# HQC-Net: Hybrid Quantum-Classical Network for Leukemia Detection

MAJOR PROJECT REPORT

Submitted in partial fulfillment of the requirements for the award of

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**In**

**COMPUTER SCIENCE AND ENGINEERING**

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DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING

V.R. SIDDHARTHA ENGINEERING COLLEGE

Autonomous and Approved by AICTE, NAAC A+, NBA Accredited

Affiliated to Jawaharlal Nehru Technological University, Kakinada

Vijayawada 520007


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# VELAGAPUDI RAMAKRISHNA SIDDHARTHA ENGINEERING COLLEGE

(Autonomous, Accredited with 'A+' grade by NAAC)

## Department of Computer Science and Engineering

## CERTIFICATE

This is to certify that the Major Project report entitled **"HQC-Net: Hybrid Quantum-Classical Network for Leukemia Detection"** being submitted by

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in partial fulfilment for the award of the Degree of Bachelor of Technology in Computer Science and Engineering to the Jawaharlal Nehru Technological University, Kakinada, is a record of bonafide work carried out under my guidance and supervision.

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**Professor & HOD, CSE**

# DECLARATION

We hereby declare that the Major Project Report entitled "HQC-Net: Hybrid Quantum-Classical Network for Leukemia Detection" submitted for the B.Tech Degree is our original work and the dissertation has not formed the basis for the award of any degree, associate ship, fellowship or any other similar titles.

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# Abstract

Acute Lymphoblastic Leukemia (ALL) is a severe blood cancer that affects both children and adults. Early and accurate detection is crucial for improving survival rates. Traditional diagnostic methods rely on manual microscopic examination, which is time-consuming and prone to human error. Deep learning-based approaches, particularly Convolutional Neural Networks (CNNs), have shown promise in automating leukemia classification. However, CNNs require large datasets and suffer from computational inefficiencies due to the high number of parameters in fully connected layers.To address these challenges, we propose HQC-Net, a Hybrid Quantum-Classical Network that integrates CNN-based feature extraction with Quantum Neural Networks (QNNs) for efficient leukemia classification. Unlike pure CNN models, which require extensive fully connected layers for classification, our approach utilizes QNNs to leverage quantum properties such as superposition and entanglement, reducing parameter count while maintaining high classification accuracy.We experiment with multiple CNN architectures, including Simple CNN and ResNet50, and optimize hyperparameters such as learning rate, qubit count, and training epochs. Our results demonstrate that HQC-Net achieves an accuracy of 94.35% on the leukemia dataset, with the potential for further improvements through quantum circuit optimization and dataset expansion.

**Keywords:** Quantum Computing, Convolutional Neural Networks, Quantum Neural Networks, Leukemia Detection, Medical Image Classification.

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# Chapter 1

# INTRODUCTION

Acute Lymphoblastic Leukemia (ALL) is among the fiercest malignancies affecting human blood, which has an evidently higher tendency to predominate in children and adults, with equally equally high mortality rates upon failure for early diagnosis and treatment [1]. Conventional leukemia diagnosis depends primarily on the manual operation of a microscope and analysis of blood smear images by pathologists[2] [3]. The process is time-consuming and susceptible to human errors that generally occur through misdiagnosis and delays in treatment. The need for the automation of the classification of leukemia, with accuracies and efficiency, has driven enormous developments in deep learning and AI applications in medical imaging.

Artificial Intelligence (AI) has been the driving force behind the motion of Industry 5.0 revolution, providing excellent automation, real-time decision-making, and data-driven problem-solving across different domains. The AI-based classification techniques have found a wide application in supervised learning, deep learning, and neural networks for increasing accuracy in applications such as image classification, text classification, or speech recognition[4]. The application of AI in the field of medical imaging, in particular, has led to breakthroughs in the diagnosis of disease and prognosis. The ongoing issues of computational sophistication, model interpretability, and datasets have put a call for hybrid AI approaches.

Cancer is a vast classification of diseases with uncontrolled cell growth, which can affect other organs and tissues. Among hematological cancers, leukemia is one of the most aggressive. According to classification, they are divided into two main types: Acute and Chronic leukemia, which in turn are classified into Lymphoblastic (ALL) and Myeloid (AML). Studies have shown that ALL is the most common type of leukemia in children, with almost 75% of pediatric leukemia cases globally[5]. On the other hand, while it enjoys higher prevalence in adults, the rate of its survival is usually dismal due to the rapidity of its progress[6]. Being drugged with high incidence rate cases and necessitating presentation for early and definite diagnosis, we would look into classification of Acute Lymphoblastic Leukemia (ALL) using AI-based models.

Acute Lymphoblastic Leukemia (ALL) is a highly aggressive blood cancer that affects much primarily white blood cells; it is a threatening disease for children and adults alike. Traditionally, leukemia is diagnosed by microscopic viewing of images obtained from blood smear, which is tedious, subjective, and prone to possible error. The AI-based approach in automating the classification of leukemia, specifically the Convolutional Neural Networks (CNNs), has shown great promise. Several studies have taken up CNN-based models for leukemia detection: A Abhishek et al.[7] proposed an ensemble learning approach using the Gompertz function, achieving an 88.80% accuracy for leukemia classification

Quantum computing is being increasingly spotlighted as a possible shift in the very foundation of AI and deep learning. Quantum Neural Networks (QNNs) use quantum principles like superposition and entanglement to perform computations efficiently with few parameters and retain high accuracy. QNNs have been demonstrated to provide value-added services with high accuracy in medical imaging: A Elaraby et al. showed that QNNs exhibited comparably accurate results as classical deep learning architectures but with fewer parameters.

The pure quantum models, however, are still constrained due to hardware limitations. Thus, the more reasonable alternative will be to innovate hybrid quantum-classical models that combine features extracted via CNNs and categorized via QNNs, thereby obviating the merits from these two computing paradigms.

## 1.1 Basic Concepts

### 1.1.1 Convolutional Neural Networks

Convolutional Neural Networks (CNNs) are a specialized class of deep learning models designed for image processing and classification. They are particularly effective in medical imaging applications, including leukemia detection, as they can automatically extract and learn features from blood smear images.

A CNN consists of multiple layers, with convolutional layers acting as the core feature extractors. These layers apply filters to input images, detecting essential patterns such as edges, textures, and complex structures. As the network deepens, it captures more abstract and high-level features, enabling accurate classification of diseased and healthy cells. Pooling layers help reduce the spatial dimensions of feature maps while preserving important information. This process improves computational efficiency and prevents overfitting. Finally, fully connected layers interpret the extracted features and make predictions by mapping them to output labels.

A popular CNN architecture, ResNet50, is widely used in medical imaging due to its ability to train deeper networks without performance degradation. It employs residual connections to bypass layers, solving the vanishing gradient problem and ensuring stable learning. However, CNNs require large datasets and extensive computational resources, especially when using fully connected layers for classification. This limitation makes them less efficient for complex tasks with limited data, necessitating alternative approaches like Quantum Neural Networks (QNNs).

### 1.1.2 Quantum Neural Networks (QNNs)

Quantum Neural Networks (QNNs) combine deep learning with quantum computing principles to enhance computational efficiency. Unlike classical neural networks, which rely on sequential data processing, QNNs leverage quantum states such as superposition and entanglement to perform computations in parallel. This allows them to process large amounts of information with fewer parameters, making them an attractive alternative to traditional deep learning models.

In QNNs, qubits serve as the fundamental units of computation, replacing classical bits. Unlike traditional bits, which exist as either 0 or 1, qubits can exist in multiple states simultaneously due to superposition. This property enables QNNs to explore multiple solutions at once, leading to faster convergence and improved efficiency in tasks such as medical image classification. Quantum circuits, composed of quantum gates, manipulate qubits to perform computations. These gates transform quantum states in ways similar to activation functions in classical neural networks, allowing the model to learn complex patterns from input data. Optimizing these circuits is crucial for improving classification accuracy while minimizing computational overhead.

In leukemia classification, Hybrid Quantum-Classical Networks (HQC-Net) integrate CNN-based feature extraction with QNN-based classification. Instead of relying on fully connected layers, HQC-Net utilizes quantum circuits to process extracted features, reducing the number of parameters while maintaining high accuracy. This approach not only improves efficiency but also demonstrates the potential of quantum computing in advancing AI-driven medical diagnostics.

## 1.2 Motivation

- Acute Lymphoblastic Leukemia (ALL) is a common blood cancer affecting both children and adults, with high mortality rates if not detected early. Manual diagnosis is slow and prone to errors, necessitating automated solutions for faster and more accurate detection.

- While CNN-based leukemia classification has shown effectiveness, it suffers from computational inefficiencies and large parameter sizes, making it resource-intensive and dependent on extensive datasets.

- QNNs leverage quantum properties for efficient classification with fewer parameters, making hybrid models a promising solution for medical imaging.

## 1.3 Problem Statement

This project aims to develop an efficient leukemia classification system by integrating classical deep learning with quantum computing. Traditional CNN-based models, while effective, require large datasets and suffer from computational inefficiencies due to high parameter counts. To address these challenges, this work proposes HQC-Net, a Hybrid Quantum-Classical Network that combines CNN-based feature extraction with Quantum Neural Networks (QNNs) for classification. By leveraging quantum properties such as superposition and entanglement, the model reduces computational overhead while maintaining high classification accuracy.

## 1.4 Objectives

The objectives of our project are:

1. Collect and preprocess a dataset of blood smear images containing both ALL-positive and healthy cells to ensure high-quality input for model training.

2. Develop a CNN-based feature extractor to analyze microscopic blood smear images and extract relevant patterns for leukemia classification.

3. Integrate a Quantum Neural Network (QNN) to enhance classification efficiency by leveraging quantum computing principles such as superposition and entanglement.

4. Compare the performance of the hybrid model against traditional CNN-based classifiers and optimize it for practical deployment in medical diagnostics.

## 1.5 Scope

The scope of our project is:

1. The dataset consists of BMP format blood smear images.

2. Our Project focuses on binary classification (ALL-positive vs. healthy).

## 1.6 Advantages

1. Enhanced Computational Efficiency: By integrating Quantum Neural Networks (QNNs) with CNN-based feature extraction, the model reduces the number of parameters, leading to lower computational costs and faster processing compared to traditional deep learning models.

2. Improved Classification Accuracy: Leveraging quantum properties such as superposition and entanglement allows the model to efficiently distinguish between ALL-positive and healthy cells, enhancing overall classification performance.

3. Scalability for Medical Diagnostics: The hybrid quantum-classical approach enables effective leukemia detection with fewer resources, making it a viable solution for real-world medical applications, even in settings with limited computational power.

# Chapter 2

# LITERATURE REVIEW

This chapter contains a list of research papers that we have studied under literature survey. We focused on the approaches for maintaining accuracy in these papers. Our study included the techniques used for developing and training the model.

## 2.1 Ensemble learning using Gompertz function for leukemia classification[7]

The study utilized a CNN-based classification approach with transfer learning to analyze 1,250 microscopic blood smear images. [7] To enhance model robustness, image preprocessing techniques such as normalization and augmentation were applied. The VGG16 architecture, integrated with a Squeeze-and-Excitation (SE) block, was fine-tuned to improve feature extraction capabilities. The dataset was split into an 80:20 ratio, with 80% allocated for training and the remaining 20% for testing. The model was trained using the Stochastic Gradient Descent with Momentum (SGDM) optimizer to ensure stable convergence and optimal performance.

To further enhance classification accuracy, ensemble learning techniques were explored. Majority Voting, Weighted Average, and a Fuzzy Rank-based Ensemble approach leveraging the Gompertz function were compared to assess their effectiveness in improving model predictions. The performance of each method was evaluated using key metrics, including accuracy, precision, recall, F1-score, and Matthews Correlation Coefficient (MCC).This comprehensive evaluation framework ensured a rigorous assessment of the proposed approach, highlighting the impact of advanced ensemble techniques on microscopic blood smear image classification.

**Advantages:**

1. The proposed CNN achieved 88.80% accuracy, surpassing other ensemble techniques.

2. The SE block helped capture fine-grained features in blood smear images, enhancing classification.

**Disadvantages:**

1. Pre-trained models require careful fine-tuning to prevent overfitting on medical datasets.

2. The study focuses only on blood smear images, excluding other leukemia detection methods.

## 2.2 LEU3: An Attention Augmented-Based Model for Acute Lymphoblastic Leukemia Classification[8]

The study focused on developing a CNN-based classification model enhanced with an attention mechanism to analyze 484 peripheral blood smear (PBS) images.[8] To ensure consistency and improve model generalization, preprocessing steps included resizing images to 224×224 pixels, normalization, and data augmentation techniques such as rotation, shifting, zooming, and flipping. The proposed model, LEU3, employed convolutional layers to extract spatial features while integrating an attention module to highlight critical regions within the images, thereby improving classification accuracy.The Adam optimizer was utilized for training, coupled with categorical cross-entropy loss to optimize model performance.

To enhance model transparency and interpretability, Explainable AI (XAI) techniques such as Local Interpretable Model-Agnostic Explanations (LIME) and Shapley Additive Explanations (SHAP) were incorporated. These techniques provided insights into the model's decision-making process by identifying significant image regions that influenced classification outcomes.[8] By leveraging attention mechanisms and explainability tools, the proposed approach aimed to improve both the accuracy and reliability of peripheral blood smear image classification, offering valuable support for clinical diagnosis and hematological analysis.

**Advantages:**

1. Attention layers improved feature extraction for better leukemia detection.

2. LIME and SHAP provided insights into model decisions, enhancing transparency.

**Disadvantages:**

1. Requires high-quality augmented data for effective training.

2. Limited to PBS images, restricting generalization to other leukemia diagnosis methods.

## 2.3 Advanced Blast Identification in ALL Using Pivot-Growing Segmentation and U-Net PLR [9]

The study developed a CNN-based segmentation and classification model to analyze 15,135 microscopic images of pediatric Acute Lymphoblastic Leukemia (ALL) patients.[9] To achieve precise image segmentation, the Pivot-Growing Segmentation (PGS) technique was implemented, which partitions blood smear images into multiple regions based on pixel intensity similarity. This process involved selecting pivot points through K-medoids clustering, followed by iterative cluster expansion using the squared Euclidean distance. By applying PGS, the segmentation step effectively isolated relevant regions, enhancing feature extraction for subsequent classification.

