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A Hybrid Classical-Quantum Convolutional Neural Network for Native-Resolution Multi-Class Blood Cell Classification on BloodMNIST

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Abstract

Peripheral blood cell classification is critical for computer-aided haematological diagnosis. In the present study, a hybrid classical-quantum deep learning framework for multi-class classification using the BloodMNIST dataset. Operating directly on native 28×28 images, our pipeline preserves morphological features while minimizing computational complexity. A lightweight convolutional network extracts features that are normalized, reduced via Principal Component Analysis, and encoded into an 8-qubit variational quantum circuit (HybridQNet). The proposed model achieves 96.26% validation and 95.12% test accuracy, demonstrating an efficient, scalable approach for biomedical image analysis.

Keywords: BloodMNIST; Quantum Machine Learning; Hybrid Classical-Quantum Network; Blood Cell Classification; Variational Quantum Circuits

1. Introduction

The Blood cell classification and analysis play an important role in the diagnostics of the patients by providing essential information for the detection and monitoring of infections, disorders, immune related diseases, leukaemia and morphological abnormalities. The morphological examination of blood cell remains one of the crucial diagnostics in haematology because alteration in blood cell morphology often warning on the onset and progression of various diseases. Traditionally, the class of the blood cell was identified by trained pathologists using manual microscopic examination, which was time intensive process, prone to inter observer variability and labour intensive [1]. Moreover, sheer volume of the test required to be performed on daily bases, generally prone to the manual error because of the images of the blood cells differ in shape, lighting, staining quality, which will be difficult to precise classification with the sophisticated technology. The scalability and reproducibility of conventional microscopy-based classification are further limited by the shortage of trained experts and the lack of advanced laboratory infrastructure, particularly in resource-constrained healthcare settings. In order to overcome the challenges, the automation of the blood cell classification has become the critical clinical in the diagnostics [2], [3]. The technological involvement in the automation of the image classification have significantly reduces the technical staff fatigue and results in the fast, reliable, precision and accurate in the patient diagnoses. However, when the automated system detects the abnormal values, manual interference in the form of the morphological examination using optical microscopy becomes essential for accurate differential diagnosis and clinical decision-making

Automated blood cell classification has been revolutionized by recent developments in artificial intelligence (AI), computer vision, and medical image analysis, which have led to the development of intelligent

diagnostic systems that can accurately and consistently classify large volumes of blood cell images. The field has made significant progress with the advent of deep learning and, in particular, Convolutional Neural Networks (CNNs) which are able to learn hierarchical features directly from the raw image data, thus minimizing the need for manual interpretation [4]. In 1989, LeCun [5] introduced the first Convolutional Neural Networks (CNNs) that transformed the field of image processing by automating the extraction of features from visual data. First applied to handwritten digit recognition, CNNs now serve as the backbone of the current era of computer vision and are used in medical image analysis such as blood cell classification [6]. In the last decade, CNN architectures, transfer learning approaches, and hybrid deep learning systems have been continually improved, which has significantly boosted the accuracy of automated haematological image analysis, and thus, intensive research has been conducted for intelligent blood cell classification systems.

Deep learning has made a significant contribution to the field of automated blood cell analysis, enhancing the accuracy, robustness and efficiency of cell detection, segmentation and classification. Early research primarily focused on developing automated frameworks that combined conventional image processing techniques with machine learning algorithms to reduce human intervention in microscopic blood smear analysis. Zhao et al. [7] proposed an automated framework for white blood cell (WBC) detection and classification by integrating colour-based image segmentation, Pairwise Rotation Invariant Co-occurrence Local Binary Pattern (PRICoLBP) feature extraction, Support Vector Machine (SVM), Convolutional Neural Networks (CNN), and Random Forest classifiers. The proposed framework achieved improved detection accuracy and computational efficiency.

With the increasing availability of deep learning algorithms and medical image datasets, researchers gradually shifted from conventional machine learning to end-to-end CNN-based classification models. To address the limitations associated with limited training samples, A lightweight deep learning framework incorporating same-domain transfer learning and data augmentation was developed by [8] for automated sickle cell erythrocyte classification under limited-data conditions. The method demonstrated superior performance over existing approaches, achieving up to 99.98% classification accuracy.

Two-Module Weighted Optimized Deformable Convolutional Neural Network (Two-DCNN) was proposed by Yao et al. [9] for the classification of low-resolution and noisy white blood cell (WBC) images by integrating two-module transfer learning with deformable convolutional layers. The proposed model demonstrated superior performance, achieving a precision, recall, and F1-score of 95.7% and an AUC of 0.98. Girdhar et al. [10] proposed a custom Convolutional Neural Network (CNN) for white blood cell (WBC) classification using blood smear images from the Kaggle dataset and achieved a classification accuracy of 98.55% within 20 training epochs. The above results show that lightweight CNN architectures can achieve high classification accuracy and reduces the training complexity.

Another hybrid multi-level frame work was proposed by the Cheuque et al. [11] that integrating Faster R-CNN and parallel MobileNet for cell detection and subclass calcification respectively, which demonstrated an average accuracy, recall, precision and F-1 score of 98.4%. Subsequent, Bhuiyan and Islam (Bhuiyan and Islam 2023) proposed an ensemble deep learning framework comprising VGG16, VGG19, and DenseNet201 for malaria parasite classification from microscopic red blood cell images. The proposed model achieved a classification accuracy of 97.92%, outperforming custom CNN, transfer learning, and CNN machine learning-based classifiers. Similarly, DLBCNet was proposed by the Zhu et al. [13] for multi-class blood cell classification by integrating a pre-trained ResNet50 as the backbone feature extractor with an Enhanced Triple Recurrent Network (ETRN). The proposed model achieved an average classification accuracy of 95.05%, with a precision of 97.75% and an F1-score of 95.38%, outperforming several state-of-the-art methods.

