

QFusionNet: A Quantum-Enhanced Hybrid Learning Framework for Intelligent Early Cancer Detection

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Abstract — Early and accurate cancer detection is essential for improving patient survival rates and enabling timely clinical intervention. However, conventional diagnostic approaches and classical machine learning techniques often encounter challenges in processing high-dimensional biomedical datasets due to feature redundancy, computational complexity, and limited predictive performance. To address these limitations, this paper proposes a quantum-assisted intelligent framework for early cancer detection by integrating advanced quantum-inspired preprocessing, feature optimization, and hybrid predictive modeling techniques. The proposed methodology employs Quantum-Normalized Adaptive Refinement (Q-NAR) to enhance data quality through effective preprocessing, Wrapper Component Attribute Analysis (WCAA) to rank significant biomedical features, and Swing L-Bee Mustard Optimization (SLBMO) to identify the optimal feature subset while reducing dimensionality. Finally, a Quantum Boosted Vector Fusion Network (QBVFN) is developed to perform accurate cancer classification and treatment outcome prediction. The proposed framework is validated using biomedical data from The Cancer Genome Atlas (TCGA) within a Python-based implementation environment. Experimental evaluation demonstrates that the proposed approach achieves superior prediction accuracy, improved feature optimization, and enhanced computational efficiency compared with conventional machine learning models. The obtained results highlight the effectiveness of integrating quantum computing principles with machine learning techniques to support next-generation intelligent cancer diagnosis and precision healthcare systems.

Keywords— Quantum Machine Learning, Early Cancer Detection, Biomedical Data Analysis, Quantum Boosted Vector Fusion Network (QBVFN), Feature Selection, Cancer Genome Atlas (TCGA), Predictive Analytics, Healthcare Intelligence, Quantum Computing, Machine Learning.

I. INTRODUCTION

Cancer continues to be one of the most significant global health challenges, accounting for millions of deaths annually despite considerable advancements in medical science. The effectiveness of cancer treatment largely depends on early diagnosis, as identifying the disease during its initial stages substantially improves patient survival rates and increases the success of therapeutic interventions. Conventional diagnostic techniques, including histopathological analysis, medical imaging, and biomarker evaluation, have contributed significantly to cancer diagnosis; however, these approaches often face limitations in handling large-scale biomedical datasets characterized by high dimensionality, feature redundancy, and computational complexity [1]–[3].

The rapid growth of healthcare technologies has resulted in the generation of massive volumes of biomedical information, including genomic sequences, clinical records, molecular biomarkers, and medical imaging data. Extracting meaningful knowledge from these heterogeneous datasets requires intelligent computational methods capable of identifying

complex biological patterns associated with cancer progression. Machine learning has emerged as a powerful tool for biomedical data analysis by enabling automated feature learning, disease classification, and clinical decision support. Classical machine learning algorithms such as Support Vector Machines, Decision Trees, Random Forests, and Artificial Neural Networks have demonstrated promising performance in cancer prediction; however, their effectiveness is often limited by redundant features, increased computational overhead, and reduced scalability when processing high-dimensional datasets [2], [3].

Recent advances in Quantum Machine Learning (QML) have introduced new opportunities for addressing these computational challenges by integrating quantum computing principles with artificial intelligence techniques. Quantum computing utilizes concepts such as superposition, entanglement, and quantum parallelism, enabling efficient processing of complex optimization and learning tasks that are computationally expensive for classical systems. The combination of quantum computing with machine learning has shown significant potential in biomedical data analysis, feature

optimization, genomic research, and intelligent clinical decision support, thereby improving prediction accuracy and computational efficiency [4]–[6], [10], [11].

Motivated by these developments, this paper proposes a Quantum-Driven Vector Fusion Network for early cancer detection that combines advanced quantum-assisted preprocessing, intelligent feature selection, optimization, and hybrid predictive modeling within a unified diagnostic framework. Initially, Quantum-Normalized Adaptive Refinement (Q-NAR) is employed to improve biomedical data quality through adaptive preprocessing. Subsequently, Wrapper Component Attribute Analysis (WCAA) ranks the most informative biomedical features, while Swing L-Bee Mustard Optimization (SLBMO) identifies the optimal feature subset by eliminating redundant attributes. Finally, the optimized data are processed using the proposed Quantum Boosted Vector Fusion Network (QBVFN) to perform accurate cancer classification and treatment outcome prediction. This integrated framework enhances feature representation, reduces computational complexity, and improves diagnostic performance for early-stage cancer detection [5], [6], [12].

