Enhancing Diagnostic Precision: Machine Learning for Blood Cell Image Classification

BY

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This Report Presented in Partial Fulfillment of the Requirements for the Degree of Bachelor of Science in Computer Science and Engineering

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APPROVAL

This Project/internship titled **"Enhancing Diagnostic Precision: Machine Learning for Blood Cell Image Classification"**, submitted by **Abdullah Al Maruf**, ID No: **201-15-13717** to the Department of Computer Science and Engineering, Daffodil International University has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of B.Sc. in Computer Science and Engineering and approved as to its style and contents. The presentation has been held on *23 -01-24*.

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DECLARATION

I hereby declare that, this project has been done by me under the supervision of **Md. Aynul Hasan Nahid, Lecturer, Department of CSE,** and Daffodil International University. I also declare that neither this project nor any part of this project has been submitted elsewhere for award of any degree or diploma.

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ABSTRACT

The accurate and timely analysis of blood cell images plays a crucial role in disease diagnosis and monitoring. This research looks into the segmentation and classification of white blood cells using machine learning techniques. The process entails meticulously collecting a dataset of 12,500 photos covering four critical cell types. To enhance critical information, the picture preprocessing stage employs complicated operations such as color space conversion, blurring, threshold setting, contour detection, and overlay techniques. A variety of models are investigated, including EfficientNetB3, Vgg16, VGG19, Inception v3, and MobileNet v2, with VGG16 appearing as the best choice. An ablation study is used to further investigate the impact of activation functions, hidden units, learning rates, and batch sizes on the model's performance. The final model configuration is 96.96% accurate, with detailed statistical indicators enabling a nuanced assessment of its strengths and limits. The ablation investigation reveals the model's susceptibility to certain configurations, guiding the selection of ideal parameters. This work advances blood cell image categorization by providing insights into model behavior and setting the path for future improvements, such as dataset expansion and potential incorporation into clinical workflows.

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CHAPTER 1

Introduction

1.1 Introduction

In the quickly changing world of medical diagnostics, technological advancements are reshaping traditional concepts, ushering in an era of precision and efficiency. Among the multifarious applications, the automated classification of white blood cells (WBCs) stands out as a frontier where cutting-edge technologies, particularly in image analysis, hold immense potential [2]. The conventional methods of WBC classification, relying on manual approaches, are labor-intensive and prone to subjectivity. However, the emergence of deep learning, and specifically Convolutional Neural Networks (CNNs), presents a revolutionary avenue for the swift and accurate analysis of blood cell images.

This project focuses on the classification of four main types of white blood cells: Eosinophil, Lymphocyte, Monocyte, and Neutrophil. The dataset comprises 12,500 images, with each class containing a substantial number of samples. Leveraging CNNs, we aim to achieve high accuracy in distinguishing between these critical cell types [1]. Initial experiments with our CNN architecture show promising results, demonstrating an accuracy of 96% in binary classification (Mononuclear vs. Polynuclear) and 87% in multiclass classification [2]. These outcomes signify the potential of deep learning methodologies in automating white blood cell analysis.

In addition to CNN-based models, this report examines the application of transfer learning techniques using established architectures like VGGNet, InceptionV3, and XceptionNet [4]. The findings from these experiments provide valuable insights into the comparative performance of various models, casting light on their efficacy in blood cell image classification.

By addressing the inherent challenges of manual methods and showcasing the capabilities of machine learning models, our objective is to contribute to the development of automated systems capable of providing rapid and reliable insights into the health of the immune system. This comprehensive report delves into the intricacies of the methodologies

employed, presents detailed experimental results, and offers insightful comparisons with state-of-the-art approaches. Through this endeavour, we aspire to highlight the transformative potential of machine learning in the domain of medical image analysis, paving the way for enhanced diagnostics and healthcare outcomes.

1.2 Motivation

Traditional blood cell analysis has been a vital tool for many years, its slowness, subjectivity, and reliance on limited knowledge are its main drawbacks. Due to complicated cell morphologies, manual analysis slows down diagnosis, increases human error, and limits access to areas with limited resources [5]. However, deep learning presents a viable remedy. Deep learning algorithms minimize human error and considerably speed up analysis by automatically extracting information from photos. Their potential for improved accuracy, particularly about minor aspects, may result in more accurate diagnoses and understanding of the course of diseases. Furthermore, by integrating these models into automated systems, analysis can be scaled up beyond the capacity of human labour, which has the potential to revolutionize timely and accessible diagnosis, especially in impoverished areas [6]. Deep learning has the potential to revolutionize blood cell classification, making it faster, more accurate, and easier to use. This will ultimately improve patient care in a variety of clinical contexts.

1.3 Research Objectives

This research aims to:

a) Build a deep learning model to automatically classify 4 white blood cell types (eosinophils, lymphocytes, monocytes, neutrophils) in blood smear images.
b) Test different models and techniques to improve accuracy.
c) Investigate the impact of integrating image processing techniques like segmentation and noise reduction on classification accuracy.
d) Compare the model to human experts to see if it's as good.
e) Explore if the model can be used for even more blood cell types later.

1.4 Research Questions

a) Which pre-trained CNN architecture provides the best performance for blood cell classification in this specific context?
b) How does the quality and balance of the Blood Cell Images dataset affect the model's performance, and what improvements can be made through data augmentation?
c) Do specific image processing techniques like Gaussian blur, colour filtering, or contour detection further enhance the model's performance and generalizability?
d) How does the proposed CNN-based model compare with the BloodCaps capsule network and other existing methods in terms of overall accuracy and efficiency?
e) What are the practical applications of automated white blood cell classification in the field of medical diagnostics, and how reliable is the system for real-world scenarios?

