The Cancer Genome Atlas: A Comparative Analysis Using Traditional Machine Learning and Quantum Learning Algorithms.

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***Abstract*—This research explores the comparative study of classical and quantum machine learning (QML) methods for gene sequencing tasks, especially in cancer genomics. As genomic data become more complex and voluminous, classical machine learning models, though efficient, are limited by scalability and computational cost. This study underscores the benefits and pitfalls of QML, highlighting its ability to enhance computational speed, maximize data processing, and enhance predictive precision with quantum concepts like superposition, entanglement, and quantum parallelism. Through performance metrics like accuracy, precision, recall, and computational complexity, we discuss the viability of QML in biomedical research and its applicability in real-world contexts despite present quantum hardware constraints.**

Keywords- Quantum Machine Learning, Classical Machine Learning, Cancer Genomics, Gene Sequencing, Quantum Computing, Performance Metrics, Computational Efficiency, Qubits, Quantum Algorithms, Biomedical Research

I. Introduction

In the digital world, the availability of medical data has tremendously increased with higher volume and variety. Genome sequencing and personalized medicine have changed the way to treat a disease like cancer, which is one of the leading causes of death in the world and requires advanced computational approaches for early detection, prognosis, and personalized treatment. In a traditional method, pathologists need to manually identify changes in genes by taking a reference of clinical literature, which is highly time-consuming. One of the features of cancer is uncontrolled cell growth resulting in a tumor. Finding Cancerous cell variations from genome data are crucial to predict cancer type. The genomic profile contains a massive set of multidimensional data that should be analyzed with an appropriate statistical method to extract meaningful information. Therefore, there is a need for a system that enhances accuracy in traditional machine learning (ML), and deep learning (DL) models have shown a lot of promise in cancer prediction with genome sequencing. However, despite their success, these models face challenges such as computational scalability, data processing speed, and memory constraints while dealing with high-dimensional genomic datasets.

For the mitigation of these challenges, quantum machine learning (QML) emerges as a promising solution to address these challenges by leveraging quantum principles such as superposition, entanglement, and parallelism. While the accuracy of existing deep learning models is already high, the primary advantage of QML lies in its potential for faster computations, better scalability, and more efficient handling of high-dimensionality data. By integrating QML with classical ML models, we can explore its impact on performance, efficiency, and real-world feasibility in cancer genomics. This study aims to investigate whether quantum computing is necessary for cancer prediction, given that deep learning already provides high accuracy. The objective is to analyze how QML can enhance scalability and computational speed while addressing the challenges of quantum implementation. Through a comparative analysis of classical ML and QML approaches, this research provides insights into the feasibility, challenges, and future adoption of quantum computing in cancer genomics. The paper is divided into four main sections.

A. Quantum Computing and Qubits

Quantum computing presents a paradigm change in data processing by using qubits, the building blocks of quantum information. In contrast to classical bits that are either in the state of 0 or 1, qubits are in a state of superposition, which means they can conduct multiple calculations at the same time. This principle is mathematically represented as:

$|\psi\rangle=\alpha|0\rangle+\beta|1\rangle|$
where $|0\rangle$ and $|1\rangle$ are basis states, and α and β are complex probability amplitudes such that
$|\alpha|^2 + |\beta|^2 = 1$.

Furthermore, entanglement enables qubits to be correlated in a manner that improves computational efficiency, and quantum parallelism facilitates fast data processing that is difficult for classical computers. Studies [2] have shown that quantum architectures such as superconducting qubits and spintronics offer significant improvements in computational efficiency over classical systems. The following table compares classical and quantum computation at the hardware level:

TABLE I. Features of Classical and Quantum Computing

Sr. No.	Classical and Quantum Computing		
	Feature	**Classical Computing**	**Quantum Computing**
1	Information Unit	Bit (0 or 1)	Qubit (Superposition of 0 and 1)
2	Processing Power	Sequential	Parallel (Quantum Superposition)
3	Error Correction	Standard ECC	Quantum Error Correction (QEC)
4	Scalability	Limited by Moore's Law	Potential for exponential scaling