For classification, the U-Net PLR model was employed, leveraging an encoder-decoder architecture with convolutional layers and skip connections to retain spatial details. The integration of Parametric Leaky ReLU (PLR) activation further improved feature extraction by addressing vanishing gradient issues. The model was trained using EfficientNet-B3, benefiting from its strong feature representation capabilities, and evaluated through cross-validation to ensure robustness. This approach aimed to enhance the accuracy and reliability of leukemia diagnosis by combining advanced segmentation techniques with deep learning-based classification.

**Advantages:**

1. PGS-based segmentation provided precise localization of blast cells.

2. The U-Net PLR model captured fine-grained features, enhancing classification.

**Disadvantages:**

1. The study is limited to microscopic images, not considering genetic or molecular biomarkers.

2. The combination of PGS, U-Net PLR, and EfficientNet-B3 increases computational overhead, making the model resource-intensive and challenging for real-time deployment on standard medical imaging systems.

## 2.4 Secretary Bird Optimization Algorithm Based on Quantum Computing and Multiple Strategies Improvement for KELM Diabetes Classification[10]

The study leveraged the Pima Indians Diabetes Dataset (PIDD) to develop an optimized diabetes classification model by enhancing the Secretary Bird Optimization Algorithm (SBOA).[10] The proposed improvement, termed the Quantum Hybrid Secretary Bird Optimization Algorithm (QHSBOA), integrated multiple enhancements to refine the optimization process. Specifically, a Particle Swarm Optimization (PSO) search mechanism was incorporated to enhance exploration capabilities, while dynamic boundary adjustment was introduced to adapt based on the best-performing individuals. Additionally, a quantum computing-based t-distribution variation was applied to improve search diversity, ensuring a more effective optimization process.

QHSBOA was employed to fine-tune the critical hyperparameters of the Kernel Extreme Learning Machine (KELM), namely the kernel penalty parameter (C) and bandwidth (c).By optimizing these parameters, the model achieved improved classification performance, leading to more accurate diabetes detection. This hybrid optimization approach demonstrated the effectiveness of integrating quantum-inspired techniques with nature-inspired algorithms, offering a novel and efficient strategy for medical data classification.

**Advantages:**

1. Achieved higher classification accuracy compared to traditional KELM models.

2. Quantum computing-based optimization improved convergence speed and reduced the risk of local optima.

**Disadvantages:**

1. Requires fine-tuning of hyperparameters, making model training more complex.

2. Performance is dataset-dependent, limiting generalization to other medical datasets without adaptation.

## 2.5 Enhanced Multi-Label Ocular Disease Identification Using a Quantum Convolutional Neural Network Approach Based on Fundus Images.[11]

The study utilized the OIA-ODIR dataset, comprising 10,000 fundus images from 5,000 patients, to develop a Quantum Convolutional Neural Network (QCNN)-based classification model for retinal disease diagnosis.[11] A comprehensive image preprocessing pipeline was implemented, including circular border cropping, resizing, contrast enhancement, noise reduction, and data augmentation to improve image quality and model generalization. The QCNN architecture integrated Quantum Convolutional Layers with traditional CNN layers, enabling the extraction of quantum-enhanced features from fundus images.

The model leveraged a hybrid approach, combining classical and quantum convolutional layers while employing entanglement-based quantum pooling for dimensionality reduction.To further enhance feature extraction, Anisotropic Diffusion Filtering was applied to smooth image textures while preserving edges, and Wavelet Transform (WT) was utilized to improve contrast and highlight critical retinal structures. By incorporating quantum computing principles, the proposed QCNN model aimed to improve classification accuracy and robustness, offering a novel approach for fundus image analysis in ophthalmology.

**Advantages:**

1. The quantum convolutional layers improved feature extraction, leading to better classification of multiple ocular diseases.

2. Enhanced contrast filtering and wavelet transform reduced noise, improving diagnostic accuracy.

**Disadvantages:**

1. The model's performance is dependent on high-quality fundus images, limiting real-world applicability in noisy environments.

2. The integration of quantum layers increases hardware dependency, limiting the model's implementation on conventional computing systems.

## 2.6 Pre-trained Quantum Convolutional Neural Network for COVID-19 Disease Classification Using Computed Tomography Images[12]

The study utilized the SARS-CoV-2 CT dataset, comprising 2,482 CT scan images from hospitals in São Paulo, Brazil, to develop a pre-trained Quantum Convolutional Neural Network (QCNN)-based classification model for COVID-19 detection.Image preprocessing steps included resizing, grayscale conversion, and data normalization to standardize input data and improve model performance[12]. The QCNN model integrated VGG16, a well-established classical CNN architecture, with a quantum computing layer to enhance feature extraction capabilities, leveraging the strengths of both classical and quantum paradigms.

To facilitate quantum feature representation, Quantum Feature Encoding using ZZFeatureMap and RealAmplitudes Ansatz circuits was applied, embedding CT scan data into quantum space.This hybrid approach aimed to improve classification accuracy by capturing complex patterns in medical imaging. By incorporating quantum computing principles, the proposed model sought to enhance diagnostic reliability, demonstrating the potential of quantum-classical hybrid architectures for medical image analysis.

**Advantages:**

1. The quantum-enhanced feature extraction improved classification performance.
2. Low computational complexity, making it suitable for real-world deployment.

**Disadvantages:**

1. Requires specialized quantum computing hardware, limiting accessibility.
2. The dataset is limited to CT scan images, reducing generalizability to other medical imaging modalities.

## 2.7 H-QNN: A Hybrid Quantum–Classical Neural Network for Improved Binary Image Classification[13]

The study leveraged three binary image classification datasets from Kaggle to develop a Hybrid Quantum–Classical Neural Network (H-QNN) for improved classification performance.[13] The preprocessing pipeline involved resizing images to

720×720 pixels, normalization, and augmentation to enhance generalization. The H-QNN architecture combined a classical CNN with a two-qubit quantum circuit, enabling quantum-assisted feature extraction. The quantum module incorporated parameterized quantum gates, including Hadamard and Ry gates, to transform image features into quantum space, enhancing pattern recognition capabilities.

To enable seamless integration, the hybrid module connected classical CNN layers with the quantum circuit, utilizing PyTorch's autograd function for efficient backpropagation.The model was trained using gradient-based optimization, employing the parameter-shift rule to update quantum parameters effectively. By leveraging quantum computing principles, the H-QNN model aimed to improve classification accuracy while exploring the advantages of quantum-enhanced feature transformations in deep learning applications.

**Advantages:**

1. Quantum-enhanced feature extraction improved classification accuracy compared to CNN.
2. The model showed better generalization on small datasets, reducing overfitting.

**Disadvantages:**

1. The model requires quantum simulators or specialized quantum hardware.
2. Limited to binary classification, requiring modifications for multi-class tasks.

## 2.8 Hybrid Quantum–Classical Neural Networks for Efficient MNIST Binary Image Classification[14]

The study employed the MNIST dataset, a widely recognized benchmark for handwritten digit classification, to develop a Hybrid Quantum–Classical Neural Network (H-QNN) aimed at enhancing image classification performance [14].The preprocessing steps included resizing, standardization, and quantum feature encoding to ensure effective data representation. The quantum layer incorporated ZZFeature Map for embedding image data into quantum space and utilized Real Amplitudes Ansatz circuits to perform quantum transformations, enabling enhanced feature extraction.

The hybrid architecture integrated classical CNN layers with quantum circuits containing parameterized rotation gates (RY) and CX entanglement gates, leveraging quantum computing to improve learning efficiency.The training process was optimized using the Adam optimizer, with gradient-based parameter tuning to refine both classical and quantum components. By combining the strengths of deep learning and quantum computing, the H-QNN model aimed to explore quantum-assisted feature learning, demonstrating its potential for advancing image classification tasks.

**Advantages:**

1. Quantum-enhanced feature mapping improved pattern recognition and reduced computational complexity.
2. Required fewer parameters compared to conventional CNNs, making it more resource-efficient.

**Disadvantages:**

1. Restricted to binary classification, requiring modifications for multi-class tasks.
2. The reliance on quantum circuits increases computational overhead and limits scalability due to the constraints of current quantum hardware.

# Chapter 3

# Analysis and Design

Software design is a stage within a software development methodology that results in a concise explanation of the optimal solution to address the current problem when implemented.

## 3.1 Software Development Life Cycle

In our project, we adopt the **Scrum framework** , a subset of the Agile process model, by dividing development into iterative **sprints**, as shown in Figure 3.1. Each sprint focuses on tasks such as designing the CNN backbone, integrating the quantum neural network (QNN) module, tuning hyperparameters, and evaluating model performance. This iterative cycle supports the progressive enhancement of the HQC-Net model.The Scrum framework image used in Figure 3.1 is adapted from StartInfinity's online resource [15].

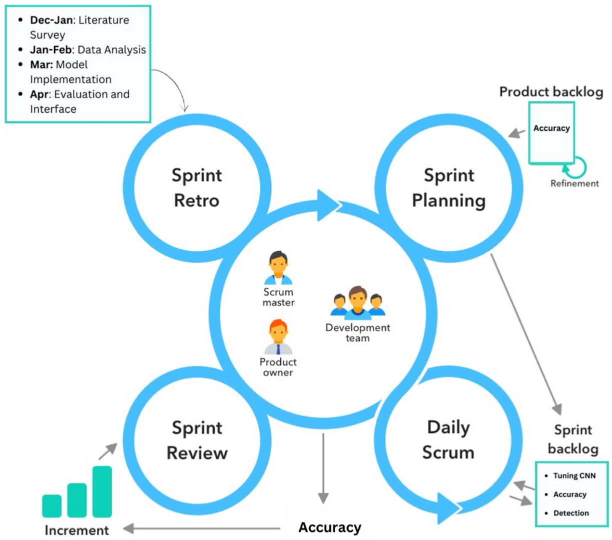


Figure 3.1: Scrum Framework for HQC-Net Project[15]

- Scrum events like **Sprint Planning, Daily Scrum, Sprint Review**, and **Sprint Retrospective** help us adapt to advancements in quantum computing and deep learning throughout the project lifecycle.
- The roles of **Scrum Master, Product Owner**, and the **Development Team** promote collaboration between classical and quantum computing experts, ensuring seamless integration.

- Regular feedback and visible progress through **incremental prototypes** after each sprint enable early detection of challenges and alignment with stakeholder expectations.

## 3.2 Use Case Diagram

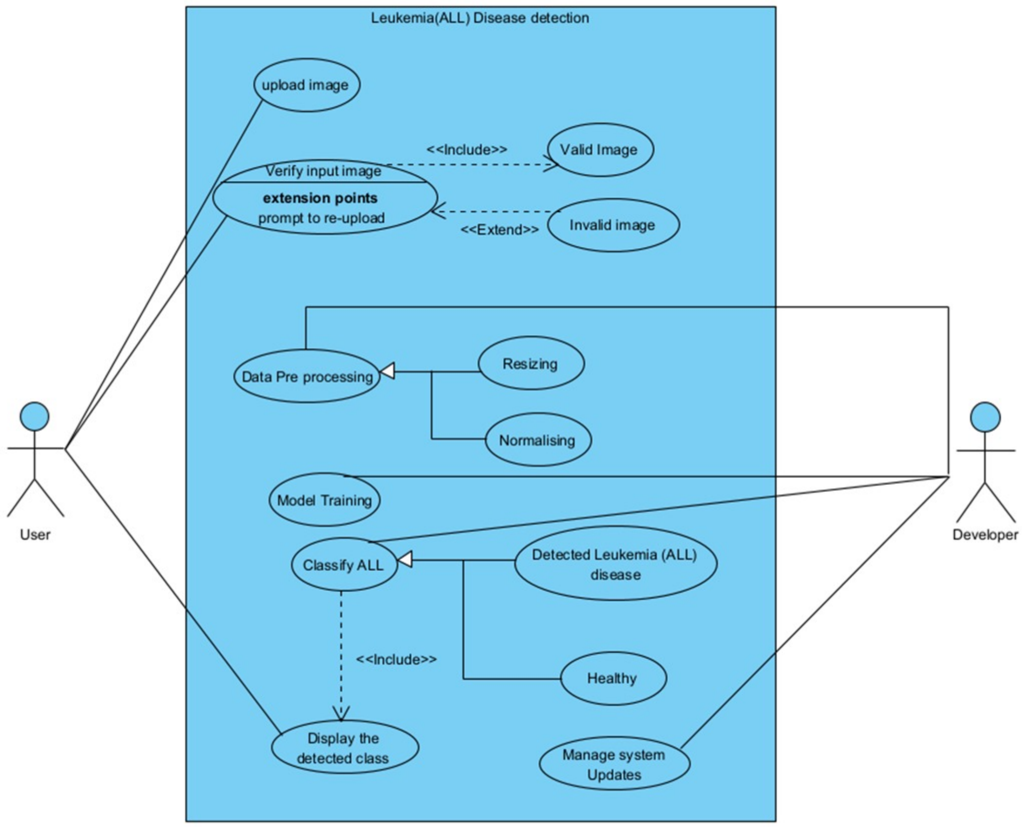


Figure 3.2: Use Case Diagram

The workflow of the system as depicted in Figure 3.2 can be described through the following key use cases:

1. **Image Upload:**
   The diagnostic process begins with the user uploading a microscopic blood smear image to the system.

2. **Image Verification:**
   The uploaded image is checked for validity in terms of format and clarity.

   - If the image is valid, the workflow proceeds to preprocessing.
   - If the image is invalid, the system prompts the user to re-upload a suitable image.

3. **Data Preprocessing:**
   This step ensures that the input image is properly prepared for analysis and includes the following sub-processes:

   - **Resizing:** Adjusting the image dimensions to meet model requirements.
   - **Normalization:** Scaling pixel values for consistent input and improved model performance.

4. **Model Training:**
   Developers are responsible for training the Hybrid Quantum-Classical Network (HQC-Net) on labeled leukemia datasets to ensure accurate classification.

5. **Classification:**
   The preprocessed image is passed through the HQC-Net model, which integrates CNN-based feature extraction and Quantum Neural Networks (QNNs) to classify the sample.

   - The model determines whether the image indicates signs of **Acute Lymphoblastic Leukemia** or the **Healthy** class.

6. **Display of Results:**
   The system displays the classification result to the user, specifying whether the input image corresponds to a healthy sample or one showing signs of ALL.

7. **System Management and Updates:**
   Developers manage model and system updates to improve accuracy and integrate new features, such as enhanced preprocessing or advanced quantum circuit optimizations.