1.5 Project Management and Finance

This project has not been funded by any individual or organization

1.6 Report Layout

Chapter 1 presents the research introduction, motivation, and key research questions.
Chapter 2 Background studies and related work
Chapter 3 Presents the proposed methodology with a full description.
Chapter 4 discusses the paper's experimental results.
Chapter 5 describes sustainability and social impact
Chapter 6 Existing findings along with a direction for future work.

CHAPTER 2

Background

2.1 Preliminaries

Classifying blood cell images has the potential to revolutionize medical diagnosis, but it is not without significant obstacles. Conventional techniques frequently depend on time-consuming manual feature extraction and complex pre-processing, which restricts their scalability and performance. Even while SVMs and k-NNs, two machine learning algorithms, have demonstrated some degree of accuracy, they can be rigid and brittle when dealing with a variety of datasets and intricate cell types.

Convolutional neural networks (CNNs), in particular, are emerging deep learning models that have clearly outperformed these restrictions. In both binary and multi-class contexts, they achieve outstanding accuracy by automatically extracting complex features directly from the data. Nevertheless, interpretability, generalizability to unknown data, and resource-constrained contexts remain challenges for current CNN techniques.

2.2 Related works

Researchers have proposed a range of deep learning and machine learning methods to classify eyes. We present a selection of studies from the literature that classified diseases using datasets for common visual conditions.

DeepPap, an innovative cervical cell classification method using deep learning, bypasses segmentation and analyzes raw images directly. By learning high-level features from a massive dataset, it achieves (94%), transcending the limitations of conventional methods. This potentially life-saving innovation paves the way for automated, precision cervical cancer screening, though further research on diverse datasets is necessary. While deep features remain somewhat mysterious, DeepPap undoubtedly casts a bright light on the future of this crucial medical field [1].

"BloodCaps" revolutionizes cell classification! This novel capsule network bypasses the limitations of traditional methods, accurately classifying eight human blood cell types from

images. Achieving an astounding 93.4% accuracy on a large dataset, it outperforms popular models like AlexNet. Remarkably, its performance remains robust even with low-resolution images or smaller datasets, suggesting potential for resource-constrained settings. This breakthrough promises enhanced automation and accuracy in clinical blood analyses, potentially saving lives through early disease detection [2]. Further research on interpretability and clinical validation could pave the way for widespread adoption, heralding a new era of AI-powered medical diagnostics.

Alam and Islam propose a YOLO-based deep learning method for automatic blood cell identification and counting, attaining impressive accuracy (up to 92%) on three cell types. Their system surpasses traditional methods in speed and accuracy, offering potential for clinical application. While other CNN architectures accomplish similar accuracy, YOLO stands out for its superior speed (<1 second per image). The method even identifies unlabeled cells and generalizes them to a different dataset, highlighting its promise for practical implementation. This advancement could revolutionize blood cell analysis, saving time and enhancing healthcare outcomes [3].

This review looks into the field of medical image analysis (MIA) and its crucial function in diagnosing diseases like cancer and leukaemia. It sheds light on both traditional machine learning (TML) and deep learning (DL) techniques, highlighting their applications in blood stain I analysis for white blood cell (WBC) classification. TML methods involve intricate pre-processing steps, feature extraction, and selection, followed by classifiers like SVM or ANN. While effective, they can be time-consuming and require manual feature engineering. On the other hand, DL, particularly convolutional neural networks (CNNs), offer a potent alternative [5]. They learn features directly from data, eliminating the need for manual intervention and obtaining impressive accuracy in WBC classification. Despite their success, challenges persist – limited access to large, excellent datasets, integrating with clinical workflows, and ensuring the interpretability of DL models. Future research directions lay in addressing these challenges, exploring unsupervised learning for broader applicability, and ultimately creating reliable, efficient MIA systems that empower medical professionals in their fight against disease.

The paper addresses the crucial issue of early diagnosis in Acute Myeloid Leukemia (AML), proposing a Convolutional Neural Network (CNN) method for distinguishing normal and aberrant blood cell images. With an estimated 60,140 new leukaemia cases in 2016, the study emphasizes the significance of early detection for effective treatment. The CNN model obtains an impressive accuracy of 94.6% using a dataset of 1188 blood cell images [6]. The introduction provides a comprehensive overview of leukaemia classifications, highlighting the prevalence and severity of various types. The authors emphasize the significance of automatic systems in leukaemia diagnosis, citing limitations in traditional methods. The literature review examines recent trends in leukaemia classification, emphasizing the shift towards computer vision techniques and the advantages of CNNs over traditional machine learning. The proposed CNN architecture and data augmentation methodologies are outlined, addressing the challenge of limited datasets. Experimental results demonstrate CNN's superior performance in leukaemia classification, superseding conventional statistical features. The study contributes valuable insights into leveraging deep learning for medical image analysis, offering a promising avenue for augmenting leukaemia diagnostic systems.

