Quantum-Classical Hybrid Classification for Malaria Cell Images

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***Abstract*—This work compares the performance of classical deep learning models and hybrid quantum-classical systems for malaria cell classification problem, based on a publicly available Kaggle dataset of 27,558 labelled images. The pipeline combines classical feature extraction with quantum feature mapping and variational quantum circuits (2, 3 and 4 qubits) through angle encoding and strongly entangling layers. All the models have been trained over 40 epochs with a 70-15-15 train-validation-test split and accuracy, precision, recall, and F1-score have been evaluated. Classical cNN achieved 92.93% accuracy, ResNet18 and MobileNetV2 achieved.87.87% and 60.67% respectively. 4-qubit QCNN achieves the highest score of 93.47%, surpassing all the classical bases. The hybrid MobileNetV2 achieved an accuracy of 87.07%, which is a significant improvement compared with its classical counterpart, indicating that quantum feature transformation can repurpose weak classical representations. The findings demonstrate the great possibility to apply quantum layers to lightweight or ineffective classical models to analyze biomedical images, stimulate noise-sensitive training, and real-hardware simulations in future studies.**

***Index Terms*—Quantum-classical algorithms, Variational Quantum Circuit, Entangling layers, Feature mapping, Resnet, Mobilenet**

I. INTRODUCTION

Human health continues to be shaped by the persistent coexistence of communicable and non-communicable diseases across the globe. Communicable diseases are the diseases caused by infectious agents (bacteria, viruses, parasites, etc.). Meanwhile, non-communicable illnesses, including diabetes, cardiovascular diseases, and cancers, have long-term health care costs on health care system, economies, and individuals. As a result, there has been increased interest in the world to improve the accuracy and availability of diagnosis, especially on conditions that are characterized by high morbidity and mortality.

Malaria is among the most prevalent and affective parasitic infections in the category of communicable diseases. In Africa, Asia, and South America, malaria has been endemic despite decades of efforts by the control programs. Global health reports have indicated that millions of cases of malaria are still being reported every year, and that, the disease has particularly been disproportionate in the vulnerable population especially the children below the age of five, and pregnant women. Several factors lead to the persistence of the malaria disease, among them climatic factors, the distribution of mosquito vectors, human movement, and constraint in medical care services. It is these issues that require successful diagnosis and timely treatment to minimize transmission and deaths [1].

The manual diagnosis of malaria is performed by light microscopy even though effective in the hands of skilled specialists, has a number of limitations. It is tedious, subject to human error and is sensitive to the quality of staining and slide preparation. Machine learning (ML) has become an effective approach to help with medical image analysis due to the growth of computational approaches in healthcare. Despite the promising results of these methods, manual feature engineering proved to be tedious.

The history of deep learning (DL) had changed the nature of medical image recognition when models started learning hierarchical representations directly out of raw images. CNNs, especially, were chosen as the architecture of choice when dealing with tasks that utilized spatial patterns, textures, and shapes, which microscopic blood smear images contain. CNNs remove the human task of extracting features and have always been better than the older ML methods in accuracy and resilience. A number of studies have demonstrated that classical CNN architectures can be used to detect malaria with high-performance, which is a solid platform to base automated diagnostic systems [2].

Besides the custom CNNs, the application of the pretrained deep learning models, like ResNet and MobileNet has significantly expedited the advancement of medical imaging systems. The benefit of these architectures is transfer learning, in which the experience of large-scale natural image data sets are reused in specialized medical tasks. Their thick hierarchical structure and their remnants enable them to detect small visual elements and as a result, they are suitable to detect the morphological features of malaria parasites [3].

Although classical DL architectures have been quite successful, recent progress in quantum computing has provided opportunities to improve machine learning processes even more. The concept of quantum machine learning (QML) opens up the potential of using quantum circuits to encode data into Hilbert spaces, which classical networks might be unable to learn. Though being in its nascent stages, such approaches promise to be promising sources of new diagnostic technologies in the future [4].

