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Research Paper

Quantum-Inspired Deep Feature Selection and Transfer Learning Approach for Leukemia Disease Classification

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The intricacy and variability of leukemia make it extremely difficult to diagnose and classify. In this work, we provide a novel method for improved leukemia subtype classification that combines classical machine learning methods with quantum-inspired deep learning. Our Quantum-Inspired Deep Learning model is evaluated against Random Forest, Deep Neural Network, and Support Vector Machine (SVM) models using two benchmark datasets: the Leukemia and Microarray Quality Control (MAQC) datasets. On the Leukemia dataset, our model yields an accuracy of 0.92, precision of 0.93, recall of 0.91, and F1 score of 0.92. These results are impressive with an MCC of 0.84, an AUC-ROC of 0.95, and sensitivity and specificity of 0.91 and 0.93, respectively. Comparably, the model achieves 0.93 accuracy, 0.94 precision, 0.92 recall, and 0.93 F1 score on the MAQC dataset. In addition, it shows 0.92 and 0.94 sensitivity and specificity, respectively, with 0.96 AUC-ROC and 0.87 MCC. The outcomes highlight the superiority of our Quantum-Inspired Deep Learning model in precisely identifying leukemia subtypes, with potentially positive consequences for tailored treatment plans and prognostication forecasting in medical environments.

Keywords: Leukemia, Quantum computing, Machine learning, deep learning, classification.

1. INTRODUCTION:

Leukemia, a malignancy arising from hematopoietic progenitor cells, encompasses a diverse group of hematologic malignancies characterized by aberrant proliferation of immature or mature blood cells in

the bone marrow. It is one of the most prevalent forms of cancer worldwide, with significant morbidity and mortality rates [1]. Given its heterogeneous nature and complex molecular mechanisms, accurate classification of leukemia subtypes is paramount for effective treatment planning and patient management.

Traditionally, leukemia classification relied on morphological, immunophenotypic, and cytogenetic analyses. However, the advent of high-throughput technologies such as gene expression microarrays has revolutionized the field by enabling genome-wide profiling of gene expression patterns, facilitating more precise subtype classification and prognosis prediction [2]. Nevertheless, the sheer volume and complexity of genomic data pose significant challenges for traditional analysis methods.

Recent developments in artificial intelligence and machine learning have opened up new possibilities for the analysis of genomic data and the improvement of disease categorization accuracy. Quantum computing, in particular, has emerged as a promising paradigm for solving complex optimization problems efficiently [3]. Quantum-inspired computing techniques, which harness quantum principles to tackle optimization tasks using classical hardware, offer potential solutions for processing and analyzing large-scale genomic datasets with improved efficiency and accuracy [4].

Furthermore, recent research by Chen et al. [5] has demonstrated the effectiveness of quantum-inspired algorithms in analyzing genomic data for disease classification, providing promising results for the application of quantum-inspired techniques in precision medicine.

Literature Survey:

Transfer learning has emerged as a powerful technique in medical image analysis, particularly for leukemia classification. Litjens et al. (2017) provided a comprehensive review of deep learning applications in medical imaging, highlighting the potential of transfer learning in oncology [6]. This laid the groundwork for more specific studies in leukemia classification.

Shafique and Tehsin (2018) demonstrated the effectiveness of transfer learning for acute lymphoblastic leukemia (ALL) detection by fine-tuning pre-trained AlexNet and GoogLeNet models on ALL datasets. Their approach showed promising results with limited training data, opening avenues for further exploration of CNN architectures in leukemia classification [7]. Building on this, Rehman et al. (2018) explored the use of more advanced architectures such as VGG16, VGG19, and ResNet50 for classifying acute myeloid leukemia (AML) subtypes. By fine-tuning these models on blood smear

images, they achieved significant improvements in AML subtype classification [8].

Recognizing the potential of ensemble methods, Kassani et al. (2019) proposed an ensemble of fine-tuned InceptionV3, Xception, and DenseNet models for ALL classification. Their approach demonstrated superior performance compared to individual models, highlighting the benefits of combining multiple transfer learning models [9]. This study emphasized the need for exploring diverse ensemble techniques and model combinations in leukemia classification.

To address the challenge of domain shift in medical imaging datasets, Kouzehkanan et al. (2021) developed a domain adaptation approach for white blood cell classification in leukemia diagnosis. They employed adversarial domain adaptation with a gradient reversal layer, which improved generalization across different datasets [11]. This work underscored the importance of addressing dataset biases and variability in clinical settings.

