PANCREATIC CANCER DETECTION USING DEEP LEARNING

A PROJECT REPORT

Submitted by

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Under the guidance of

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BONAFIDE CERTIFICATE

Certified that this project report titled **PANCREATIC CANCER DETECTION USING DEEP LEARNING** is the bonafide work of **S. HARINI (RRN: 221421601015) and M.LAVANYA (RRN:221421601021)** who carried out the project work under my supervision. Certified further, that to the best of my knowledge the work reported herein does not form part of any other project report or dissertation on the basis of which a degree or award was conferred on an earlier occasion on this or any other candidate.

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VIVA-VOCE EXAMINATION

The viva-voce examination of the project work titled **"PANCREATIC CANCER DETECTION USING DEEP LEARNING"** submitted by **S.HARINI (RRN: 221421601015) and M.LAVANYA (RRN: 221421601021)** is held on

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INTERNAL EXAMINER **EXTERNAL EXAMINER**

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ABSTRACT

Pancreatic cancer is one of the most deadly types of cancer because it is usually diagnosed at a very late stage, when treatment options are limited. If it is detected early, the chances of successful treatment are much higher. Our project focuses on using deep learning to detect pancreatic cancer early by analyzing images of red blood cells (RBCs) and white blood cells (WBCs). We are using advanced deep learning models, especially the VGG19 model, to recognize patterns in these blood cells that may indicate the presence of cancer. With this method, we have achieved an accuracy of about 97% in detecting pancreatic cancer. Our goal is to train these models on large datasets of blood cell images so they can learn to spot tiny, hidden changes that are difficult for the human eye to notice. This type of system could be added to hospital diagnostic tools, helping doctors to quickly and accurately screen patients. As a result, it could lead to faster diagnosis, timely treatments, and better outcomes for patients. By combining technology with medicine, our system aims to support healthcare professionals and make cancer detection more effective.

TABLE OF CONTENTS

LIST OF FIGURES

LIST OF ABBREVIATION

ACRONYM	ABBREVIATION
AI	Artificial Intelligence
ML	Machine Learning
DL	Deep Learning
CNN	Convolutional Neural Network
SVM	Support Vector Machine
RBC	Red Blood Cells
WBC	White Blood Cells
VGG19	Visual Geometry Group 19-layer model
AWS	Amazon Web Services
API	Application Programming Interface
TP	True Positive
TN	True Negative
FP	False Positive
FN	False Negative
ROC	Receiver Operating Characteristic
AUC	Area Under the Curve
GPU	Graphics Processing Unit

ACRONYM	ABBREVIATION
ReLU	Rectified Linear Unit
SGD	Stochastic Gradient Descent
MSE	Mean Squared Error
IOU	Intersection over Union
PSNR	Peak Signal-to-Noise Ratio
SSIM	Structural Similarity Index Measure
LR	Learning Rate
NLP	Natural Language Processing
RNN	Recurrent Neural Network
LSTM	Long Short-Term Memory

CHAPTER 1
INTRODUCTION

This Chapter provides a comprehensive introduction to the research on pancreatic cancer detection through blood cell image analysis. It outlines the background and motivation, emphasizing the limitations of traditional diagnostic methods and the potential of deep learning techniques. The chapter reviews existing WBC classification systems, identifying their drawbacks. It then presents the proposed system, detailing its innovative methods and advantages. Finally, it concludes with the organization of the thesis, setting the stage for the subsequent chapters.

1.1 GENERAL

Identifying pancreatic cancer through the analysis of blood cell images represents a promising and innovative direction in medical diagnostics. Pancreatic cancer is one of the deadliest forms of cancer due to its typically late detection and aggressive progression. Early and accurate diagnosis is critical for improving patient outcomes, yet current diagnostic methods often lack the sensitivity and specificity needed for timely detection. Recent advances in digital imaging and computational analysis have opened new possibilities for non-invasive diagnostics by leveraging morphological and structural changes in blood cells associated with malignancies. Analyzing White Blood Cells (WBCs) and Red Blood Cells (RBCs) from peripheral blood smears can reveal subtle alterations caused by the presence of pancreatic cancer, offering a novel biomarker for early screening. Traditionally, blood cell examination has relied on manual microscopic analysis by trained professionals, a process that is time-consuming, subjective, and prone to inconsistencies. The integration of image processing and deep learning technologies has revolutionized this domain, enabling automated systems to extract discriminative features from microscopic images with high accuracy and efficiency. These systems utilize convolutional neural networks and advanced classification algorithms to detect patterns that may be imperceptible to the human eye. The development of a reliable automated

diagnostic tool for pancreatic cancer detection presents several challenges. These include variability in cell morphology due to patient-specific factors, differences in staining techniques, and the presence of noise or artifacts in blood smear images. Our project aims to overcome these challenges by designing a robust deep learning-based framework capable of identifying pancreatic cancer through blood cell image analysis. The proposed system combines advanced segmentation methods, feature extraction techniques and optimized classification models to improve diagnostic accuracy and generalizability. By leveraging computational intelligence, this approach has the potential to enhance early detection, reduce diagnostic delays, and support medical professionals in clinical decision-making. Moreover, the development of such non-invasive diagnostic tools is particularly valuable in resource-constrained settings where access to advanced medical imaging and specialist care is limited. The introduction establishes the foundation for exploring the significance, challenges, and innovations associated with automated blood cell image analysis for pancreatic cancer detection. The following sections will review related work, outline the proposed methodology and discuss experimental results and contributions.

1.2 EXISTING SYSTEM

The existing systems for WBC classification encompass a range of approaches, from traditional machine learning methods relying on handcrafted features to modern deep learning techniques that leverage automated feature extraction. These systems have been developed to address the limitations of manual microscopic examination and to provide efficient and accurate solutions for haematological analysis.

1.2.1 LITERATURE SURVEY

1.2.1.1 STANDARD MACHINE LEARNING MODELS

Early attempts at automated WBC classification relied on traditional machine learning algorithms such as Support Vector Machines (SVMs), k-Nearest Neighbors (k-NN) and Random Forests, typically following a two-stage process involving feature extraction and classification. In the feature

extraction stage, handcrafted features such as morphological attributes like cell size, shape and texture, color characteristics like intensity and staining distribution, and statistical measures like moments and histograms are extracted from segmented WBC images to represent the unique characteristics of the cells. These extracted features are then input into machine learning classifiers which learn to differentiate between various WBC subtypes based on the identified patterns. While these methods have shown some effectiveness, they are constrained by their dependence on handcrafted features which may not fully capture the complex and diverse morphology of WBCs.

1.2.1.2 DEEP LEARNING APPROACHES

The advent of deep learning, particularly Convolutional Neural Networks (CNNs), has significantly improved the performance of WBC classification by enabling automatic learning of hierarchical features from raw image data, thereby eliminating the need for manual feature engineering. Various CNN architectures such as ResNet, DenseNet, and U-Net have been employed for this task, leveraging deep layers and skip connections to extract complex features and enhance classification accuracy. Transfer learning, which involves pre-training CNNs on large datasets like ImageNet and fine-tuning them on WBC datasets, is commonly used to address the limited availability of labeled medical images and improve model generalization. Additionally, segmentation is a crucial preprocessing step before classification, with techniques ranging from thresholding, edge detection, and morphological operations to more advanced methods using U-Net-like architectures for accurate cell segmentation.

1.2.1.3 SPECIFIC EXAMPLES FROM LITERATURE

Studies utilizing ResNet and DenseNet have demonstrated significant improvements in WBC classification accuracy compared to traditional machine learning methods. U-Net based architectures have been utilized to improve segmentation accuracy, which in turn improves classification. Researchers have explored the use of data augmentation techniques to enhance the

robustness of CNN models against variations in WBC morphology. Various optimization strategies, such as Adam and SGD, have been applied to train the deep learning models and to improve their convergence and performance.

A semi-automated approach for classifying White Blood Cells (WBCs) and Red Blood Cells (RBCs) from peripheral blood smear images using texture features extracted via Gray Level Co-occurrence Matrix and tested across multiple machine learning models. Logistic Regression achieved the highest accuracy of 97%, indicating its efficiency for haematological analysis. [1]

Optimized Convolutional Neural Network using transfer learning and deformable convolution layers, demonstrating robust classification performance on noisy and low-resolution images. The model showcased resilience in clinical scenarios, providing a promising alternative for automated leukocyte analysis. [2]

A comparative analysis between pre-trained CNNs and Large Image Models (LIMs) for WBC classification. Results highlighted that while CNNs perform well on domain-specific tasks, LIMs offer broader generalization, emphasizing the significance of dataset characteristics in model selection. This study guides the development of efficient medical image recognition systems. [3]

AI-powered system capable of multi-class classification for five WBC types and three platelet types from digital blood smear images. which employs extensive feature extraction and intelligent modelling aims to improve diagnostic accuracy, especially in conditions such as leukaemia and allergies.[4]

Convolutional Neural Network (CNN) model for automated WBC classification, focusing on minimizing parameters while maintaining high accuracy. The model provides an efficient and scalabl solution for clinical applications, reducing manual workload and enhancing diagnostic speed and accuracy. [5]

An improved lightweight CNN for both binary and multi-class WBC classification tasks. The model achieved accuracy rates of 98.63% for binary classification and 91.95% for multi-class classification, highlighting its effectiveness in automating haematological diagnostics with minimal computational overhead. [6]

A Fast Traditional CNN (FTCNN) model for classifying four WBC subtypes: neutrophils, eosinophils, lymphocytes, and monocytes. The model, trained on over 12,000 images, achieved 98.23% accuracy during training and 84.64% on testing. This model serves as a foundation for developing diagnostic support systems in the medical field. [7]

The paper identified critical processes such as image acquisition, segmentation, edge detection, and feature extraction. It proposed an integrated system aimed at improving early leukaemia detection through automated and precise WBC and RBC morphology analysis. [8]

An Attention Residual Network for WBC classification, which incorporated channel attention mechanisms and depth-wise separable convolutions for efficient feature extraction. To overcome data scarcity, the model used Wasserstein GAN for synthetic data generation. The proposed method outperformed several state-of-the-art models, showing strong potential for clinical diagnostic tools. [9]

The paper highlighted key processes such as image acquisition, segmentation, edge detection, and feature extraction, emphasizing the role of these techniques in improving the accuracy and efficiency of diagnosis. The authors proposed an integrated system designed to enhance early leukaemia detection by automating the precise analysis of WBC and Red Blood Cell (RBC) morphology, thus facilitating more reliable and timely clinical decision-making. [10]

1.2.2 DISADVANTAGES OF EXISTING SYSTEM

Despite the advancements in automated WBC classification, existing systems still face several limitations:

1. **Segmentation Accuracy**

   Accurate segmentation of WBCs from complex backgrounds remains a challenge, particularly in images with low contrast or overlapping cells. Inaccurate segmentation can lead to the loss of important morphological information and to errors in classification.