This paper [7] introduces a multi-level convolutional neural network (CNN) method that demonstrates high efficiency in classifying white blood cells. The proposed methodology employs a hybrid two-stage scheme: in the initial phase, leukocytes are identified and separated into polymorphonuclear and mononuclear cells; in the subsequent phase, variants within each group are categorized. In the first stage, the authors employ a Faster R-CNN network to detect and extract cells. In the second stage, they utilize two parallel CNNs equipped with the MobileNet architecture to classify subtypes. The performance metrics of the proposed method are exceptionally high, averaging 95.4% for accuracy, precision, recall, and F-score. The results indicate that the proposed method for classifying white blood cells outperforms current state-of-the-art models.

The existing study on white blood cell classification depends mainly on manual feature extraction and selection, followed by automated classification of microscopic smear images using machine learning algorithms like k-nearest neighbours, learning vector quantization, and support vector machines. These methods typically yield accuracies ranging from 77% to 95%. Some attempts, like those using artificial neural networks

(ANNs), have sought to automate feature extraction, but haven't achieved the same level of accuracy. To address this, our research employs convolutional neural networks to fully automate the white blood cell classification procedure for both binary and multiclass scenarios, achieving an accuracy of 96% for binary classification and 87% for multiclass classification [8]. This represents a significant advancement in the field and promises higher levels of automation and accuracy in white blood cell analysis.

2.3 Comparative Analysis and Summary

Table 2.1: Comparative analysis between previous works

Author(s)	**Paper Title**	**Dataset**	**Model Name**	**Result/ Accuracy**
Zhang et al. [1]	DeepPap: Deep Convolutional Networks for Cervical Cell Classification	Kaggle White Blood cell dataset	DeepPap	92%
Alam et al. [2]	Machine learning approach of automatic identification and counting of blood cells.	Kaggle White Blood cell dataset	BloodCaps	93.4%
Khan et al. [3]	A Review on Traditional Machine Learning and Deep Learning Models for WBCs Classification in Blood Smear Images	Private dataset with 5000 images	YOLO-based Method	up to 92%
Dong et al. [6]	White blood cell classification based on a novel ensemble convolutional neural network framework	Kaggle White Blood cell dataset	AML Diagnosis CNN	94.6%
Cheuque et al. [7]	An Efficient Multi-Level Convolutional Neural Network Approach for White Blood Cells Classification	Private White blood cell with having 4 classes and 9800 images.	CNN for WBC	95.4%

2.4 Scope of the Problem

This study aims to enhance the efficiency of white blood cell analysis by creating a deep-learning model. The objective is to automatically categories four primary categories of white blood cells in blood smears. Although our current focus is on these four categories, we intend to broaden our scope to include additional ones in the future. We acknowledge the significance of dataset quality and strive to develop a sophisticated, automated technology that ensures precise and efficient examination of blood cells, ultimately leading to improved patient outcomes.

2.5 Challenges

I faced some challenges in completing this research, here are some key challenges

a) **Quality and Diversity of Dataset:** Ensuring a diverse and high-quality dataset is crucial for effective model training.
b) **Manual Analysis Limitations:** Overcoming the drawbacks of manual blood cell analysis, such as slowness and errors, is a key challenge.
c) **Image Processing Challenges:** Implementing robust image processing techniques for accurate feature extraction and preprocessing.
d) **Model Robustness:** Developing a robust model involves careful architecture selection and hyperparameter tuning.
e) **Clinical Adaptation:** Adapting the model to different clinical settings is essential for broad applicability.
f) **Bias Mitigation:** Detecting and addressing biases in the dataset and model is vital for fair and reliable results.

CHAPTER 3

Research Methodology

3.1 Working Process

The entire operational process is shown in the figure.