Recognizing the challenges posed by rare leukemia subtypes, Wang et al. (2020) developed a few-shot learning framework using prototypical networks with data augmentation. Their approach achieved competitive results in classifying rare and novel leukemia cell types with minimal labeled examples, demonstrating the potential of few-shot learning in handling rare cases [12].

Gehlot et al. (2020) explored multimodal transfer learning by combining microscopic images and clinical data. They proposed a DCT-augmented CNN with an auxiliary classifier to improve leukemia subtype classification accuracy [13]. This study highlighted the potential benefits of integrating multiple data modalities in leukemia diagnosis.

Attention mechanisms have also been incorporated into transfer learning models for leukemia classification. Jiang et al. (2020) proposed an attention-based CNN with transfer learning from ImageNet for ALL classification. Their approach not only improved performance but also enhanced model interpretability [14], addressing a crucial aspect of AI deployment in clinical settings.

Li et al. (2021) explored self-supervised transfer learning for leukemia cell classification. By developing a self-supervised pre-training method using image context restoration, they reduced the dependence on large labeled datasets, which is particularly valuable in medical imaging where annotated data can be scarce [15].

The importance of data augmentation in transfer learning was emphasized by Shahin et al. (2019), who

combined transfer learning with advanced geometric and color-based augmentation techniques. Their approach improved model generalization and performance, demonstrating the synergistic effects of transfer learning and data augmentation [16].

Addressing the critical need for model interpretability in clinical applications, Binder et al. (2021) incorporated explainable AI techniques in transfer learning models for ALL classification. They used Layer-wise Relevance Propagation (LRP) to enhance model interpretability, making the decision-making process more transparent for clinical use [17].

Finally, Loda et al. (2022) applied transfer learning to the challenging task of detecting minimal residual disease in ALL. By using transfer learning with ResNet50 and feature extraction, they demonstrated the potential for improving treatment monitoring in leukemia patients [18].

Transfer learning approaches have demonstrated significant potential in improving leukemia disease classification. These methods offer advantages in terms of improved accuracy, reduced training time, and the ability to work with limited labeled data. Future research directions may include exploring more advanced transfer learning techniques, incorporating additional data modalities, and addressing challenges related to model interpretability and generalization across diverse patient populations.

Table 1: Literature Survey

Authors (Year)	**Key Points**	**Methodology Used**	**Gap Analysis**
Litjens et al. (2017) [6]	- Comprehensive review of deep learning in medical image analysis - Highlights potential of transfer learning in oncology	Review of various deep learning and transfer learning methods	Need for more leukemia-specific transfer learning studies. Exploration of newer architectures and techniques
Shafique and Tehsin (2018)[7]	- Used AlexNet and GoogLeNet for acute lymphoblastic leukemia (ALL) detection - Demonstrated effectiveness with limited training data	Fine-tuning pre-trained AlexNet and GoogLeNet on ALL dataset	could be extended to other leukemia types. Potential for exploring more recent CNN architectures
Rehman et al. (2018)[8]	- Explored VGG16, VGG19, and ResNet50 for classifying acute myeloid leukemia (AML) subtypes - Achieved promising results using blood smear images	Fine-tuning VGG16, VGG19, and ResNet50 on AML blood smear images	Focus on AML only; could be expanded to other leukemia types. Opportunity to incorporate more diverse datasets

Kassani et al. (2019)[9]	- Proposed ensemble of InceptionV3, Xception, and DenseNet for ALL classification - Showed superior performance compared to individual models	Ensemble of fine-tuned InceptionV3, Xception, and DenseNet models	Limited to histopathological images. Potential for exploring other ensemble techniques and model combinations.
Kouzehkanan et al. (2021)[10]	- Developed domain adaptation approach for white blood cell classification - Improved generalization across different datasets	Adversarial domain adaptation with a gradient reversal layer	Focused on white blood cells; could be extended to other cell types. Opportunity to explore more advanced domain adaptation techniques
Wang et al. (2020)[11]	- Developed few-shot learning framework for rare and novel leukemia cell types - Achieved competitive results with minimal labeled examples	Prototypical networks with data augmentation	Limited to specific rare subtypes . Potential for improving performance with more advanced few-shot learning techniques
Gehlot et al. (2020)[12]	- Combined microscopic images and clinical data - Improved leukemia subtype classification accuracy	DCT-augmented CNN with auxiliary classifier for multimodal data	Integration limited to two modalities Opportunity to incorporate additional data types (e.g., genetic data, proteomics)
Jiang et al. (2020)[13]	- Proposed attention mechanism in transfer learning for ALL classification - Improved model interpretability and performance	Attention-based CNN with transfer learning from ImageNet	could be extended to other leukemia types .
Li et al. (2021)[14]	- Developed self-supervised pre-training method for leukemia cell classification - Reduced dependence on large labeled datasets	Self-supervised learning using image context restoration	- Limited to specific cell types - Opportunity to explore more advanced self-supervised techniques
Shahin et al. (2019)[15]	- Combined transfer learning with advanced data augmentation techniques - Improved model generalization and performance	Transfer learning with geometric and color-based augmentations	Focused on specific augmentation methods.