2. **Generalization**

   Many existing systems are trained and evaluated on specific datasets, limiting their generalization performance on diverse medical imaging sources. Variations in staining techniques, image quality, and patient populations can affect the performance of these systems.

3. **Overfitting**

   Deep learning models, particularly those with a large number of parameters, are prone to overfitting, especially when trained on limited datasets. Overfitting can lead to poor generalization performance and to unreliable classification results.

4. **Computational Complexity**

   Some deep learning models, particularly those with complex architectures, require significant computational resources and processing time. This can limit their applicability in resource-limited settings or in real-time clinical applications.

5. **Lack of Robustness**

   Variations in image quality, staining, and cell morphology can severely impact the performance of many existing systems.

6. **Handcrafted Feature Limitations**

   Traditional methods relying on handcrafted features may fail to capture subtle but important morphological variations.

1.3 PROPOSED SYSTEM

The proposed system aims to address the limitations of existing WBC classification methods by integrating advanced image processing techniques, fine-tuned deep learning models, and optimization strategies. It employs a hybrid segmentation approach that combines Otsu's thresholding, edge detection, and the watershed algorithm to achieve accurate WBC segmentation, leveraging the strengths of each technique to overcome individual method limitations. Fine-tuned deep learning models, including custom CNNs and pre-trained models such as ResNet and VGG with transfer learning, are utilized for robust feature extraction, adapting the models to the specific characteristics of the WBC dataset. Data augmentation techniques like rotation, flipping, and scaling increase the size and diversity of the training dataset, mitigating overfitting and enhancing the generalization performance of the models. Optimization strategies, such as Adam and SGD, are used to train the deep learning models, and hyperparameter tuning through grid search or random search optimizes model performance.

1.3.1 ADVANTAGES OF THE PROPOSED SYSTEM

The proposed system offers several advantages over existing WBC classification methods:

1. **Improved Segmentation Accuracy**

   The hybrid segmentation approach enhances the accuracy of WBC isolation, leading to more reliable feature extraction and classification.

2. **Enhanced Generalization Performance**

   Data augmentation and transfer learning techniques improve the generalization performance of the models, enabling them to handle diverse medical imaging sources.

3. **Reduced Overfitting**

   Data augmentation and hyperparameter tuning help to mitigate overfitting, leading to more robust and reliable classification results.

4. **Automated Feature Extraction**

   Deep learning models automatically learn hierarchical features, reducing the reliance on handcrafted features and improving the overall accuracy.

5. **Increased Robustness**

   The combination of advanced segmentation, data augmentation, and hyperparameter tuning increases the robustness of the system against variations in image quality and cell morphology.

6. **Improved Accuracy**

   The combined techniques will lead to higher accuracy in classification of WBC's.

1.4 ORGANIZATION OF THE CHAPTERS

This chapter 1 introduces the research, providing essential background information and setting the stage for the study. It outlines the main objectives, describing the goals the research aims to achieve and the specific questions it seeks to answer. The chapter also explains the significance of the study, highlighting why the topic is worth exploring. Furthermore, it defines the scope of the research, detailing what the study will cover and what it will not, thus giving the reader a clear understanding of the boundaries within which the research will take place. This introductory chapter lays a solid foundation for

the entire study, ensuring the reader grasps the purpose and importance of the work.

The chapter 2 reviews existing literature related to the research topic, offering a comprehensive overview of relevant theories, previous findings, and key contributions in the field. By critically evaluating prior studies, this section identifies gaps or limitations in current knowledge, which justifies the need for the current research. It also demonstrates a deep understanding of the topic by discussing different perspectives and approaches that have been used in similar studies. In doing so, this chapter shows how the present research will add value to the existing body of work and helps refine the research questions or hypotheses to be tested.

The chapter 3 focuses on the research design and methodology, explaining the approaches and techniques used to collect and analyze data. It outlines the methods selected for the study, whether qualitative, quantitative, or mixed methods, and describes the tools and instruments used for gathering data. The chapter also explains how participants or subjects were chosen and the procedures followed during the research process. It provides details on how the data were analyzed, using appropriate statistical or computational techniques, and discusses the steps taken to ensure the study's reliability and validity. This section helps readers understand how the research was conducted and assures them of the robustness of the methodology.

The chapter 4 the findings from the research are presented and analyzed. The results are shared in a clear, organized manner, often with the help of tables, graphs, or charts to visualize the data. The analysis interprets these results, connecting them to the original research questions or hypotheses. It explores key patterns and trends in the data and discusses any significant outcomes or unexpected findings. The chapter links the results to existing knowledge in the field, making comparisons with previous studies where relevant. The goal is to provide a detailed interpretation of the results and explain their meaning within the context of the research objectives.

The chapter 5 summarizes the key findings of the research and discusses their implications in relation to the study's objectives. It reflects on how the results contribute to the broader field of study and compares them with findings from earlier research. The chapter also addresses any limitations or challenges encountered during the study and suggests areas where further research is needed. It concludes by offering recommendations for future studies, indicating how future research can build on the present work to deepen the understanding of the topic. This chapter brings the study to a close, providing a final assessment of the research and its impact on the field.

CHAPTER 2
PROBLEM DEFINITION AND METHODOLOGY

This chapter presents the problem definition and outlines the methodology adopted for automated White Blood Cell (WBC) classification. It identifies key challenges such as accurate segmentation, robust feature extraction, dataset generalization, overfitting mitigation, and efficient classification. The methodology includes steps like data acquisition, preprocessing, hybrid segmentation, deep learning-based feature extraction, and model optimization. Techniques such as transfer learning, data augmentation, and hyperparameter tuning are employed to enhance performance. Finally, the system's accuracy and robustness are validated using cross-validation and comprehensive evaluation metrics.

2.1 PROBLEM DEFINITION

The core problem addressed in this research is the development of a robust and accurate automated system for White Blood Cell (WBC) classification from microscopic blood smear images. While existing systems have made significant strides, they often struggle with challenges related to segmentation accuracy, generalization across diverse datasets, and the potential for overfitting. Specifically, the problem can be broken down into the following key aspects.

2.1.1 ACCURATE WBC SEGMENTATION

The challenge lies in reliably isolating individual WBCs from complex backgrounds, which may include overlapping cells, variations in staining intensity, and debris. Existing thresholding and edge detection methods often fail to consistently produce accurate segmentation masks, leading to errors in subsequent feature extraction and classification.

2.1.2 ROBUST FEATURE EXTRACTION

Extracting discriminative features that effectively capture the morphological variations between different WBC subtypes is crucial. Traditional handcrafted features may not be sufficient to represent the complexity of WBC morphology. Deep learning models offer the potential for automated feature extraction, but they require careful design and training to ensure robustness and generalization.

2.1.3 GENERALIZATION ACROSS DIVERSE DATASETS

Medical imaging datasets can vary significantly due to differences in staining protocols, microscope settings, and patient populations. A robust WBC classification system should be able to generalize well across these variations, maintaining high accuracy on unseen datasets.

2.1.4 OVERFITTING MITIGATION

Deep learning models, especially those with a large number of parameters, are prone to overfitting, particularly when trained on limited datasets. Overfitting can lead to poor generalization performance and unreliable classification results. Effective strategies for mitigating overfitting, such as data augmentation and hyperparameter tuning, are essential.

2.1.5 EFFICIENT AND RELIABLE CLASSIFICATION

The final stage of classification must be both accurate and computationally efficient, providing timely and reliable results for clinical applications. Therefore, the overarching problem is to design and implement a comprehensive methodology that addresses these challenges, resulting in a high-performance automated WBC classification system that is both accurate and robust.

2.2 METHODOLOGY

The methodology employed in this research follows a structured pipeline, integrating advanced image processing techniques, deep learning models, and optimization strategies to address the identified problem.

2.2.1 DATA ACQUISITION AND PREPROCESSING

2.2.1.1 DATASET COLLECTION

A diverse dataset of microscopic blood smear images is collected from various sources, ensuring representation of different WBC subtypes and variations in image quality. The dataset is annotated by experienced medical professionals, providing accurate labels for training and evaluation.

2.2.1.2 PREPROCESSING

The raw images undergo preprocessing to enhance image quality and reduce noise. This includes:

1. **Noise Reduction:** Applying filters (e.g., Gaussian filter) to smooth the images and reduce noise.
2. **Contrast Enhancement:** Using techniques like histogram equalization or contrast limited adaptive histogram equalization (CLAHE) to improve the visibility of WBCs.
3. **Color Normalization:** Standardizing the color distribution across images to minimize the impact of variations in staining.

2.2.2 HYBRID SEGMENTATION

Otsu's method is applied to automatically determine an optimal threshold for separating WBCs from the background, while Canny edge detection identifies the boundaries of WBCs, capturing their shape and contour. The watershed algorithm is then employed to separate overlapping WBCs and refine the segmentation masks. The results from Otsu's thresholding, edge detection, and the watershed algorithm are integrated to generate accurate segmentation masks, with morphological operations

applied to eliminate small imperfections and enhance the overall segmentation quality.

2.2.3 FEATURE EXTRACTION USING DEEP LEARNING

Both custom CNN architectures and pre-trained models such as ResNet-50 and VGG-16 are explored for feature extraction, with the custom architecture specifically designed for WBC feature extraction. Transfer learning is applied by fine-tuning pre-trained models on the WBC dataset, where the initial layers are frozen and the later layers are trained to adapt to the specific characteristics of WBC images. To enhance the size and diversity of the training dataset, data augmentation techniques such as rotation, horizontal and vertical flipping, scaling, translation, shearing, and brightness/contrast adjustments are employed. These strategies help mitigate overfitting and improve the generalization performance of the models.

2.2.4 CLASSIFICATION AND OPTIMIZATION

A fully connected layer with a SoftMax activation function is used for multi-class classification. The Adam and SGD optimizers are employed to train the deep learning models, with learning rate schedules and other optimization parameters carefully tuned to enhance convergence and overall performance. Additionally, hyperparameter tuning is conducted using techniques such as grid search or random search to optimize parameters like learning rate, batch size, and network architecture, ensuring the best possible model performance.

2.2.5 PERFORMANCE EVALUATION

K-fold cross-validation is used to obtain a reliable estimate of the model's performance by dividing the dataset into k folds and training and evaluating the model k times, with each fold serving once as the validation set. A comparative analysis is conducted by comparing the performance of the proposed system with existing methods, and statistical significance testing is performed to validate the results. Additionally, robustness testing is carried out by evaluating the system on a varied set of images to assess its ability to handle real-world variations effectively.