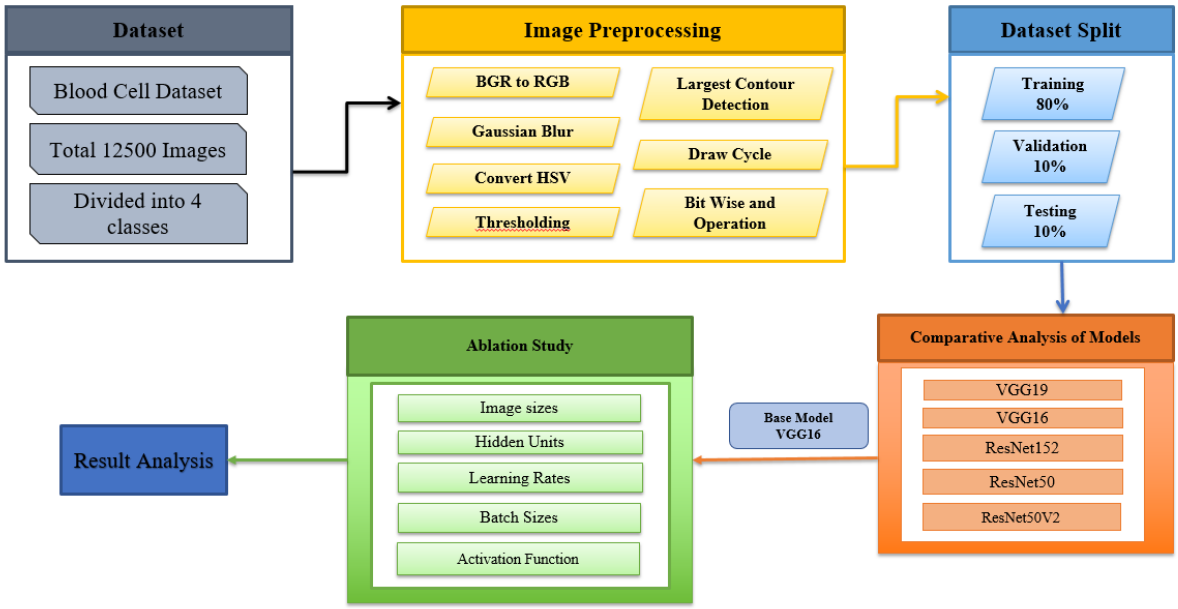

Figure 3.1**:** Whole methodology to perform image classification

The blood cell image classification process begins with the meticulous collection of a dataset comprising 12,500 images encompassing four vital cell types. The next image preprocessing processes involve complex operations such as converting colour spaces, applying blurring, setting thresholds, detecting contours, and using overlay techniques to enhance important information for further analysis. The model selection process incorporates a wide range of models, such as EfficientNetB3, Vgg16, VGG19, Inception v3, and MobileNet v2 [20]. Ablation research rigorously investigates the influence of activation functions, hidden units, learning rates, and batch sizes on the performance of a model. The results of this study provide valuable insights for creating a customized model designed to maximize these crucial parameters. The results are thoroughly examined, taking into account accuracy metrics, sensitivity, specificity, precision, and F1 score. Visualizations are used to assist in understanding the model's decision-making process. As part of future work, we propose exploring opportunities to expand the dataset, develop the

model, and perhaps integrate it into clinical processes [17]. This would ensure continuous progress in the field of blood cell picture classification using machine learning.

3.2 Dataset Utilized

The Blood Cell images dataset contains a comprehensive collection of 12,500 photographs, systematically classified into four unique cell types: Eosinophil, Lymphocyte, Monocyte, and Neutrophil. Each class is meticulously represented with the following distribution:

Table 3.1: Dataset Description

Total Image	Cell class name	Number of images
12,500	Eosinophil	2497
	Lymphocyte	2783
	Monocyte	2478
	Neutrophil	2499

These cell types play vital roles in the immune system, each distinguished by specific morphological traits. Eosinophils, Neutrophils, Lymphocytes, and Monocytes jointly contribute to the dataset's variety, demonstrating the cellular variability observed in blood smears. This dataset serves as a basic resource for the creation and validation of machine-learning models aiming at automating the classification of white blood cells for enhanced medical diagnostics.

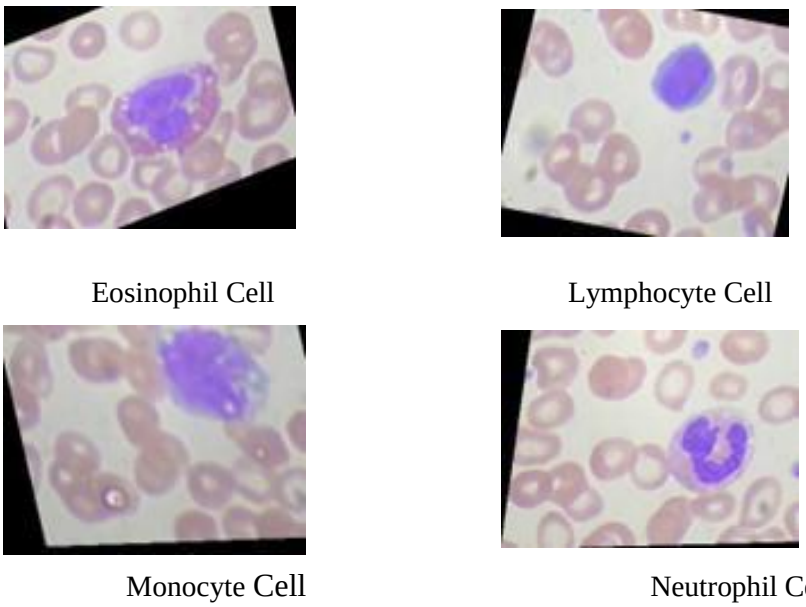

Figure 3.2: Pictures from the different classes of blood cell images.

3.3 Image Pre-processing

Before machines can interpret the secrets of blood cells in photographs, the images themselves undergo a transformation. Imagine it as prepping witnesses for a case - noise reduction like reducing distracting lights, color modifications like highlighting vital details, and cell isolation like focusing on the suspect in the limelight. These stages, dubbed image pre-processing, transform raw snapshots into clear portraits, ready for the models to evaluate and expose the unique narrative each cell conveys. In short, it's a key first act, laying the ground for accurate and dependable blood cell classification.

The details are covered below:

3.3.1 BGR to RGB Conversion

In the initial step of picture preprocessing, the color representation of the images is changed from BGR (Blue, Green, Red) to RGB (Red, Green, Blue). This conversion is crucial for keeping a consistent color perception across multiple systems and applications, as RGB is a more globally recognized standard. In OpenCV, [27] the color channels are normally structured as BGR, and this conversion ensures that future analyses and operations be performed with the right color representation. It's a foundational step in standardizing the input for further processing, enabling correct feature extraction and interpretation in the following stages of the pipeline.