The proposed framework is evaluated using biomedical datasets obtained from The Cancer Genome Atlas (TCGA), and its performance is assessed using standard classification metrics. Experimental results demonstrate that the integration of quantum-assisted preprocessing, intelligent feature optimization, and hybrid predictive modeling significantly improves cancer detection accuracy while maintaining computational efficiency. The proposed approach contributes to the advancement of intelligent healthcare systems by providing a scalable and reliable framework capable of supporting precision medicine, personalized treatment planning, and next-generation cancer diagnosis [4]–[6], [12].

II. LITERATURE SURVEY

Recent advancements in Artificial Intelligence (AI) and Machine Learning (ML) have significantly transformed healthcare by enabling intelligent analysis of complex biomedical data for disease diagnosis and clinical decision support. Machine learning algorithms have demonstrated remarkable success in identifying hidden patterns from genomic data, medical images, and electronic health records, thereby assisting healthcare professionals in the early detection of cancer and improving treatment planning. The integration of AI-driven predictive models into healthcare has substantially enhanced diagnostic accuracy while reducing human intervention in medical decision-making [1]–[3].

Conventional machine learning techniques, including Support Vector Machines (SVM), Decision Trees, Random Forests, Artificial Neural Networks (ANNs), and ensemble learning methods, have been extensively applied to cancer diagnosis and biomedical data analysis. These algorithms are capable of learning discriminative patterns from high-dimensional datasets and have shown promising performance in predicting various types of cancer. However, their effectiveness is often limited by redundant biomedical features, increased computational complexity, and scalability challenges when processing large genomic datasets. Consequently, efficient preprocessing and feature optimization techniques have become essential components of intelligent cancer detection systems [2], [3].

The emergence of quantum computing has introduced new opportunities for addressing computational challenges associated with biomedical data analysis. Unlike classical computing, quantum computing exploits principles such as superposition, entanglement, and quantum parallelism to efficiently solve complex optimization problems. Researchers have demonstrated the potential of quantum computing in healthcare applications, including genomic analysis, radiotherapy optimization, and clinical decision support, highlighting its capability to process high-dimensional biomedical datasets more efficiently than conventional computational approaches [4], [5].

The integration of quantum computing with machine learning has led to the development of Quantum Machine Learning (QML), an emerging research area that combines quantum computational principles with intelligent predictive models. QML techniques have shown considerable promise in improving feature extraction, dimensionality reduction, optimization, and classification performance for biomedical applications. Hybrid quantum–classical learning models have been reported to enhance computational efficiency while maintaining high predictive accuracy when analysing complex healthcare datasets [6].

Several studies have further explored the application of quantum-assisted algorithms in oncology and precision medicine. Quantum-inspired optimization techniques have been successfully employed for radiotherapy planning, adaptive treatment optimization, genomic sequence analysis, and bioinformatics research. These approaches demonstrate the capability of quantum-based methodologies to improve feature selection, identify clinically significant biomarkers, and support accurate disease prediction in cancer diagnosis [7]–[11].

More recently, researchers have investigated intelligent quantum-based predictive frameworks that integrate advanced optimization techniques with machine learning models to improve clinical decision-making. These hybrid frameworks combine efficient preprocessing, optimized feature selection, and predictive modelling to enhance disease classification accuracy and computational performance. Such developments indicate that quantum-assisted machine learning has considerable potential to support next-generation intelligent healthcare systems and precision medicine applications [12].

Although significant progress has been achieved, existing cancer detection systems continue to face challenges related to high-dimensional biomedical data, redundant feature representation, computational overhead, and limited scalability. Motivated by these limitations, the proposed research introduces a Quantum-Driven Vector Fusion Network that integrates Quantum-Normalized Adaptive Refinement (Q-NAR), Wrapper Component Attribute Analysis (WCAA), Swing L-Bee Mustard Optimization (SLBMO), and a Quantum Boosted Vector Fusion Network (QBVFN) to improve feature optimization, prediction accuracy, and computational efficiency for early cancer detection [4]–[6], [12].