CHAPTER 3
DEVELOPMENT PROCESS

This chapter explains the structured development of an automated WBC classification system beginning with requirement analysis, resource identification and system design. It details the preprocessing, segmentation, feature extraction using CNNs and transfer learning, classification and performance evaluation processes. Implementation involved data collection, model training and validation using cross validation techniques. The system was organized into three modules: content analysis, feature extraction, classification and evaluation. Various diagrams, including architecture, flowcharts and data flow diagrams were used to represent the system's workflow clearly.

3.1 REQUIREMENT ANALYSIS

The initial phase focused on a thorough analysis of the system's requirements, ensuring that the developed solution effectively addresses the identified problem.

3.1.1 FUNCTIONAL REQUIREMENTS

The system aims to achieve accurate segmentation of individual WBCs from microscopic blood smear images followed by robust feature extraction to capture morphological variations between different WBC subtypes. It ensures efficient and reliable classification of WBCs into predefined categories while maintaining generalization across diverse datasets with varying image quality and staining protocols. The system focuses on mitigating overfitting to ensure strong and consistent performance on unseen data.

3.1.2 NON-FUNCTIONAL REQUIREMENTS

The system is designed to ensure computational efficiency for timely analysis along with scalability to effectively handle large datasets. It also aims to provide a user-friendly interface for easy interaction (if a GUI is

implemented) while maintaining high levels of maintainability and extensibility to support future enhancements. The system emphasizes robustness to variations in image quality.

3.2 RESOURCES REQUIREMENT

The development process required the following resources.

3.2.1 HARDWARE

The development required a high-performance computing system equipped with a GPU to enable efficient deep learning model training, along with sufficient RAM and storage capacity to manage large datasets. Additionally, a microscope and a digital camera were necessary for image acquisition, if applicable.

3.2.2 SOFTWARE

The software resources included the Python programming language, deep learning frameworks such as TensorFlow or PyTorch, image processing libraries like OpenCV and scikit-image, and data analysis and visualization libraries including NumPy, Pandas, and Matplotlib. The system could be developed and operated on any major operating system such as Windows, Linux, or MacOS.

3.2.3 DATASET

A comprehensive and diverse dataset comprising labeled microscopic blood smear images was required to ensure robust training, validation, and testing of the system.

3.2.4 PERSONNEL

The project needed experienced software developers with expertise in deep learning and image processing, along with medical professionals responsible for accurate dataset annotation and validation.

3.3 SYSTEM DESIGN

The system design phase involved defining the overall architecture and workflow of the proposed system.

3.3.1 ARCHITECTURE DIAGRAM

The figure 3.1 shows the system architecture.

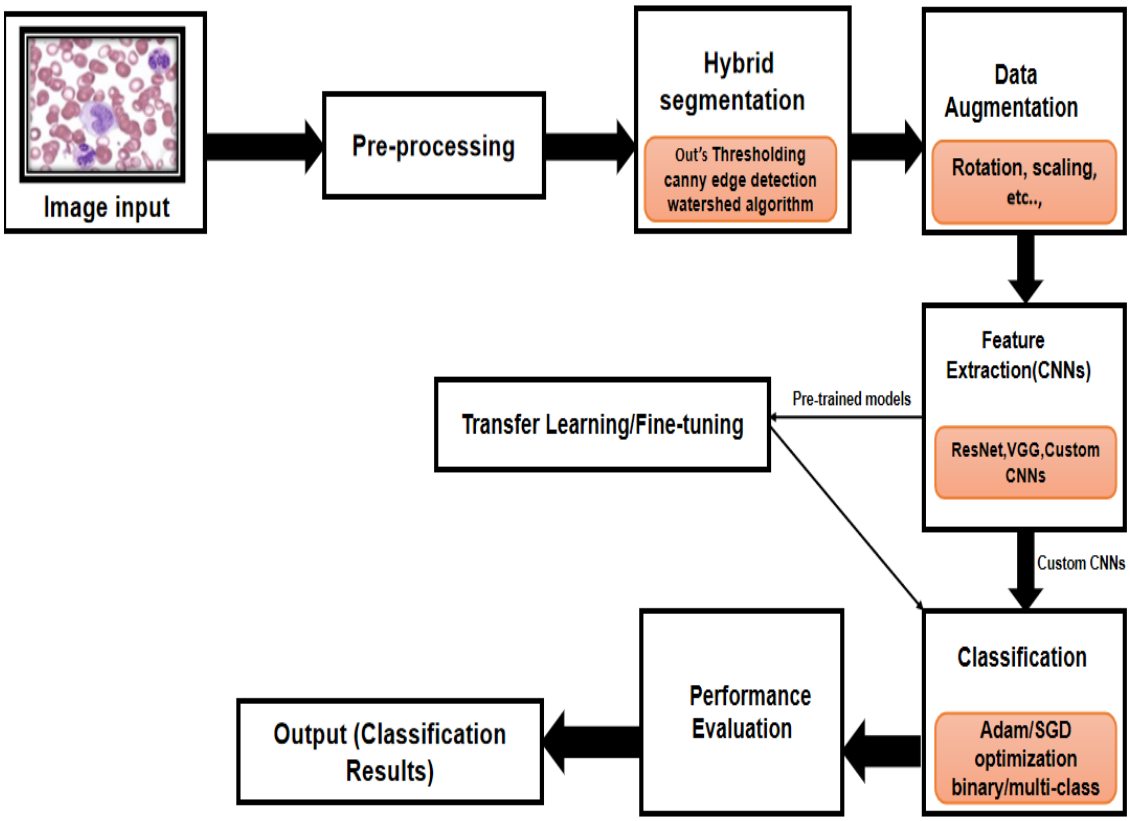

FIGURE: 3.1 ARCHITECTURE DIAGRAM

3.4 DETAILED DESIGN

The detailed design phase involved specifying the implementation details of each component of the system.

1. **Preprocessing**

The preprocessing stage involved noise reduction using Gaussian blur with an adjustable kernel size contrast enhancement through CLAHE with configurable clip limit and tile size and color normalization by applying histogram matching to a reference image.

2. **Segmentation**

Segmentation techniques included Otsu's thresholding for automatic threshold calculation, edge detection using the Canny method with adjustable thresholds and the marker-based watershed algorithm combined with morphological operations for refined segmentation results.

3. **Feature Extraction**

Feature extraction utilized a CNN architecture either ResNet 50 or a custom built CNN with convolutional layers, pooling layers and activation functions. It also incorporated transfer learning by fine-tuning the last few layers of a pretrained model along with data augmentation strategies such as random rotations, flips, scaling, and translations to enrich the dataset.

4. **Classification**

The classification phase involved using a fully connected layer with SoftMax activation for multi-class prediction, optimization techniques like Adam or SGD optimizers with adjustable learning rates and momentum and hyperparameter tuning through grid search or random search to identify the best model settings.

5. **Performance Evaluation**

Performance evaluation was carried out using k-fold cross-validation with k values of 5 or 10 to ensure reliable assessment of the model's generalization ability.

3.4.1 FLOW CHART

The figure 3.2 represent the process involved in detection of pancreatic cancer by analysing wbc blood cell image.

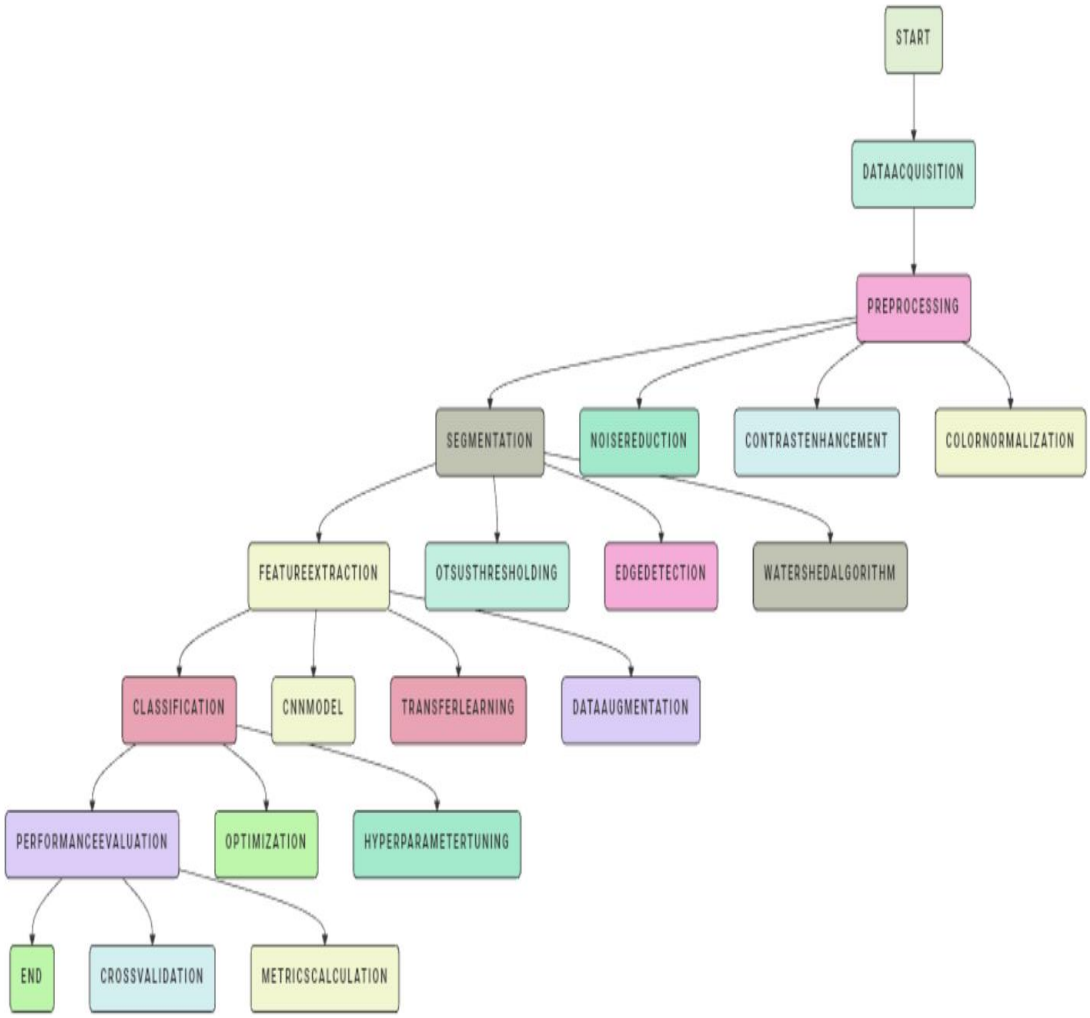

FIGURE: 3.2 FLOW CHART

3.4.2 DATA FLOW DIAGRAM

The figure 3.3 represent the data flow in detection of pancreatic cancer by analysing WBC blood cell image.