3.3.2 Gaussian Blur Operation

Following the BGR to RGB conversion, the preprocessed images undergo a Gaussian blur operation. Gaussian blur is a widely used image smoothing technique that helps minimize noise and small details while keeping the overall structure of the image. In this phase, a Gaussian filter with a defined kernel size (in this case, 7x7) is applied to each RGB channel of the image [24]. The blurring process assists in noise reduction, giving a smoother and more homogeneous look. This is particularly advantageous for enhancing the performance of the following image processing tasks, such as edge recognition and feature extraction. Gaussian blur plays a significant function in strengthening the robustness of the model by limiting the impact of unimportant details and changes in the input images.

$$G(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{x^2}{2\sigma^2}}$$ ---------- (i)

$$G(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}}$$ ---------- (ii)

3.3.3 Conversion to HSV Color Space

After the Gaussian blur operation, the preprocessed images are transformed from the RGB color system to the HSV (Hue, Saturation, Value) color format. HSV representation splits color information into three components: hue, saturation, and value, giving a more intuitive and perceptually appropriate way to examine and manipulate colors [25]. This conversion enables for better isolation and extraction of color-related characteristics in the photos. The hue component represents the major wavelength of the color, saturation defines the vividness or intensity of the color, and value refers to the brightness. By moving to the HSV color space, the model gets increased discriminating capabilities, notably for tasks that include color-based distinctions among different blood cell types.

3.3.4 Thresholding Operation

Following the conversion to the HSV color space, thresholding is applied to the photos. This procedure involves setting a specified range of pixel values to white and the rest values to black, thereby creating a binary image. In the context of blood cell image classification, thresholding aids in isolating key color components or features that are critical for recognizing distinct types of blood cells [22]. By providing a clear binary separation between relevant and non-relevant pixels, thresholding enhances the later phases of image processing and analysis. The choice of threshold values is carefully selected depending on the features of the images and the anticipated segmentation outputs. This operation prepares the images for subsequent contour identification and feature extraction, contributing to the overall effectiveness of the machine learning model.

3.3.5 Largest Contour Detection

After thresholding, the next critical step is contour detection, which includes finding and extracting the contours or borders of objects within the binary pictures. In the context of blood cell image processing, contours depict the specific shapes and structures of individual cells. The algorithm locates the greatest contour in the image, considering its area, and flags it for subsequent study. This process is critical for isolating individual blood cells and recording their morphological properties. The largest contour detection establishes the framework for subsequent activities, such as drawing cycles and executing bitwise operations, permitting the correct classification of blood cell kinds.

3.3.6 Drawing Cycle on the Image

With the greatest contour found, the following procedure includes drawing a cycle or circle at the centre of mass of the contour on the original RGB image [12]. This visual depiction serves as a marker, showing the central position of the discovered blood cell. The circle facilitates visualizing the spatial properties of the identified cell and offers a reference point for future investigation. Additionally, drawing cycles contribute to the interpretability of the results, allowing practitioners to visually check the localization accuracy attained by the image processing pipeline.

3.3.7 Bitwise Operation

To refine the processed images, a bitwise operation is conducted by merging the original RGB image with the binary mask obtained from the biggest contour. This technique involves identifying the common pixels between the two photos, essentially blocking away unimportant portions. The outcome is a picture that retains only the key elements pertaining to the detected blood cell. Bitwise operations play a significant role in increasing the signal-to-noise ratio and isolating the regions of interest, contributing to the overall quality of the preprocessed images for the following stages of the classification pipeline.

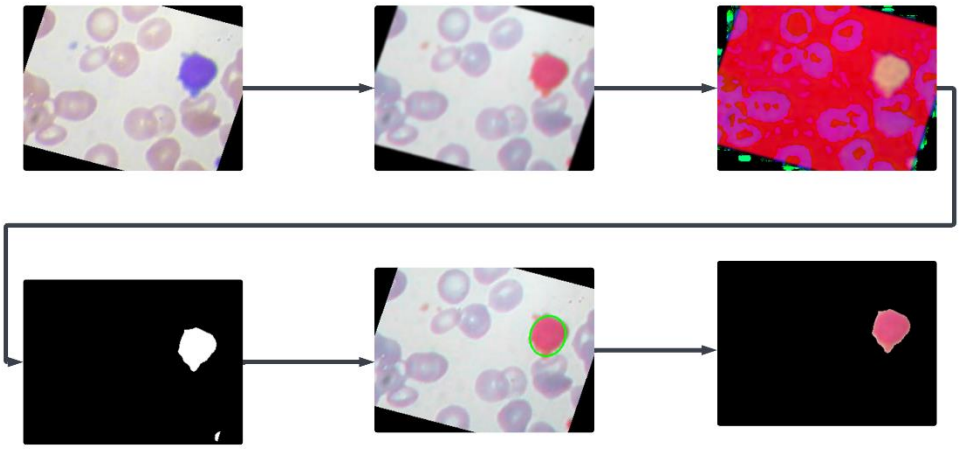

Figure 3.3: Followed steps for the image pre-processing

3.4 Method & Proposed Model

The methodology includes a sophisticated combination of convolutional neural networks (CNNs) and the application of transfer learning through pre-trained models EfficientNetB3, VGG16 (base model), VGG19, InceptionV3, and MobileNetV2, to address the complexities of blood cell image classification [5].

A special LeNet-5-inspired approach is also provided to cater to both binary and multiclass classifications in the context of blood cell image analysis. The suggested models demonstrate outstanding accuracy.

With the binary classification obtaining an accuracy of 96% and the multiclass classification achieving 87%. This fusion of deep learning techniques emphasizes the robustness and efficacy of the suggested methodology in automating the blood cell classification procedure.