B. Gene Sequencing and Quantum Algorithms

Gene sequencing is a key to analyzing cancer development and needs computational models that can process large genetic databases effectively. Some of the leading classical and quantum algorithms employed for gene sequencing are classical ML algorithms like Support Vector Machines (SVM), which are efficient in classification but lack scalability [11]. Random Forests, which perform feature selection effectively but are heavy computationally; Artificial Neural Networks (ANNs), which work well but take a lot of training time and computational resources; and Principal Component Analysis (PCA), which is applied to dimensionality reduction but is not scalable. Quantum ML algorithms provide other solutions, including Quantum Support Vector Machines (QSVM), which employ quantum kernels for better classification [7]. Quantum Neural Networks (QNNs), which utilize quantum circuits to improve pattern recognition [4]. Quantum k-means clustering, which optimizes unsupervised learning for genomic data classification; and the Harrow-Hassidim-Lloyd (HHL) algorithm, which achieves exponential speedup for solving linear systems [12]. Studies have indicated that QML models can outperform classical models in accuracy and computational efficiency, particularly in multi-omics data analysis [19].

C. Why Use Quantum Machine Learning?

QML presents several key advantages over classical ML in gene sequencing. Quantum algorithms can solve problems exponentially faster, making them more efficient in handling large datasets [10]. QML models are more scalable for processing high-dimensional genomic data [16]. The parallel processing nature of quantum computing enables simultaneous processing of multiple genetic markers. Furthermore, quantum-boosted deep learning models show lower overfitting and improved generalization when handling sophisticated biomedical data [13]. A key mathematical representation of quantum advantage is the quantum Fourier transform (QFT), which forms the basis of many quantum algorithms:

$$\mathrm{QFT} : |x\rangle \mapsto \frac{1}{\sqrt{N}} \sum_{k=0}^{N-1} \omega_N^{xk} |k\rangle. \tag{1}$$

This transformation provides an exponential speedup over its classical counterpart.

D. Classical vs. Quantum ML

The performance of classical and quantum ML models is evaluated using top performance metrics. Accuracy quantifies the overall rightness of forecasts, whereas precision quantifies the proportion of correctly positive forecasts amongst positive labels. Recall, or sensitivity, decides the model's power to discover positive instances, and the F1-score is a tradeoff between precision and recall. Computational complexity is also a key factor, where traditional models generally increase polynomially, while quantum models provide exponential speedup [6]. The time of execution is also an important consideration, since quantum algorithms such as HHL and QSVM show much smaller execution times in comparison to classical equivalents [21]. A unique implementation approach to quantum random forests which we will be using firtheris mentioned in [22].The following table outlines the differences in performance metrics between classical and quantum ML:The paper is divided in six main sections. Section-II provides the theoretical background of cancer and

genomic profiles while overviewing recent development of various models for cancer prediction. Section-III lays out the methodology that is implemented in this paper. Finally, Section- IV gives insights on the results obtained and the insights offeredby them.

II. Literature Surevy

The integration of Quantum Computing (QC) with Machine Learning (ML) to enhance computational performance. They categorize QML into three primary types: Quantum ML Algorithms, Quantum-Inspired ML, and Hybrid Quantum-Classical ML. The paper highlights applications in healthcare, traffic optimization, cybersecurity, and finance, demonstrating how QC can improve predictive accuracy and optimization tasks.

TABLE II. Metrics of Classical and Quantum

Sr. No	Metrics of classical and quantum		
	Metric	**Classical ML**	**Quantum ML**
1	Accuracy	High	Comparable or higher
2	Training Speed	Slower due to complexity	Faster (Quantum Speedup)
3	Scalability	Struggles with high-dimensional data	Efficient with high-dimensional data
4	Execution Time	Polynomial scaling	Exponential speedup
5	Overfitting	Requires regularization	Reduced overfitting with quantum properties