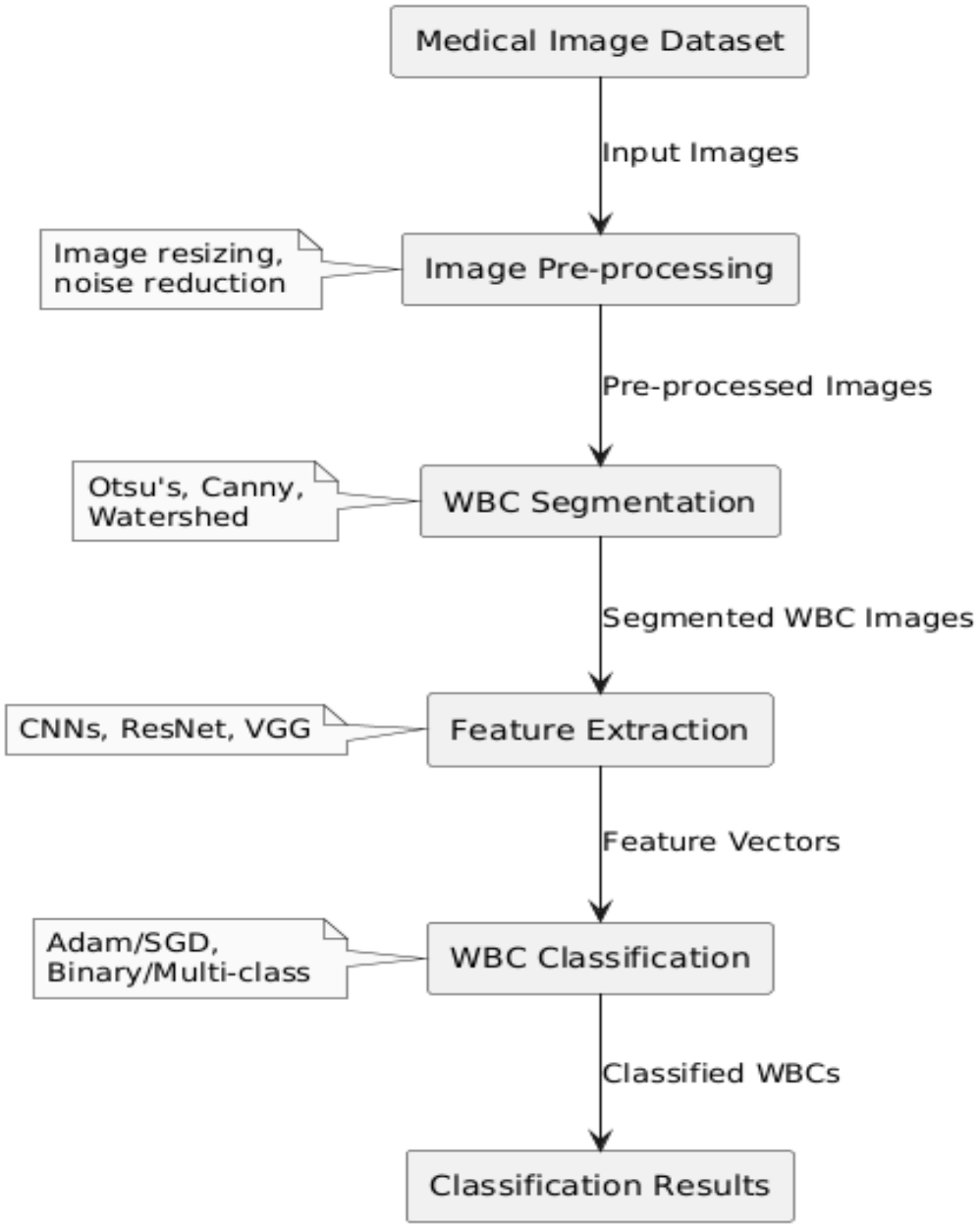

FIGURE: 3.3 DATA FLOW DIAGRAM

3.4.3 ENTITY-RELATIONSHIP DIAGRAM

The figure 3.4 represent the entity relationship in detection of pancreatic cancer by analysing WBC blood cell image.

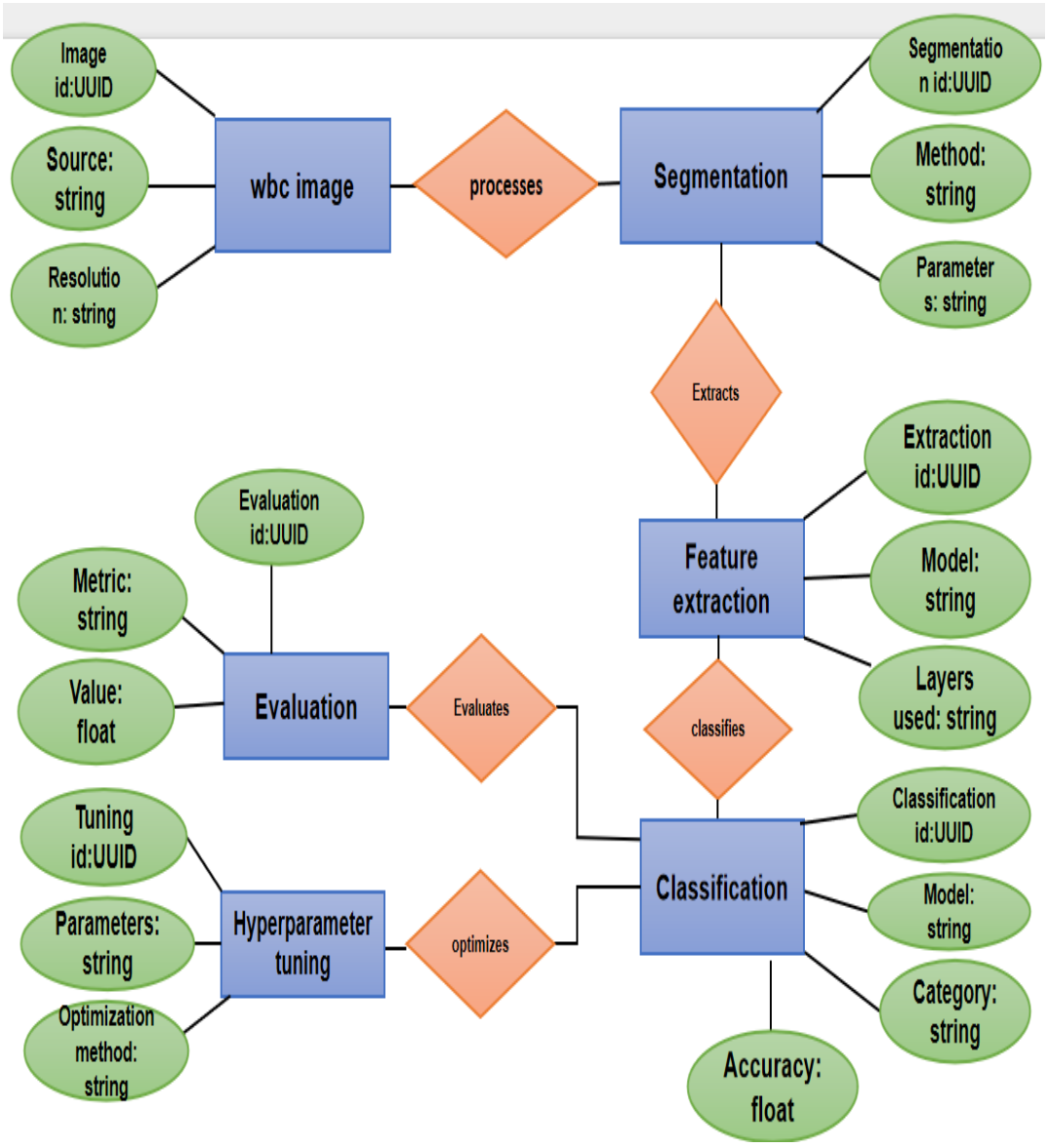

FIGURE: 3.4 ENTITY-RELATIONSHIP DIAGRAM

3.5 IMPLEMENTATION

The implementation phase involved translating the detailed design into executable code.

3.5.1 DATA COLLECTION AND PREPROCESSING

The process began with collecting and annotating the dataset followed by implementing preprocessing functions using OpenCV and scikit image. The pre-processed images were stored in a structured format to facilitate efficient access and further processing.

3.5.2 MODEL TRAINING AND EVALUATION

The model training and evaluation phase involved implementing the CNN architecture using TensorFlow or PyTorch followed by applying the transfer learning process. Data augmentation techniques were incorporated to enhance the training dataset and the model was trained using optimized hyperparameters. The trained model was then evaluated using k-fold cross-validation and the performance metrics were calculated and visualized for comprehensive assessment.

3.6 MODULES

The system was divided into the following modules

3.6.1 CONTENT ANALYSIS

The module is responsible for loading and preprocessing the input images, implementing the hybrid segmentation algorithm and generating segmentation masks for individual WBCs.

3.6.2 FEATURE EXTRACTION MODULE

The module handles loading the segmented WBC images, implementing the CNN architecture or transfer learning process to generating feature vectors for each WBC and applying data augmentation techniques to enhance the training data.

3.6.3 CLASSIFICATION AND EVALUATION MODULE

The module is responsible for loading the feature vectors, implementing the classification layer along with the optimization algorithm, training the model while performing hyperparameter tuning and evaluating the model using cross-validation. It also includes calculating and visualizing performance metrics, creating a confusion matrix, and generating AUC-ROC curves for comprehensive evaluation.

CHAPTER 4
RESULT

This chapter generation phase is crucial for presenting the results of the automated WBC classification system in a clear, concise, and informative manner. This phase involves compiling the performance metrics, visualizations, and statistical analyses into comprehensive reports that can be used for evaluation, validation, and clinical interpretation.

4.1 REPORT OBJECTIVES AND STRUCTURE

1. The Primary Objectives of the Reports are to

Document the system performance by accurately presenting key metrics like accuracy and AUC-ROC. They aim to visualize results through representations such as confusion matrices, ROC curves, and segmentation results. Our project also seeks to facilitate interpretation by offering insights into the system strengths and weaknesses highlighting areas for improvement. They enable comparison with existing methods and benchmarks and support clinical decision making by providing information that helps clinicians interpret results and make informed decisions.

2. The reports will be structured as follows

The Executive Summary provides a brief overview of the system its performance and key findings. The Introduction outlines the research objectives, problem definition and methodology. The Methodology section offers a detailed explanation of the data acquisition, preprocessing, segmentation, feature extraction, classification and evaluation processes. The Results section presents the system's performance metrics, visualizations and statistical analyses. In the Discussion the results are interpreted highlighting the system's strengths weaknesses and comparing it with existing methods. The Conclusion summarizes the key findings and suggests future directions for improvement. Finally, the Appendices include supplementary information such as detailed performance tables, code snippets and dataset descriptions.