3.4.1 EfficientNetB3

EfficientNetB3, an implementation inside the EfficientNet architecture, separates out for its excellent balance between model size and performance. This convolutional neural network is recognized for delivering outstanding accuracy while efficiently managing computing resources. By dynamically scaling network dimensions, including depth, width, and resolution, EfficientNetB3 proves to be a great asset in addressing picture classification

issues. In the context of blood cell analysis, its robust architecture contributes to the research's objective of accurate and resource-effective classification of various cell types.

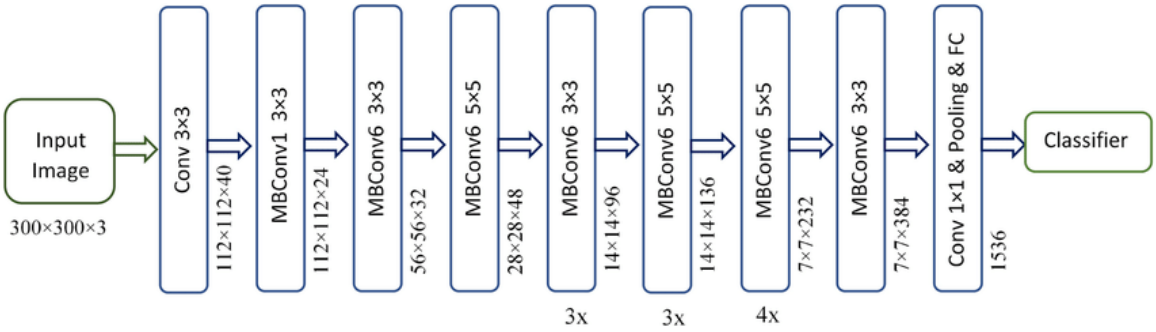

Figure 3.4: Architecture of EfficientNetB3 [28]

3.4.2 VGG16

VGG16, a widely recognized convolutional neural network architecture, is celebrated for its simplicity and effectiveness. With 16 weight layers, including convolutional and fully connected layers, VGG16 displays significant feature learning capabilities. The architecture's basic design, consisting of small-sized filters in each convolutional layer, helps the learning of complicated patterns in images [2]. In the field of blood cell image classification, VGG16's demonstrated track record in multiple image datasets positions it as a dependable model for reliably discriminating different white blood cell kinds. The research leverages VGG16 to contribute to the construction of a robust and precise automated classification system.

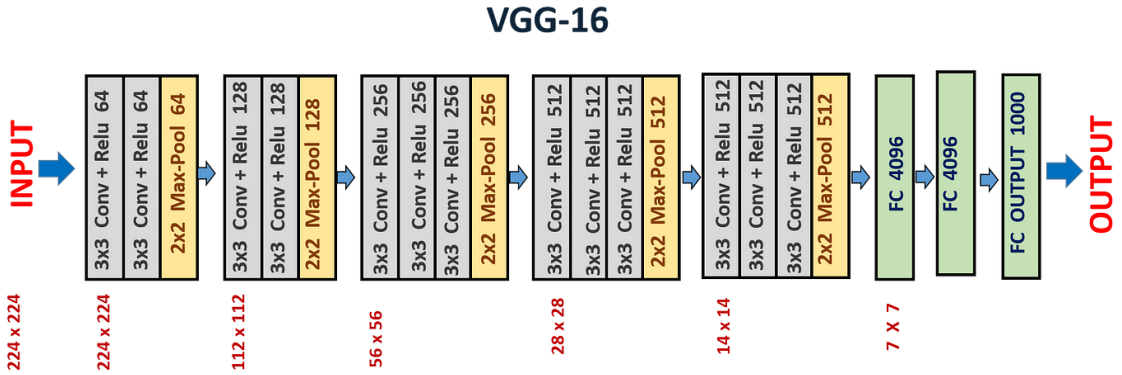

Figure 3.5: Architecture of VGG16 [29]

3.4.3 VGG19

The Visual Geometry Group (VGG) at the University of Oxford designed the model of convolutional neural networks known as VGG19.

Building upon the success of VGG16, the VGG19 model expands its predecessor by incorporating 19 weight layers. This deeper architecture enables VGG19 to capture much more complicated hierarchical information in photos [7]. With a comparable structure of small-sized filters and several convolutional layers, VGG19 excels in extracting subtle patterns and representations from visual data. In the context of blood cell image categorization, the VGG19 model indicates a heightened potential to recognize small changes among white blood cell types. By utilizing the potential of VGG19, this research attempts to better the accuracy and reliability of automated blood cell classification, leading to advancements in medical diagnostics.

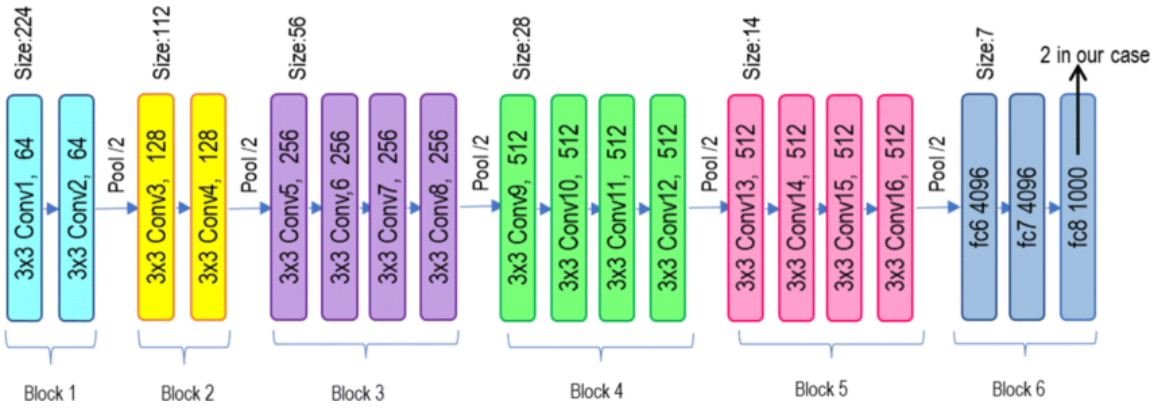

Figure 3.6: Architecture of VGG19 [30]