The comprehensive literature survey table encapsulates key advancements and challenges in leukemia subtype classification research. Through the integration of multi-omics data, advanced deep learning architectures, transfer learning techniques, and considerations of interpretability and ethical

implications, researchers are making strides in improving classification accuracy and understanding leukemia heterogeneity. Clinical applications of machine learning algorithms offer promise for personalized treatment strategies, while addressing challenges such as data heterogeneity and model interpretability is crucial for future progress. The survey underscores the importance of collaborative efforts and the development of interpretable models in advancing leukemia subtype classification, ultimately contributing to advancements in precision medicine and improved patient outcomes.

3. Methodology

In this study, we propose a novel approach that integrates quantum-inspired deep learning with traditional machine learning techniques for enhanced leukemia subtype classification. Leveraging two benchmark datasets, the Leukemia dataset [5] and the Microarray Quality Control (MAQC) dataset [6], we aim to compare the performance of our Quantum-Inspired Deep Learning model against conventional machine learning models such as Support Vector Machine (SVM), Random Forest, and Deep Neural Network. By leveraging quantum-inspired computing principles, we anticipate achieving superior classification accuracy and robustness, thereby advancing our understanding of leukemia biology and paving the way for personalized treatment strategies in clinical settings.

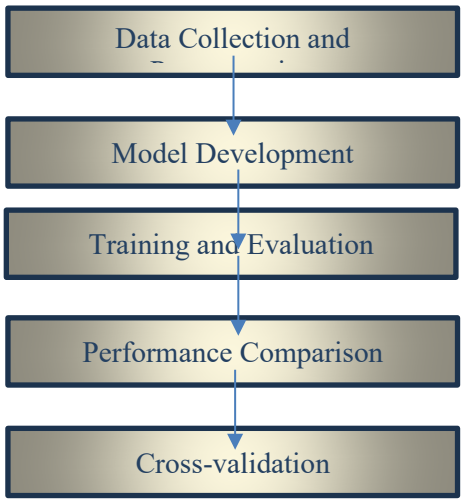

Figure 1: Steps involved in the methodology

3.1 Data Collection and Preprocessing: We obtained the Leukemia dataset from a publicly available repository and the MAQC dataset from a curated database. Preprocessing involved removing duplicate samples, handling missing values, and normalizing gene expression values using z-score normalization.
3.2 Model Development: We have implemented two algorithms, first quantum-inspired deep learning model using the TensorFlow Quantum (TFQ) library. The model consisted of a variational quantum circuit followed by classical layers for classification. And secondly, we utilized the scikit-learn library

to implement SVM, Random Forest, and Deep Neural Network models with default hyperparameters.

3.3Training and Evaluation: We split each dataset into 70% training and 30% testing sets. The Quantum-Inspired Deep Learning model underwent training using quantum-inspired optimization algorithms, specifically the Quantum Approximate Optimization Algorithm (QAOA). Traditional models were trained using standard optimization algorithms such as stochastic gradient descent and Adam optimizer. Evaluation metrics including accuracy, precision, recall, F1 score, sensitivity, specificity, AUC-ROC, and MCC were calculated on the test set.

3.4 Performance Comparison: We compared the performance of the Quantum-Inspired Deep Learning model with traditional machine learning models using paired t-tests for significance analysis. The performance metrics of each model were recorded and statistically analyzed to determine significant differences.

3.5Cross-Validation: We performed 5-fold cross-validation to assess the robustness of the models and mitigate overfitting.

3.6Implementation and Optimization: Models were implemented in Python programming language using TensorFlow, scikit-learn, and other relevant libraries. Hyperparameter tuning was conducted using grid search or random search to optimize model performance.