Hybrid classical-quantum neural networks enable classical backbones (CNNs, ResNet, MobileNet, etc.) to extract preliminary features, which are consequently processed by quantum circuits that can model nonlinear relationships and multi-feature correlations. This increases the representational power of the model in a way that does not overrule classical terms and thus, QML is a useful supplement to existing deep learning models [5].

Although quantum approaches are a promising avenue emerging, their use on malaria classification is still not well exploited. The vast majority of the available literature is dedicated to the classical deep learning only, and limited literature examines the idea of whether quantum circuits can offer extra opportunities to differentiate between parasitized and uninfected cells. Moreover, successful hybrid models require sensitive architectural design such as the proper dimensionality of feature, embedding approaches and circuit organizations. This leaves a gap in the research where systematic comparisons of purely classical models with hybrid classical-quantum models can provide interesting information [5].

Hence, within the framework of the proposed work, we create a unified model of malaria cell classification, or both the classical deep learning model and classical-quantum hybrid model. The system analyses the various model families such as custom CNNs and pretrained ResNet and MobileNet models and investigates how quantum layers can be used to improve classification performance should they be incorporated into the feature extraction pipeline. It is not only aimed at substituting classical models but evaluating whether quantum-enhanced representations are measurably better on the same experimental conditions. The study will help fill both practical and conceptual knowledge gaps in the intersection of quantum computing and medical imaging by comparing these architectures in a side-by-side analysis of them.

Therefore, the major contributions of this work are:

- A comparison of classical CNNs, pretrained deep networks and hybrid quantum-classical networks to classify malaria cell images with a standardized training and testing set of parameters.
- The analysis and implementation of quantum-enhanced feature transformations with variational quantum circuits with classical backbones, which allow a systematic comparison of representational abilities.

II. Related Works

The paper by [6] utilises pre-trained convolutional neural networks in feature extraction to enhance detection of malaria parasites in images of thin blood smears. The study states that with ImageNet-based CNNs fine-tuned on the NIH dataset, performance improvement over handcrafted features is significant because of more detailed transfer-learned features. The technique is also resistant to staining variation and morphological variation. Major drawbacks include computational cost, an ImageNet bias, and low generalization in cases where the conditions of real-world situations are highly dissimilar with the training distribution.

The article [7] introduces an end-to-end CNN that was trained directly on images of thin blood smears without any handcrafted preprocessing. Findings indicate that the accuracy is high and it is accurate across experiments, and it is more accurate than previous automated systems but is computationally efficient. The paper reflects the power of hierarchies of deep features trained on data. Limitations consist of decreased resilience to divergent microscopes and vulnerability to overfitting because of monolithic datasets.

The authors of the article [8] compare a variety of deep architectures: ResNet, VGG variants, and Xception to determine which types of models are effective in the field of malaria image classification. It has been shown that residual networks of greater depth are more accurate because they reuse features better and have a stable gradient. The experiment gives systematic compares and contrasts of precision, intricacy and the inference expenditure among structures. The weaknesses are a small diversity of the datasets, poor cross-site generalization, and lack of interpretability mechanisms.

Research paper [9] is an exploration of MobileNet and other small CNNs to allow the diagnosis of malaria on edge devices with constrained resources. The methodology realizes significant model reduction and latency as well as accuracy loss reduction and is applicable to the field. The article highlights the importance of depthwise-separable conv Run-Time Diagnostic Systems The article focuses on the advantages of depthwise-separable convolutions to portable diagnostic systems. The main problems are the decrease in capacity compared to larger CNNs, sensitivity to image noise, and high hyperparameters tuning.

The authors in work [10] develop a hybrid malaria detection pipeline that is based on the residual attention learning and the use of SVM-based classification. Attention modules enhance concentration on areas of interest of the parasite and SVMs boost decision boundaries on limited data. The accuracy is improved as compared to standard CNN baselines in experiments. Significant weaknesses include added complexity in architecture, slow training, and difficulty in tuning deep features to classical SVM integration.

The paper [11] presents a transformer-driven malaria detection model which utilizes multi-head self-attention to extract global context that traditional CNNs are not able to extract. The approach proves to be competitive and has better interpretability through the visualizations of attention maps. The benefits of this model can be determined by the fact that the model has the ability to model long-range relationships between the various cellular structures. Nevertheless, training transformers needs datasets that are large, needs considerable compute resources, and needs to be carefully regularized, which makes it hard to apply in the real clinical setting.