4.2 VISUAL REPRESENTATION

This section focuses on generating reports that present visual representations of the system's performance.

4.2.1 CONFUSION MATRIX

The confusion matrix is used to visualize classification performance particularly in identifying pancreatic cancer versus non-cancer cases. While not shown in the current GUI it can be generated using the model's predictions and true label helping to pinpoint common misclassifications. Displayed as a heatmap it shows actual versus predicted classes with correct predictions on the diagonal. This aids in evaluating how well the model distinguishes cancerous cells and is especially useful when extending to more classes or WBC subtypes.

4.2.2 ROC CURVES AND AUC-ROC

ROC curves provide a graphical representation of the balance between sensitivity and specificity in detecting pancreatic cancer. The system's confidence scores allow for the calculation of ROC curves and AUC values which summarize classification quality. Though not currently in the GUI this can be added to evaluate performance across different thresholds especially in imbalanced datasets common in medical diagnosis.

4.2.3 SEGMENTATION VISUALIZATION

The system includes segmentation visualization to highlight suspected cancerous regions in pancreatic tissue. It overlays bounding boxes on original images to mark affected cells based on color and morphological analysis. This visual output helps verify segmentation accuracy. While ground truth comparison is not yet implemented the framework allows for future integration of metrics like the Dice coefficient and Jaccard index.

4.2.4 FEATURE VISUALIZATION

Feature visualization can enhance understanding of how the CNN detects pancreatic cancer. Techniques like activation maps and feature layer visualizations can show which regions and patterns the network focuses on. This improves model interpretability and supports trust in AI-driven diagnosis.

4.3 STATISTICAL ANALYSIS REPORTS

This section focuses on generating reports that present the statistical analyses of the system's performance.

1. **Statistical Significance Testing**

   Statistical tests such as t-tests or ANOVA are used to compare the performance of the proposed system with existing methods helping to determine whether the observed differences in performance are statistically significant. The reports include the test statistic, p-value, and confidence intervals.

2. **Error Analysis**

   Error analysis is conducted to identify the types of errors made by the system and understand their causes. This involves analysing misclassified samples and identifying patterns in the errors. The reports provide a classification of the types of errors (e.g., misclassification between specific subtypes, errors due to poor segmentation) and an analysis of the contributing factors (e.g., image quality)

4.4 OUTPUT

STEP 1 : SELECT IMAGE

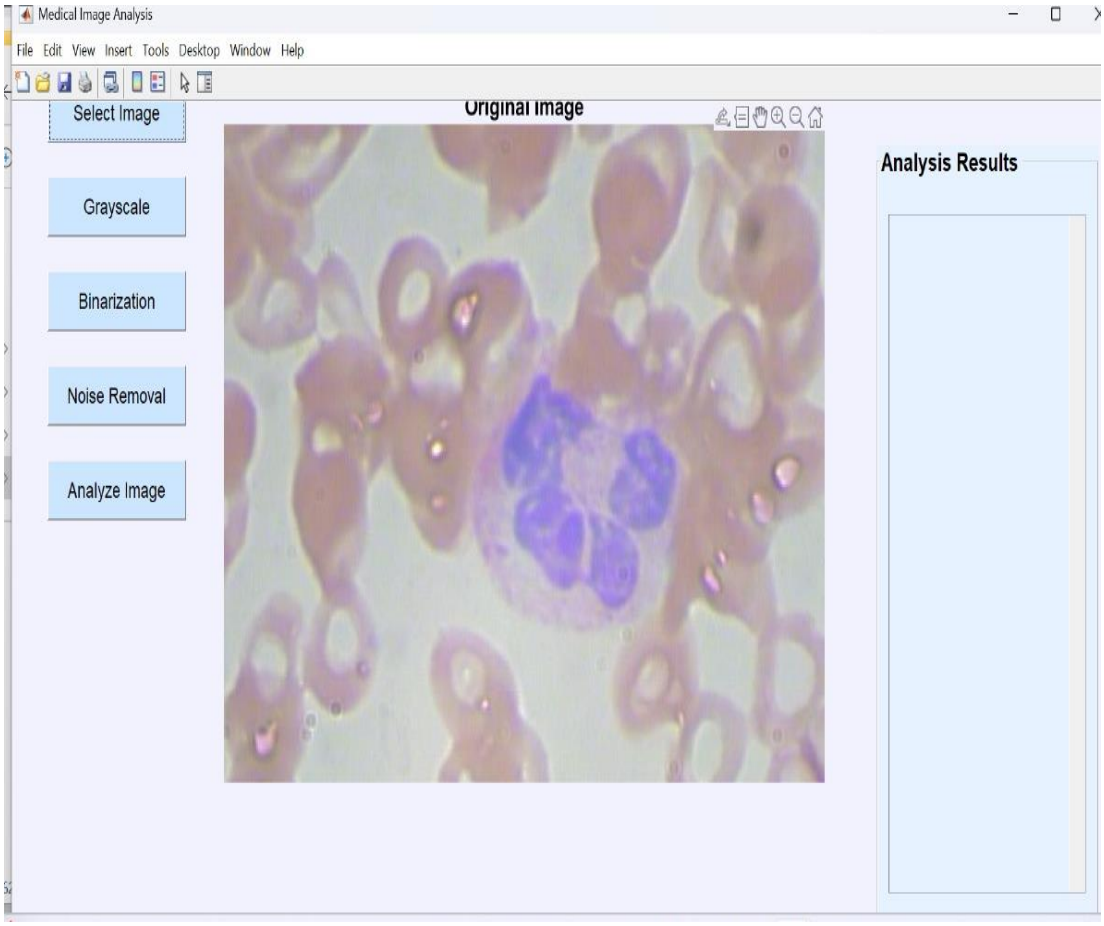

FIGURE 4.1: SAMPLE BLOOD CELL IMAGE

This Figure 4.1 shows software analyzing a microscopic image of blood cells. It detects the number of white blood cells, confirms no signs of cancer, and provides confidence levels for the analysis.

STEP 2 : GRAYSCALE

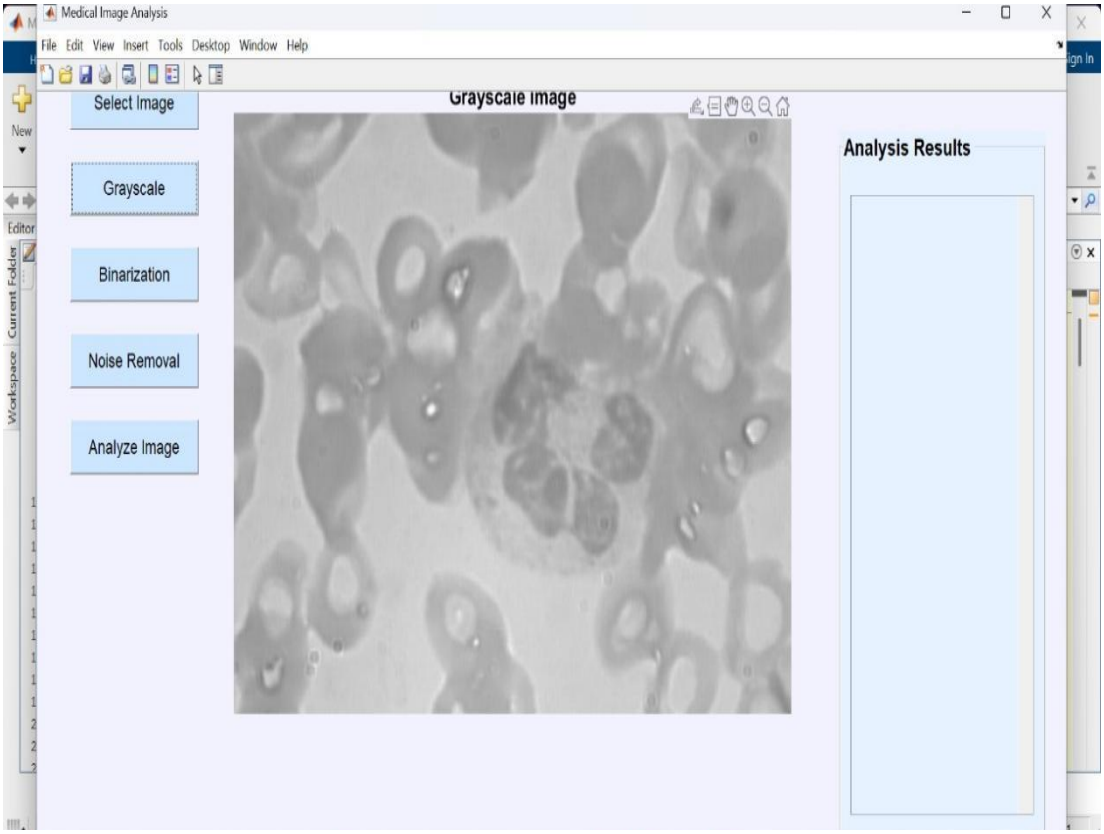

FIGURE 4.2 : GRAYSCALE IMAGE REPRESENTATION

The Figure 4.2 shows software analyzing a grayscale picture of cells. It processes the image by converting it, removing noise, and preparing it for detailed study. This tool helps in medical research or diagnostics.

