability of candidate i, and f_i is its fitness score.

Table.5. Selection Probability

Candidate	Fitness Score	Selection Probability
P1	0.805	0.334
P2	0.795	0.330
P3	0.805	0.334

This selection process ensures that the best-performing candidates have guided the subsequent evolution iterations.

After convergence, the best candidate has been decoded to generate the final segmentation mask, representing the delineated tumor regions. This step has translated the probabilistic representation into a deterministic mask suitable for clinical interpretation.

The Candidate Decoding is defined as:

$$S_{\text{opt}}(x,y)=\begin{cases}1, & \text{if} |\alpha_i^{\text{final}}|^2 > |\beta_i^{\text{final}}|^2\\ 0, & \text{otherwise}\end{cases}$$

Table.6. Final Segmentation Decision

Pixel	α² (Final)	β² (Final)	Segmentation Label
(10,10)	0.78	0.22	1 (Tumor)
(15,20)	0.34	0.66	0 (Healthy)
(12,18)	0.81	0.19	1 (Tumor)

The final mask demonstrates precise delineation of tumor boundaries, which has validated the robustness of the proposed framework.

5. RESULTS AND DISCUSSION

The experiments are conducted using MATLAB R2023b simulation environment to implement the quantum-inspired evolutionary segmentation framework. The convolutional backbone and quantum evolutionary operators are integrated within the same platform to ensure seamless evaluation.

5.1 EXPERIMENTAL SETUP AND PARAMETERS

The framework is configured with parameters optimized for robust segmentation across heterogeneous MRI scans. The population size, quantum rotation angle, and maximum iterations have been tuned empirically to balance exploration and convergence. The convolutional backbone uses three convolutional layers with kernel sizes and strides set to extract hierarchical features while preserving spatial resolution.

Table.7. Experimental Parameters and Values

Parameter	Value / Setting	Description
Population Size (N)	30	Number of quantum candidates per iteration
Maximum Iterations (T)	100	Number of evolutionary generations
Quantum Rotation Angle (θ)	Adaptive (0–π/4)	Angle for probability amplitude update
Convolution Layers	3	Layers in segmentation backbone
Kernel Size	3x3	Convolution kernel size for feature extraction
Learning Rate	0.001	For CNN backbone weight update
Mutation Probability	0.1	Likelihood of amplitude mutation
Crossover Probability	0.8	Likelihood of candidate combination
Dice–Boundary Weights (α, β)	0.6, 0.4	Weighting for fitness computation

These parameters have been chosen to ensure stable convergence while preserving diversity among the quantum candidates (Table.7).

5.2 PERFORMANCE METRICS

The performance of the proposed method is evaluated using five metrics:

- **Dice Similarity Coefficient (DSC):** Measures the volumetric overlap between predicted segmentation and ground truth. Higher values indicate better overlap.
- **Jaccard Index (JI):** Quantifies similarity between predicted and actual tumor regions by comparing intersection over union.
- **Sensitivity (Recall):** Evaluates the proportion of actual tumor pixels correctly identified, highlighting detection capability.
- **Specificity:** Measures the proportion of non-tumor pixels correctly classified, indicating robustness against false positives.
- **Accuracy:** Represents the overall proportion of correctly classified pixels, balancing tumor and background predictions.

These metrics collectively provide a comprehensive evaluation of segmentation performance in terms of precision, recall, overlap, and overall correctness.

5.3 DATASET DESCRIPTION

The experimental evaluation utilizes the BraTS 2021 multi-modal MRI dataset, which contains T1, T1c, T2, and FLAIR sequences. The dataset includes high-grade and low-grade gliomas with manual annotations provided by expert radiologists. Images have been preprocessed with skull-stripping, intensity normalization, and resizing to a uniform 240×240×155 voxel resolution for compatibility with the segmentation backbone.

Table.8. Dataset Description

Attribute	Description
Dataset Name	BraTS 2021
Modalities	T1, T1c, T2, FLAIR
Number of Patients	335 (Training set)
Tumor Types	High-grade glioma (HGG), Low-grade glioma (LGG)

Preprocessing Steps	Skull-stripping, normalization, resizing
Annotation	Manual expert segmentation
Image Resolution	240×240×155 voxels

The dataset provides comprehensive coverage of tumor heterogeneity and allows evaluation across multiple imaging modalities (Table 2).

Results and Discussion

The performance of the proposed quantum-inspired evolutionary framework is evaluated against three existing methods: Fully Convolutional Network (FCN), Attention U-Net, and Particle Swarm Optimization (PSO)-based segmentation. The evaluation is performed using Dice–Boundary weights $\alpha = 0.6$ and $\beta = 0.4$. Separate tables are presented for each metric with values to illustrate comparative performance.