## 3.3 Activity Diagram

The activity diagram shown in Figure 3.3 illustrates the workflow of a diagnostic system for Parkinson's Disease, involving two primary actors: the user and the developer. The process starts with the user uploading an image, which is then verified by the system. If the image is invalid, the process terminates by displaying an "Image Invalid" message to the user. If the image is valid, it proceeds to the next stage for classification.

On the developer's side, the verified image is passed through a customized CNN (Convolutional Neural Network) model. This model analyzes the image to

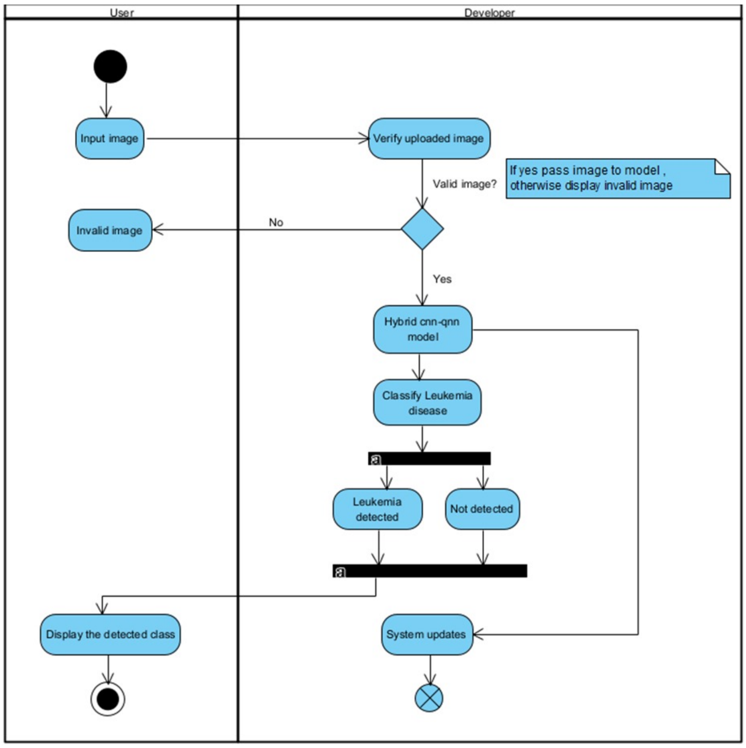


Figure 3.3: Activity Diagram

classify whether the patient has Parkinson's Disease (PD) or not. Based on the classification outcome, the system either detects PD or confirms the absence of it. The result is then displayed to the user. Additionally, system updates are managed by the developer to ensure the model remains accurate and efficient over time.

## 3.4 Class Diagram

This class diagram shown in Figure 3.4 illustrates the structural components of a medical image classification system using a Customized CNN (Convolutional Neural Network) model. The system begins with the User uploading medical images (e.g., spiral, meander, or wave images) through the Interface, which interacts with the backend by obtaining input from the user and communicating with the model to return the diagnosis report. The Image Input class stores and manages various types of images and their attributes, enabling the system to process healthy and all categorized images for diagnosis.

The Customized CNN Model class serves as the core engine for image analysis and is linked to the EvaluationMetric class, which records performance metrics such as accuracy, precision, recall, and F1-score. These metrics are essential for validating model effectiveness. A Developer class is responsible for monitoring models, managing updates, and logging system changes, ensuring the reliability

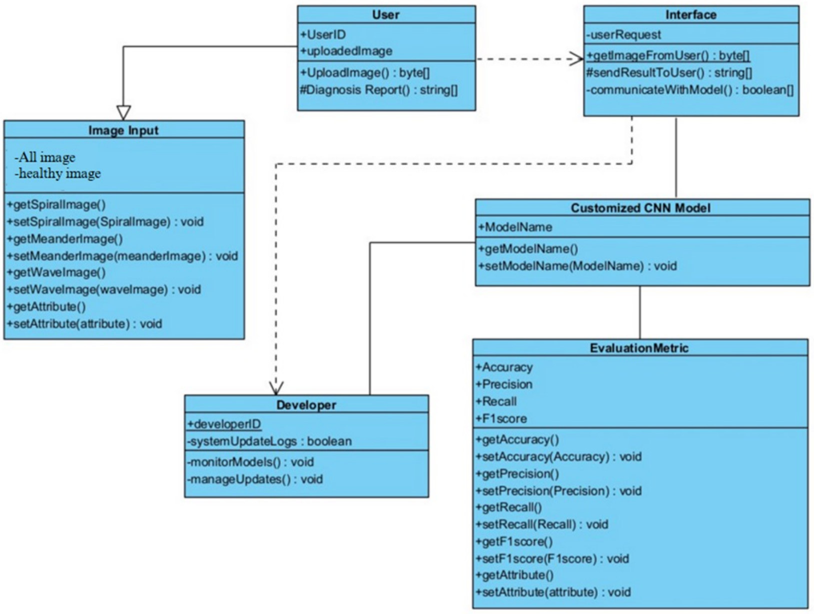


Figure 3.4: Class Diagram

and maintenance of the system. This modular design ensures clear separation of roles—user interaction, image processing, model evaluation, and system management—enhancing scalability and maintainability.

# Chapter 4

# Requirement Analysis

## 4.1 Functional and non-functional requirements

### 4.1.1 Functional requirements

**Image Upload:** The system shall allow users (e.g., lab technicians, radiologists) to upload blood smear images for analysis.
**Image Preprocessing:** The system shall preprocess uploaded images using techniques such as resizing, normalization, and noise removal.
**Feature Extraction:** The system shall extract features from the preprocessed images using CNN-based architectures like Simple CNN or ResNet50.
**Quantum-Enhanced Classification:** The system shall classify images using a Quantum Neural Network (QNN) integrated with the CNN feature extractor to detect the presence of Acute Lymphoblastic Leukemia (ALL).
**Result Display:** The system shall display the classification result (e.g., "ALL Detected" or "Healthy") to the user.
**Model Training and Validation:** The system shall support training and evaluation of the HQC-Net model with adjustable hyperparameters such as learning rate, qubit count, and epochs.
**Performance Metrics Reporting:** The system shall generate performance metrics such as accuracy, precision, recall, and F1-score after training.

### 4.1.2 Non-Functional requirements

**Performance:** The system should provide classification results within an acceptable time frame, leveraging quantum efficiency to reduce computation overhead.
**Accuracy:** The system should maintain a high classification accuracy (e.g., around or above 94.35%) and aim for continuous improvement through hyperparameter tuning.
**Scalability:** The system should support scalability to include additional leukemia types or larger datasets in future iterations.
**Reliability:** The system should handle large medical image datasets and return consistent results across multiple runs.
**Security:** Patient data and medical images should be securely stored and transmitted to maintain privacy and confidentiality.

**Usability:** The interface should be user-friendly and accessible to healthcare professionals with minimal technical knowledge.
**Maintainability:** The system should be easy to maintain and update, especially for improving models or integrating new quantum components.

## 4.2 Hardware Requirements

**Local Machine:** A personal computer or laptop with internet connectivity is required to develop, train, and deploy the hybrid deep learning and quantum model. It should support Python development environments and necessary ML/QML libraries such as TensorFlow, PennyLane, and Flask.
**Processor (CPU):** A modern multi-core processor (Intel i5/Ryzen 5 or higher) is recommended for handling parallel tasks such as image preprocessing and Flask-based web server operations.
**GPU (Graphics Processing Unit):** For training the CNN part of the model efficiently, an NVIDIA GPU with CUDA support (e.g., NVIDIA GTX 1650 or better) is highly beneficial. Although quantum simulation (via PennyLane's default.qubit) is CPU-based, GPU acceleration significantly reduces training time for the classical layers.
**RAM:** A minimum of 8GB RAM is required; 16GB or more is recommended to smoothly handle model training, dataset loading, and quantum circuit simulation without memory bottlenecks.
**Storage:** At least 20GB of free storage is necessary for datasets, model checkpoints, and logs.
**Operating System:** Windows 10/11, Ubuntu 20.04+, or macOS that supports Python 3.10+, TensorFlow 2.x, and other relevant packages.

## 4.3 Software Requirement

**Visual Studio Code:** Use Visual Studio Code for developing and training the deep learning model. Install python libraries for model implementation.
**TensorFlow and Keras:** Employ TensorFlow and Keras as the primary deep learning frameworks for model development. Verify compatibility with architecture for feature extraction.
**Tensorflow:** Implement TensorFlow Lite for optimizing the deep learning model for deployment on edge devices.
**OpenCV:** OpenCV is used to extract frames from video to feed into models and can extract facial features efficiently.OpenCV can be used to overlay text or bounding boxes on images to display model predictions and evaluation metrics.

# Chapter 5

# Methodology

## 5.1 Data Collection

The dataset of this research includes microscopic images of blood smears classified into Acute Lymphoblastic Leukemia (ALL) positive and healthy ones [16]. The training dataset consists of two distinct folders: one with diseased and the other healthy images. The validation dataset includes one folder containing samples of mixed images with the respective labels provided in a CSV file. The test dataset contains unlabeled images that serve to evaluate two types of final model evaluation. The images start out at 450×450 pixels and are reduced to 64×64 pixels to suit the CNN and QNN models. Normalization and augmentation are performed before training on the data to help generalize model. The dataset is from ALL Challenge at ISBI 2019, which was made public via The Cancer Imaging Archive (TCIA) having 10k+ images.

## 5.2 Data Preprocessing

To ensure uniformity and improved model performance, the raw microscopic blood smear images are put through multiple preprocessing steps before being fed into the Hybrid CNN-QNN model. Such images in the dataset include training, validation, and test images, wherein the training images comprise two folders namely, Healthy and Diseased. A total of 4,000 images belonging to 2 classes were found and provided for training. On the other hand, validation and test images follow the mixed format. All images are, at the outset, 450×450 pixels and hereon, are resized to 64×64 pixels to meet the requirements of the model with reduced computational complexity. Moreover, normalization of the pixel values is done to the range [0,1] to improve the convergence of the model while training.

For the case of validation data, images were provided without separate class folders; hence, labels had to be extracted from a CSV file consisting of the image filenames and their corresponding class labels (0 for Healthy, 1 for Diseased). Using this mapping of image names to class labels, images are loaded, resized, and normalized before storing them as NumPy arrays for easy processing. Validation labels were loaded successfully, and a total of 1,867 images were prepared for validation through this process. A similar approach is applied to test images by checking whether the filenames have valid formats (.bmp or .png), resizing and normalizing them accordingly before converting them into arrays. This procedure ultimately resulted in a total of 2,586 test images, which were later used to evaluate the generalization performance of the model.

Further, to enhance model robustness while curbing overfitting, data augmentation is carried out on the training images. Techniques like rotation, width and height shifting, zooming, and horizontal flipping enable the external expansion of the dataset, allowing the model to learn invariant features. These preprocessing steps enhance feature extraction, leading to improved model accuracy and enabling efficient hybrid quantum-classical classification for Acute Lymphoblastic Leukemia (ALL) detection.

## 5.3 Combined Model

### 5.3.1 Combined Hybrid Classical-Quantum Model Architecture

The proposed model integrates the capabilities of classical deep learning and quantum computing through a hybrid architecture, designed specifically for effective classification of leukemia (ALL) from blood smear images.

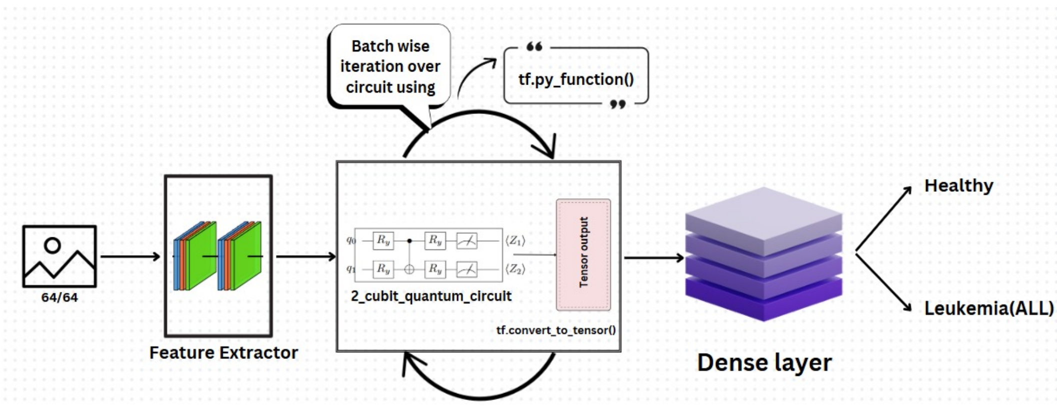


Figure 5.1: Hybrid Classical-Quantum Model Architecture

The pipeline begins with a classical Convolutional Neural Network (CNN)-based feature extractor as shown in Figure 5.1. Input images of size $64 \times 64$ pixels are processed through a sequence of convolutional and pooling layers, allowing the network to extract spatial features that capture both low-level textures and high-level structures from the blood smear images.

The output from the CNN is then reshaped and passed to a 2-qubit parameterized quantum circuit. This circuit comprises three core layers:

- **Angle Embedding Layer:** Classical features are encoded into quantum states using parameterized $R_y$ rotation gates.
- **Entanglement Layer:** Qubits are entangled using controlled-NOT (CNOT) gates to model correlations between features.
- **Measurement Layer:** Each qubit is measured using the Pauli-Z operator to obtain expectation values $\langle Z_1 \rangle$ and $\langle Z_2 \rangle$.

To integrate the quantum circuit into the TensorFlow workflow, we utilize the `tf.py_function()` API to iterate over each batch and pass the output through the quantum node. The resulting values are converted into a tensor using `tf.convert_to_tensor()` and reshaped into the form $(\text{batch\_size}, 2)$.

These two-dimensional outputs, representing the expectation values from the quantum circuit, are then fed into a classical dense layer for final classification. The dense layer outputs predictions indicating whether the input corresponds to a **Healthy** subject or a patient with **Leukemia (ALL)**.

This hybrid approach combines the representational power of classical CNNs with the quantum circuit's ability to explore complex, high-dimensional feature spaces, potentially leading to improved performance, especially in settings with limited training data or noisy inputs.

### 5.3.2 Classical Feature Extractor Using CNN

The classical feature extractor in the proposed hybrid architecture utilizes a Convolutional Neural Network (CNN) to efficiently extract meaningful spatial features from the input microscopic blood smear images.