Work [12] suggests that a hybrid quantum-classical convolutional network (QCNN) can be used to detect malaria, and quantum circuits can be employed as a substitute to conventional convolution layers. The method shows that feature extraction based on QCNN can be competitive with relatively lower trainable parameters because of quantum entanglement. It seems promising with respect to simulated quantum hardware findings. There are drawbacks such as those in NISQ devices: noise, and the cost of simulation is expensive and fails to scale to large imaging datasets.

The researchers of the article [13] give the comparative analysis of quantum convolutional neural networks and classical CNNs on malaria cell data. Findings indicate that QCNNs are able to be equivalent or better than classical models in certain environments with significantly fewer parameters through quantum encoding efficiencies. The article is one of the earliest systematic comparisons of QCNNs in medical imaging. The limitations are the lack of qubits, the long execution time of existing quantum computers and the discrepancy between simulation and actual hardware.

The article [14] introduces a long hybrid quantum-classical ensemble of malaria detection that is a combination of quantum convolutional layers and classical deep modules. The model represents the multi-scale correlations with the help of parameterized quantum circuits and is more robust than the classical-only baselines. The method makes emphasis on the promise of quantum- enhancing feature space. Nevertheless, the problem of optimization, the lack of hardware maturity and memory constraints in quantum circuits do not allow realistic scaling.

Research [15] applies variational quantum classifiers to malaria-related biomedical tasks such as compound screening and molecular classification. The approach has the advantage of the expressiveness of high-dimensional quantum state spaces and fewer parameters than classical neural networks. The work extends quantum ML application to the wider antimalarial study pipelines other than imaging. The main shortcomings are that optimization is vulnerable to noise, hardware noise is a problem, and that quantum workflows are at an early stage of their development.

The article [16] also explores the efficiency of quantum convolutional neural networks (QCNNs) in malaria cell classification by directly comparing them with classical CNN models. This paper will look at the performance of quantum circuit based feature extraction compared to conventional convolutional filters in terms of representational efficiency and robustness. Findings indicate that QCNNs are capable of reaching competitive accuracy levels (with fewer parameters than classical CNNs) and thus indicate that quantum state encoding has the potential to be helpful in biomedical imaging. Among the benefits of the approach, the authors note that it can simplify the model further and achieve quantum parallelism, but they also realize that the current hardware is limited in the number of qubits, and is highly sensitive to quantum noise, and the majority of tests are done on simulated and not physical quantum processors.

The authors of [17] give a quantum-convolutional network (QCN) to detect malaria parasites in a microscopic blood smear with the use of an automated detector. The model combines quantum convolution operations to acquire small image representations and is compared to classical CNN baselines. The results of experiments have shown that the QCN can have competitive or even better classification performance using fewer parameters, which underlines its potential in the low-resource biomedical image analysis. The authors highlight the advantages of quantum entanglement and amplitude encoding in the process of detecting complicated spatial correlations. Nevertheless, the article also admits major limitations, such as the use of quantum simulators since, at present, large-scale quantum machines are scarcely available, higher training times of hybrid models, and the inability to scale the method to higher-resolution images due to the qubit limitation.

III. Dataset Description

The dataset of the malaria cell images that has been used in the present study is provided by National Institutes of Health (NIH) and has become a popular reference to study automated malaria detection. It contains 27,558 microscopic cell images with an equal distribution of 13,779 parasitized and 13,779 uninfected samples which were extracted on thin blood smear slide images. Each image is of a solitary red blood cell that has been isolated and cut of entire microscopic fields to concentrate on particular cell morphological disparities that are linked to the malaria sickness. The trustworthiness and quality of the dataset have been supported by the previous academic articles like Rajaraman et al. (2018) who have proved that it is useful in creating malaria parasite detection systems based on deep-learning. The data is organized into two folders namely, Parasitized and Uninfected in respect to two diagnostic classes necessary to perform supervised classification. This dataset is also publicly available on Kaggle, which allows easy access by researchers, educators, and practitioners involved in medical image analysis. It is balanced in class distribution, has a large sample size and high-quality annotations, which make it suitable to train and evaluate classical machine learning, deep learning, and new hybrid quantum-classical models. The dataset can also be useful in the research directed to the enhancement of early malaria diagnosis with the help of automated diagnostic systems based on image.