III. SYSTEM ANALYSIS

1. Related Work

Conventional cancer detection systems primarily rely on classical machine learning algorithms and standard diagnostic methodologies to analyze biomedical datasets, including genomic sequences, histopathological images, clinical records, and molecular biomarkers. Widely adopted algorithms such as Support Vector Machines (SVM), Decision Trees (DT), Random Forests (RF), Naïve Bayes (NB), and Artificial Neural Networks (ANNs) have been extensively utilized to classify cancerous and non-cancerous samples. These models assist clinicians by learning predictive patterns from labeled biomedical data, thereby supporting automated disease diagnosis and clinical decision-making [2], [3].

Although these techniques have improved diagnostic performance, they often encounter significant challenges when processing high-dimensional biomedical datasets. Genomic and molecular datasets typically contain thousands of features, many of which are redundant or irrelevant, leading to increased computational complexity and reduced prediction accuracy. Traditional preprocessing and feature selection methods are frequently insufficient to identify the most informative biomarkers, resulting in inefficient learning and limited model generalization [4], [5].

Recent studies have explored the application of quantum computing and Quantum Machine Learning (QML) to overcome these computational limitations. Quantum-assisted algorithms exploit principles such as superposition and entanglement to accelerate optimization and improve feature selection. While these approaches demonstrate promising performance in biomedical data analysis, many existing frameworks remain focused on individual optimization techniques and do not provide an integrated pipeline that combines quantum-assisted preprocessing, feature optimization, and hybrid predictive modeling for early cancer detection [4]–[6], [10], [11].

2. Proposed Approach

To address the limitations of conventional cancer detection methods, the proposed research introduces a Quantum-Driven Vector Fusion Network (QBVFN) that integrates quantum-assisted preprocessing, intelligent feature selection, bio-inspired optimization, and hybrid predictive modeling into a unified diagnostic framework. The proposed architecture is specifically designed to improve early cancer detection by enhancing feature representation, reducing computational complexity, and increasing prediction accuracy for high-dimensional biomedical datasets [4]–[6].

Initially, biomedical data obtained from The Cancer Genome Atlas (TCGA) undergo preprocessing using Quantum-Normalized Adaptive Refinement (Q-NAR), which improves data quality by eliminating noise, handling inconsistencies, and generating normalized feature representations suitable for machine learning analysis. Subsequently, Wrapper Component Attribute Analysis (WCAA) evaluates and ranks biomedical attributes according to their contribution to cancer prediction, enabling the identification of clinically significant biomarkers while removing redundant features [5], [6].

To further optimize the feature space, the proposed framework employs Swing L-Bee Mustard Optimization (SLBMO), a bio-inspired optimization algorithm that determines the optimal subset of informative features. This optimization process reduces dataset dimensionality while preserving essential predictive information, thereby improving computational efficiency and model generalization [6], [7].

Finally, the optimized biomedical features are processed using the proposed Quantum Boosted Vector Fusion Network (QBVFN), which integrates quantum computing principles with machine learning techniques to perform accurate cancer classification and treatment outcome prediction. The hybrid predictive model effectively captures complex nonlinear relationships within biomedical data, resulting in improved

diagnostic performance, enhanced scalability, and reliable clinical decision support. Experimental evaluation demonstrates that the proposed framework provides superior accuracy, efficient feature optimization, and reduced computational overhead compared with conventional machine learning approaches [5], [6], [12].

IV. SYSTEM DESIGN

1. System Architecture

Below diagram depicts the whole system architecture.

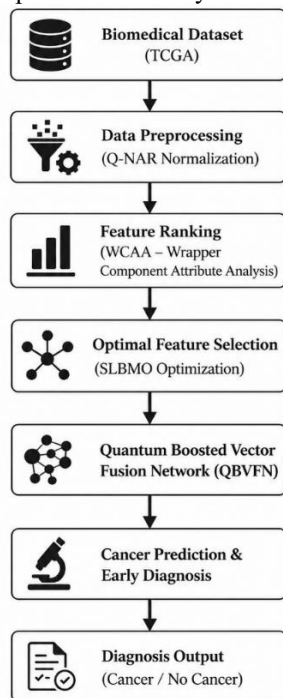


Fig 1. Methodology followed for proposed model

V. SYSTEM IMPLEMENTATION

1. Modules

The proposed Quantum-Driven Vector Fusion Network (QBVFN) framework is implemented through a sequence of interconnected modules that collectively perform biomedical data acquisition, preprocessing, feature optimization, predictive modeling, and cancer diagnosis. Each module is designed to improve computational efficiency, reduce feature redundancy, and enhance prediction accuracy for early cancer detection.