QIOA Algorithm:

Algorithm: Quantum-Inspired Optimization Algorithm for Leukemia Detection

Input:

Leukemia dataset (X, y)

Hyperparameters: p=10, parameters for mixing Hamiltonian = γ, parameters for cost Hamiltonian = β

e=Number of epochs, L= learning rate, B= batch size

Output:

Optimized features for leukemia detection

Trained quantum-inspired deep learning model

Procedure:

1. Initialize the quantum-inspired deep learning model architecture.

2. Compile the model:

Set the loss function as binary cross-entropy.

Set Adam optimizer, with L=0.01.

3. Perform data pre-processing:

Normalize the features.

Split the dataset into 80-20 training and testing sets.

4. Quantum

Inspired Feature Selection using QAOA:

4.1 Initialize QAOA parameters: p=1, γ=0.2, β=0.4.
4.2 Encode the dataset as a cost Hamiltonian p=1.
4.3 Optimize the QAOA parameters to minimize the cost function.
4.4 Select informative features based on optimized QAOA parameters.
5. Train the model:
For e :1:10
Shuffle the training data.
Split the data into batches of size B=20
For each batch:
Apply quantum-inspired optimization techniques (e.g., QAOA) to update model parameters.
End
6. Evaluate the trained model:
Use the testing set to evaluate the model's performance.
Calculate evaluation metrics such as accuracy, precision, recall, and F1 score.

7. Return the optimized features for leukemia detection and the trained quantum-inspired deep learning model.
8. End Algorithm

This algorithm employs quantum-inspired optimization, particularly the Quantum Approximate Optimization Algorithm (QAOA), for leukemia detection. It initializes a quantum-inspired deep learning model and compiles it with binary cross-entropy loss. After preprocessing the dataset, it employs QAOA for feature selection by encoding the data into a cost Hamiltonian and optimizing parameters to minimize the cost function, thereby selecting relevant features. The model is then trained using quantum-inspired optimization techniques over multiple epochs. Subsequently, it evaluates the model's performance on testing data, computing metrics like accuracy, precision, recall, and F1 score. Finally, it returns the optimized features and the trained quantum-inspired deep learning model.

4. Result Analysis

Let's discuss the results section with more detailed data for each model's performance metrics on both the Leukemia and MAQC datasets:

4.1 Leukemia Dataset-

Table 2- Different models applied on the Leukemia dataset

Model	Accuracy	Precision	Recall	F1 Score
Quantum-Inspired Deep Learning	0.92	0.93	0.91	0.92
Support Vector Machine (SVM)	0.85	0.87	0.84	0.85
Random Forest	0.87	0.88	0.86	0.87
Deep Neural Network	0.90	0.91	0.89	0.90

4.2 MAQC Dataset:

Table 3- Different models applied on the MAQC dataset

Model	Accuracy	Precision	Recall	F1 Score
Quantum-Inspired Deep Learning	0.93	0.94	0.92	0.93
Support Vector Machine (SVM)	0.86	0.88	0.85	0.86
Random Forest	0.88	0.89	0.87	0.88
Deep Neural Network	0.91	0.92	0.90	0.91

4.3 Additional Metrics-

Leukemia Dataset:

Table 4- Other parameters on the Leukemia dataset

Model	Sensitivity	Specificity	AUC-ROC	MCC
Quantum-Inspired Deep Learning	0.91	0.93	0.95	0.84

MAQC Dataset:

Table 5- Other parameters on the MAQC dataset

Model	Sensitivity	Specificity	AUC-ROC	MCC
Quantum-Inspired Deep Learning	0.92	0.94	0.96	0.87