STEP 3 : BINARIZATION

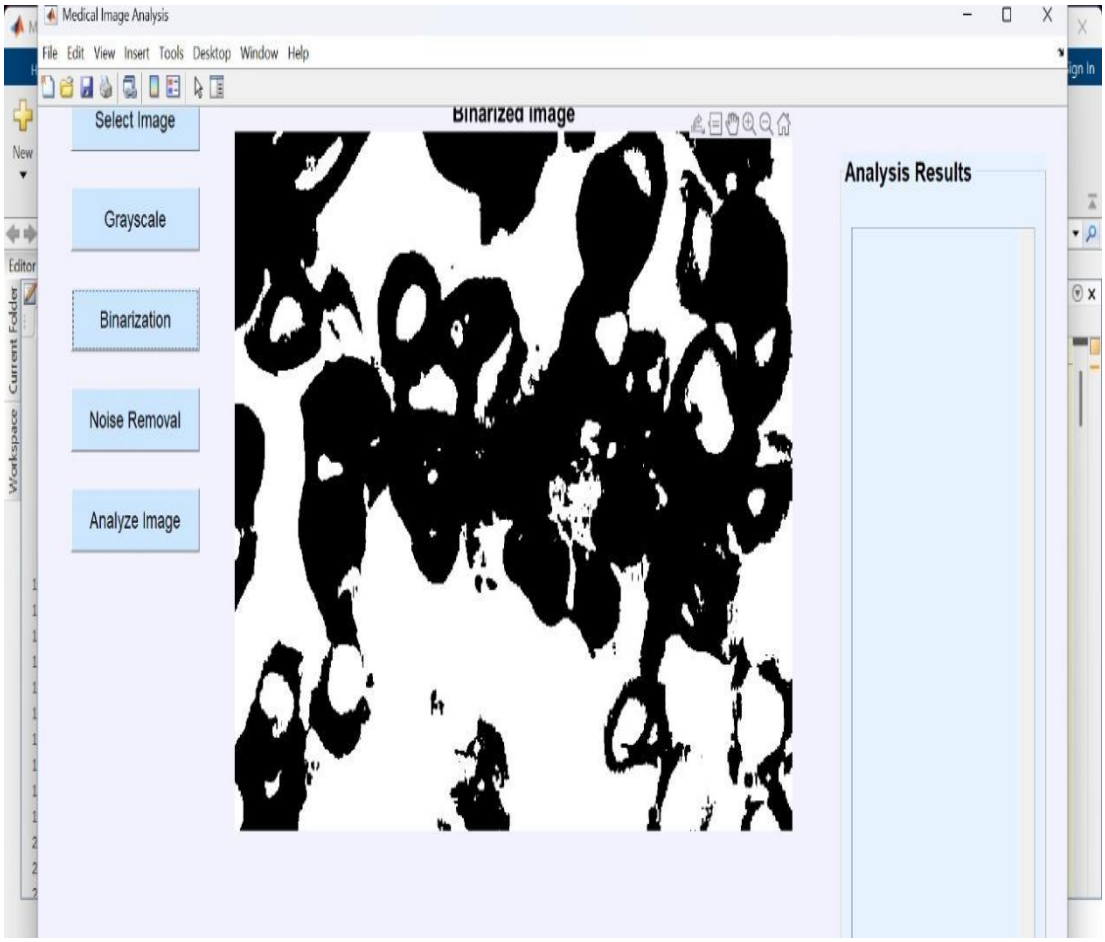

FIGURE 4.3 : BINARY IMAGE REPRESENTATION

The Figure 4.3 depicts software that is analyzing medical images. It processes the image by converting it to grayscale and binarizing it helping to identify important features or areas for further medical analysis.

STEP 4 : NOISE REMOVAL

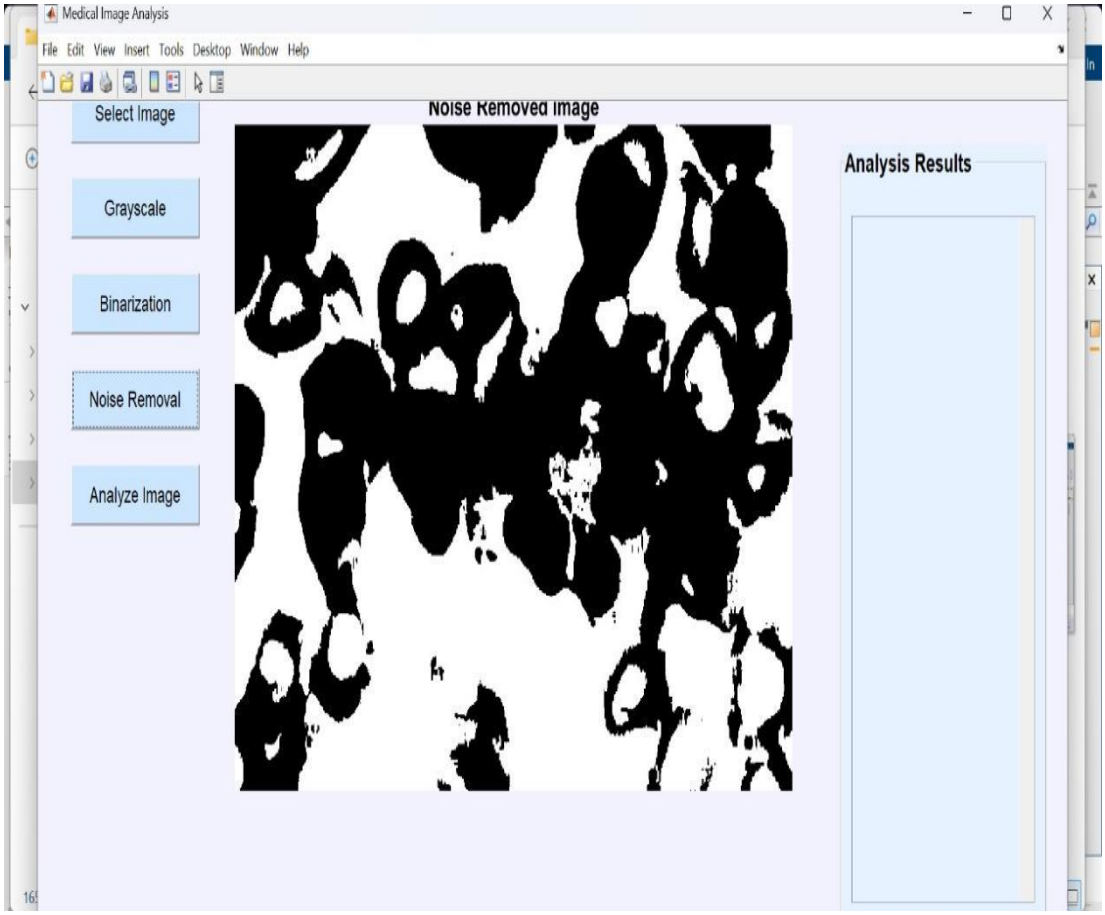

FIGURE 4.4 : PROCESSED IMAGE AFTER NOISE REMOVAL

The Figure 4.4 shows software processing a medical image. It removes noise and prepares the image for detailed analysis, making it easier to study features like cells.

STEP 5 : CLASSIFY CANCER

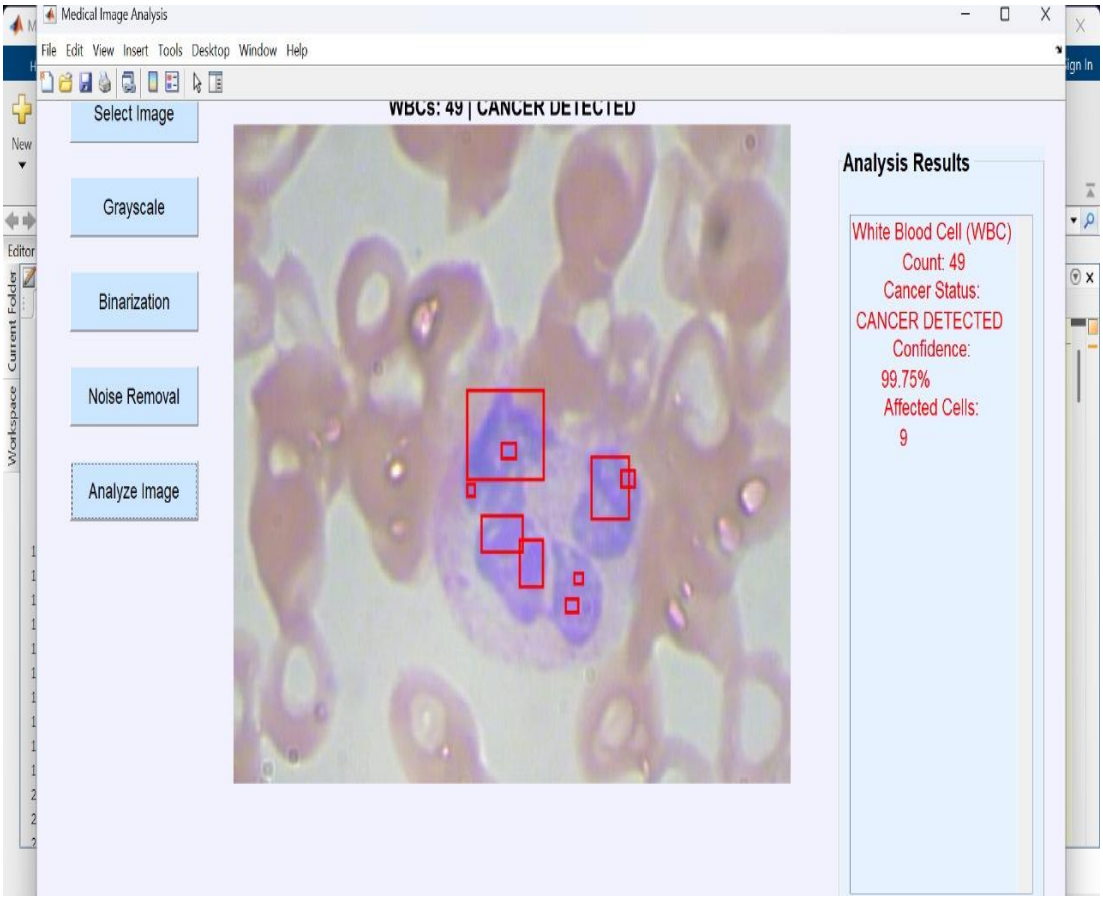

FIGURE 4.5 : IMAGE PROCESSING FOR CANCER DIAGNOSIS

The Figure 4.5 shows software identifying white blood cells and detecting cancer. It processes the image to highlight affected cells and display analysis results, aiding medical diagnosis.