Biomedical Data Collection Module

The Biomedical Data Collection Module is responsible for acquiring high-dimensional biomedical datasets from reliable

healthcare repositories, particularly The Cancer Genome Atlas (TCGA). The collected data include genomic information, gene expression profiles, clinical attributes, and biomarker records associated with various cancer types. These datasets provide comprehensive biological information required for training intelligent predictive models and are organized into a structured format before further processing [3], [10], [11].

Quantum-Assisted Data Preprocessing Module

The collected biomedical data often contain missing values, noise, inconsistencies, and redundant information that can adversely affect prediction performance. To address these challenges, the proposed framework employs Quantum-Normalized Adaptive Refinement (Q-NAR) for data preprocessing. This module performs data cleaning, missing value handling, normalization, and refinement to improve data quality while preserving significant biomedical characteristics. The preprocessing stage ensures that the dataset is suitable for efficient feature analysis and predictive learning [4]–[6].

Feature Ranking and Engineering Module

Biomedical datasets generally contain thousands of features, many of which contribute minimally to disease prediction. This module applies Wrapper Component Attribute Analysis (WCAA) to evaluate the importance of each biomedical feature and rank them according to their contribution to cancer diagnosis. In addition, feature engineering techniques are employed to eliminate redundant attributes and generate an optimized feature representation that improves model interpretability and reduces computational complexity [5], [6], [12].

Optimal Feature Selection Module

Following feature ranking, the proposed framework utilizes Swing L-Bee Mustard Optimization (SLBMO) to identify the optimal subset of informative biomedical features. This bio-inspired optimization algorithm effectively minimizes dataset dimensionality while preserving critical biomarkers required for accurate cancer prediction. The optimized feature subset significantly enhances computational efficiency, improves learning capability, and reduces unnecessary processing overhead during model training [6], [7].

Quantum Boosted Vector Fusion Network Module

The optimized biomedical features are provided as input to the Quantum Boosted Vector Fusion Network (QBVFN), which serves as the core predictive model of the proposed framework. QBVFN integrates quantum computing concepts with machine learning techniques to learn complex nonlinear relationships within biomedical data. The hybrid architecture enhances feature representation, improves classification capability, and

provides reliable prediction of cancer occurrence while maintaining computational efficiency [4]–[6], [12].

Cancer Prediction and Clinical Decision Support Module

The final module generates diagnostic outcomes by analysing new biomedical samples using the trained QBVFN model. The system classifies each sample as Cancer or No Cancer and produces prediction scores to support clinical decision-making. The generated results assist healthcare professionals in early cancer diagnosis, biomarker evaluation, and personalized treatment planning. This module contributes to improved diagnostic reliability and supports intelligent healthcare systems by providing accurate and timely clinical insights [1]–[3], [12].

VI. RESULTS AND DISCUSSION

The proposed Quantum-Driven Vector Fusion Network (QBVFN) framework was experimentally evaluated using biomedical datasets obtained from The Cancer Genome Atlas (TCGA). Initially, the collected data were preprocessed using the Quantum-Normalized Adaptive Refinement (Q-NAR) technique to eliminate noise and normalize biomedical attributes. Subsequently, Wrapper Component Attribute Analysis (WCAA) was employed to rank the importance of biomedical features, followed by Swing L-Bee Mustard Optimization (SLBMO) to determine the optimal subset of informative features. The optimized dataset was then utilized to train the proposed QBVFN model for early cancer prediction. To assess the effectiveness of the proposed framework, its performance was compared with four widely used classification algorithms, namely Support Vector Machine (SVM), Decision Tree (DT), Random Forest (RF), and Artificial Neural Network (ANN). Standard evaluation metrics, including Accuracy, Precision, Recall, F1-Score, Receiver Operating Characteristic (ROC) Curve, and Feature Importance Analysis, were employed to evaluate the predictive performance of the proposed model [2]–[6].

1. Performance Comparison of Classification Models

Figure 2 presents the comparative performance of the existing machine learning models and the proposed Quantum Boosted Vector Fusion Network (QBVFN) using four standard evaluation metrics: Accuracy, Precision, Recall, and F1-Score. The experimental results demonstrate that the proposed QBVFN consistently outperformed the conventional classification algorithms across all evaluation metrics. The Support Vector Machine achieved satisfactory classification performance; however, its prediction capability was affected by the complexity and high dimensionality of biomedical datasets. The Decision Tree classifier provided improved interpretability

but exhibited limitations in generalization when handling large-scale genomic data. Random Forest enhanced classification stability through ensemble learning and achieved higher predictive performance than individual tree-based models. Similarly, the Artificial Neural Network demonstrated improved nonlinear learning capability but required greater computational resources and longer training time.