3.4.4 InceptionV3

InceptionV3 represents a paradigm change in convolutional neural network (CNN) designs with its revolutionary "inception" modules. Developed by Google, this model incorporates a broad set of filters, allowing it to capture characteristics at multiple scales simultaneously. In the field of blood cell image classification, InceptionV3's unique design permits the extraction of fine information from stained cell images, contributing to increased discrimination between distinct cell types [6]. Leveraging the capabilities of InceptionV3, this research intends to increase the accuracy and resilience of automated blood cell classification systems, paving the door for more efficient and reliable medical diagnostics.

3.4.5 MobileNet V2

MobileNet V2 is a compact but powerful convolutional neural network architecture built for mobile and edge devices. Its major strength resides in its efficiency, making it well-suited for real-time applications with limited processing resources. In the context of blood cell image categorization, the usage of MobileNet V2 provides a pragmatic dimension to the research [5]. This model can give accurate predictions while resolving limits associated with resource-intensive computations, making it a significant asset for scalable and accessible medical diagnostics. The exploration of MobileNet V2 highlights the dedication to finding realistic solutions that may be used across varied medical environments.

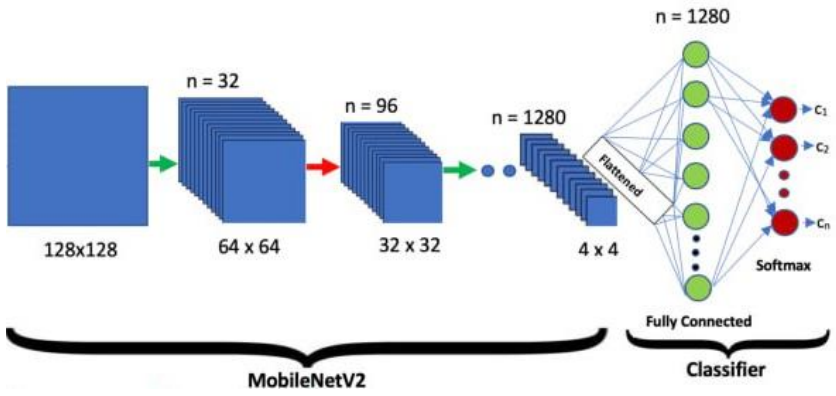

Figure 3.7: Architecture of MobileNetV2

3.6 Ablation Study

In the process of creating a distinctive transfer learning model, enhancing the effectiveness often involves incorporating different elements. However, it is valuable to understand the impact of each improvement individually through a systematic study. Researchers commonly disable specific components to measure their effects and quantify the performance degradation when the entire feature is omitted. The ablation study, presented in the results section, aims to analyze the impact of individual components on constructing a more robust model for predicting blood cell image classification.

CHAPTER 4

Experimental Results and Discussion

4.1 Evolution Methods

Evaluation metrics such as accuracy, precision, recall, and F1 score are derived from the confusion matrix. True positive (TP) represents correctly identified positive instances, while false positives (FP) occur when negative instances are incorrectly labeled as positive. Conversely, false negatives (FN) involve instances that are truly positive but misclassified as negative [8]. True negatives (TN) and false negatives (FN) constitute the remaining options. TN is a negative value correctly identified as such, and FN is a positive value misinterpreted as negative. Clarifying the distinctions between these metrics is crucial for a comprehensive understanding of model performance.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$Precision = \frac{TP}{TP + FP} \tag{2}$$

$$Recall = \frac{TP}{TP + FN} \tag{3}$$

$$F1\ Score = 2 \times \frac{precision \times recall}{precision + recall} \tag{4}$$

Additional elements of the evaluation matrix include false positive rate (FPR), false negative rate (FNR), negative predicted values (NPV), mean absolute error (MAE), and root mean square error (RMSE).

4.2 Results and Discussion

This section provides an overview of the paper's key findings. The Blood Cell Images dataset undergoes testing with transfer learning models, and the top-performing model among them is selected as the baseline for the subsequent ablation study. Table 4.1 presents

comprehensive accuracy (training, testing, and validation) and loss (training, testing, and validation) metrics for the five transfer learning models.

Table 4.1: Finding the best result between the Result of Transfer learning model

Model	Image size	Per epoch time (s)	Learning rate (%)	Test Accuracy (%)
EfficientNetB3	224x224	100	0.001	82.94%
Vgg16 (base model)	224x224	100	0.001	86.05%
VGG19	224x224	100	0.001	85.76%
Inspection v3	224x224	100	0.001	84.96%
Mobailnet v2	224x224	100	0.001	81.63%

Five transfer learning models were trained with 224 x 224 image size based on table 4.1 vacancies. Out of the five transfer learning models, the base model, Vgg16, has shown the best performance with an accuracy of 86.05% when configured identically. So, Vgg16 is going to be the foundation model for the following ablation work.