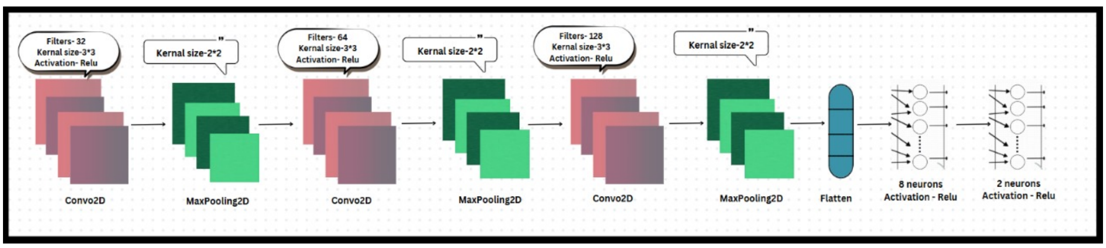


Figure 5.2: CNN-based Feature Extractor Architecture

As shown in Figure 5.2, the input image of dimension $64 \times 64$ is passed through multiple convolutional and pooling layers:

- **Conv2D Layer 1:** 32 filters of size $3 \times 3$ with ReLU activation.
- **MaxPooling2D Layer 1:** Pooling with kernel size $2 \times 2$.

- **Conv2D Layer 2:** 64 filters of size $3 \times 3$ with ReLU activation.
- **MaxPooling2D Layer 2:** Pooling with kernel size $2 \times 2$.
- **Conv2D Layer 3:** 128 filters of size $3 \times 3$ with ReLU activation.
- **MaxPooling2D Layer 3:** Pooling with kernel size $2 \times 2$.

The output from the final MaxPooling2D layer is flattened into a one-dimensional vector, which is then passed through two dense layers:

- **Dense Layer 1:** Fully connected layer with 8 neurons and ReLU activation.
- **Dense Layer 2:** Fully connected layer with 2 neurons and ReLU activation, serving as a compressed representation of the input features.

These 2-dimensional features are then forwarded to the quantum circuit block as input for quantum processing. This lightweight CNN design is tailored for medical image data with limited resolution, enabling efficient and effective extraction of visual biomarkers while reducing computational complexity.

### 5.3.3 Quantum Circuit Design

The quantum component of the hybrid model utilizes a 2-qubit quantum circuit that encodes features into quantum states, entangles the qubits, and extracts information via measurement. The schematic of the circuit is shown in Figure 5.3.

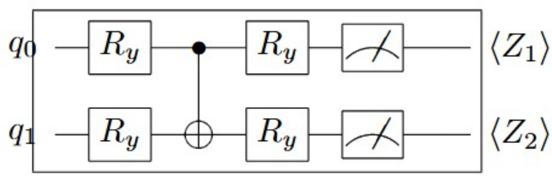


Figure 5.3: 2-Qubit Quantum Circuit used in the Hybrid Model

**Circuit Description:**

- **Input Encoding:** The 2-dimensional classical feature vector obtained from the CNN is encoded into the quantum circuit using the $R_y$ (rotation around Y-axis) gates applied to each qubit ($q_0$ and $q_1$).
- **Entanglement:** A controlled-NOT (CNOT) gate is applied between the qubits ($q_0$ as control and $q_1$ as target), enabling entanglement which allows the circuit to capture quantum correlations between features.

- **Parameterized Quantum Operation:** Another set of $R_y$ rotations are applied to both qubits, with trainable angles. These rotations introduce learnable quantum parameters that are optimized during training.

- **Measurement:** Expectation values of the Pauli-Z operator $\langle Z_1 \rangle$ and $\langle Z_2 \rangle$ are measured on qubit $q_0$ and $q_1$, respectively. These expectation values are real numbers between -1 and 1 and serve as quantum-transformed features.

**Tensor Conversion and Output:** The measured expectation values are converted into a tensor using `tf.convert_to_tensor()` and reshaped to (batch_size, 2) format. This tensor is then passed to the final classical dense layer for binary classification (Healthy vs. Leukemia (ALL)).

This simple yet effective quantum circuit enables the integration of quantum computing advantages into the classical deep learning pipeline, enhancing the model's ability to extract richer patterns from microscopic images.

## 5.4 Proposed Methodology

The proposed hybrid classification framework integrates classical deep learning and quantum computing techniques for the efficient detection of leukemia from microscopic blood smear images. The methodology consists of five major stages: Data Collection, Preprocessing, Dataset Splitting, Feature Extraction with CNN, and Quantum Classification using a Quantum Neural Network (QNN). The overall workflow is shown in Figure 5.4.

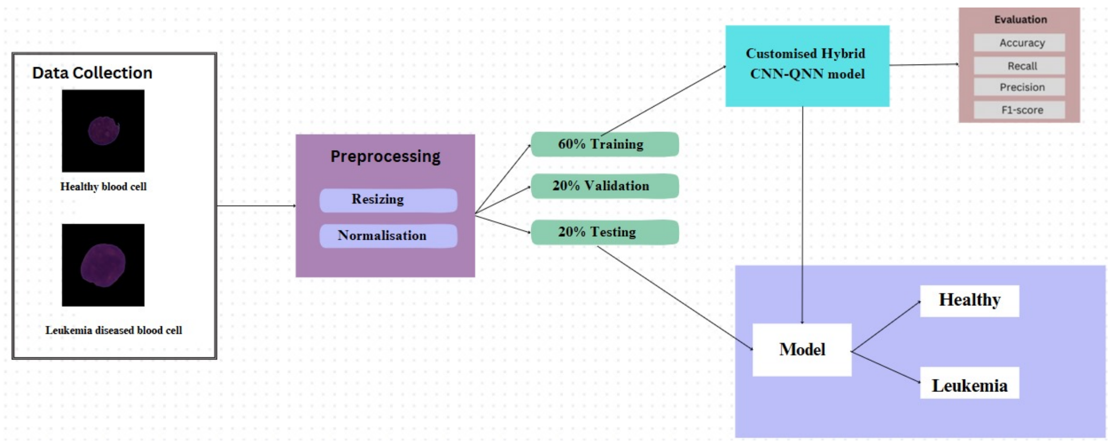


Figure 5.4: Proposed methodology: Hybrid CNN-QNN pipeline for leukemia classification

### 5.4.1 Feature Extraction using CNN

A custom Convolutional Neural Network (CNN) is used to extract high-level features from the input images. The architecture consists of three convolutional layers with ReLU activations and max-pooling, followed by a flatten layer and dense layers. The output is a compact 2-dimensional feature vector representing the image.

### 5.4.2 Quantum Classification using QNN

The extracted 2-dimensional feature vector is fed into a 2-qubit quantum circuit. The quantum circuit employs angle encoding with $R_y$ rotations, entangling gates (CNOT), and Pauli-Z measurements. The expectation values $\langle Z_1 \rangle$ and $\langle Z_2 \rangle$ are calculated and used as input to the final classification layer.

### 5.4.3 Model Evaluation

The performance of the proposed Hybrid CNN-QNN model is evaluated using standard classification metrics:

- Accuracy
- Precision
- Recall
- F1-Score

This methodology combines classical and quantum paradigms to leverage the best of both domains—deep learning's feature extraction capabilities and quantum circuits' representational power—for robust medical image classification.

## 5.5 Algorithm

The algorithm used for this project is outlined below Algorithm 1

**Algorithm 1** Hybrid CNN-QNN Based Leukemia Classification

**Input:** Blood smear image dataset $D = \{(x_i, y_i)\}$, where $x_i$ is an image and $y_i \in \{\text{Healthy}, \text{Leukemia}\}$

**Output:** Predicted class label for each image

**procedure** TrainHybridModel

  Resize all images to $64 \times 64$

  Normalize pixel values to [0, 1]

  Split dataset: 60% Train, 20% Validation, 20% Test

**CNN Feature Extraction**

  **for** each image $x_i \in D$ **do**

    Extract features using CNN:

- Conv2D (32 filters, 3x3, ReLU) → MaxPooling2D (2x2)
- Conv2D (64 filters, 3x3, ReLU) → MaxPooling2D (2x2)
- Conv2D (128 filters, 3x3, ReLU) → MaxPooling2D (2x2)
- Flatten → Dense (8, ReLU) → Dense (2, ReLU)

    Obtain 2-D feature vector $f_i$

  **end for**

**Quantum Classification**

  **for** each feature vector $f_i$ **do**

    Encode $f_i$ into quantum circuit via $R_y$ rotations

    Apply entangling CNOT gates

    Measure in Pauli-Z basis to get expectations $\langle Z_1 \rangle, \langle Z_2 \rangle$

    Convert outputs to tensor using tf.convert_to_tensor()

  **end for**

  Pass quantum outputs to Dense layer with Softmax

  Train using cross-entropy loss and backpropagation

**end procedure**

**procedure** PredictClass(image $x$)

  Apply preprocessing and CNN to get $f$

  Process $f$ using quantum circuit

  Classify with trained Dense layer

  **return** Predicted label

**end procedure**

# Chapter 6

# Result and Analysis

## 6.1 Interpretation of Accuracy and Loss Graphs

The analysis of accuracy and loss graphs serves as a critical component in understanding the performance and behavior of machine learning models. In the context of this study, the accuracy and loss graphs depict the evolution of model performance over successive epochs during the training process.

### 6.1.1 Accuracy Graphs

As shown in the Figure 6.1 the training accuracy, represented by a relatively stable blue line, fluctuates slightly between 0.49 and 0.50 across all five epochs. This steady trend indicates that the model maintains a consistent performance on the training data but shows minimal signs of significant learning or improvement. Such flatness in the training accuracy curve suggests that the model might be in the initial learning phase or encountering difficulties in effectively extracting complex patterns from the dataset.

On the other hand, the validation accuracy, depicted by the orange line, exhibits noticeable fluctuations throughout the epochs. Initially starting from a lower value of approximately 0.35, the validation accuracy increases in the second epoch but drops significantly in the third, before gradually rising and peaking in the final epoch at around 0.62. These sharp variations point toward instability in the model's generalization capability, which may be attributed to insufficient training epochs, high sensitivity to the data, or underfitting. The difference between the training and validation accuracy patterns underscores the need for further optimization in model architecture, learning rate, or data preprocessing techniques to ensure improved and consistent performance on unseen data.

### 6.1.2 Loss Graphs

As illustrated in the Figure 6.2, the training loss curve, shown in blue, demonstrates a marginal upward trend with values ranging narrowly around 0.693. This nearly flat trajectory suggests that the model is not undergoing significant improvement during training, potentially indicating a saturation point where the current learning setup—such as weights, bias updates, or optimizer configurations—fails to drive meaningful changes in performance. In contrast, the validation loss, represented by the orange line, begins with a relatively high value of approximately 0.696 and initially drops in the second epoch, indicating a slight improvement in the model's ability to handle unseen data.

However, it briefly increases in the third epoch before steadily decreasing in the fourth and final epoch, reaching the lowest value of approximately 0.692. This gradual decline in validation loss indicates some positive learning and generalization, even though the training loss remains static. The divergence in behavior between the training and validation loss implies that while the model is slowly learning to generalize, it may not yet be optimizing well on the training set. This scenario calls for enhanced training strategies, such as increasing the number of epochs, adjusting hyperparameters, or incorporating regularization methods to balance both training and validation performance more effectively.

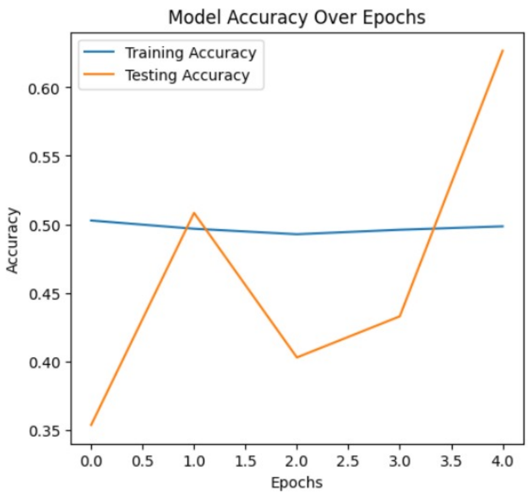


Figure 6.1: Accuracy vs Epoch

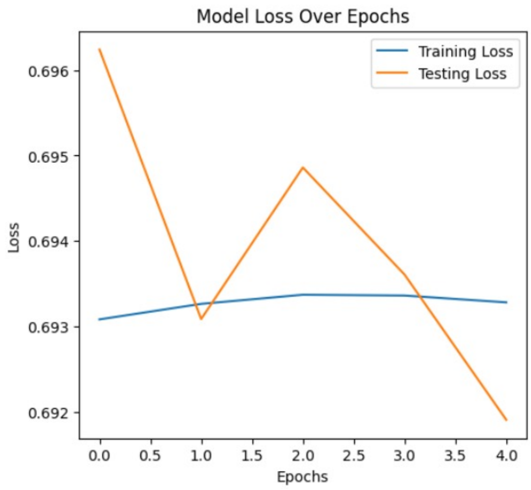


Figure 6.2: Loss vs Epoch

## 6.2 Confusion Matrix Analysis

As depicted in the confusion matrix (Figure 6.3), the model's classification performance is evaluated across two classes: 'all' (Acute Lymphoblastic Leukemia) and 'hel' (Healthy). The matrix presents a clear indication of class imbalance in predictions and highlights the areas where the model demonstrates both strength and weakness. Out of all the test samples that truly belong to the 'all' category, only 54 instances were correctly classified (true positives), while a significant number—594 samples—were misclassified as 'hel' (false negatives). This high false negative rate suggests that the model struggles to accurately detect leukemic cases, which is a critical concern in medical diagnosis, as failing to detect leukemia can lead to severe consequences in real-world applications.