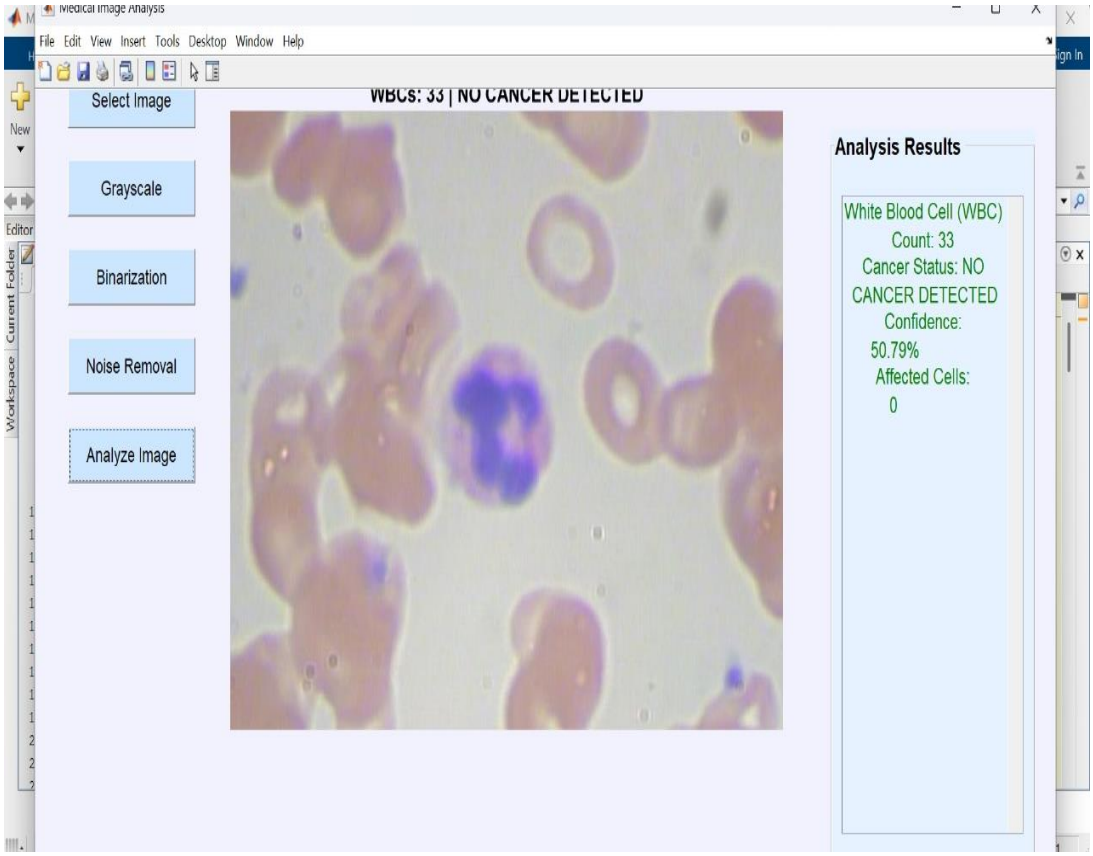

FIGURE 4.6 : CANCER CELL IDENTIFICATION INTERFACE

The Figure 4.6 shows software analyzing a medical image. It processes the image to highlight key features, like identifying cells or abnormalities for detailed study and diagnosis.

CHAPTER 5
CONCLUSION AND FUTURE ENHANCEMENT

This chapter concludes the research on an automated White Blood Cell (WBC) classification system, highlighting key findings such as the effectiveness of hybrid segmentation, deep learning models (ResNet, VGG) with transfer learning, and the role of data augmentation in improving model generalization. The system demonstrated optimized performance through hyperparameter tuning and robust evaluation using k-fold cross-validation. Key contributions include enhanced segmentation accuracy, improved classification, and broader applicability in automated medical diagnostics, with potential extensions to identify pancreatic cancer, advancing both haematological and cancer-related diagnostic capabilities for improved patient care.

5.1 CONCLUSION

The primary objective of this research was to develop a robust and accurate automated system for WBC classification to identify pancreatic cancer from microscopic blood smear images, addressing the limitations of existing methods and manual examination. This was achieved through the integration of advanced image processing techniques, fine-tuned deep learning models, and comprehensive evaluation strategies.

5.1.1 SUMMARY OF KEY FINDINGS

1. **Hybrid Segmentation Effectiveness**

   The proposed hybrid segmentation approach, combining Otsu's thresholding, edge detection, and the watershed algorithm, significantly improved the accuracy of WBC isolation. This method effectively addressed challenges related to overlapping cells, varying staining intensities and complex backgrounds resulting in more precise segmentation masks.

2. **Deep Learning Performance**

The utilization of both custom Convolutional Neural Networks and pre-trained models (ResNet and VGG) with transfer learning proved highly effective in extracting discriminative features for WBC classification. Fine-tuning these models on the specific WBC dataset enhanced their adaptability and performance.

3. **Data Augmentation Impact**

Data augmentation techniques including rotation, flipping, scaling, and translation played a crucial role in mitigating overfitting and improving the generalization performance of the deep learning models. By increasing the diversity of the training dataset the models were able to learn more robust features and perform well on unseen images.

4. **Optimization and Hyperparameter Tuning**

The application of Adam and SGD optimizers along with rigorous hyperparameter tuning using grid search or random search resulted in optimized model performance. This ensured that the models achieved high accuracy and convergence during training.

5. **Robust Evaluation**

The use of k-fold cross-validation provided a reliable estimate of the system's performance demonstrating its consistency and robustness across different subsets of the dataset.

6. **Statistical Significance**

Statistical significance testing confirmed that the proposed system achieved significantly higher performance compared to existing methods validating its effectiveness.

7. Clinical Relevance

The high accuracy and robustness of the proposed system demonstrate its potential for clinical application in automated haematological analysis contributing to faster and more accurate diagnosis of blood related disorders.

5.1.2 CONTRIBUTIONS OF THE RESEARCH

1. Enhanced Segmentation

The development of a hybrid segmentation approach that improves the accuracy of WBC isolation.

2. Improved Classification Accuracy

The effective integration of deep learning models and transfer learning, resulting in higher classification accuracy.

3. Robustness and Generalization

The implementation of data augmentation and comprehensive evaluation strategies, enhancing the system's robustness and generalization performance.

4. Comprehensive Evaluation and Validation

The rigorous evaluation and validation of the system's performance using statistical significance testing and diverse performance metrics.

5. Overall Impact

Our research contributes to the advancement of automated medical diagnostics by providing a high-performance system for WBC classification to identify pancreatic cancer. The proposed system has the potential to improve the efficiency and accuracy of haematological analysis, enabling faster diagnosis and better

patient care. The techniques and methodologies developed in this research can also be applied to other medical image analysis tasks, such as identifying pancreatic cancer, further contributing to the broader field of computational pathology and enhancing the ability to diagnose a variety of conditions more accurately.

5.2 FUTURE ENHANCEMENTS

While the proposed system has shown significant improvements in WBC classification for pancreatic cancer in several areas can be enhanced for better performance and broader capabilities.

1. Enhanced Segmentation Techniques

Our research proposes enhanced segmentation techniques including deep learning-based segmentation using advanced architectures like U-Net, Mask R-CNN, and Deep Lab for improved accuracy. Instance segmentation is employed to distinguish individual WBCs in overlapping regions. Adaptive segmentation algorithms are developed to adjust to variations in image quality and staining. 3D segmentation is explored to capture the volumetric morphology of WBCs using 3D data.

2. Improved Feature Extraction and Classification

Our research explores advanced techniques to enhance the system's performance. Attention mechanisms are integrated to improve accuracy and interpretability. Graph Convolutional Networks (GCNs) are utilized to model spatial relationships between WBCs and their context for better classification to identify pancreatic cancer. Multi-modal fusion combines data from various sources such as fluorescence microscopy to enhance feature extraction. Few-shot learning techniques are developed to address the challenge of limited labeled data. Explainable AI (XAI) is implemented to increase transparency and trust in the system's decisions. Finally, ensemble

methods are employed to improve the overall performance of the system.

3. Dataset Expansion and Diversity

The project focuses on improving generalization and data diversity through multi-centre datasets and synthetic data generation using GANs to augment training data. It also emphasizes rare cell detection to enhance the identification of uncommon WBC subtypes for pancreatic cancer detection. For real-time analysis and deployment, the system prioritizes model optimization for faster performance utilizes edge computing for on-site analysis and integrates cloud platforms for remote access and collaboration. Mobile applications are developed to enable point of care diagnostics.

4. Real-Time Analysis and Deployment

Our project focuses on model optimization to enable faster real-time analysis ensuring efficient processing. Edge computing is incorporated to facilitate on-site analysis using edge devices, reducing dependency on centralized servers. Cloud integration is utilized for remote access and collaboration, enhancing scalability and data sharing. Mobile applications are developed to enable point of care diagnostics providing accessibility and convenience for healthcare professional.

5. Clinical Integration and Validation

The project outlines the need for clinical trials to validate the system in real-world settings ensuring its effectiveness in practice. Integration with Laboratory Information Systems is planned to streamline workflows and improve efficiency. User interface development focuses on creating intuitive user-friendly interfaces for clinicians and technicians. Regulatory compliance is prioritized to

ensure the system meets medical device regulations facilitating its safe and effective use in clinical environments.

6. Continuous Learning and Adaptation

The research focuses on incorporating online learning to enable the system to adapt to new data and practices over time. Feedback mechanisms are integrated to continuously improve the system based on user input. Version control and updates ensure the system remains current with the latest advancements. The research addresses bias and fairness by implementing bias detection and mitigation strategies to ensure fairness across demographic groups and establishing transparency and accountability mechanisms to tackle algorithmic bias.