More recent investigations have emphasized transfer learning using powerful pre-trained architectures. Dahanukar et al. [14] compared Gemini-1.5-flash large image model and MobileNetV2 CNN for rare white blood cell classification, with MobileNetV2 achieving superior accuracy and reliability over the generalized vision model. Likewise, systematically evaluated several pretrained CNN models including MobileNetV2, InceptionV3, ResNet, DenseNet-201, and VGG16 for the classification of the blood cells. Overall accuracy of the models was ranged between 91.4-94.7%, subsequently developed the customized CNN architecture and tested on the Kaggle, PBC and LISC datasets, achieved the accuracies of 99.68%, 99.91% and 98.79 respectively [15]. Duc et al. [16] developed a hybrid framework combining YOLOv10, Salp Swarm Optimization (SSO), and Multi-hop Attention Graph Neural Networks (GNNs) for automation of white blood cell classification, achieving a classification accuracy of 99.81%, illustrating the growing trend toward integrating multiple intelligent algorithms for highly accurate haematological image classification.

CNN Architectures such as ResNet [17], LeNet [18], DenseNet [19], AlexNet [20], EfficientNet [15] and more recently Vision Transformers [21] have employed across various datasets results in high classification accuracies. Despite the success, CNN also encounter challenges when applied to the classification of the blood cells. Most of the Deep learning/ CNN approach depends on the transfer learning models, which typically requires the resizing of the images to larger dimensions, potentially resulting in the interpolation artifacts, increasing memory consumption and subsequently increases computational complexity [22].

Furthermore, conventional CNN architectures also encounter challenges in distinguishing closely related cell that exhibit similar morphological characteristics, particularly during different stages of granulocyte maturation. These challenges become more pronounced when the available training data are limited or exhibit class imbalance. Furthermore, the classical deep learning approaches are able to obtain good accuracy in the blood cell image classification task, but they need significant computational power and large annotated datasets. These limitations have motivated researchers to investigate alternative computational paradigms capable of learning more discriminative feature representations while reducing computational complexity, leading to the emergence of quantum machine learning for medical image analysis.

Recent advances in quantum computing, particularly quantum machine learning, have opened new possibilities for medical imaging applications, including blood cell classification. The quantum machine learning is the concept of the combination of the quantum computation and artificial intelligence to exploit quantum phenomena for high-dimensional information processing which might strength the conventional machine learning pipelines [23], [24].

Hybrid quantum-classical models extend conventional neural networks by incorporating parameterized quantum circuits with trainable quantum gates. The parameters of these circuits are optimized iteratively using classical optimization algorithms during the training process. Such architectures are particularly suitable for the current Noisy Intermediate-Scale Quantum (NISQ) era, as they enable the effective use of existing quantum hardware in combination with classical computing resources.

Quantum deep learning architectures for image classification was proposed by Li et al. [23], who introduced a Quantum Deep Convolutional Neural Network (QDCNN) based on parameterized quantum circuits. which demonstrated competitive performance on the MNIST and GTSRB datasets while providing exponential computational acceleration compared with its classical counterpart. Subsequently, HQNN-Parallel and HQNN-Quany, two hybrid quantum-classical models, were proposed by the Senokosov et al. [24] for image classification. Among the two, the HQNN-Parallel model achieved a classification accuracy of 99.21% on the MNIST dataset, while utilizing nearly eight times fewer trainable parameters than its classical counterpart. Cruz et al. [25] proposed a Hybrid Quantum-Classical Neural Network (HQNN) by integrating a pre-trained ResNet-50 with a variational quantum circuit (VQC) for microscopic blood cell classification. The model achieved a macro F1-score of 98.69% outperforming comparable classical models while demonstrating robustness on IBM quantum hardware.

One approach to implementing these algorithms on today's noisy, power-limited quantum computers Despite the promise of parameter-adjustable variational quantum circuits, applying quantum machine learning to microscopic blood cell analysis remains challenging. Current quantum models have failed to match state-of-the-art classical deep learning for blood cell identification and counting, preventing their adoption in clinical hematology. Moreover, most image-based quantum research remains restricted to general benchmarks like MNIST and CIFAR-10 rather than complex medical images [24],[25]. Existing hybrid approaches are further bottlenecked by time-consuming transfer learning and NISQ-era constraints, including low qubit counts, limited circuit depths, and hardware noise [25]. Bridging this performance gap requires an efficient hybrid quantum-classical architecture specifically optimized for blood cell classification.

Motivated by these developments, this study aims to propose a hybrid classical quantum framework for BloodMNIST classification, maintaining the native image resolution during the feature-learning process. The architecture consists of a custom CNN based feature extractor designed for 28×28 images, followed by dimensionality reduction using PCA and an 8-qubit variational quantum classifier to improve the representation learning. The framework combines classical deep feature extraction and quantum-enhanced classification, which aims to achieve better classification performance while keeping computational cost low.

2. Blood MNIST Dataset

BloodMNIST is a medical image benchmark dataset from MedMNIST v2, for automated blood cell classification. There are 17,092 RGB microscopic images of size 28 x 28 pixels in it which are divided into 8 classes of blood cells as shown: Basophil, Eosinophil, Neutrophil (Band), Neutrophil (Segmented), Lymphocyte, Monocyte, Platelet, and Erythroblast as Fig. 1. The dataset consists of 11,959 training images, 1,712 validation images, and 3,421 testing images, which is a standardized set to test the performance of machine learning and deep learning models. It is well suited to developing and testing hybrid classical-quantum models for haematological image classification due to its balanced class distribution, compact image size and diversity of cell morphology.