IV. Proposed Methodology

A. Research workflow

This research for cell classification for malarial diseases has a structured workflow, from data preparation, feature extraction, quantum processing, and the final classification. The images are resized to 64 x 64 and normalized. The images are then into one of three classical backbone networks: CNN, ResNet18 or MobileNetV2, for feature extraction. The processed feature vectors are then dimensionally aligned following the classical processing through the available quantum resources. Normalization of these features is then done by scaling operation which operates on tanh that scales the outputs to valid rotation angles in quantum gate operations. The system then feeds the scaled values into a quantum-aware preprocessing algorithm which decides whether to use X-axis rotation or a mix of X and Y rotation. The system examines the statistical relationships between the features with the help of correlation matrix prior to the design of the quantum circuit. In case the strength of correlation between any two features surpasses a set parameter, the system turns on entanglement and uses the XY form of angle encoding. The encoded attributes are fed into a variational quantum circuit (VQC) of two layers of parameterized rotation in addition to controlled entangling interactions. The measurements of the qubits respectively produce a quantum-transformed feature-vector. The last phase of the pipeline converts quantum outputs into a classical classifier. In the case of hybrid models, the observed expectation values of each of the qubits are fed through a small multilayer perceptron (MLP) with ReLU activation and dropout regularization to produce the final binary classification result. In the case of classical baselines, the quantum layer is completely removed and the backbone outputs are the direct input to the classifier. The final stage of the workflow consists of training, validation, and evaluation.

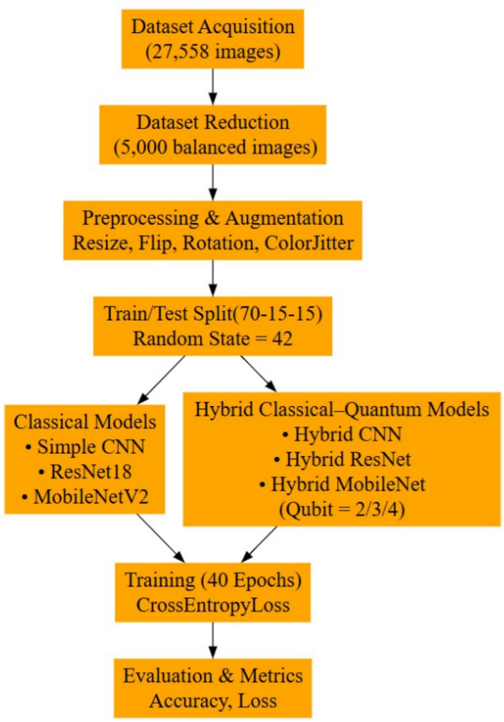

Fig. 1. The research workflow

B. *Classical architectures utilized in this study*

Three backbone architectures have been used namely, SimpleCNN, ResNet18, and MobileNetV2. SimpleCNN is a small feature extractor that consists of 3 convolutional layers with ReLU activations, max-pooling layers and adaptive average pooling operation. Its architecture is ended with three output channels that are flattened into a three dimensional feature space and is aligned to the number of available qubits in its corresponding hybrid model. The model is carefully chosen to be lightweight to give a shallow baseline and test quantum performance with minimal classical preprocessing. The second architecture is ResNet18 which uses pretrained ImageNet weights and uses the skip connections to learn in a residual form. All the pretrained convolutional layers are frozen and the last fully connected layer is substituted with a linear layer that yields four output features. Such alteration makes ResNet18 a frozen feature extractor that produces a small representation that is optimized to compute on four qubits of a quantum computer. The backbone obtains high-level semantic and morphological data of the input images and simplifies the training process. The third classical model is MobileNetV2 that is pretrained as well and operates on inverted residual blocks with depthwise-separable convolution to make it computationally efficient. Just like ResNet18, the final linear layer of its classifier is swapped with a four-feature output head to align with the quantum requirements. The architecture of MobileNetV2 provides a mobile-efficient variant that can extract features fast with low memory and computation costs and thus can be used to implement hybrid models.