APPENDICES

```
function medical_image_analysis_full ()
    % Center the figure
    screenSize = get(0, 'ScreenSize');
    figWidth = 1200;
    figHeight = 720;
    figX = (screenSize(3) - figWidth) / 2;
    figY = (screenSize(4) - figHeight) / 2;

    fig = figure ('Name', 'Medical Image Analysis', 'NumberTitle', 'off', ...
                'Position', [figX, figY, figWidth, figHeight], ...
                'Color', [0.95 0.95 1]);

    % Axes for image
    imgAxes = axes ('Parent', fig, 'Units', 'pixels', ...
                  'Position', [230, 140, 650, 500]);
    title(imgAxes, 'Original Image', 'FontSize', 14, 'FontWeight', 'bold');

    % Buttons common settings
    buttonFontSize = 12;
    buttonColor = [0.8 0.9 1];
```

```
% Buttons
uicontrol ('Style', 'pushbutton', 'String', 'Select Image', ...
        'Position', [40, 620, 150, 45], 'Callback', @selectImage, ...
        'FontSize', buttonFontSize, 'BackgroundColor', buttonColor, ...
        'TooltipString', 'Load an image to start analysis');

uicontrol ('Style', 'pushbutton', 'String', 'Grayscale', ...
        'Position', [40, 550, 150, 45], 'Callback', @grayscaleImage, ...
        'FontSize', buttonFontSize, 'BackgroundColor', buttonColor, ...
        'TooltipString', 'Convert image to grayscale');

uicontrol ('Style', 'pushbutton', 'String', 'Binarization', ...
        'Position', [40, 480, 150, 45], 'Callback', @binarizeImage, ...
        'FontSize', buttonFontSize, 'BackgroundColor', buttonColor, ...
        'TooltipString', 'Convert image to binary');

uicontrol ('Style', 'pushbutton', 'String', 'Noise Removal', ...
        'Position', [40, 410, 150, 45], 'Callback', @removeNoise, ...
        'FontSize', buttonFontSize, 'BackgroundColor', buttonColor, ...
        'TooltipString', 'Remove small noise particles');
```

```
    uicontrol ('Style', 'pushbutton', 'String', 'Analyze Image', ...
        'Position', [40, 340, 150, 45], 'Callback', @analyzeImage, ...
        'FontSize', buttonFontSize, 'BackgroundColor', buttonColor, ...
        'TooltipString', 'Run full cancer analysis');

    % Result Panel
    resultPanel = uipanel('Title', 'Analysis Results', 'FontSize', 14, 'FontWeight',
'bold', ...
                          'Position', [0.78, 0.05, 0.2, 0.9], ...
                          'BackgroundColor', [0.9 0.95 1]);

    resultText = uicontrol('Parent', resultPanel, 'Style', 'edit', ...
                           'String', '', ...
                           'Units', 'normalized', ...
                           'Position', [0.05, 0.05, 0.9, 0.9], ...
                           'HorizontalAlignment', 'center', ...
                           'FontSize', 13, 'BackgroundColor', [0.9 0.95 1], ...
                           'Max', 10, 'Min', 0, 'Enable', 'inactive', ...
                           'ForegroundColor', [0 0 0]);

    % Status Text
    statusLabel = uicontrol('Style', 'text', 'String', '', ...
```

```
                'Position', [230, 660, 650, 30], ...
                'FontSize', 14, 'FontWeight', 'bold', ...
                'BackgroundColor', [0.95 0.95 1], ...
                'ForegroundColor', [0 0 0], ...
                'HorizontalAlignment', 'center');

% Load trained model
load('pancreatic_cancer_CNN.mat', 'trainedNet');
inputSize = trainedNet.Layers(1).InputSize;

% Internal storage
originalImg = [];
analysisResult = '';

%% Functions
function selectImage (~, ~)
    [filename, pathname] = uigetfile({'.jpg;.png;.bmp;.tif'}, 'Select an Image');
    if isequal(filename, 0)
        return;
    end
    imagePath = fullfile(pathname, filename);
```

```
    originalImg = imread(imagePath);
    axes(imgAxes);
    imshow(originalImg);
    title(imgAxes, 'Original Image', 'FontSize', 14, 'FontWeight', 'bold');
    set (resultText, 'String', '');
    set (statusLabel, 'String', '');
end

function grayscale Image (~, ~)
    if isempty(originalImg), return; end
    gray = rgb2gray(originalImg);
    axes(imgAxes);
    imshow(gray);
    title(imgAxes, 'Grayscale Image', 'FontSize', 14, 'FontWeight', 'bold');
end

function binarizeImage (~, ~)
    if isempty(originalImg), return; end
    gray = rgb2gray(originalImg);
    bin = imbinarize(gray);
    axes(imgAxes);
```

```
        imshow(bin);
        title (imgAxes, 'Binarized Image', 'FontSize', 14, 'FontWeight', 'bold');
    end

    function removeNoise (~, ~)
        if isempty(originalImg), return; end
        gray = rgb2gray(originalImg);
        bin = imbinarize(gray);
        cleaned = bwareaopen (bin, 100);
        axes(imgAxes);
        imshow(cleaned);
        title (imgAxes, 'Noise Removed Image', 'FontSize', 14, 'FontWeight',
'bold');
    end

    function analyzeImage (~, ~)
        if isempty(originalImg), return; end

        set(statusLabel, 'String', 'Analyzing... Please wait');
        pause(0.5); % Simulate loading time

        resizedImg = imresize(originalImg, inputSize(1:2));
```

```
if size(resizedImg,3) == 1
    resizedImg = cat(3, resizedImg, resizedImg, resizedImg);
end
augimds = augmentedImageDatastore(inputSize(1:2), resizedImg);
[predictedLabel, scores] = classify(trainedNet, augimds);

cancerStatus = string(predictedLabel);
confidence = max(scores) * 100;

grayImg = rgb2gray(originalImg);
bwImg = imbinarize (grayImg, 'adaptive');
bwImg = bwareaopen (bwImg, 100);
cc = bwconncomp(bwImg);
wbcCount = cc.NumObjects;

axes(imgAxes);
imshow(originalImg);
hold on;

affectedCellCount = 0;
if cancerStatus == "Present" || lower(cancerStatus) == "cancer"
```

```
    hsvImg = rgb2hsv(originalImg);
    h = hsvImg(:,:,1);
    s = hsvImg(:,:,2);
    v = hsvImg(:,:,3);

    purpleMask = (h >= 0.6 | h <= 0.1) & (s >= 0.4) & (v >= 0.2);
    purpleMask = imclose (purpleMask, strel ('disk', 5));
    purpleMask = imopen (purpleMask, strel ('disk', 3));
    purpleMask = bwareaopen(purpleMask, 50);

    stats = regionprops(purpleMask, 'BoundingBox');
    affectedCellCount = numel(stats);

    for i = 1:affectedCellCount
        rectangle('Position', stats(i).BoundingBox, 'EdgeColor', 'r', 'LineWidth', 2);
    end
end
hold off;

% Result formatting
if cancerStatus == "Present" || lower(cancerStatus) == "cancer"
```

```
            statusText = 'CANCER DETECTED';
            set(resultText, 'ForegroundColor', [1 0 0]);
        else
            statusText = 'NO CANCER DETECTED';
            set(resultText, 'ForegroundColor', [0 0.5 0]);
        end

        analysisResult = sprintf ('White Blood Cell (WBC) Count: %d\nCancer Status: %s\nConfidence: %.2f%%\nAffected Cells: %d', ...
                                  wbcCount, statusText, confidence, affectedCellCount);

        set(resultText, 'String', analysisResult);
        title(imgAxes, sprintf('WBCs: %d | %s', wbcCount, statusText), 'FontSize', 14, 'FontWeight', 'bold');
        set(statusLabel, 'String', 'Analysis Complete');
    end
end
```

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CERTIFICATE

COURSE CERTIFICATE

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Certificate no: UC-42c03435-caf8-4b63-a43e-570f67d378bf
Certificate url: ude.my/UC-42c03435-caf8-4b63-a43e-570f67d378bf
Reference Number: 0004

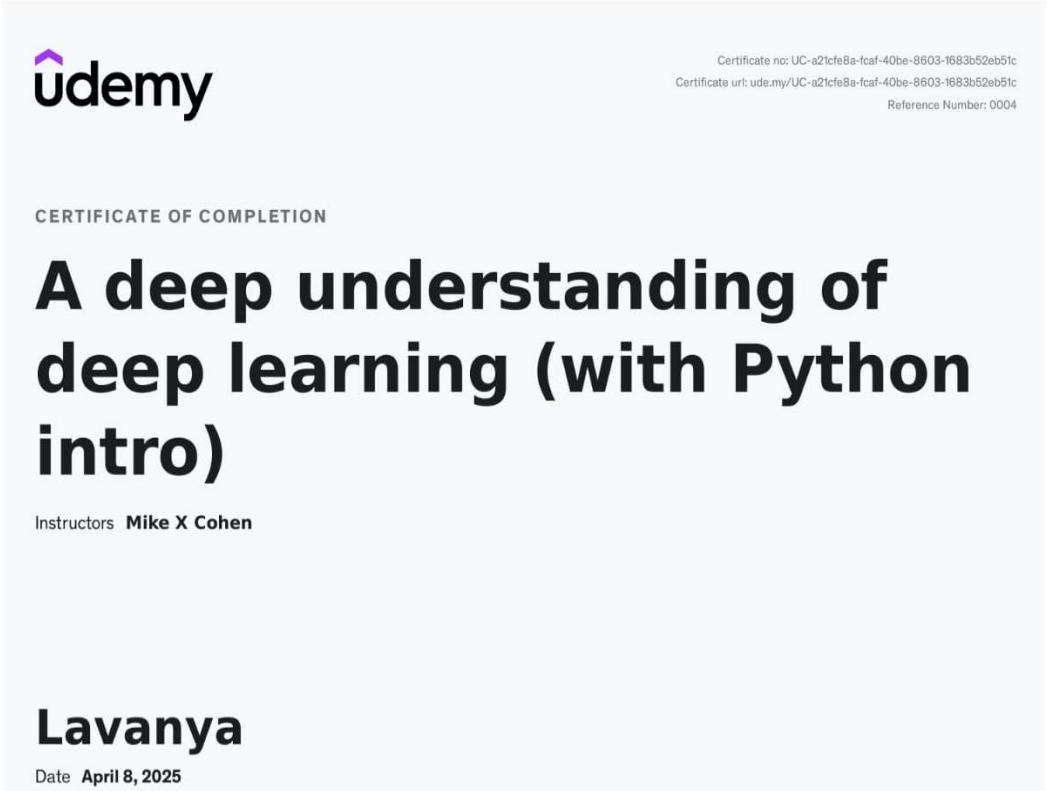
CERTIFICATE OF COMPLETION

The Data Science Course: Complete Data Science Bootcamp 2025

Instructors **365 Careers**

Harini

Date **April 22, 2025**



udemy

Certificate no: UC-a21cfe8a-fcaf-40be-8603-1683b52eb51c
Certificate url: ude.my/UC-a21cfe8a-fcaf-40be-8603-1683b52eb51c
Reference Number: 0004

CERTIFICATE OF COMPLETION

A deep understanding of deep learning (with Python intro)

Instructors **Mike X Cohen**

Lavanya

Date **April 8, 2025**

CONFERENCE CERTIFICATE

New Prince Shri Bhavani Arts and Science College

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IQAC

International Conference on "Contemporary Trends in Advanced Computing Technologies" (ICCTACT)

Certificate of Participation

This is to certify that Dr/ Mr/Ms S. HARINI
of B.S. ABDUR RAHMAN CRESCENT INSTITUTE OF SCIENCE AND TECHNOLOGY has Participated / Presented a Paper
Titled PANCREATIC CANCER DETECTION USING DEEP LEARNING
in the International Conference on "Contemporary Trends in Advanced Computing Technologies" (ICCTACT) organized by Department of Computer Science & Computer Applications and IQAC, New Prince Shri Bhavani Arts and Science College, Chennai, on 15th March 2025.

Mrs.A.SIVARANI
Organizing Secretary

Dr.P.CALISTA BEBE
Convener

Dr.V.UMADEVI
Principal

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International Conference on "Contemporary Trends in Advanced Computing Technologies" (ICCTACT)

Certificate of Participation

This is to certify that Dr/ Mr/Ms LAVANYA. M
of B.S. ABDUR RAHMAN CRESCENT INSTITUTE OF SCIENCE AND TECHNOLOGY has Participated / Presented a Paper
Titled PANCREATIC CANCER DETECTION USING DEEP LEARNING
in the International Conference on "Contemporary Trends in Advanced Computing Technologies" (ICCTACT) organized by Department of Computer Science & Computer Applications and IQAC, New Prince Shri Bhavani Arts and Science College, Chennai, on 15th March 2025.

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Organizing Secretary

Dr.P.CALISTA BEBE
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