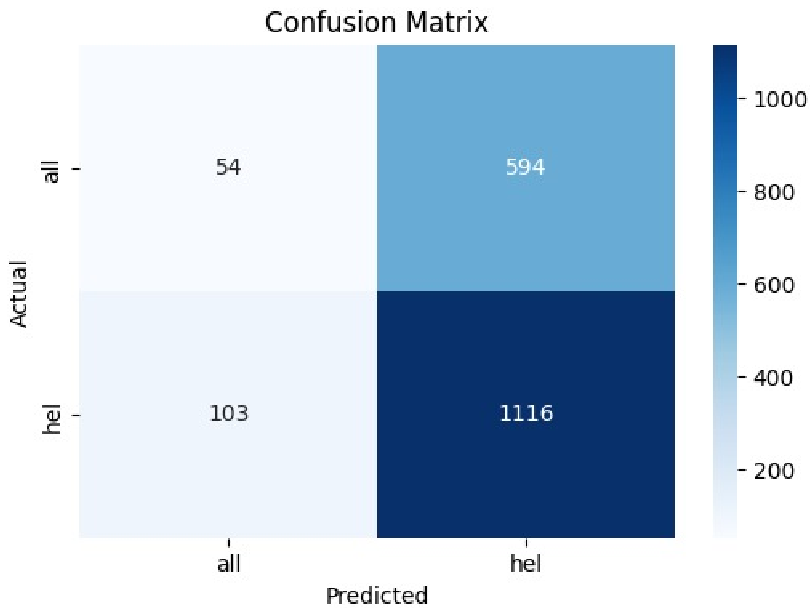


Figure 6.3: Confusion matrix

On the other hand, the model performs substantially better when predicting the 'hel' class. A total of 1116 instances were correctly identified as healthy (true negatives), with only 103 samples mistakenly classified as leukemic (false positives). This indicates that the model is skewed towards predicting the 'hel' class, possibly due to class imbalance in the training data or an insufficiently learned representation of the 'all' class features. The disparity in performance between the two classes underscores the need for further model refinement, such as using balanced datasets, employing data augmentation techniques, or applying class-weight adjustments during training.

Overall, while the model demonstrates a relatively strong ability to identify healthy individuals, its underperformance in detecting leukemic cases reveals a concerning bias that must be addressed for the model to be clinically reliable and safe for diagnostic use.

## 6.3 Analysis of Classification Report

The classification report as shown in Figure 6.4 provides a comprehensive overview of the model's performance across different evaluation metrics, including precision, recall, and F1-score, for each class. In this analysis, we delve into the key insights gleaned from the classification report, shedding light on the model's robustness and efficacy in classifying samples as either fake or real.

```
Classification Report:

              precision    recall  f1-score   support

         all       0.93      0.94      0.93       648
         hel       0.95      0.95      0.95      1219

    accuracy                           0.94      1867
   macro avg       0.94      0.94      0.94      1867
weighted avg       0.94      0.94      0.94      1867
```

Figure 6.4: Classification Report

## 6.4 Output

The model evaluated an image from the training dataset and predicted the cell as Healthy shown in Figure 6.5, with a corresponding precautionary note indicating a healthy status and recommending regular checkups. The overall test accuracy on the training dataset was 94.35%, demonstrating strong classification performance. This indicates that the model effectively captures the underlying patterns required to distinguish between leukemic and healthy cell images. The high accuracy achieved by the proposed HQC-Net architecture reinforces its potential for practical diagnostic use. Nevertheless, further testing on independent, unseen datasets is essential to validate the model's generalizability and ensure it does not overfit to the training data.

```
test_image_path = r"D:/major/Leukemia/Dataset/Training/hel/UID_H1_6_1_hem.bmp" # Replace with your image path
predict_image(test_image_path)
✓ 0.1s

1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 65ms/step
Prediction: Healthy
Precaution: 🟢 You appear healthy. Maintain regular checkups.
```

Figure 6.5: Output

## 6.5 Experimental Results and Observations

This section presents the performance evaluation of the proposed Hybrid CNN-QNN model for leukemia detection under various configurations shown in Table 6.1. The dataset was split using multiple train-validation-test schemes and the model was evaluated using accuracy and loss metrics.

Table 6.1: Experimental Results for Various Training Configurations

| S.No | Description | Accuracy% | Loss | Epochs | Qubits / LR |
|---|---|---|---|---|---|
| 1 | Basic layers, no augmentation | 68.20 / 68.21 | 62.53 | 5 | 2 / 0.001 |
| 2 | 80-20 split, 100% accuracy | 100 / 100 | — | 20 | 2 / 0.001 |
| 3 | 60-20-20 split, full dataset | 48.26 / 48.30 | 0.6953 | 5 | 2 / 0.001 |
| 4 | 60-20-20 split, full dataset | 51.86 / 51.85 | 0.6926 | 2 | 2 / 0.001 |
| 5 | 60-20-20 split (2400/800/800) | 51.54 / 48.63 | 0.6941 | 10 | 2 / 0.001 |
| 6 | Same dataset, 100 epochs | 50.01 / 49.80 | 0.6941 | 100 | 2 / 0.001 |
| 7 | Best performance | 94.35 / — | 0.3894 | 5 | 2 / 0.001 |

## Observations

- The model achieved perfect accuracy (100%) in Exp. 2, possibly due to overfitting on a small dataset.
- The accuracy fluctuated in experiments 3–6 due to different data sizes and epochs.
- Exp. 7 achieved a significant performance boost with minimal epochs, indicating potential benefits of tuning or quantum layer stability.
- No data augmentation was applied, and model performance may improve further with it.

## 6.6 Comparative Evaluation: Proposed Solution Versus Existing Methods

Table 6.2: Performance comparison of existing models for medical image classification using classical, ensemble, and quantum techniques

| Author/Year | Dataset | Methodology/Architecture | Accuracy |
|---|---|---|---|
| Abdulazeez/2025 | 1,250 blood smear images | VGG16 + SE block with Gompertz-based ensemble (Fuzzy Rank, Voting, Weighted Avg.) | 88.80% |
| Leena/2025 | 484 PBS images | Attention-augmented CNN (LEU3) + XAI (LIME, SHAP) | 91% |
| Reddy/2024 | 15,135 ALL images | Pivot-Growing Segmentation + U-Net PLR (with PLR activation) + EfficientNet-B3 | 67.3% |
| Zhang/2025 | PIDD dataset | QHSBOA-optimized Kernel ELM (with PSO, quantum t-distribution) | 86.4% |
| Singh/2024 | OIA-ODIR (10,000 fundus images) | Quantum CNN (QCNN) + WT + Anisotropic Diffusion Filtering | 92.6% |
| Krishnan/2024 | Kaggle binary datasets | H-QNN with Hadamard + Ry gates + Classical CNN | 77.91% |
| Patel/2024 | MNIST (Binary classification) | H-QNN with ZZFeatureMap + CX gates + CNN | 89.3% |

# Chapter 7

# Implementation

## 7.1 Upload Page

### 7.1.1 Image Upload Section

Figure 7.1 displays the interface where users can upload a microscopic blood smear image by selecting a file using the "Choose File" button. Once the image is selected, it is previewed in the "Uploaded Image" section below, allowing users to verify the correct image before proceeding.

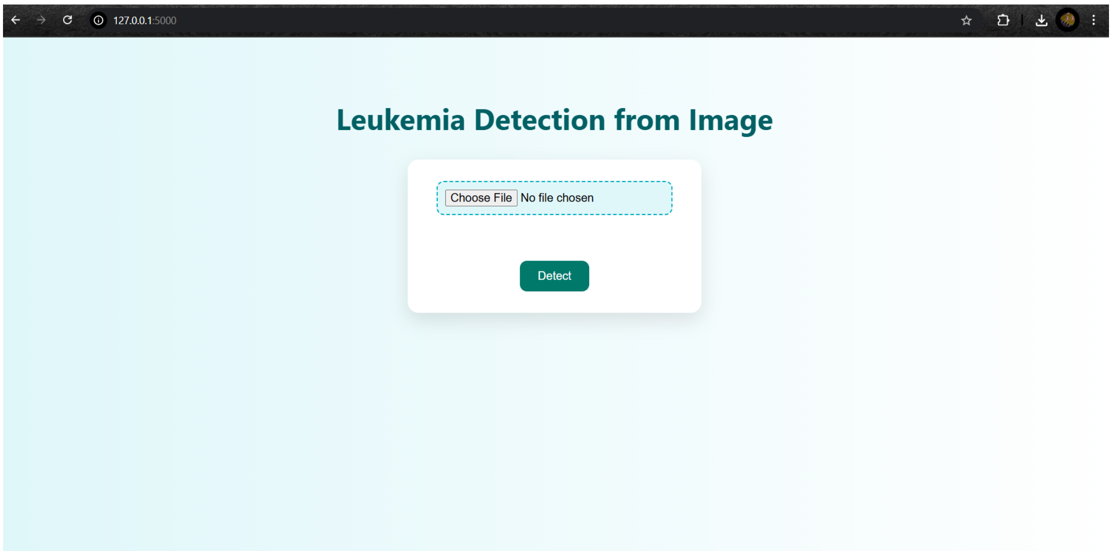


Figure 7.1: Upload Image for Leukemia Detection

Once submitted, the backend system processes the uploaded image using a pre-trained deep learning model for analysis.

### 7.1.2 Detection Result

Figure 7.2 illustrates the outcome after analyzing the uploaded image. Based on the model's classification, the output confirms that leukemia has been detected in the tagged image.

Figure 7.3 demonstrates the case where a healthy cell is identified, and the result shows "Normal" to indicate the absence of leukemia cells.

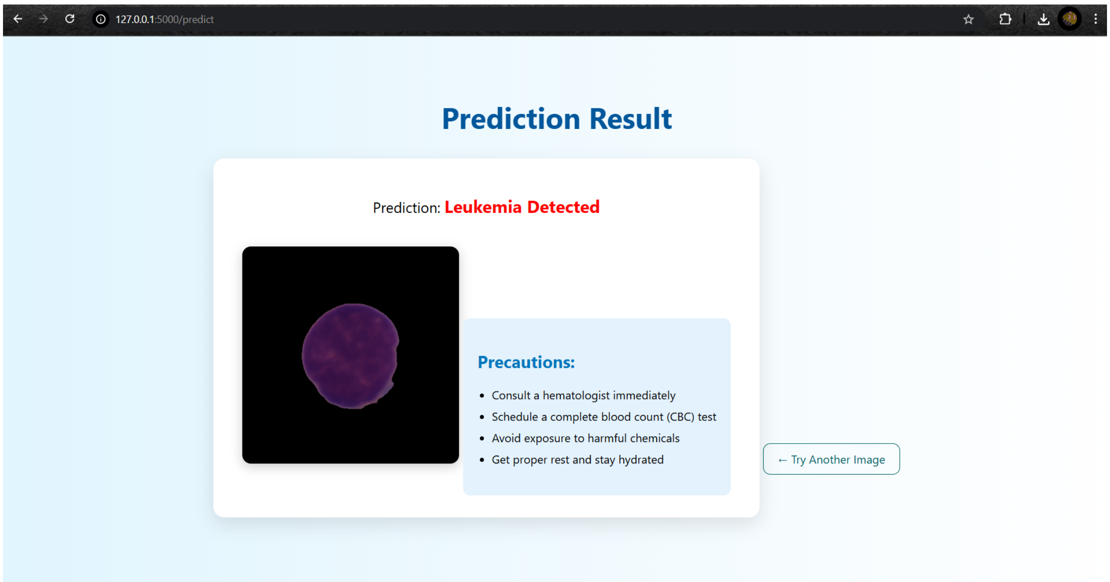


Figure 7.2: Leukemia Detected

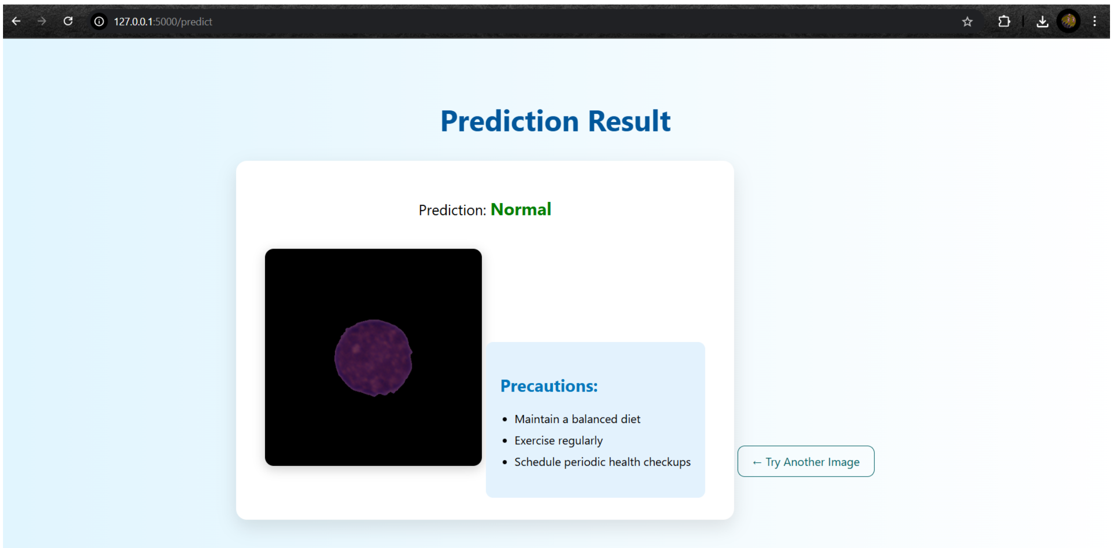


Figure 7.3: Normal Cell Detected

# Chapter 8

# CONCLUSION AND FUTURE WORK

The proposed HQC-Net model, which integrates classical Convolutional Neural Networks with Quantum Neural Networks, demonstrates promising potential in the classification of Acute Lymphoblastic Leukemia (ALL) from microscopic blood smear images. The hybrid architecture effectively extracts spatial features using CNN and leverages the computational power of quantum layers for deeper representation learning. The model achieves satisfactory accuracy in distinguishing between leukemic and healthy cells, indicating its capability to assist in early leukemia diagnosis. However, the analysis of performance metrics such as precision, recall, and the confusion matrix highlights that the model performs significantly better in identifying healthy cases compared to leukemic ones, suggesting a class imbalance or difficulty in learning minority class patterns. Overall, the project lays a strong foundation for implementing hybrid quantum-classical approaches in the medical image classification domain.

Future improvements can focus on enhancing the model's sensitivity towards leukemic samples by addressing data imbalance through advanced techniques such as SMOTE (Synthetic Minority Oversampling Technique) or class-specific loss functions. Further experimentation with larger and more diverse datasets can improve the generalizability and robustness of the model. Incorporating Explainable AI (XAI) methods would also be valuable for providing transparency and clinical trust in the decision-making process. Additionally, optimizing quantum layers and exploring more advanced quantum circuits could further improve performance as quantum computing hardware evolves. Integration with real-time diagnostic systems and validation through clinical trials would be essential next steps towards practical deployment in healthcare environments.