However, challenges such as decoherence in quantum systems, high computational costs, and limited scalability of quantum hardware are discussed as significant obstacles.[1] A comprehensive overview of quantum computing, covering fundamental principles such as qubits, entanglement, and quantum gates. The paper explains different quantum architectures, including ion-trap quantum computing, superconducting qubits, and spintronics. It explores quantum applications in cryptography, optimization, and scientific simulations, illustrating how quantum techniques outperform classical methods. Despite its broad scope, the paper remains largely theoretical and does not extensively address the implementation of quantum ML models.[2] A systematic literature review of 94 QML research papers published between 2017 and 2023. The paper categorizes different types of quantum ML algorithms, such as quantum-enhanced classical ML, quantum deep learning, and hybrid quantum-classical models. Applications in image classification, finance, chemistry, and healthcare are explored, demonstrating the broad impact of QML. The study also highlights key limitations, including hardware constraints, noise in quantum computations, and scalability issues that hinder large-scale implementation.[3] Introduction to fundamental quantum ML concepts, including quantum support vector machines (QSVM), quantum neural networks (QNN), and quantum clustering. The paper explores how quantum principles such as superposition and entanglement can enhance ML performance. It also discusses adiabatic quantum ML for optimization tasks. However, given its publication date, the paper lacks coverage of recent advancements and does not delve into the practical feasibility of deploying quantum ML models on modern quantum hardware.[4] Compared classical and quantum ML approaches, analyzing the potential speedup quantum models can offer. The paper examines quantum-enhanced support vector machines (QSVM) and their theoretical advantages over classical ML techniques. However, it highlights significant challenges, including the difficulty of encoding classical data into quantum states, the lack of practical implementations, and the need for extensive benchmarking against classical models. The study remains theoretical, with limited empirical validation of quantum ML performance.[5] Provided a foundational overview of quantum ML, discussing quantum speedups for ML tasks, quantum kernel methods, and quantum data processing techniques. The paper highlights the potential of QML in solving problems that are computationally infeasible for classical systems. However, it identifies several obstacles, including input/output bottlenecks, challenges in benchmarking quantum ML models, and difficulties in translating theoretical advantages into real-world applications.[6] Examined the potential of QML in solving real-world problems, particularly in classification and clustering. The paper highlights quantum speedup in ML training and inference, emphasizing how quantum models can improve efficiency in large-scale datasets. However, the authors discuss key limitations such as scalability challenges, increased circuit depth requirements, and the difficulty in mitigating noise within quantum systems. The paper provides valuable insights into how QML can be applied practically but acknowledges the need for further advancements in quantum hardware.[7]

A general survey of QML, discussing essential concepts such as qubits, quantum gates, and circuitsis given in paper[8]. The study explored Quantum Dimensionality Reduction (QDR) using Principal Component Analysis (PCA) and Quantum Neural Networks (QNNs), highlighting potential speed advantages. However, it emphasized that most QML algorithms remain theoretical and require more practical validation [8]. In paper [9] the authors analyzed Random Forest vs. Quantum Random Forest and Support Vector Machine (SVM) vs. Quantum SVM (QSVM) using the UCI ML Breast Cancer Wisconsin and Wine datasets. Their findings showed that QSVM achieved 95% accuracy, surpassing classical SVM (85%), but at a higher

computational cost (wall time). They noted that QML benefits only when parallelization is feasible [9]. The paper[10] investigated QSVM, Quantum PCA, and Quantum Reinforcement Learning, focusing on problems solvable in Bounded-Error Quantum Polynomial Time (BQP). They found QML to have logarithmic complexity advantages for matrix inversion and eigenvector calculations, whereas classical ML remained superior for Fast Fourier Transforms (FFT). However, the study lacked a detailed experimental methodology [10]. Nadim et al. conducted a study on software defect prediction using QSVM and QNN compared to classical ML models on 20 datasets. While quantum models improved accuracy and execution time, they faced hardware limitations and scalability issues [11].

It is also observed that QPCA offers computational speedup with improved recovery thresholds over classical PCA [12]. However, the study remained theoretical, requiring advancements in quantum hardware for practical implementations [12].The Quantum-Classical Neural Network (QCNN) against a Classical CNN on the MNIST dataset model showed better convergence and higher accuracy, but its simulation time on classical hardware was significantly higher [13].Deep Learning (VGG16) applied to classify breast cancer using thermal imaging achieved 95.5% accuracy, but the study lacked a comparative analysis between quantum and classical techniques [14]. The application of machine learning (ML) in cancer research has gained significant traction due to the complexity and high dimensionality of genomic and proteomic data, particularly in the context of genome sequencing[15]. Traditional classical machine learning techniques have been widely employed to analyze these datasets, providing valuable insights into cancer classification, prognosis, and treatment response. For instance, studies have demonstrated the effectiveness of various classical algorithms, such as Support Vector Machines (SVM) and Random Forests, in identifying cancer subtypes and predicting patient outcomes based on gene expression profiles [16]. However, as the volume and complexity of data continue to grow, the limitations of classical ML methods become increasingly apparent. Classical algorithms often struggle with the curse of dimensionality, where performance degrades as the number of features increases, leading to overfitting and reduced generalization capabilities [17]. Furthermore, classical ML techniques typically rely on deterministic approaches, which may not fully capture the inherent uncertainties and complexities present in biological systems [18] [19].