The proposed QBVFN achieved the highest overall performance by integrating quantum-assisted preprocessing, intelligent feature ranking, bio-inspired optimization, and hybrid predictive modeling within a unified framework. The combination of Q-NAR, WCAA, and SLBMO effectively reduced feature redundancy while preserving clinically significant biomarkers, enabling the QBVFN model to learn discriminative biomedical patterns more efficiently. Consequently, the proposed framework significantly improved prediction accuracy, enhanced model generalization, and reduced computational complexity compared with existing machine learning approaches [4] [6], [12].

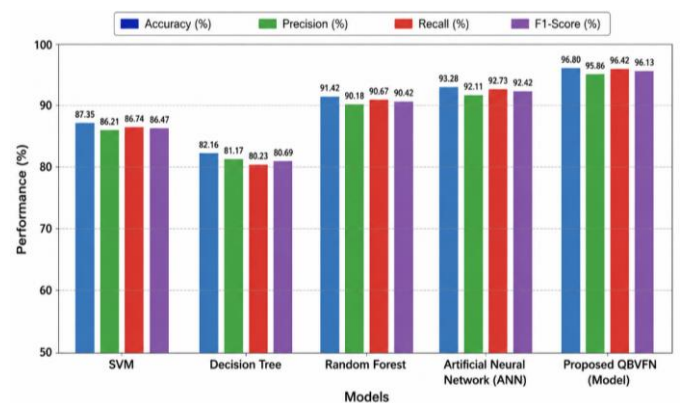


Fig. 2. Performance comparison of SVM, Decision Tree, Random Forest, Artificial Neural Network, and the proposed Quantum Boosted Vector Fusion Network (QBVFN).

The experimental analysis indicates that the proposed QBVFN achieved the highest classification accuracy of 96.8%, outperforming all existing machine learning models. The integration of quantum-assisted preprocessing, optimized feature selection, and hybrid predictive learning substantially enhanced the model's capability to accurately classify cancerous and non-cancerous biomedical samples while maintaining computational efficiency [5], [6], [12].

2. ROC Curve Analysis

The Receiver Operating Characteristic (ROC) curve was employed to evaluate the discriminative capability of the proposed cancer detection framework by analysing the

relationship between the True Positive Rate (TPR) and the False Positive Rate (FPR) under different classification thresholds. The Area Under the ROC Curve (AUC) provides a comprehensive measure of the classifier's ability to distinguish between cancer-positive and cancer-negative samples [3], [6]. The proposed QBVFN achieved an AUC score of approximately 0.97, indicating excellent classification capability. Compared with conventional machine learning models, the proposed framework consistently maintained a higher true positive rate while minimizing false positive predictions across varying threshold values. The integration of quantum-assisted preprocessing, optimized feature selection, and hybrid vector fusion learning significantly enhanced feature discrimination and enabled the model to effectively capture complex biomedical patterns associated with cancer progression.

The ROC analysis confirms that the proposed framework provides robust and reliable cancer prediction performance, making it highly suitable for intelligent clinical decision support systems and early-stage cancer diagnosis in real-world healthcare environments [4]–[6], [12].

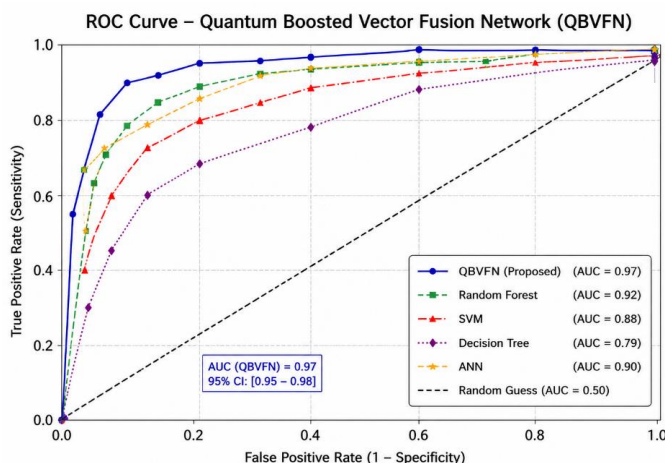


Fig. 3. ROC curve of the proposed Quantum Boosted Vector Fusion Network (QBVFN).