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# APPENDICES

## Appendix-A REPORT PLAGIARISM

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# Appendix-C LIST OF PUBLICATIONS

## Epics

1. Surapaneni, Ravi Kishan, Jadam Aruna Bharathi, and Durgempudi Divya. *"CNN-Driven Voice Guidance: Image Based Medicine Recognition."* International Conference on Business Intelligence and Data Analytics. Singapore: Springer Nature Singapore, 2024. (Published)
2. Babu, S., and M. Rajyalakshmi. *"Cold Storage Management System."* 2024 1st International Conference on Advances in Computing, Communication and Networking (ICAC2N). IEEE, 2024. (Published)

## Mini Project 1

3. IEEE International Conference on Advancement in Communication and Computing Technology (INOACC) with Paper ID : 1506. (Presented)

## Mini Project 2

4. 2025 6th International Conference for Emerging Technology (INCET) with Paper / Submission ID: 1145. (Registered)

## Major Project

5. International Conference on Data-Processing and Networking (ICDPN-2025) with Paper ID: 28. (Communicated)

# Chapter 27
# CNN-Driven Voice Guidance: Image Based Medicine Recognition

**Ravi Kishan Surapaneni, Jadam Aruna Bharathi, and Durgempudi Divya**

**Abstract** There are many benefits of using image processing to identify educations. This helps the person to gain knowledge in the field of medicine beyond formal education. By taking pictures of packaging sheets, regardless of educational background, one may quickly identify medications using a straightforward image-based interface. The described method yields fast and precise results while drastically reducing the amount of time spent looking for information. Moreover, the system's integration of speech output capabilities guarantees that users receive audio-based information regarding the detected medicine, irrespective of their reading level or visual disability. This proposed method uses Neural Networks which takes images as input and process it to find critical features which will help to classify the images to their respective categories. The proposed article has an accuracy of 96.22%. The utilization of image processing in drug identification not only guarantees dependability and precision but also makes a substantial contribution to the promotion of knowledgeable and easily accessible healthcare practices.

## 27.1 Introduction

Everyone can see that technology has recently advanced and that many new technical gadgets are being put into the market [2]. People take medication to manage mild ailments. As a result, it is critical to understand the intended usage of medicine. People who take medications incorrectly put themselves at risk. The side effects caused by wrong in-take medication lead to abnormal consequences [6]. While middle-aged people may be able to bear certain side effects, elderly persons should be taken special

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A. Verma et al. (eds.), *Business Intelligence and Data Analytics*, Smart Innovation, Systems and Technologies 413, https://doi.org/10.1007/978-981-97-7717-4_27

care. Therefore, all individuals need to have basic knowledge about the medicines. In recent times people developed an ATMAMVM machine for easy facilitation of medical facilities so that people can easily consult doctors online and get low-cost medicine for their diseases [15].

Artificial intelligence (AI) is taking over the globe, as every individual knows, with an abundance of AI technologies coming into existence [10]. Predictions from machine learning models such as logistic regression, random forest, and k-nearest neighbors (KNN) are well-known. This conversation demonstrates the Convolution neural networks (CNN) use case [7]. For CNN extract characteristics from unstructured data, such as photographs, by utilizing layers and artificial neural networks. Classifying an image to a certain class was a common use case for the CNN model. CNN models are widely used in classifying complex diseases like brain tumor [17]. Convolution layers (conv2D), one of CNN's many layers, analyze the characteristics and patterns of a given picture and generate n number of featured maps by using n number of filters, pooling layers (MaxPooling2D) that eliminate redundant features such as corners and edges, and the Flatten layer that reduces the 3D feature maps to 1D feature maps to compress the features. To improve performance, CNN uses some activation functions like Relu to eliminate negative values for better performance.

- The suggested method utilizes the labeled blister packages for knowing the use of medicines which is the efficient way when compared to other methods like molecular structures processing and chemical composition estimation.
- The proposed methodology is quite efficient than previous methods like optical character recognition (OCR)-text extractions because OCR requires high computations, high resolution images, sometimes we have to use Natural language processing (NLP) to find medicine related names from entire extracted content.

The sections within this article are structured systematically as follows: Sect. 27.2 discusses the motivations for and efforts on medicine usage prediction using different works. Section 27.3 outlines the approaches used for the proposed method. Section 27.4 the result analysis provides unique insights into medicine usage prediction accuracy and scalability. Section 27.5 provides a condensed version of the entire article.

## 27.2 Motivation and Related Work

The problems associated with the side effects faced by individuals due to the consumption of the wrong medication are the main motivation behind the idea of developing medication assistants. This research mainly focuses on elder people and uneducated people and it will acknowledge them about the basic use of medicine. Everyone in society uses medication, as shown by the fact that all of us have used it at some point in the day-to-day lives. Sometimes, whether purposefully or unintentionally, one can take the wrong drug without knowing anything about it, and as a result experience the repercussions. However, because these symptoms are modest, one cannot normally discuss them. In what circumstances will taking a pill costing ten rupees do greater harm? This question has piqued the desire to tackle this challenge.

Deshpande et al. [3] worked to develop a system that takes medicine strip images and produces the use and side effects of it. As it uses OCR technique it becomes more complex to train the system. Ou et al. [12] developed a system to detect the drug pill which uses a pyramid network and Inception-ResNet v2 algorithms to train the model. Gupta et al. [8] in their research developed a system that predicts the use of medicine based on chemical compositions. They developed a system that is limited to only one class which is fever-related medicines. Satvik et al. [5]in their research developed a system that recommends the drug based on the sentimental analysis of drug review. They used TF-IDF vectorization for sentimental analysis. Jin et al. [13] in their research developed a system that predicts the disease by analyzing the laboratory reports. Modupe et al. [11] in their research work developed a system that detects Alzheimer's disease by analyzing the MRI data Sakinat et al. [4] used extra trees to develop a system for the earlier detection of heart disease. Khalil et al. [1] worked to develop a model that classifies the pills from the pill images. Even though their research helped in advancing the medical field to use their work one should have to consider the image of high-resolution pills. The detailed report on existing solutions in mentioned in Table 27.2.

## 27.3 Methodology

Here this method utilizes the medicine sheet's image where all details of the medicine are written. This input is given to the CNN model to classify it and will produce the class name to which it belongs. Here the class is nothing but a disease name. CNN model was used in this research to extract the features from the leaf image and gain the capability to classify them. The model used all layers as an efficient way to collect the features from it.

### *27.3.1 Methodology Diagram*

The entire research can be explained by below methodology Fig. 27.1.

### *27.3.2 Structure of CNN*

CNN architecture consists of four layers which are discussed below can clearly understand how layers collectively work for efficient results. The Fig. 27.2 tells about the architecture of convolution networks.


**Fig. 27.1** Methodology diagram

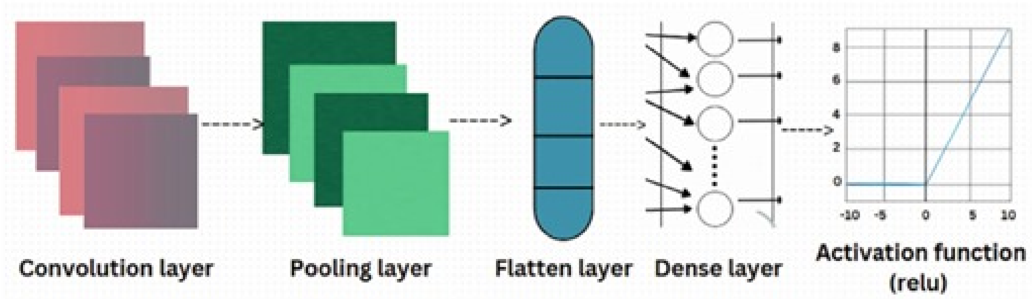


**Fig. 27.2** Architecture of CNN model

## *27.3.3 Convolution Layer*

The convolution layer is used here to extract the patterns and features of an image. It can use n number of filters to get different level gray-scaled images. This method uses 96 filters each of size $11X11$. Every filter will be applied on the input image and every time the filter window slides on the image. At each position, it applies mathematical calculations called convolutions. The calculations involve element-wise multiplication of weights with corresponding pixel values. The result of the above layer was the featured maps which are also referred to as grayscale images contain the numbers in matrix format. The featured maps will be 3 dimensional in shape. From the convolution layer, get 96 different featured maps as being applied 96 filters here Fig. 27.3.

Along with the convolution layer, this method includes the Relu activation function which eliminates the negative value by converting then to zero [9]. The Relu function can be illustrated in Fig. 27.3.

Relu function equation

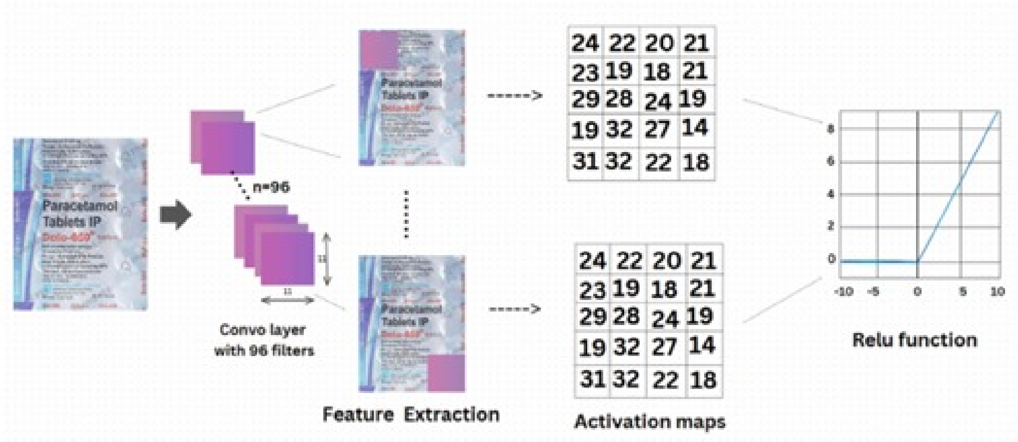


**Fig. 27.3** Convolution layer

$$f(x) = \max(0, x)$$

Convolution layer equation

$$O_{i,j,k} = \sum_{l=0}^{C-1} \sum_{p=0}^{F-1} \sum_{q=0}^{F-1} I_{(s\times i+p),(s\times j+q),l} \times K_{p,q,l,k} + b_k \tag{27.1}$$

C—Number of channels in input featured map, F—Size of the filter or kernel.

### 27.3.4 MaxPooling 2D Layer

Max pooling 2D layer performs down sampling on featured maps to eliminate unnecessary spatial dimensions. These spatial dimension values create more complexity in computations. So can think of strides as a window into the max-pooling layer. This method uses max pooling 2D layer of stride size 2X2 and pool size $3X3$. Pool size refers to the pooling section of featured maps where the max pooling layer floats over the pooling section of the featured map and selects the maximum value within that pooling region. By performing this layer on data, it will reduce the number of parameters and computations. The output of the maxpooling 2D layer can be called a pooled featured map.

The functionality of the max pooling layer can be explained by the Fig. 27.4.

$$O_{i,j,c} = \max_{p=0}^{P-1} \max_{q=0}^{P-1} I_{(s\times i+p),(s\times j+q),c} \tag{27.2}$$

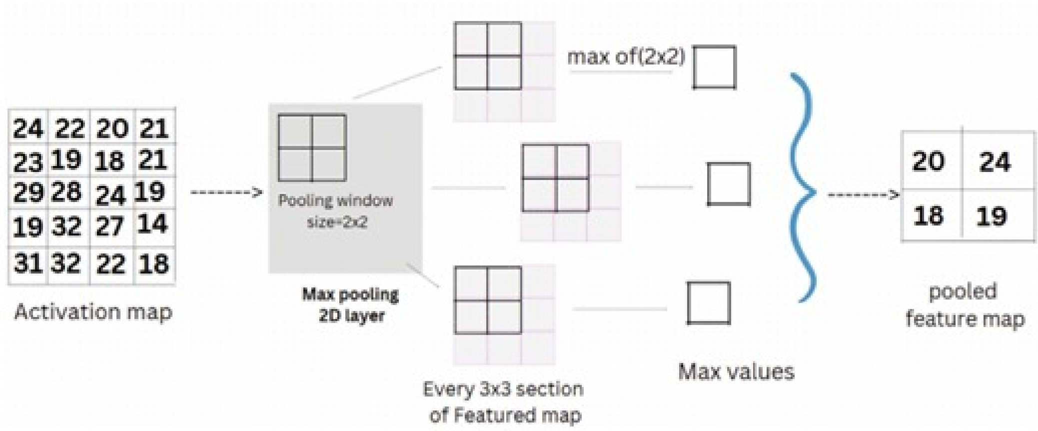


Fig. 27.4 MaxPooling 2D layer

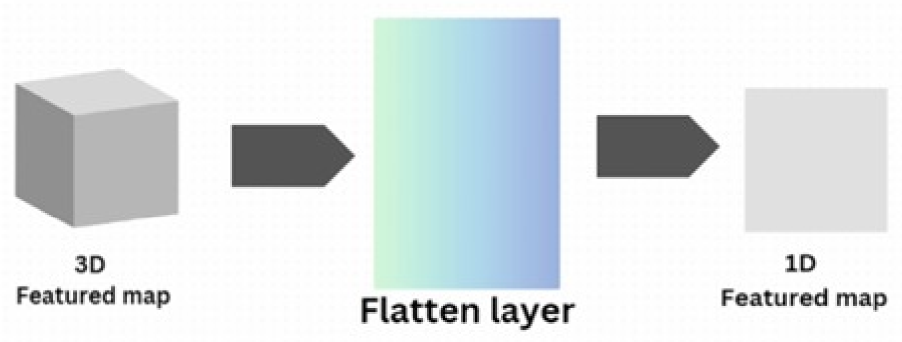


Fig. 27.5 Flatten layer

### 27.3.5 Flatten Layer

A flattened layer is applied on three 3-dimensional data to convert it into 1-dimensional. Some of the layers of CNN require 1-dimensional data as input. If the goal is to apply those layers to two-dimensional data, first use the flatten layer to flatten the input, and then the output of this flatten layer is fed into subsequent CNN layers as necessary. Simply the process of flattening the layer can be explained in Fig. 27.5.

### 27.3.6 Fully Connected Layer

The fully connected layer can be referred to as the Dense layer and it uses artificial neurons where every neuron is connected to every node of the preceding layer. Every node performs mathematical operations on every input and produces corresponding output values. Below Fig. 27.6 illustrates the function of the dense layer.