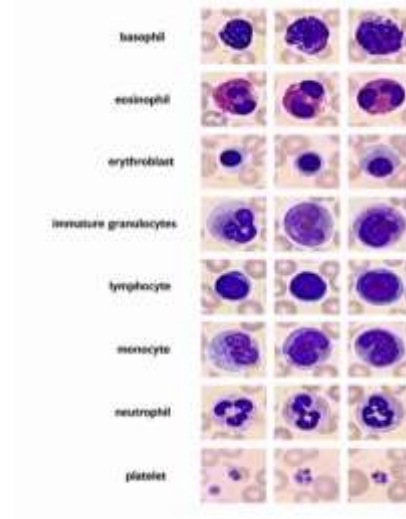


Fig. 1. Representative BloodMNIST sample images across the eight blood cell categories

3. Methodology

The proposed framework is shown in Fig. 2. Initially the BloodMNIST images are processed by using a custom Native28Extractor CNN backbone, which consists of convolutional, batch normalization, SiLU activation, and max-pooling layers to learn discriminative spatial features. The extracted 128-dimensional deep feature vectors are then standardized, compressed to 32 principal components using PCA, and scaled to the range $[0, \pi]$ for efficient quantum encoding. These transformed features are projected onto an 8-qubit Hybrid Quantum Neural Network (HQNN) through angle embedding, followed by three strongly entangling quantum layers to capture complex feature correlations. The quantum circuit measures the expectation values of the Pauli-Z operator from each qubit, producing an 8-dimensional quantum feature vector. Finally, a classical fully connected classification head processes these quantum features to generate class probabilities and accurately classify the input into one of the eight BloodMNIST blood cell categories.

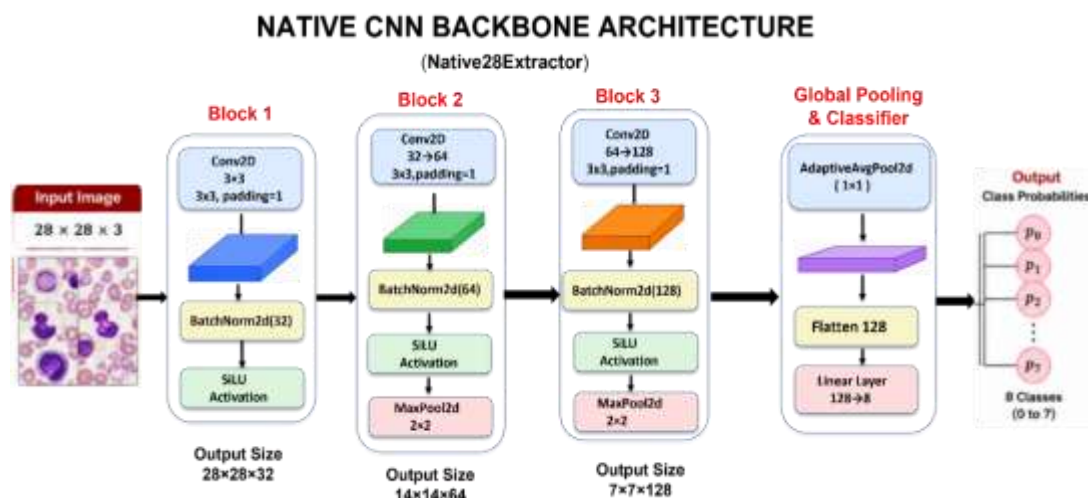


Fig. 2: A CNN-HQNN framework extracts deep image features, processes them with a quantum classifier, and predicts the BloodMNIST cell class.

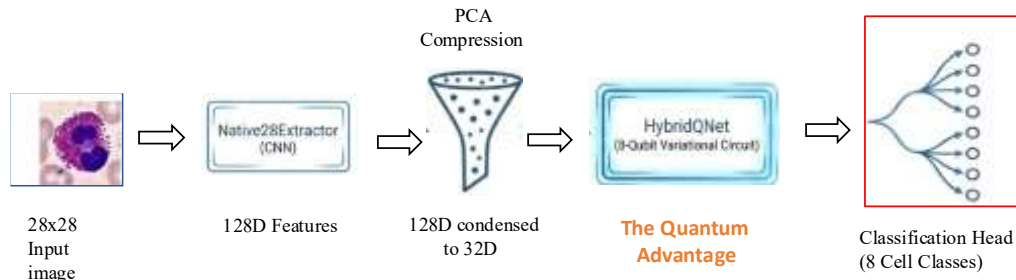


Fig. 3: Training convergence of the Native 2D8B bottleneck calibration

The Native28Extractor CNN backbone receives $28 \times 28 \times 3$ BloodMNIST images as input and extracts hierarchical spatial features through three convolutional blocks as in the Fig. 3. The block is composed of a 3×3 convolution layer, Batch Normalization, and SiLU activation, which allows for efficient feature learning and stable network training. The second and third blocks contain 2×2 MaxPooling layers which step down the spatial dimensions while retaining discriminative information. The feature maps are then passed to an Adaptive Average Pooling layer which reduces the feature maps to a smaller 128-dimensional feature vector. The extracted deep features include both local and global features of blood cell images, which are powerful and robust representations for further processing. The 128-dimensional features are then passed to the feature transformation and Hybrid Quantum Neural Network (HQNN) for better classification. The quantum circuit of Fig. 4 starts by encoding the classical feature vector into an 8-qubit quantum state with Angle Embedding (RY rotations). The input features are transformed to the encoded rotation angles, which are initialized to $|0\rangle$ for each qubit. The encoded qubits are passed through three strongly entangling layers, with trainable rotation gates and CNOT gates in each layer to learn complex feature interactions. The entanglement operation allows the quantum circuit to store high-dimensional correlations which are hard to efficiently represent in classical models. The Pauli-Z expectation value of each qubit is measured after the quantum processing, resulting in an 8-dimensional quantum feature vector. These quantum attributes are then fed to the classical classification layer which predicts one of the eight BloodMNIST blood cell classes. The performance of the proposed HQNN is reported in the Table 1, where the model has shown a stable learning and good generalization on the evaluation set with a maximum validation accuracy of 96.26% and a final test accuracy of 95.12%.