The second architecture we designed is ResNet18, which we configured using pretrained weights on ImageNet that uses skip connections during residual learning. We froze all the pretrained conv layers and replaced the final fully-connected layer with a linear layer with four features. In essence, we convert ResNet18 into a frozen feature extractor, thereby obtaining a representation compatible with 4 qubits.

We utilized MobileNetV2 with pretrained weights which takes advantage of inverted residual blocks and depth-separable convolutions as well that are cheap to compute. Similar to the ResNet we replaced its final linear layer by the one which produces four values thus aligning it to the quantum side.

C. *Quantum-Classical architectures utilized in this study*

We trained hybrid systems, consisting of a combination of traditional DNNs and parameterised quantum circuits in a single pipeline. The hybrid architecture begins with a classical feature extractor which resizes the microscope images. CNN - hybrid provides us with a representation compatible for 2,3 and 4 qubits, for comparing which gives the best results. As, it was found that 4 qubits performed best, ResNet18 and MobileNetV2 were trained with 4 qubits.

Once we extract the features, the features undergo a non-linear scaling which constrains the value of the features to the range of [-π, π]. That puts them in correspondence with the rotation gates applied to quantum angle based embedding. Then we check the feature-correlation to optimize the quantum circuit. On a mini-batch of the outputs, we compute a correlation matrix, on a backbone each. When two or more features are highly interdependent to 0.3, we consider the feature space to be interdependent. If the qubits were independent, we have utilized Strongly Entangling Layers, along with X and Y rotations.

The quantum feature mapping is used to map the scaled classical features to the quantum states. In case the features are not correlated, every single one merely undergoes a Y-axis rotation on its qubit. When they are correlated, complex set of trainable rotation and entanglement operations is distributed over the Bloch sphere.

After encoding the features we run two trainable layers of the quantum bits through a variational circuit. The variational layers allow the quantum section to shape the incorporated information to a new feature space that is adjusted in conjunction with the standard classic classifier.

The expectation values of Pauli -z are produced by the variational circuit per qubit, producing a quantum -transformed feature vector of the same size as the qubits. As continuous numbers we sort them out into the final classic head. This head has an FC layer which maps to a latent sensor, a nonlinear tweak and dropout to ensure that we do not over-fit followed by the output layer which votes on whether the slide is malaria-positive or not.

In classical baselines, we simply project the characteristics of the backbone directly to the same conventional classifier that the hybrids are relying on. In that case, the quantum transformation is the only variable that is present or absent. The architectures of hybrid quantum-classical utilized have been shown.

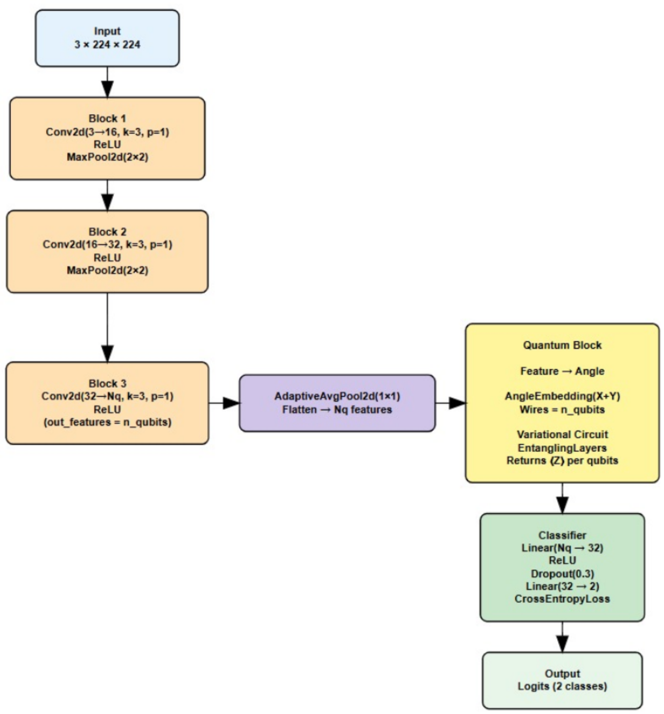

Fig. 2. Hybrid CNN

V. Results and analysis

The evaluation of the performance of the models is shown in Table I In the case of the classical baselines, it has been observed that CNN has the highest accuracy of 92.93%, which is quite remarkable considering the light weight structure. ResNet18 also scores 0.8787, although not much better than