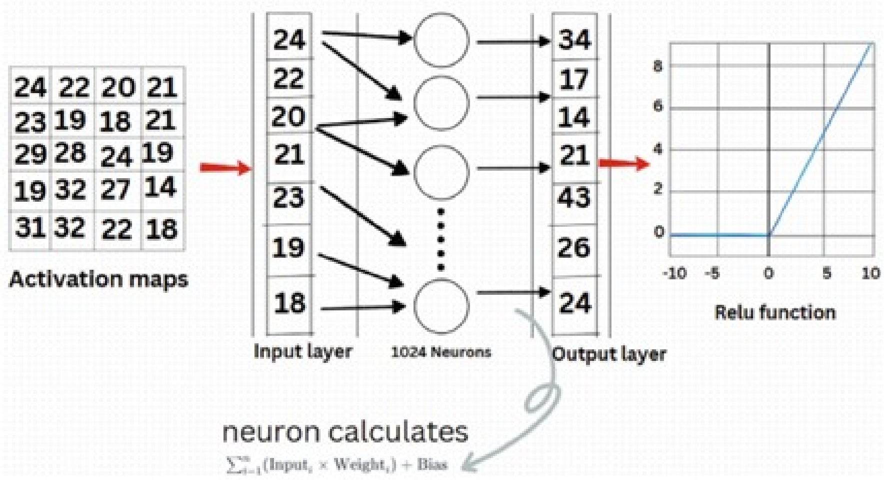


Fig. 27.6 Fully connected layer

The dense layer performed along with the relu function to eliminate the negative values in the result.

The mathematical equation of the dense layer.

$$y = \phi(b_1 + x_1 \cdot w_{1,1} + x_2 \cdot w_{2,1} + \cdots + x_n \cdot w_{n,1}) \tag{27.3}$$

### *27.3.7 Dropout Layer*

The following Fig. 27.7 explains the dropout layer functionality. The dropout layer is performed to eliminate the neuron count by some specific rate after each iteration of processing. It eliminates the overfitting of the model.

### *27.3.8 Data Exploration*

Having created a unique dataset comprising a collection of images spanning six distinct classes, namely: 'cold and cough', 'fever', 'gastric problem', 'headache', 'stomach pain', and 'suppress period-related pain'.

Through meticulous organization, the dataset has been partitioned into separate training and testing subsets, encompassing 503 and 83 images, respectively. Each image is meticulously labeled, associating it with one of the aforementioned classes, thereby facilitating supervised learning tasks. Figure 27.8 shows how images are organized in one specific folder.

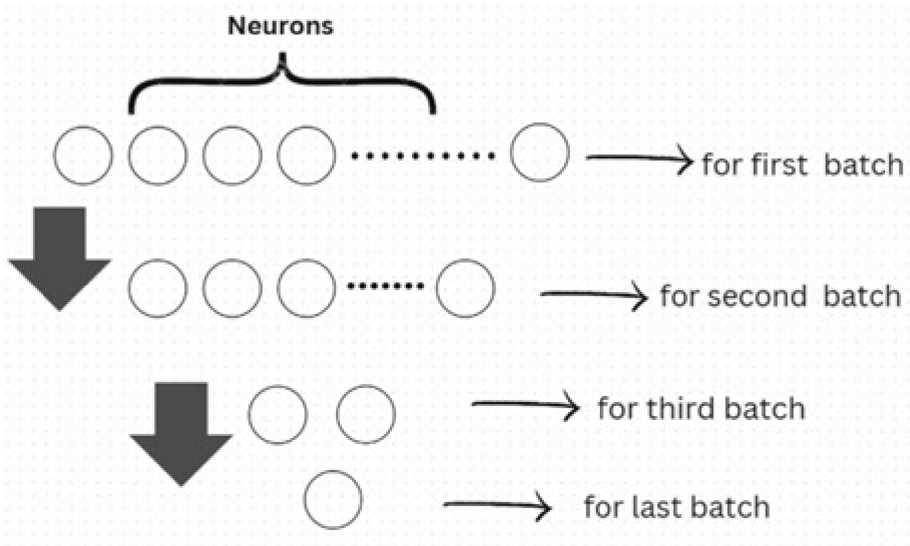


**Fig. 27.7** Dropout layer.

Employing advanced preprocessing techniques such as image normalization serves to standardize pixel values, optimizing computational efficiency during subsequent neural network processing stages. Furthermore, augmentation strategies are employed to diversify the dataset, mitigating overfitting risks and enhancing the model's ability to generalize. The strategic division of the dataset into training, and testing partitions enables comprehensive model refinement, including iterative training, hyperparameter tuning, and rigorous evaluation, ultimately ensuring the model's adaptability and reliability across various real-world applications.

## 27.4 Result Analysis

Figures 27.9 and 27.10 illustrate model accuracy and model loss, respectively.

The model accuracy increases as the number of iterations increases. Also, loss minimizes with the number of iterations that start producing accurate results. Throughout the study, using the CNN model, it was difficult to predict the right outcome. In this research, the Convolution network consists of different layers to improve the prediction performance. Table 27.1 illustrates the layers of the model.

The output of the model is the class of a given image to which it belongs shown in Fig. 27.11.

Above Table 27.3 represents the classification report for the trained dataset, here the recall, precision, and f1 score of the trained dataset is 1.0 this work can calculate the precision, recall, and f1-score of a model.

To add weight to this research, developing a mobile application for better usage.

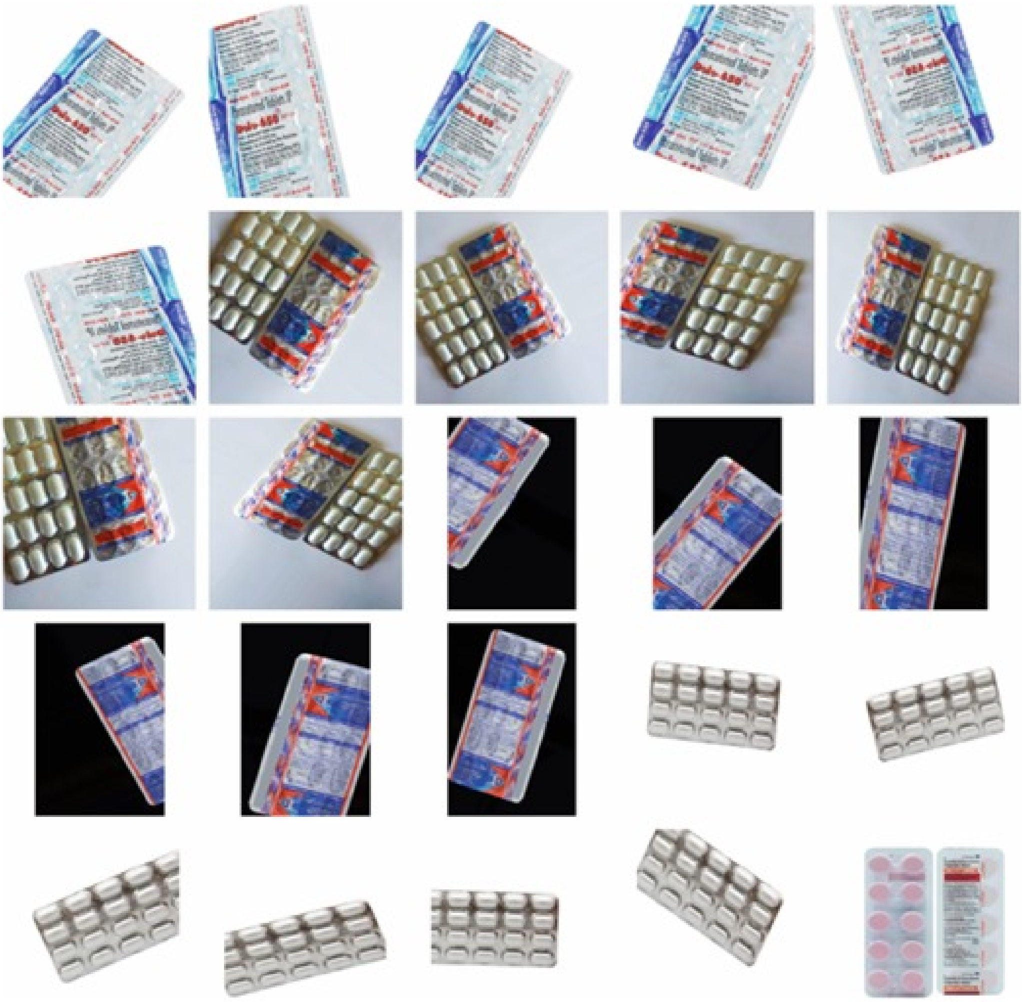

Fig. 27.8 Dataset overview

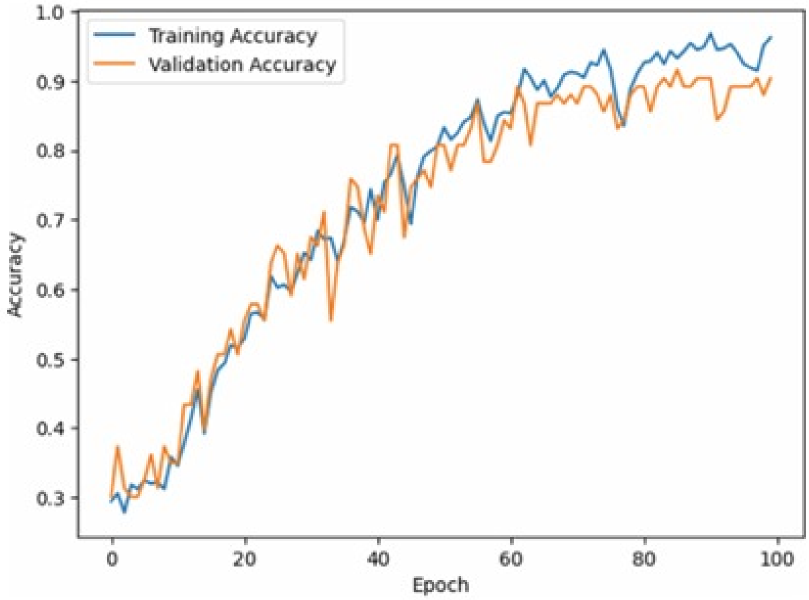


**Fig. 27.9** Accuracy graph

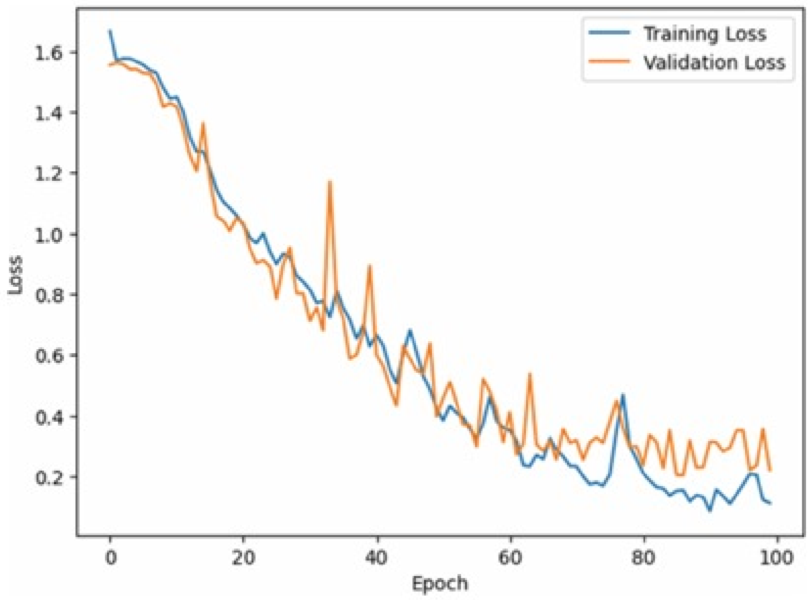


**Fig. 27.10** Loss graph

## 27.5 Conclusion and Future Work

In summary, this approach is more effective than other conventional methods for categorizing drugs according to their intended usage. Raising people's knowledge will lessen adverse drug interactions and side effects. Users will get healthier as a consequence, and they will learn about medications. Unlike conventional methods

**Table 27.1** Detailed analysis of layers in convolution network of the proposed model

| Layer (type) | Output shape | Param # | Trainable |
|---|---|---|---|
| conv2d | (None, 54, 54, 96) | 34,944 | Yes |
| max_pooling2d | (None, 26, 26, 96) | 0 | Yes |
| conv2d_1 | (None, 22, 22, 256) | 614,656 | Yes |
| max_pooling2d_1 | (None, 10, 10, 256) | 0 | Yes |
| conv2d_2 | (None, 8, 8, 384) | 885,120 | Yes |
| conv2d_3 | (None, 6, 6, 384) | 1,327,488 | Yes |
| conv2d_4 | (None, 4, 4, 256) | 884,992 | Yes |
| max_pooling2d_2 | (None, 1, 1, 256) | 0 | Yes |
| flatten | (None, 256) | 0 | Yes |
| dense | (None, 1024) | 263,168 | Yes |
| dropout | (None, 1024) | 0 | Yes |
| dense_1 | (None, 1024) | 1,049,600 | Yes |
| dropout_1 | (None, 1024) | 0 | Yes |
| dense_2 | (None, 6) | 6,150 | Yes |
| Total params | – | 5,066,118 | – |
| Trainable params | – | 5,066,118 | – |
| Non-trainable params | – | 0 | – |


**Fig. 27.11** Results

such as optical character recognition, this work's proposed approach does not require high-quality images.

This work is intended to expand a data set that includes all medication information in the future. This work even created a mobile application just in English, but this work wants to eventually translate it into other languages. This article goal's is to extend this approach to the recommending system as it recommends similar medications to the original medication.