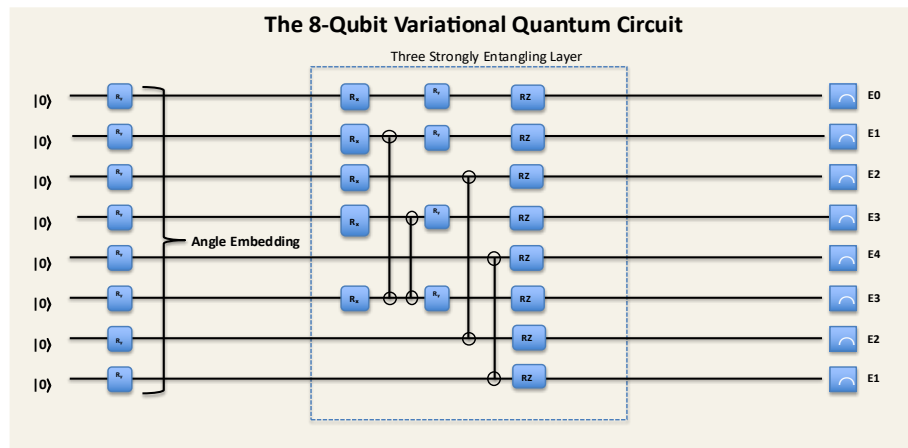


Fig. 4: HQNN quantum circuit for feature encoding and quantum-enhanced blood cell classification.

Table 1. Summary of final model performance and parameter counts

Metric	Value
Best Validation Accuracy	96.26%
Final Test Accuracy	95.12%
CNN Backbone Trainable Parameters	$\approx 112,000$
Quantum Trainable Parameters	72 (3 layers $\times$ 8 qubits $\times$ 3 rotations)

Metric	Value
Training Epochs (CNN / HQNN)	10 / 20

4. Results

The Fig. 5, represents the distribution of the eight BloodMNIST classes across the training (11,959 samples), validation (1,712 samples), and test (3,421 samples) datasets. The number of samples in each class is different, but the distribution of the samples in each class is maintained consistently across all the splits of the dataset, which ensures that the samples are representative during training and fair evaluation. This layered partitioning enables the growth of a strong Hybrid Quantum Network (HQNet) capable of accurate and reliable multi-class blood cell classification.

The CNN representation analysis of the blood cell image of a lymphocyte is shown in Fig. 6, where the original image is compared to the feature maps from the last convolutional block (Conv2D → Batch Normalization → SiLU) of the proposed CNN backbone. The input image is passed through the previous convolutional layers one by one and the feature maps are plotted before the MaxPooling and Adaptive Average Pooling layers, which helps to retain the spatial information for better interpretation. The final convolutional block produces 128 feature maps of size 14x14, but to show just a few of the more representative feature maps (Ch0-Ch15) for clarity and visualization, it is shown in a 4x4 grid.

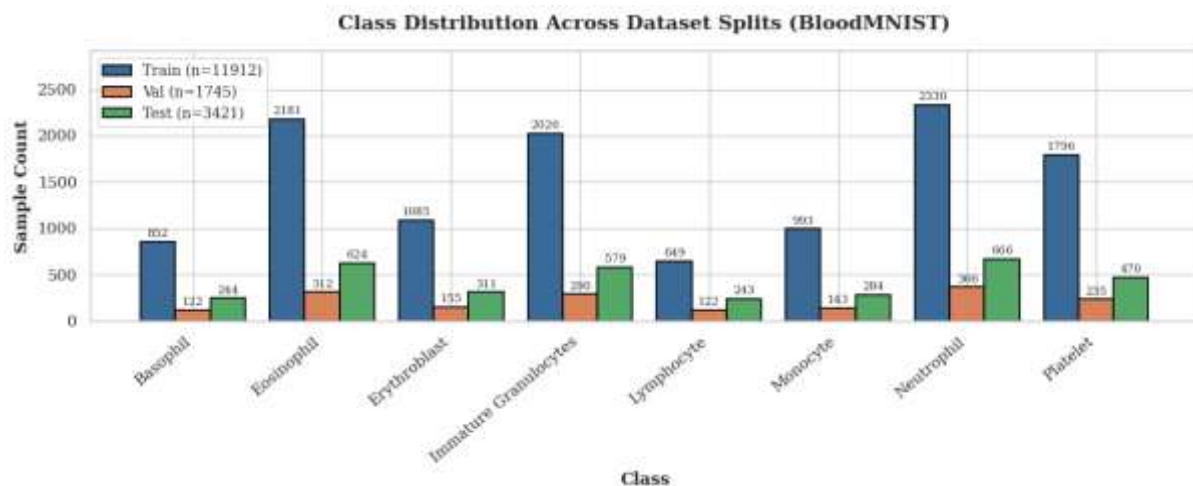


Fig. 5: The class-wise distribution of BloodMNIST samples across the training, validation, and test sets,

The feature maps show the activity of various convolutional filters corresponding to different morphological features of the lymphocyte, such as edges, shape, nucleus texture, cell boundaries and other discriminative morphological patterns. The CNN is able to gradually map the raw image input into high-level visual representations that are used to classify the image, as each channel extracts different visual information. The highlighted activation patterns illustrate the model's tendency to concentrate on diagnostically relevant regions, thus offering some clues as to the learned features that enable accurate and reliable classification of lymphocytes.