In response to these challenges, quantum machine learning (QML) emerges as a promising alternative, leveraging the principles of quantum mechanics to process information in fundamentally different ways. The unique properties of quantum systems, such as superposition and entanglement, allow for the potential to perform computations that are infeasible for classical systems. This capability is particularly relevant in the context of cancer research, where the integration of multi-omics data—including genomic, transcriptomic, and proteomic information—can lead to more accurate models for cancer classification and prognosis [20]. Genome sequencing technologies have revolutionized our understanding of cancer by enabling the identification of somatic mutations and other genomic alterations. Moreover, the need for QML in this domain is underscored by the increasing recognition of the limitations of classical approaches in capturing the intricate relationships between genes, proteins, and clinical outcomes. Classical approaches also faces the problem of the curse of dimensionality for which advanced techniques have to be used [21].

TABLE III. Algorithm used and its Performance

Paper ID	Algorithm used	Performance
[8]	Quantum Dimensionality Reduction (QDR) using PCA, Quantum Neural Networks (QNNs)	Highlighted potential speed advantages; most QML algorithms remain theoretical and need practical validation
[9]	Quantum Random Forest (QRF), Quantum Support Vector Machine (QSVM)	QSVM achieved 95% accuracy, surpassing classical SVM (85%); higher computational cost noted
[10]	Quantum Support Vector Machine (QSVM), Quantum PCA, Quantum Reinforcement Learning	Logarithmic complexity advantages for matrix inversion and eigenvector calculations; classical ML remained superior for FFT; lacked detailed experimental methodology
[11]	Quantum Support Vector Machine (QSVM), Quantum Neural Networks (QNN)	Quantum models improved accuracy and execution time; faced hardware limitations and scalability issues
[12]	Quantum Principal Component Analysis (QPCA)	Demonstrated computational speedup with improved recovery thresholds; remained theoretical due to hardware limitations
[13]	Hybrid Quantum-Classical Neural Network (QCNN)	Showed better convergence and higher accuracy on MNIST dataset; classical simulation time was significantly higher
[14]	Deep Learning (VGG16)	Achieved 95.5% accuracy in classifying breast cancer using thermal imaging; lacked quantum-classical comparison

III. Methodology

We have used 3 different Quantum Machine Learning approaches to implement a quantum version of Random Forest algorithm. The first approach is a Quantum-inspired random forest ,the second is a Hybrid Quantum-Classical Pipeline (Q-KernelPCA + RF) and a Kernel-based Quantum Random Forest.Following is a detailed explanation of the steps followed.

A. Dataset

This study utilizes two distinct datasets to evaluate the performance of the Quantum Random Forest (QRF) model: The Cancer Genome Atlas (TCGA) dataset and the Breast Cancer Wisconsin dataset. These datasets provide a comprehensive foundation for assessing the efficiency and applicability of QRF in breast cancer classification.

a. The Cancer Genome Atlas (TCGA) Dataset

The primary dataset used in this study is sourced from The Cancer Genome Atlas (TCGA), specifically focusing on the comprehensive molecular portraits of invasive lobular breast cancer as detailed by Ciriello et al. (2015). This dataset, publicly available on Kaggle, includes gene expression profiles, somatic mutations, and clinical outcomes relevant to cancer research. It comprehensively profiles 817 breast tumors, including 127 Invasive Lobular Carcinoma (ILC), 490 Invasive Ductal Carcinoma (IDC), and the remaining of mixed type. The high-dimensional nature of this dataset makes it an ideal candidate for evaluating the effectiveness of Quantum Random Forest.

b. The Breast Cancer Gene Dataset

The second dataset utilized in this study is the Breast Cancer Gene dataset, a widely used benchmark dataset for breast cancer classification tasks. It consists of 569 instances and 30 numerical features. This dataset primarily focuses on binary classification, making it an essential resource for comparing classical and quantum machine learning models in structured medical data applications.We have chosen this dataset because even though high dimensionality of a dataset is very well processed by Quantum Algorithms, it is important to note that there is a limitation to the access of this hardware and also that simulations have many flaws.