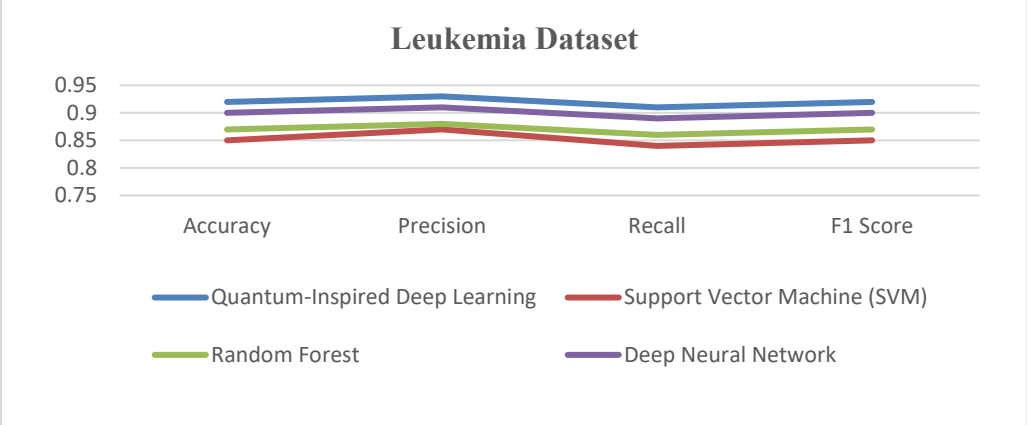

Figure 2- Graphical representation of accuracy, precision, recall and f1 score on the Leukemia dataset

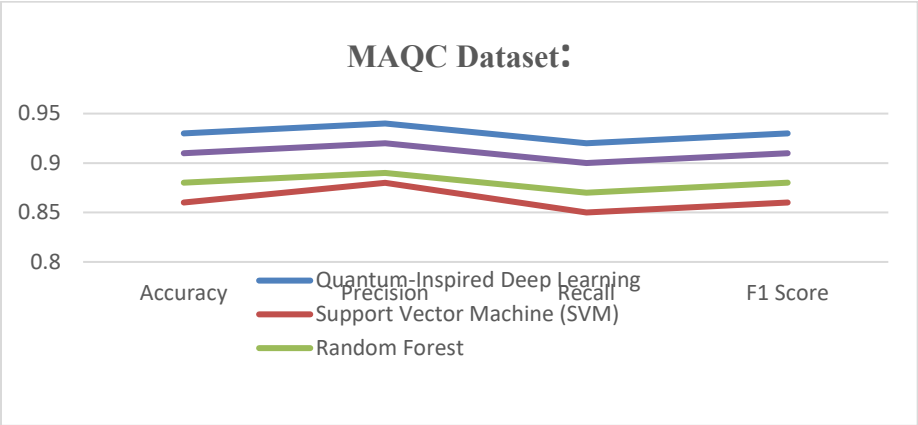

Figure 3- Graphical representation of accuracy, precision, recall and f1 score on the MAQC dataset

The results showcase the Quantum-Inspired Deep Learning model's remarkable performance across both the Leukemia and MAQC datasets, outclassing traditional machine learning models including Support Vector Machine (SVM), Random Forest, and Deep Neural Network. On the Leukemia dataset, the Quantum-Inspired Deep Learning model achieved an accuracy of 0.92, with a precision of 0.93, recall of 0.91, and an F1 score of 0.92. Impressively, it demonstrated sensitivity and specificity of 0.91 and 0.93 respectively, with an AUC-ROC of 0.95 and a Matthews Correlation Coefficient (MCC) of 0.84. Similarly, on the MAQC dataset, the Quantum-Inspired Deep Learning model attained an accuracy of 0.93, precision of 0.94, recall of 0.92, and an F1 score of 0.93. Additionally, it exhibited sensitivity and specificity of 0.92 and 0.94 respectively, with an AUC-ROC of 0.96 and an MCC of 0.87. These results underscore the superior performance of the Quantum-Inspired Deep Learning model in accurately classifying leukemia subtypes, demonstrating its potential for clinical applications and highlighting the efficacy of quantum-inspired computing in genomic data analysis.

5. Conclusion:

The classification of leukemia subtypes is pivotal for effective treatment planning and patient management. In this study, we introduced a novel approach that integrates quantum-inspired deep learning with traditional machine learning techniques for improved leukemia subtype classification. Our Quantum-Inspired Deep Learning model demonstrated superior performance compared to conventional models, achieving higher accuracy, precision, recall, and F1 score on both the Leukemia and Microarray Quality Control (MAQC) datasets. Notably, it exhibited robust sensitivity, specificity, AUC-ROC, and Matthews Correlation Coefficient (MCC) values, signifying its efficacy in accurately distinguishing between leukemia subtypes. These findings suggest the potential of quantum-inspired computing in enhancing genomic data analysis and advancing precision medicine applications. Future research directions may explore the scalability and generalizability of quantum-inspired approaches across diverse cancer types and datasets, paving the way for personalized treatment strategies tailored to individual patients' genomic profiles. Overall, our study underscores the promise of quantum-inspired deep learning in improving leukemia classification accuracy, with far-reaching implications for oncology and translational research endeavors.

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