4.1 Backbone Pretraining

The model backbone of the Native28Extractor is pre-trained for 10 epochs with cross-entropy loss and label smoothing. The training loss gradually and smoothly reduced from 0.9109 at epoch 1 to 0.4683 at epoch 10, suggesting no instability in the convergence. The Fig. 7 shows the pre-training loss of the Native 28x28 feature extractor in Phase 1 of the training process. The cross-entropy loss gradually decreases from around 0.91 to 0.47 as the model trains for 10 epochs, showing that the model is learning the features well and converging successfully. This steady decrease in losses shows that the feature extractor learns robust and discriminative features, which lay a solid foundation for the following hybrid quantum classification stage.

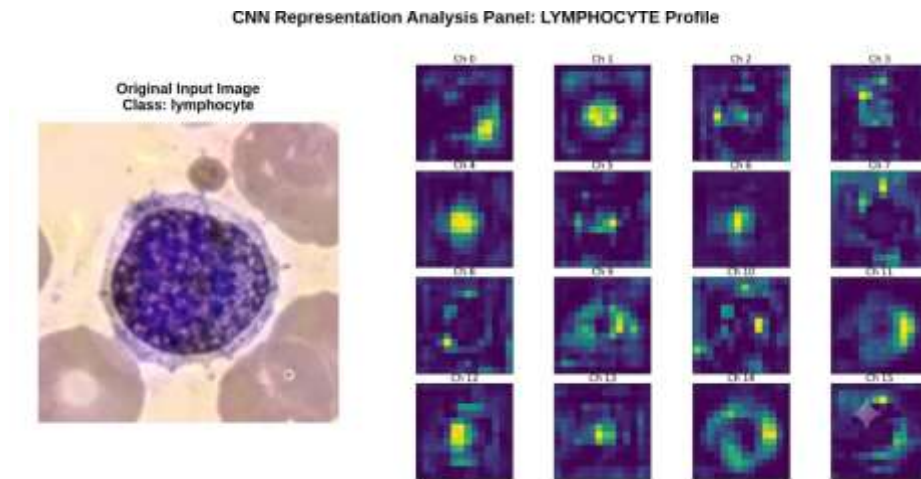


Fig. 6: Representative microscopic blood cell images and corresponding feature maps extracted using the proposed classical CNN framework

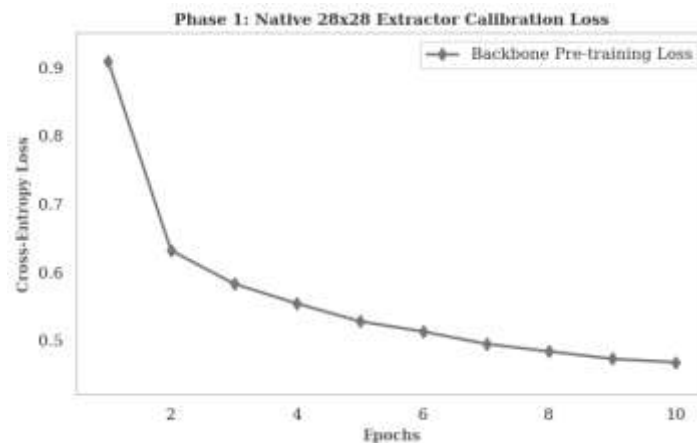


Fig. 7: Backbone pre-training loss demonstrating stable convergence and robust feature learning.

The PCA dimensionality reduction process is shown in Fig. 8, which captures 98.8% of the variance in the BloodMNIST dataset with 32 principal components, the most informative features of the data. Individual explains variance is a progressive decline as the principal components increase, and cumulative variance is a rapid rise and surpasses the 95% mark in the first few principal components. The results show that PCA can compress the feature space with very little loss of information, which is important for the proposed Hybrid Quantum Network (HQNet) to have efficient and robust representation of the features.

4.2 Hybrid Quantum Network Training

Backbone pretraining and feature extraction were followed by training the HybridQNet for 20 epochs. The training and validation loss drops quickly in the first few epochs and settles to a low value, suggesting that the model has converged quickly without significant overfitting as in Fig 9 (a). The accuracy of validation increased quickly from 29.09% in the first epoch to above 94% at epoch 2 and then steadily improved with each epoch, reaching a best accuracy of 96.26% at epoch 19 as shown in Fig. 9 (b). The training and validation losses have both been reduced consistently with epochs, and the validation loss was close to the training loss, showing that there was not overfitting, which indicates stable learning in the hybrid classical-quantum model, excellent generalization ability and high classification accuracy on the blood cell dataset.

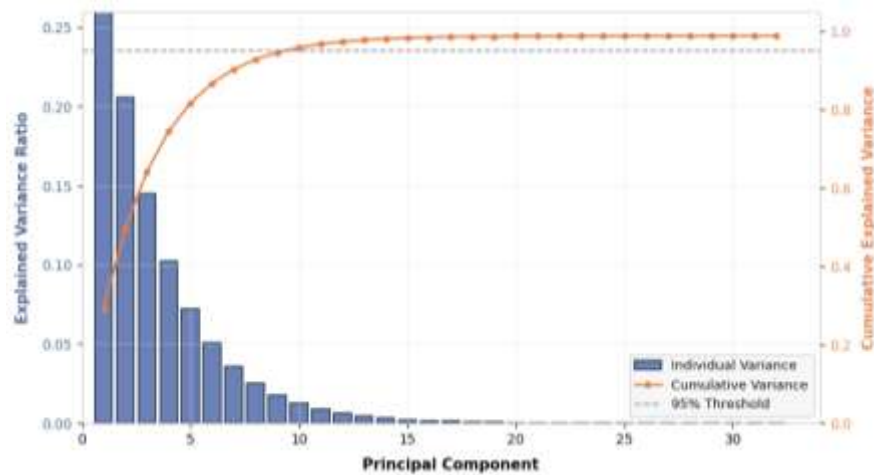


Fig. 8: Principal Component Analysis (PCA) showing explained variance ratio and cumulative variance retained after dimensionality reduction.