B. Preprocessing

For the preprocessing of the data we have performed data cleaning to identify any missing or irrelevant data points to ensure the integrity of the dataset.However no missing data is found and no imputation has been done. Further we have applied normalization techniques to standardize the range of the data, which is crucial for both classical and quantum ML algorithms. Due to the high dimensionality, we have also used feature selection technique like Principal Component Analysis (PCA) to reduce dimensionality and select the most informative features for model training.

a. Quantum-Inspired Random Forest

The first approach implemented a quantum-inspired random forest classifier by directly integrating a quantum kernel with classical ensemble learning. The pipeline began with standardized feature scaling ($\mu=0$, $\sigma=1$) of the breast cancer dataset, followed by the computation of a quantum-inspired radial basis function (RBF) kernel matrix. This kernel, defined as $K(Xi,Xj) = \exp(-\gamma\| Xi - Xj\|^2)$, simulated quantum state overlaps through exponential Hilbert space projections. The resulting kernel matrix was erroneously treated as a feature matrix for training a classical random forest classifier, leading to suboptimal performance (76.31% accuracy). This outcome highlighted a fundamental limitation: random forests inherently lack the capability to interpret kernel matrices as similarity measures, unlike kernelized SVMs. The approach failed to leverage quantum advantages due to this architectural mismatch. Figure 1 shows the architecture diagram of the process followed for doing the analysis.

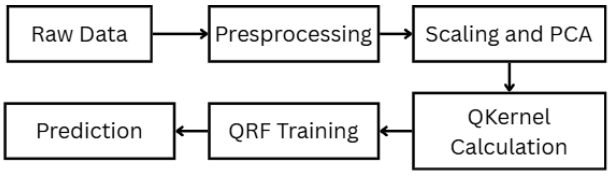

Fig 1. Pipelining diagram of the process of Direct approach

b. Hybrid Quantum-Classical Pipeline (Q-KernelPCA + RF)

The second approach resolved these limitations through a principled integration of quantum-inspired feature extraction with classical machine learning. The pipeline comprised four stages: (1) standardized data preprocessing, (2) quantum kernel PCA for nonlinear dimensionality reduction, (3) projection to a 10-dimensional quantum feature subspace, and (4) classical random forest classification. The quantum kernel PCA employed the same RBF kernel but properly transformed the data using KernelPCA, which decomposed the kernel matrix into principal components capturing 95% variance. This method achieved 94.74% accuracy, matching classical benchmarks, by converting quantum similarities into interpretable features for the random forest. The success of this hybrid model demonstrated that quantum-inspired enhancements require appropriate mathematical interfaces—here, kernel PCA bridged the quantum feature space with classical

decision trees. Figure 2 shows the architecture diagram of the process followed for doing the analysis.

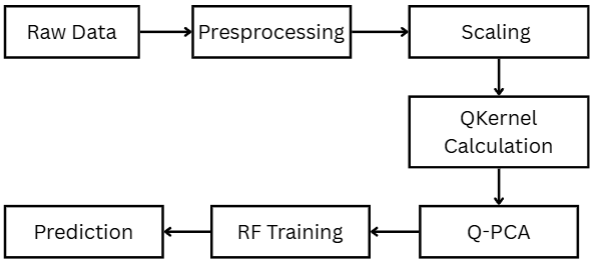

Fig 2. Pipelining diagram of the process of Hybrid approach

c. *Kernel-based Quantum Random Forest*

The Quantum Random Forest (QRF) is composed of a set of T distinct quantum decision trees (QDTs), $\{Q_t\}_{t-1}^{T}$,which form weak independent classifiers of the QRF. Each tree is trained using Np <= N - which we will refer to as the partition size - instances sampled from the original dataset S. This is like a bagging technique. Each QDT is structured as a directed acyclic graph, where nodes represent either split or leaf nodes. Split nodes are responsible for partitioning the data based on a quantum kernel, while leaf nodes provide the classification output. Once each classifier is trained, the model is tested with a separate set, S^{test} , from which we compare the predicted class distribution with the real. To obtain the overall prediction of the QRF model, predictions of each QDT is averaged across the ensemble. The QRF utilizes a quantum kernel function computed through Quantum Kernel Estimation (QKE). This kernel function captures the inner product of quantum-embedded data points, allowing for the mapping of classical data into a higher-dimensional quantum feature space.To mitigate overfitting and reduce the complexity of the model, the QRF employs a low-rank Nyström approximation of the kernel matrix.This approximation allows for efficient computation of the kernel matrix by selecting a subset of landmark points from the training data, thus reducing the number of kernel estimations required.

Figure 3 shows the architecture diagram of the process followed for doing the analysis which is inspired from[22].