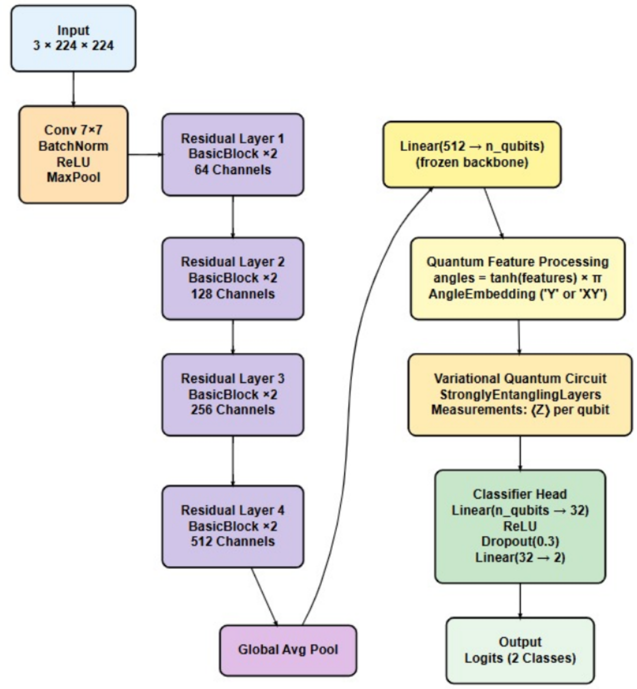

Fig. 3. Hybrid Resnet

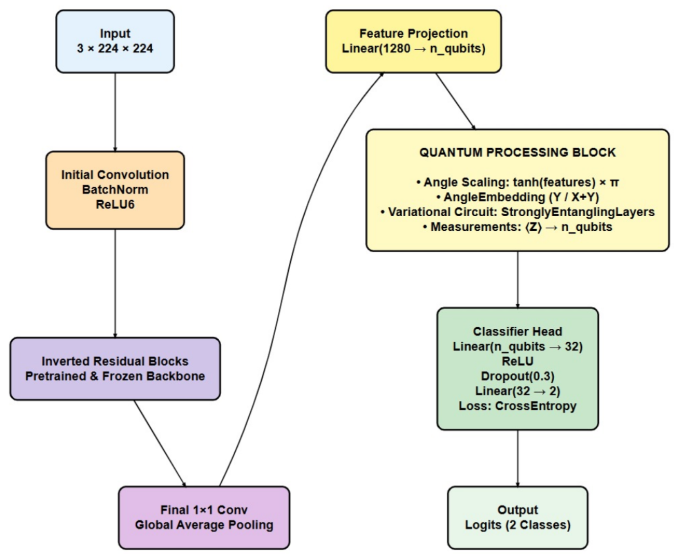

Fig. 4. Hybrid Mobilenet

CNN, and this is likely due to the fact that its pretrained backbone is frozen, thus not allowing it to learn the specific attributes of microscopy images. On the other hand, MobileNetV2 is the slowest with the lowest accuracy of 60.67%, primarily due to the frozen feature extractor. That is, it is not able to learn adequately to differentiate malaria cells.

The hybrid quantum-classical models prove to be stronger in some cases, that is, by adding quantum layers to them we can improve performance in case they are paired with

TABLE I
PERFORMANCE COMPARISON OF CLASSICAL AND HYBRID QUANTUM-CLASSICAL MODELS.