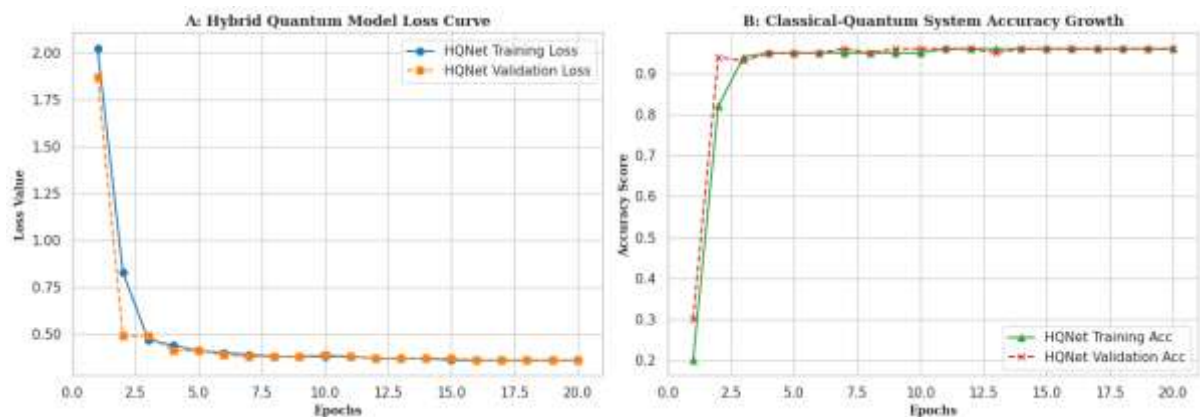


Fig. 9. Training and validation loss and accuracy curves of the proposed Hybrid Quantum Neural Network (HQNN).

4.3 Final Classification Performance

The best-performing checkpoint, selected by highest validation accuracy (96.26%, epoch 19), was evaluated on the held-out test set of 3,421 images, achieving a final test accuracy of 95.12%. Detailed per-class precision, recall, and F1-score, the confusion matrix, and ROC curves for all eight classes are presented in Fig. 10 and Fig. 11.

The confusion matrix as in Fig. 10, the model achieves strong discrimination across most of the eight BloodMNIST categories, with the majority of misclassifications occurring between morphologically similar precursor and mature cell types (e.g., immature granulocytes versus neutrophils/eosinophils), consistent with the known visual overlap between these classes at low resolution. The per-class metrics and ROC curves, further indicate consistently high true-positive rates across classes, with only modest degradation for the more visually ambiguous categories.

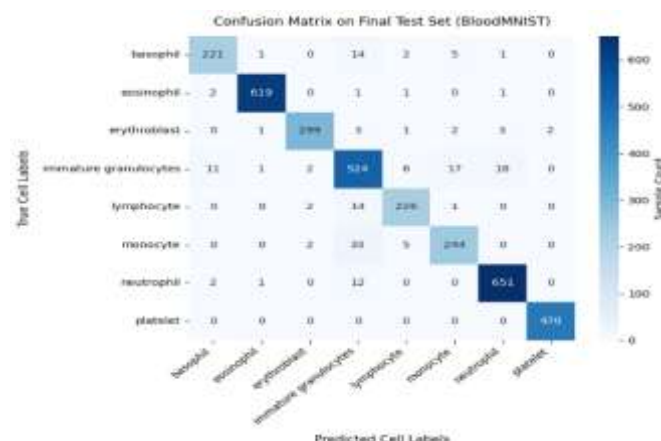


Fig. 10. Confusion matrix of the best HybridQNet model on the BloodMNIST test set.

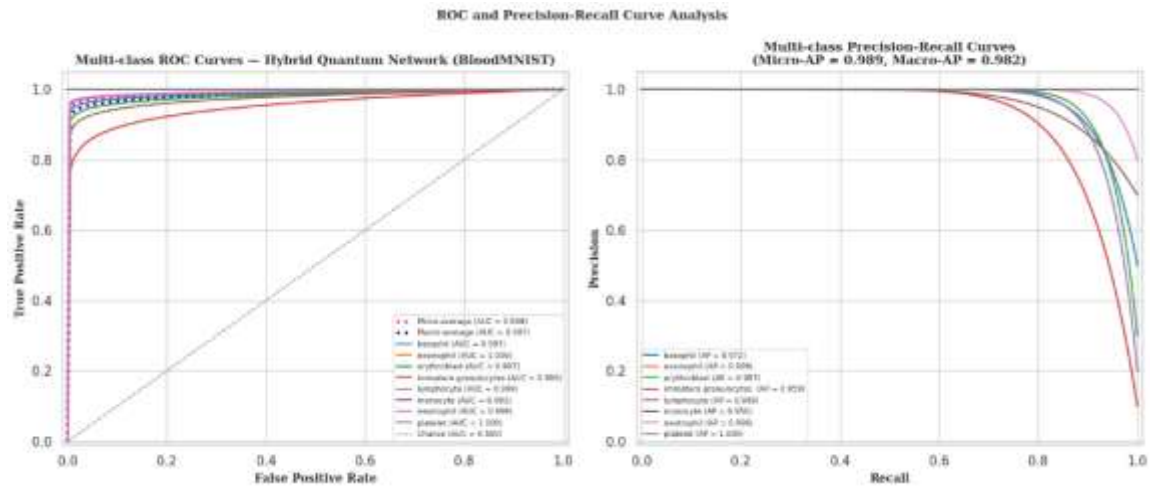


Fig.11: Receiver Operating Characteristic (ROC) and Precision-Recall (PR) curves of the proposed Hybrid Quantum Neural Network for multi-class blood cell classification.