Table.9. Dice Similarity Coefficient (DSC)

Method / Modality	T1	T1c	T2	FLAIR
FCN	0.85	0.87	0.84	0.83
Attention U-Net	0.88	0.90	0.86	0.85
PSO-based	0.81	0.83	0.80	0.79
Proposed Method	0.91	0.93	0.89	0.88

The proposed method achieves the highest DSC across all MRI modalities, demonstrating improved overlap with the ground truth. The integration of quantum-inspired evolutionary optimization has enhanced tumor boundary delineation, especially in heterogeneous regions.

Table.10. Jaccard Index (JI)

Method / Modality	T1	T1c	T2	FLAIR
FCN	0.74	0.76	0.73	0.71
Attention U-Net	0.77	0.79	0.75	0.74
PSO-based	0.70	0.72	0.69	0.68
Proposed Method	0.81	0.84	0.79	0.78

Jaccard index confirms that the proposed framework consistently achieves higher intersection over union. The quantum-inspired population diversity prevents premature convergence that affects FCN and PSO-based methods.

Table.11. Sensitivity (Recall)

Method / Modality	T1	T1c	T2	FLAIR
FCN	0.83	0.86	0.82	0.81
Attention U-Net	0.86	0.89	0.84	0.83
PSO-based	0.78	0.81	0.77	0.75
Proposed Method	0.90	0.92	0.88	0.87

The proposed method demonstrates superior sensitivity, indicating that tumor pixels are detected more reliably, even in low-contrast regions such as FLAIR images.

Table.12. Specificity

Method / Modality	T1	T1c	T2	FLAIR
FCN	0.88	0.89	0.87	0.86
Attention U-Net	0.90	0.91	0.89	0.88
PSO-based	0.85	0.86	0.84	0.83
Proposed Method	0.93	0.94	0.91	0.90

Specificity results highlight that the proposed framework minimizes false positives, accurately distinguishing tumor and healthy tissue across all modalities.

Table.13. Accuracy

Method / Modality	T1	T1c	T2	FLAIR
FCN	0.86	0.88	0.85	0.84
Attention U-Net	0.88	0.90	0.87	0.86
PSO-based	0.82	0.84	0.81	0.80
Proposed Method	0.92	0.94	0.90	0.89

5.4 DISCUSSION OF RESULTS

The proposed quantum-inspired evolutionary segmentation framework demonstrates consistently superior performance across all evaluated metrics and MRI modalities. As shown in Table.9, the Dice similarity coefficient achieves 0.91 for T1, 0.93 for T1c, 0.89 for T2, and 0.88 for FLAIR, surpassing FCN (0.85–0.87) and Attention U-Net (0.86–0.90). Similarly, the Jaccard index in Table.10 confirms improved intersection over union, reaching 0.81–0.84 across modalities, which represents approximately 4–8% improvement over the best existing method. Sensitivity values in Table.11 indicate robust tumor detection, with 0.90 in T1 and 0.92 in T1c, demonstrating enhanced identification of low-contrast tumor regions. Specificity results in Table.12 remain high (0.90–0.94), showing minimal false positive segmentation and confirming reliable distinction between tumor and healthy tissue. Overall accuracy in Table.13 ranges from 0.89 in FLAIR to 0.94 in T1c, reflecting an average improvement of ~5% over existing methods. These results indicate that the integration of quantum-inspired probabilistic encoding with evolutionary optimization effectively balances exploration and exploitation, allowing consistent convergence toward optimal segmentation. Moreover, the adaptive mutation and crossover mechanisms maintain candidate diversity, which ensures resilience under heterogeneous MRI data and imaging artifacts. Collectively, the numerical outcomes validate that the proposed method significantly enhances both volumetric and boundary accuracy compared to conventional CNN and PSO-based approaches.

6. CONCLUSION

The study presents a quantum-inspired evolutionary framework for robust brain tumor segmentation that effectively combines deep feature extraction with probabilistic evolutionary optimization.

Experimental evaluation demonstrates that the framework achieves high segmentation performance across multi-modal MRI data, with Dice similarity coefficients reaching 0.91–0.93, Jaccard index values of 0.81–0.84, and sensitivity up to 0.92. Specificity and overall accuracy remain high (0.90–0.94), indicating precise tumor delineation and minimal false positives. The probabilistic representation of candidates using quantum bits, along with adaptive evolutionary operators, enables efficient exploration of the solution space, preventing premature convergence and enhancing robustness under heterogeneous and noisy imaging conditions. Compared to existing methods such as FCN, Attention U-Net, and PSO-based segmentation, the proposed framework consistently outperforms both deep learning and traditional optimization strategies. These findings confirm that the integration of quantum-inspired evolutionary principles with convolutional networks provides a reliable and accurate approach for clinical brain tumor segmentation. The framework offers potential for broader applications in medical imaging tasks that require both high boundary precision and volumetric accuracy, establishing a foundation for future developments in intelligent and adaptive segmentation methodologies.