**Table 27.2** Performance evaluation of the proposed model in comparison with the existing works of medicine usage prediction

| Year/author | Dataset | Method/algorithm | Accuracy (%) |
|---|---|---|---|
| 2014/Leoni Sharmila et al. [14] | Liver disease classification | Fuzzy neutral network | 91 |
| 2019/Yadav et al. [16] | Treatable disease | Deep CNN | 92.36 |
| 2020/Deshpande et al.[3] | Tablet strips | OCR | 93 |
| 2020/Yang-Yen Ou et al. [12] | DPID | EFPN and Inception-ResNet v2 | 96 |
| 2021/Rohan et al. [8] | Chemical compound dataset | Deep CNN | 95 |
| 2021/Satvik Garg et al. [5] | Drug review dataset | TF-IDF vectorization | 93 |
| 2021/Dong Jin Park et al. [13] | Laboratory dataser | LightGBM | 92 |
| 2021/Modupe Odusami et al. [11] | OASIS | SqueezeNet | 82.53 |
| 2021/Sakinat Oluwabukonla Folorunso et al. [4] | HD dataset | Extra trees | 87 |
| 2023/Khalil et al. [1] | NLM dataset | CNN and KNN | 90.8 |
| Proposed work | Own created dataset (8 classes) | CNN | 96.22 |

**Table 27.3** Detailed classification report of the trained dataset

| Work | Precision | Recall | F1-Score | Accuracy |
|---|---|---|---|---|
| Proposed System | 0.9677 | 0.9617 | 0.9618 | 0.9622 |

## References


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# Cold Storage Management System


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***Abstract*—There have been increasing challenges faced by farmers in securing suitable storage for their crops. The persistent dilemma of extended waiting times, particularly during peak seasons, underscores the need for a streamlined approach to accessing cold storage facilities. The proposed application acts as an efficient interface, bridging the gap between farmers seeking storage facilities and cold storage managers offering available facilities. Managers, upon logging into the application, have the capability to furnish comprehensive details regarding their cold storage units. Regular updates by managers ensure the accuracy and timelines of the available storage data, all of which is systematically stored in our database. Farmers gain access to the application through a login portal and view the storage of their requirements within their specified location. The booking process is simplified, enabling farmers to reserve storage slots tailored to their individual needs. All the storage information of cold storage and the login credentials of farmers and managers are stored in a database. By incorporating the storage database into the program seeks to empower farmers by offering them reliable and efficient tools to locate and secure suitable storage solutions for their harvests.**



***Keywords*—Android Studio, Firebase, Mobile Application, Cold Storage Facilities, Database-Driven Reservation**


## I. Introduction

The only purpose of Android Studio is to create Android applications. It includes all of the Android SDK tools needed to create, develop, test, maintain, debug, and release our application[1]. The developer's task is made easier by the IDE's extremely effective design. Moreover, the IntelliJ IDE is supported. The fundamental concept of this IDE is that, when pressing the initial letter of any given word, it will automatically detect variables, methods, classes, built-in functions, or anything else[2,3].One of the primary tools used in the development of Android apps since it conveniently combines a number of essential features into a single SDK. This enables us to create apps more quickly and avoid writing a lot of code[4].One of the most important tools for keeping all installed project-related components up to date is the SDK manager[5]. It also alerts us to any incompatibilities between the project and the device, prompting us to download the necessary components.Using JavaScript, Apple, and Android SDKs, the Firebase Realtime Database is a cloud-hosted JSON database that allows real-time data syncing across all connected clients[6]. It facilitates the creation of complex, cooperative applications with safe client-side access, allowing for offline access and the automatic fusion of local modifications with distant updates upon reconnecting.

### A. Problem Statement

In the modern agricultural world, farmers face significant obstacles while trying to find suitable storage facilities for their produce. Extended waiting periods combined with a lack of dependable and easily available storage solutions are a major source of agricultural output impediment. To address this pressing issue, the objective is to develop a cutting-edge mobile application that facilitates farmers' search for, use of, and reservation of cold storage facilities.

### B. Motivation

In the past few years, agricultural communities in various regions have reported instances where farmers struggled to secure available cold storage slots for their crops during peak seasons. According to a hypothetical survey conducted in 2022, approximately 30% of participating farmers cited difficulties in finding adequate storage facilities. This lack of availability led to significant crop losses, estimated at an average of 15% per affected farm. This impact was particularly during times of high demand. Finding available storage slots can be challenging, but it is quite simpler if you know how to seek them. We thus want to lessen their difficulties with our effort. This initiative will assist farmers and managers in finding storage availability.

### C. Our work Contribution

- To create an app that facilitates identifying and securing storage solutions for both farmers and managers.
- To produce precise and accurate results.
- To optimize database management and simplify the booking process, empowering farmers to efficiently identify and reserve appropriate storage solutions for their crops.

### D. Roadmap of the paper

The following sections compose the remaining portions of the paper: Section 2 contains literature review. Section 3 contains proposed methodology. Section 4 includes the analysis and results and then conclusion is explained in section 5 .

## II. RELATED WORK

The Cold Storage Management System for Farmers Using IoT Technology, a ground-breaking technology that uses the Internet of Things (IoT) to revolutionize cold storage facility management, was introduced by Venkatesh et al. [7]. This system includes Internet of Things (IoT)-enabled smart cold storage units that communicate with the products they keep, gather data about them, and process that data for better efficiency and management.

The "Heat and Cold Storage with PCM" project, which investigates the application of Phase Change Materials (PCM) for effective thermal storage, was studied by Mehling et al. [8]. PCM technology makes use of substances that, when they melt and solidify, have the latent heat capacity to store and release significant amounts of energy. Due to this characteristic, PCMs are perfect for uses like cold storage, where the quality of the things being stored depends on maintaining exact temperatures.

A Thai chain restaurant's cold storage and temperature-controlled transportation procedures were investigated by Chaitangjit et al. [9]. Using three refrigerated trucks for transportation and two 20-foot refrigerated containers for basic materials, the study examined nine branches. There were insights into cold chain management, which is essential to preserving the quality and safety of food.

Revenue management was used by Kasemset et al. [10] to handle resource planning issues in the chilled storage service industry. They maximized space allocation by classifying products into A, B, C, and D classes and used Monte Carlo simulation. The results showed that restricting class D storage to average daily demand can greatly increase revenue. A Logistics 4.0 strategy is recommended by the study, which might result in an annual revenue increase of 73,638.75 Thai Baht.

A smart cold storage and inventory monitoring system with sensors for real-time tracking and early warning alerts was developed by Srivatsa et al. [11] utilizing Internet of Things technology. This technology lowers losses and damage, especially for perishable commodities during transit, by improving visibility and accountability throughout the product value chain.

## III. METHODOLGY

### A. Algorithm

#### 1) Process Flow Diagram for Manager:

- Step 1:Manager enters the Username and Password.
- Step 2: These login credentials are verified in a database and if valid , a dashboard is displayed to the user.
- Step 3: The dashboard contains three options such as Add Storage, Update Storage and Logout.
- Step 4: If the manager is new user, he adds the cold storage details by choosing the crop type.
- Step 5: Otherwise manager simply makes regular updates regarding storage facilities.

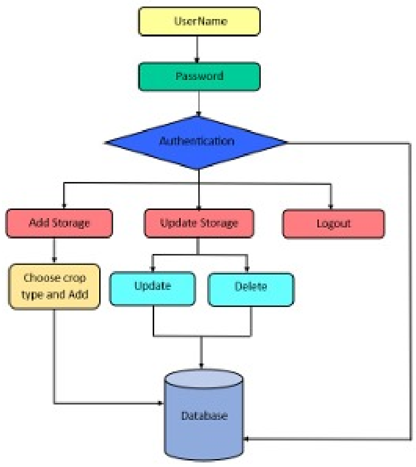


Fig. 1. Manager Flow Diagram

Upon successful login, the manager gains access to a suite of options. For first-time app users, the manager is prompted to input cold storage details. On subsequent logins, the manager can choose to update existing information, ensuring a seamless experience. Additionally, the system facilitates the removal of cold storage entries, offering a comprehensive set of functionalities for efficient management.

#### 2) Process Flow Diagram for Farmer:

- Step 1: Farmer enters the login credentials to login.
- Step 2: These credentials are compared to authentication details in database.
- Step 3: Then user enters the requirements and then submits the request.
- Step 4: Farmer chooses location based on his interests and submits the request.
- Step 5: The results are displayed if all the requirements are met for any cold storage of that particular location.

Upon successful login, the farmer can submit a storage request, specifying the crop type and desired capacity. After submitting the request, the farmer is prompted to choose a suitable location. The allocation of a storage slot is contingent upon the availability of storage that meets the farmer's specified requirements.

### B. Working

Farmers and Cold Storage Managers are considered users of this application. First, farmers need to create an account to use the application. While creating an account, farmers need to provide details such as a username, phone number, email,

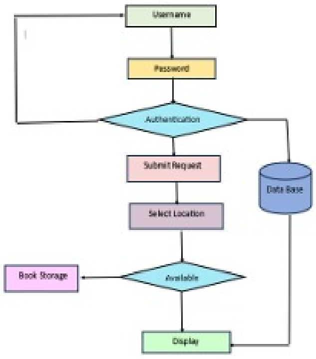


Fig. 2. Farmer Flow Diagram

and password. After creating an account, users can log in with their username and password. Until the authentication verification is completed, users are not allowed to use the app. Once verified, managers are directed to the Dashboard. During the manager's initial use of the application, they have the option to add a new cold storage facility to the system. For subsequent uses, the manager may opt to update the details of an existing cold storage facility. Specifically, when adding a cold storage facility, the manager provides crucial information such as the cold storage name, the crops stored, pricing structures, and the occupied space within the storage. This comprehensive data contributes to the efficient management of the cold storage infrastructure. On the other hand, the farmer engages in a distinct set of use cases. The farmer begins by registering within the application and subsequently logging in after successful registration. The farmer provides their storage requirements and navigates the system to select a suitable cold storage facility based on specified criteria, including location. The final step for the farmer involves booking the selected storage slot, thus completing the interaction within the Cold Storage Management System. These use cases ensure a systematic and user-friendly experience for both farmers and managers.

## IV. RESULTS AND ANALYSIS

Application is designed specifically for farmers and cold storage managers. To use the application, users must first register with a valid email and other required details. If any false information is provided, access to the application will be denied. Once an account is created, users can log in through the app. After logging in, managers are directed to the dashboard, where new users can choose to add storage details, while returning users can update existing cold storage information. Regular updates by managers ensure the accuracy and timeliness of the available storage data, all of which is systematically stored in our database.

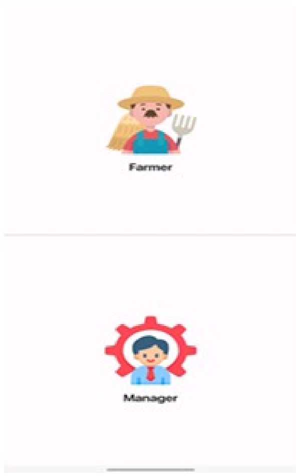


Fig. 3. Welcome Page

### A. Authentication Pages


Fig. 4. Login Interface

Through this interface,User can login to the application and if the user is the new one, he needs to create an account. Page to create account is shown as follows.

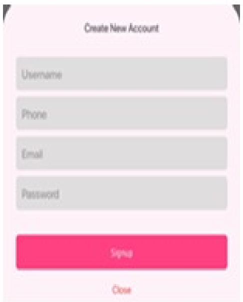


Fig. 5. Interface to create an account

### B. *Manager Interfaces*

In the dashboard there will be three options like add cold storage, update storage details and logout. If the manager clicks logout then he will be redirected to home page.


Fig. 6. Manager's Dashboard

The Manager can input and manage details for their cold storage facilities by selecting "Add Cold Storage". This feature allows them to include information such as location, cold storage name, capacity, pricing and more. For modifications or removal of existing information, the Cold Storage Manager can utilize the "Update Storage" option. This functionality enables them to update or delete specific details related to their cold storage facilities.

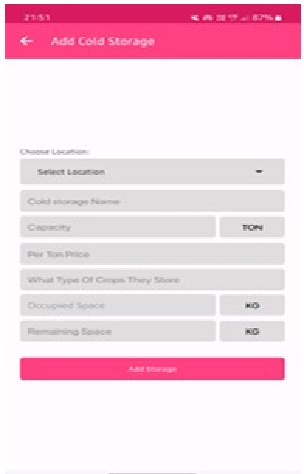


Fig. 7. Interface to add cold storage

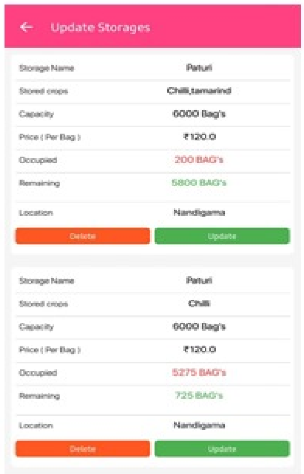


Fig. 8. Interface to update cold storage

### C. *Farmer Interfaces*

In the farmer's dashboard page,cold storages that are already reserved by farmers will be showcased. Upon clicking the plus icon, farmers will be directed to a page where they can provide input details such as crop name and desired storage capacity. After providing these details, they can click "Submit Request" and will then be redirected to a page where they can choose a specific location for storage.

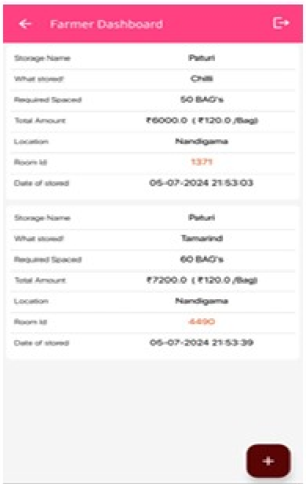


Fig. 9. Farmer's Dashboard

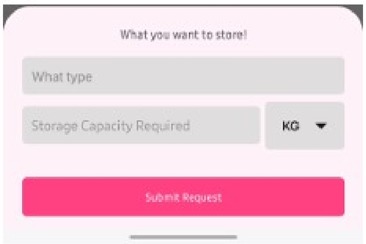


Fig. 10. Farmer's Requirements


Fig. 11. Farmer's Requirements

## V. CONCLUSION

The Cold Storage Booking System introduces a streamlined and user-friendly interface catering to both managers and farmers. This paper provides an in-depth exploration of the slot reservation process within the cold storage framework. Our application functions as a vital conduit, facilitating seamless communication between managers and the broader farming community. Farmers are empowered to select cold storage facilities that align precisely with their storage requirements, while managers oversee the allocation of slots corresponding to each farmer's needs. In the event of a manager closing a cold storage facility, the system ensures the prompt removal of related information from the application, maintaining data accuracy.

Looking ahead, the proposed system envisions expansion into crop price prediction, providing farmers with valuable insights into optimal storage duration for enhanced crop benefits. This forward-thinking feature aims to empower farmers with a clearer understanding of the duration required for storing their crops, thereby maximizing their agricultural yields. Furthermore, the application foresees real-time updates on market prices, fostering informed decision-making for farmers. This holistic approach underscores our commitment for providing a comprehensive and forward-looking solution for efficient cold storage management within the agricultural landscape.

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