Model	Accuracy (%)	Precision	Recall	F1-Score
Classical CNN	**92.93**	0.9375	0.9200	0.9287
Classical MobileNetV2	60.67	0.6020	0.6293	0.6154
Classical ResNet18	87.87	0.8515	0.9173	0.8832
QCNN (2 qubits)	87.60	0.8597	0.8987	0.8787
QCNN (3 qubits)	92.67	0.9103	0.9467	0.9281
QCNN (4 qubits)	**93.47**	0.9223	0.9493	0.9356
Q-MobileNetV2 (4q)	87.07	0.8620	0.8827	0.8722
Q-ResNet18 (4q)	86.00	0.8444	0.8827	0.8631

classical feature extraction. In the case of the QCNN, the maximum accuracy increased very noticeably, as high as 87.60% with 2 qubits and a high of 0.93.7 with 4 qubits. The hybrid MobileNetV2 achieved accuracy of 87.07%, which is much higher compared to the 60.67% of the pure classical counterpart. This is attributed to the fact that the quantum circuit is a nonlinear enhancer of features, which re-projects the sparse classical features into a Hilbert space. The hybrid version is therefore a kind of recovery of lost representation power and moves towards deeper classical networks.

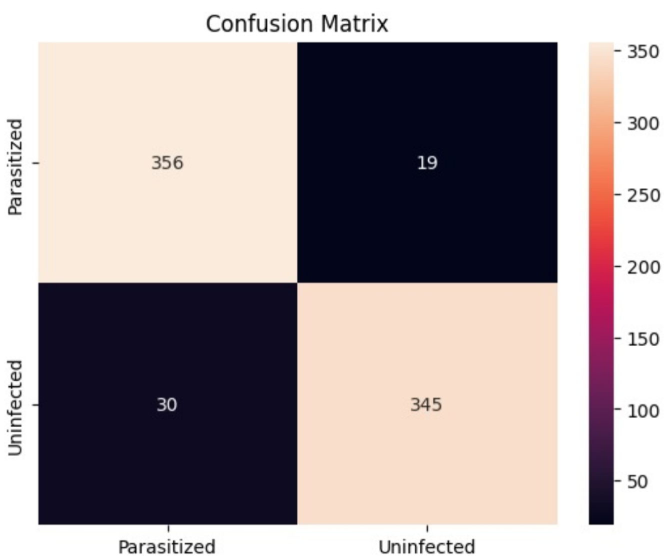

Fig. 5. Confusion matrix of the best performing model

The confusion matrix of the best performing model, 4-qubit QCNN, is shown in 5. From this, we can understand why the accuracy is so high. There were 356 uninfected cells and 353 parasitized cells that were properly called by the model, and the false positives were 19, and false negatives were 22. Such level of sensitivity and specificity is essential in medical diagnosis where each of the two types of errors can have actual clinical implications. The reduced misclassification rate of the hybrid quantum architecture over other models demonstrates that the hybrid quantum architecture does not only nail a higher overall accuracy but also maintains consistent decision boundaries. On the whole, these results highlight the fact that hybrid quantum-classical models, and variational circuits with more expressivity, can significantly increase performance on challenging biomedical imaging problems, even addressing weaknesses in classical backbones such as MobileNetV2.

VI. CONCLUSION

This paper provides an effective comparison between the various classical and hybrid quantum- classical deep learning systems in malaria cell classification. From the comparison of CNN, MobileNetV2 and ResNet18 along with quantum-enhanced counterparts, it is evident that quantum layers can be used to boost performance of a shallow or frozen classical feature extractor. The QCNN with 4 qubits has the best overall accuracy of 93.47% and outperforms all classical baselines. The hybrid MobileNetV2 also has significant increased accuracy compared to its classical counterpart indicating that variational circuits can transform weak classical representations into valuable feature representation through angle encoding and entanglement. These findings support the potential quantum processing in medical imaging that is increasingly growing, also on noisy intermediate-scale quantum (NISQ) simulators.

Future works could benefit from running the experiments on actual quantum machines to understand the effects of decoherence and sampling noise on the circuits. Scalability could also be established by bigger datasets and higher-resolution inputs. Hybrid training schemes which selectively unfreeze more profound layers of MobileNetV2 or ResNet which may form stronger quantum synergy with the quantum layers, could also be explored.

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