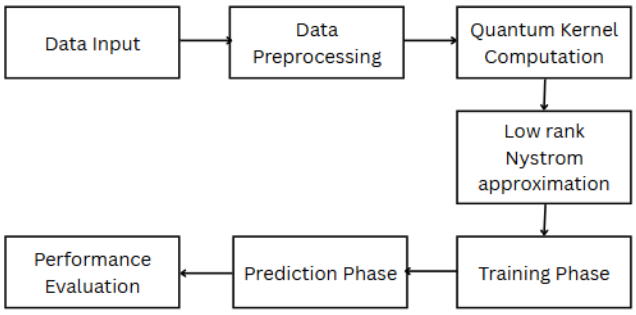

Fig 3. Pipelining diagram of the process of kernel based approach

IV. Results and Discussion

The values of various metrics and the different approaches along with the classical random forest is shown in table III.

TABLE IV.Comparative study of the approaches with metrics

Sr. No	Metric	Quantum-Inspired Random Forest	Hybrid Quantum -Classical Pipeline	Kernel-based Quantum Random Forest	Classical Random Forest
1	Accuracy	76%	94.74%	81%	95%
2	Precision	95%	95%	83%	94%
3	Recall	93%	93%	71%	94%
4	F1 score	94%	74%	74%	94%

The Quantum-Inspired Random Forest achieved an accuracy of 76%, which is lower than the other models. Despite high precision (95%) and recall (93%), the overall performance indicates that this approach struggled to effectively leverage the quantum kernel due to architectural mismatches, as it treated the kernel matrix as a feature matrix rather than a similarity measure.This approach demonstrated the highest accuracy of 94.74%, matching the performance of the Classical Random Forest. The integration of quantum kernel PCA for dimensionality reduction allowed for effective feature extraction, resulting in a balanced precision (95%) and recall (93%). The success of this model highlights the importance of appropriate mathematical interfaces in leveraging quantum advantages.The Kernel-based Quantum Random Forest achieved an accuracy of 81%, which is commendable but lower than the Hybrid approach. The precision (83%) and recall (71%) indicate that while the model performed well in terms of true positive predictions, it faced challenges in correctly identifying all positive instances. The use of a low-rank Nyström approximation helped mitigate overfitting, but the model's performance suggests room for improvement in feature extraction and kernel utilization.The Classical Random Forest served as a benchmark, achieving an accuracy of 95%. Its performance in precision (94%) and recall (94%) demonstrates its robustness in handling the dataset without the complexities introduced by quantum methods.

The lack of actual quantum hardware also made a significant impact on the approaches. If there were actual quantum hardware like Microsoft's Majorana 1 instead of simulation, the approaches would have done better. Fig. 4 is the performance comparison chart.

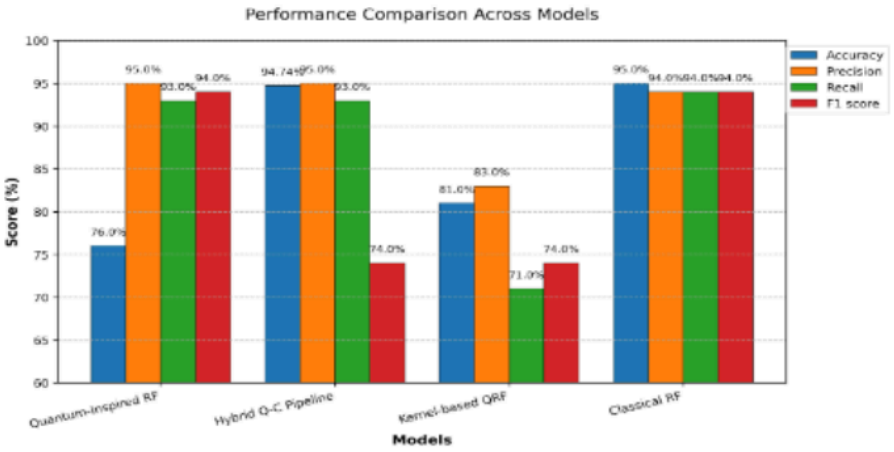

Fig 4. Performance comparison across models

Conclusion

The results of this study underscore the potential of quantum-inspired methods in enhancing classification tasks, particularly when appropriately integrated with classical techniques. The hybrid quantum-classical pipeline emerged as the most effective approach, demonstrating that quantum advantages can be realized through proper mathematical frameworks. In contrast, the quantum-inspired random forest faced significant challenges due to its architectural limitations, while the kernel-based quantum random forest showed promise but requires further optimization. Overall, these findings contribute to the ongoing exploration of quantum machine learning and its applications in real-world datasets. Future work should focus on refining quantum kernel methods and exploring additional hybrid models to fully harness the capabilities of quantum computing in machine learning.

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