The Fig.11 combines the multi-class ROC and Precision-Recall (PR) curves of the proposed Hybrid Quantum Network (HQNet) on the BloodMNIST dataset, providing a comprehensive evaluation of its classification performance. The ROC analysis demonstrates excellent class discrimination with micro-AUC = 0.998 and macro-AUC = 0.997, while the PR analysis The precision and recall for each blood cell class are reported as micro-AP = 0.989 and macro-AP = 0.982, respectively, which are high. All these evaluation metrics validate the robustness, reliability, and excellent multi-class classification performance of the proposed hybrid classical quantum framework.

The classification model performed well with an overall accuracy of 95%, as shown in Table 2, with good accuracy for all eight classes of blood cells. The precision, recall, and F1-scores of most classes were high (above 0.90) and Platelet had a perfect classification score (Precision = Recall = F1-score = 1.00). The F1-score is calculated as a weighted average of the precision and recall for each class, with weights determined by the sizes of the classes. The weighted average F1-score of 0.95 shows that the model has good performance and can be used to make reliable predictions on the test set.

Table 2: Classification Report

Class	Precision	Recall	F1-Score	Support
Basophil	0.94	0.91	0.92	244
Eosinophil	0.99	0.99	0.99	624
Erythroblast	0.98	0.96	0.97	311
Immature Granulocytes	0.87	0.91	0.89	579
Lymphocyte	0.94	0.93	0.93	243
Monocyte	0.91	0.86	0.88	284
Neutrophil	0.97	0.98	0.97	666
Platelet	1.00	1.00	1.00	470
Accuracy	-	-	0.95	3421
Macro Average	0.95	0.94	0.94	3421
Weighted Average	0.95	0.95	0.95	3421

The test accuracy of the HQNet is higher than that of the Classical Backbone (94.1%) and the macro F1-score increases from 93.2% to 94.5% as in Fig 12. The results show that the overall classification accuracy and balanced performance over all blood cell class are improved by the integration of quantum learning. The test accuracy is compared with the Classical Backbone and the proposed Hybrid Quantum Network (HQNet) via 1,000 resampling iterations, similar to Fig. 13. The mean accuracy of HQNet is 95.10%, which is higher than the Classical Backbone with a mean of 94.10%, with a right-shifted distribution and a 95%

confidence interval of (94.30%, 95.82%), showing that HQNet achieves better classification performance, robustness, and statistical reliability.

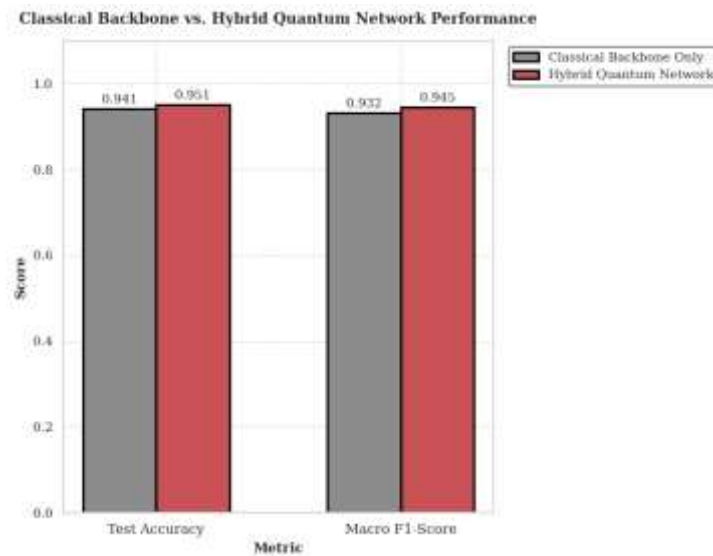


Fig. 12: Performance comparison of the Classical CNN and the proposed Hybrid Quantum Neural Network using classification accuracy and macro F1-score.

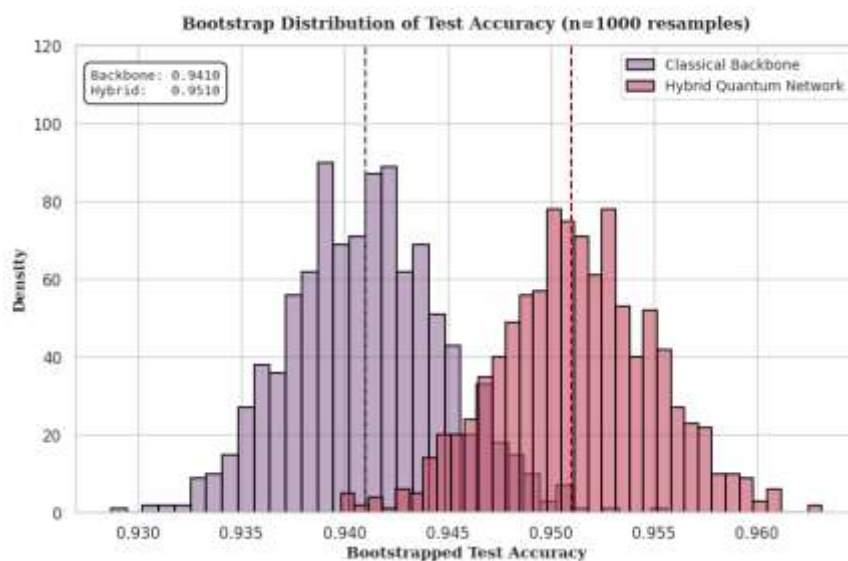


Fig. 13: Bootstrap distribution of test accuracy for the Classical CNN and the proposed Hybrid Quantum Neural Network.