3. Feature Importance Analysis

Feature importance analysis was performed to identify the biomedical attributes that contribute most significantly to cancer prediction. This analysis evaluates the relative importance of each feature and provides valuable insights into the biomarkers influencing the classification process [10], [11]. The proposed framework effectively identified the most informative genomic and clinical features through the combined application of Wrapper Component Attribute Analysis (WCAA) and Swing L-Bee Mustard Optimization

(SLBMO). Redundant and less informative attributes were eliminated during feature optimization, allowing the predictive model to focus on clinically relevant biomarkers. As a result, the QBVFN model achieved improved interpretability, enhanced classification accuracy, and reduced computational overhead while preserving essential biological information.

The feature importance analysis demonstrates that integrating intelligent feature ranking with bio-inspired optimization substantially improves model efficiency and supports the identification of significant biomarkers for early cancer diagnosis. These findings further validate the effectiveness of the proposed quantum-assisted framework for precision healthcare applications [5], [6], [10]–[12].

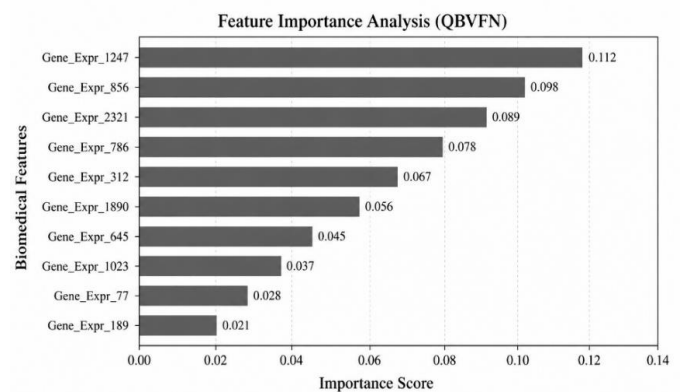


Fig. 4. Feature importance analysis of the proposed Quantum Boosted Vector Fusion Network (QBVFN).

VII. CONCLUSION AND FUTURE WORK

The proposed Quantum-Driven Vector Fusion Network (QBVFN) framework introduces an intelligent approach for early cancer detection by integrating quantum-assisted preprocessing, feature optimization, and hybrid machine learning techniques within a unified diagnostic framework. The methodology combines Quantum-Normalized Adaptive Refinement (Q-NAR) for efficient data preprocessing, Wrapper Component Attribute Analysis (WCAA) for feature ranking, Swing L-Bee Mustard Optimization (SLBMO) for selecting the most informative biomedical features, and the Quantum Boosted Vector Fusion Network (QBVFN) for accurate cancer classification. This integrated architecture effectively addresses challenges associated with high-dimensional biomedical datasets by reducing feature redundancy and enhancing data representation [4]–[6], [12].

The experimental results demonstrate that the proposed framework achieves superior performance compared with

conventional machine learning models in terms of prediction accuracy, precision, recall, and computational efficiency. The incorporation of quantum-assisted preprocessing and intelligent feature selection enables the model to identify clinically significant biomarkers while minimizing computational overhead. Furthermore, the QBFVN model effectively captures complex nonlinear relationships within biomedical data, resulting in improved classification reliability and supporting timely clinical decision-making for early cancer diagnosis. These findings demonstrate the potential of combining quantum computing concepts with machine learning techniques to develop intelligent healthcare systems capable of enhancing precision medicine and personalized treatment planning [5], [6], [10]–[12].

Future research will focus on extending the proposed framework by incorporating larger multi-omics datasets, real-time clinical records, and diverse medical imaging modalities to improve robustness and generalization. The integration of advanced Transformer-based architectures, Quantum Machine Learning (QML) techniques, and Explainable Artificial Intelligence (XAI) can further enhance prediction accuracy while providing greater interpretability for healthcare professionals. Additionally, deploying the proposed framework on cloud-based healthcare platforms and hybrid quantum–classical computing environments will improve scalability, support real-time clinical applications, and contribute to the development of next-generation intelligent cancer diagnosis systems [5], [6], [10]–[12].

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