REFERENCES

[1] T. Meenal and R. Asokan, "Quantum-Inspired Adaptive Feature Fusion for Highly Accurate Brain Tumor Classification in MRI using Deep Learning", *Biomedical Signal Processing and Control*, Vol. 112, pp. 108694-108712, 2026.

[2] R. Gupta, T.A. Kakani and K. Hudani, "Advancing Clinical Decision-Making using Artificial Intelligence and Machine Learning for Accurate Disease Diagnosis", *Proceedings of International Conference on Intelligent Communication Technologies and Virtual Mobile Networks*, pp. 164-169, 2025.

[3] R. Gupta, T.A. Kakani and K. Hudani, "Developing Predictive Models for Disease Diagnosis using Machine Learning and Deep Learning Techniques", *Proceedings of International Conference on Intelligent Communication Technologies and Virtual Mobile Networks*, pp. 158-163, 2025.

[4] V. Sharma, R.P. Shukla and D. Kumar, "A Meta Learning Approach for Improving Medical Image Segmentation with Transfer Learning", *Proceedings of International Conference on Recent Innovation in Smart and Sustainable Technology*, pp. 1-6, 2024.

[5] G. Vinuja, V. Saravanan, K. Maharajan and S. Jothi Arunachalam, "Diagnostic Device for Sustainable Medical Care using Hyperspectral Imaging", *Proceedings of International Conference on Emerging Advancements in AI and Big Data Technologies in Business and Society*, pp. 128-142, 2024.

[6] S. Bhattacharya, S. Prusty, S.P. Pande and S. Veerasamy, "Integration of Multimodal Imaging Data with Machine Learning for Improved Diagnosis and Prognosis in Neuroimaging", *Frontiers in Human Neuroscience*, Vol. 19, pp. 1552178-1552189, 2025.

[7] P. Pal, S. Bhattacharyya, J. Platos and V. Snasel, "A Brief Survey on Image Segmentation based on Quantum Inspired Neural Network", *International Journal of Hybrid Intelligence*, Vol. 2, No. 2, pp. 102-118, 2023.

[8] K. Subhashini and J. Thangakumar, "QICCNN: Quantum-Inspired Complex Convolutional Neural Network based Brain Tumor Detection from MRI Images", *Proceedings of International Conference on Intelligent Technologies*, pp. 1-5, 2024.

[9] D. Konar, S. Bhattacharyya and R. Jiang, "3-D Quantum-Inspired Self-Supervised Tensor Network for Volumetric Segmentation of Medical Images", *IEEE Transactions on Neural Networks and Learning Systems*, Vol. 35, No. 8, pp. 10312-10325, 2023.

[10] A. Bilal, M. Shafiq and H. Long, "Quantum Computational Infusion in Extreme Learning Machines for Early Multi-Cancer Detection", *Journal of Big Data*, Vol. 12, No. 1, pp. 1-27, 2025.

[11] G. Swathi, A. Altalbe and R.P. Kumar, "QuCNet: Quantum-Inspired Convolutional Neural Networks for Optimized Thyroid Nodule Classification", *IEEE Access*, Vol. 12, pp. 27829-27842, 2024.

[12] S.S. Sivasankari, J. Surendiran and R.G. Vidhya, "Classification of Diabetes using Multilayer Perceptron", *Proceedings of IEEE International Conference on Distributed Computing and Electrical Circuits and Electronics*, pp. 1-5, 2022.

[13] S.K. Roy and B. Rudra, "Quantum-Inspired Hybrid Algorithm for Image Classification and Segmentation: Q-Means++ Max-Cut Method", *International Journal of Imaging Systems and Technology*, Vol. 34, No. 1, pp. 23015-23026, 2024.

[14] S. Saumiya and A. Alvin Ancy, "ISAM-QV7Net: An Improved Segment Anything Model-2 with the Quantum-Inspired Superposition Memory and Vision-Efficient NETB7 for the Advanced Liver Tumor Prognosis", *The European Physical Journal Plus*, Vol. 140, No. 7, pp. 679-693, 2025.

[15] A.K. Shukla, S. Dwivedi, S.K. Singh and R.K. Dewangan, "Optimized Breast Cancer Diagnosis using Self-Adaptive Quantum Metaheuristic Feature Selection", *Scientific Reports*, Vol. 15, No. 1, pp. 19900-19924, 2025.

[16] S.P. Rajamohana, V. Yelamali, P. Soni and P. Prasad, "Hybrid Quantum Graph Neural Network for Brain Tumor MR Image Classification: Hybrid Quantum Graph Neural Network for Brain Tumor MR Image", *Journal of Scientific and Industrial Research*, Vol. 84, No. 1, pp. 60-71, 2025.