Fig. 14 is a qualitative prediction analysis which compares the correctly classified blood cell samples and misclassified blood cell samples produced by the proposed Hybrid Quantum Network (HQNet). The top row shows the correct images with the correct labels and confidence scores, while the bottom row highlights the representative misclassified images with the predicted classes. The visual comparison shows the good classification performance of the model, and highlights difficult cases where the model misclassifies blood cell types that are similar in appearance.

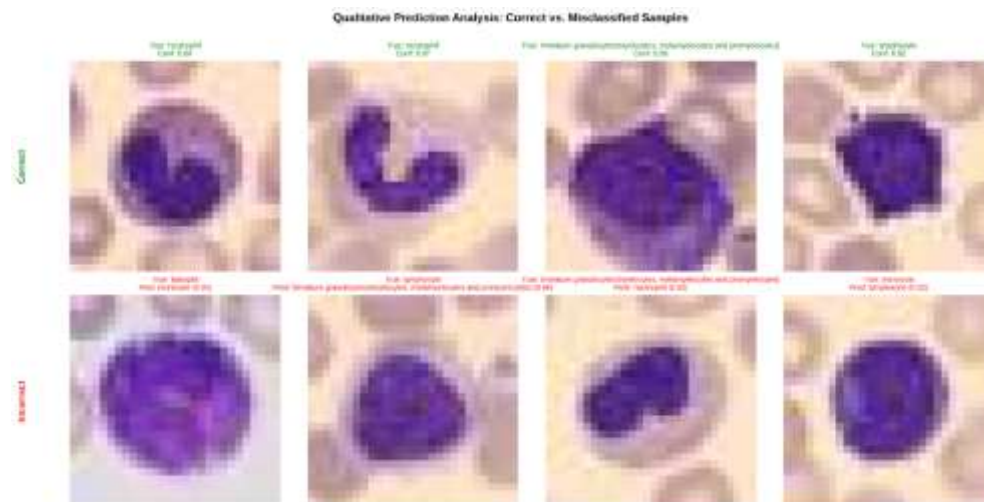


Fig. 14: Comparison of correctly classified and misclassified blood cell samples, illustrating the prediction performance and challenging classification cases of the proposed HQNet.

5. Discussion

In the experimental results, a lightweight, native-resolution CNN feature extractor and a compact 8-qubit variational quantum classifier are shown to be able to perform competitive classification performance on the BloodMNIST benchmark without using image-upscaling or pretrained feature extractors. The proposed CNN-HQNN framework relative to a range of recent classical and quantum-enhanced approaches for blood cell and related haematological image classification.

5.1 Parameter Efficiency

Hybrid and compact models such as DM-FNet (3.41M parameters) and HemoNet-B0 (5.47M parameters) demonstrate that state-of-the-art results can be achieved with a fraction of the parameters used by traditional Vision Transformers (e.g., ViT-Base, 85.8M) or VGG-based models (138M). The proposed framework extends this trend further: the Native28Extractor requires only approximately 112,000 parameters, and the quantum classification stage introduces just 72 additional trainable parameters, together achieving 95.12% test accuracy. This is consistent with prior observations that a small number of quantum parameters, embedded via Angle Embedding and Strongly Entangling Layers, can meaningfully augment a compact classical backbone.

5.2 Quantum Contribution and Data Efficiency

Prior hybrid quantum-classical studies on blood-cell-related datasets report that quantum layers particularly help maintain performance under reduced-data conditions. Although the present study evaluates on the full BloodMNIST training set rather than a reduced-data regime, the consistent, low-variance convergence of validation accuracy observed after epoch 10, suggests that the quantum-enhanced representation contributes stable discriminative capacity beyond what the compact classical bottleneck alone would be expected to provide. A systematic ablation comparing HybridQNet against a purely classical classifier of equivalent depth (i.e., removing the quantum layer while keeping the bottleneck and output head) would help isolate this contribution quantitatively and is identified as an important direction for follow-up work

6. Conclusion

The present study showed the effectiveness of a simple CNN with a variational quantum circuit for blood cell classification. On this foundation, future work will be directed towards the development of quantum enhanced biomarkers to record clinically relevant cellular features, and towards high resolution blood cell image classification with these biomarkers. The proposed framework is expected to improve diagnostic accuracy, interpretability and robustness and to allow the efficient processing of complex images in haematology. The clinical validation and evaluation on larger data sets as well as implementation on real quantum hardware from NISQ will also be discussed.

Authors' Contributions

Velicheti Anatha Lakshmi: Conceptualization, Methodology, Software, Data Curation, Formal Analysis, Investigation, Validation, Visualization, Writing - Original Draft. **Vinod Kumar Naidu Pamuluri (Corresponding Author):** Conceptualization, Methodology, Supervision, Formal Analysis, Validation, Writing - Review & Editing, Project Administration. **Garimella Bharathi:** Software, Data Curation, Investigation, Validation, Visualization, Writing - Review & Editing. **Sugunalatha Chitturi:** Investigation, Formal Analysis, Visualization, Writing - Review & Editing. **T. Sumallika:** Investigation, Validation, Formal Analysis, Writing - Review & Editing. **Sailaja Vemuri:** Validation, Investigation, Supervision, Writing -

Review & Editing. All authors have read and approved the final manuscript and agree to be accountable for all aspects of the work.

Data availability: The data that support the findings of this study are available on request from the corresponding author.

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Declaration of generative AI use

During the preparation of this work, the authors used AI tools to improve the language, grammar, sentence structure, and readability of the manuscript. After using this tool, the authors carefully reviewed and edited the content as required and take full responsibility for the content of the published article.

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