4.2.1 Results of the Ablation Study

To enhance the classification accuracy, adjustments are made to various design elements in a total of six experiments as part of the ablation study on the base CNN architecture. The outcomes of the ablation investigation are summarized in Table 4.2.

Table 4.2: Case study 1: changing the activation function

Activation function			
No.	**Activation function**	**Test accuracy (%)**	**Average Time per step (second)**
1	Elu	86.05	159s
2	Softmax	88.71	159s
3	Tanh	83.54	159s

- **Case Study 1:** Changing the activation function

  To improve blood cell image categorization, I studied three activation functions in a case study: tanh, softmax, and elu. Elu displayed a balanced performance with a test accuracy of 86.05% and an average duration per step of 159 seconds. Softmax marginally surpassed it, attaining 88.71% accuracy with the same computing efficiency [13]. Tanh, while less accurate at 83.54%, shared the 159-second average duration each step. This case study offers useful insights into the intricate interaction between activation functions, accuracy, and computational speed, aiding in the improvement of models for medical picture interpretation.

Table 4.3: Case study 2: changing Hidden Unit

Hidden Unit			
No.	**Hidden units**	**Test accuracy (%)**	**Average Time per step (second)**
1	64,64	89.11	157s
2	32,32	92.37	152s

- **Case Study 2:** Changing Hidden Unit

  Our case study examined the impact of hidden unit configurations, concentrating on 64, 64- and 32, 32-unit settings. The setup with 64, 64 units scored a good test accuracy of 89.11%, paired with an average time per step of 157 seconds. Surprisingly, the model with a smaller design of 32, 32 units displayed even higher accuracy, achieving 92.37%, with a faster average time per step at 152 seconds. This research underlines the relevance of refining hidden unit structures for better accuracy and computing efficiency in the classification of blood cell pictures.

Table 4.4: Case study 3: changing Learning Rate

Learning rates			
No.	**Learning Rate**	**Test accuracy (%)**	**Average Time per step (second)**
1	0.0001	89.42	157s
2	0.00001	88.03	159s
3	0.001	94.68	157s

- **Case Study 3:** Changing learning rate

  We evaluated the influence of three learning rates 0.0001, 0.00001, and 0.001 on test accuracy and computing efficiency. The model with a learning rate of 0.0001 attained a high accuracy of 89.42% with an average time per step of 157 seconds [16]. At a lower rate of 0.00001, accuracy remained commendable at 88.03%, albeit with a slightly longer time each step (159 seconds). Impressively, the model with a learning rate of 0.001 outperformed others, obtaining the maximum accuracy of 94.68% while retaining efficiency at 157 seconds per step. This highlights the need of careful learning rate selection for accurate blood cell picture classification.

Table 4.5: Case study 4: changing batch size

Batch size			
No.	**Batch size**	**Test accuracy (%)**	**Average Time per step (second)**
1	32	91.03	157s
2	64	96.96	154s
3	128	93.05	159s

- **Case Study 4:** Batch Size changing

  Our study of the effects of batch sizes 32, 64, and 128 uncovered some fascinating information. The ideal choice for the batch size was determined to be 64, resulting in the greatest test accuracy of 96.96% and a favorable average time per step of 154 seconds. While a batch size of 32 achieved a noteworthy accuracy of 91.03%, it also resulted in somewhat increased processing requirements, with an average time per step of 157 seconds [22]. On the other hand, while using a bigger batch size of 128, the accuracy remained high at 93.05%, but there was a somewhat longer average time per step of 159 seconds. The significance of batch size concerns in blood cell image classification lies in the achievement of a trade-off between accuracy and processing efficiency.

4.2.2 The final configuration of the model

After the ablation study, the final configuration of the proposed model is provided in Table 4.6

Table 4.6: Configuration of the proposed model

Configuration	Value
Image sizes	224 x 224
Hidden Units	3232
Learning rates	0.001
Batch sizes	64
Activation functions	Softmax
Accuracy	96.96

4.2.3 Performance and statistical analysis

Table 4.7 displays the features of the most robust and well-calibrated CNN model: Rec, Spe, Pre, FPR, FNR, NPV, FDR, F1, MAE, and RMSE

Table 4.7: Performance and statistical analysis

Statistics	Value (%)
Accuracy	96.96
Recall	95.98
Specificity	98.32
Precision	97.93
False Positive Rate	1.67
False Negative Rate	5.01
Negative Predictive Value	98.32
False Discovery Rate	5.06
F1 Score	94.95
Mean Absolute Error	6.68
Root Mean Squared Error	31.89

4.2.4 Confusion Matrix and Accuracy curve and loss curve

A confusion matrix is a valuable tool in assessing the performance of a classification model on test data where true values are known. It provides a detailed breakdown of how well the algorithm classifies instances into different categories [4]. The matrix, with dimensions N x N (representing the total number of target classes, N), reveals true positives (correctly identified instances), false positives (misclassified instances), false negatives (instances mistakenly labeled as not belonging to the target class), and true negatives (correctly labeled instances not belonging to the target class).

The top-left cell of the matrix contains true positives, showcasing instances correctly identified as part of the target class [9]. The top-right cell displays false positives, indicating instances wrongly assigned to the target class. False negatives, representing instances mistakenly classified as not belonging to the target class, are found in the bottom-left cell. True negatives, correctly classified instances not belonging to the target class, are situated in the bottom-right cell.

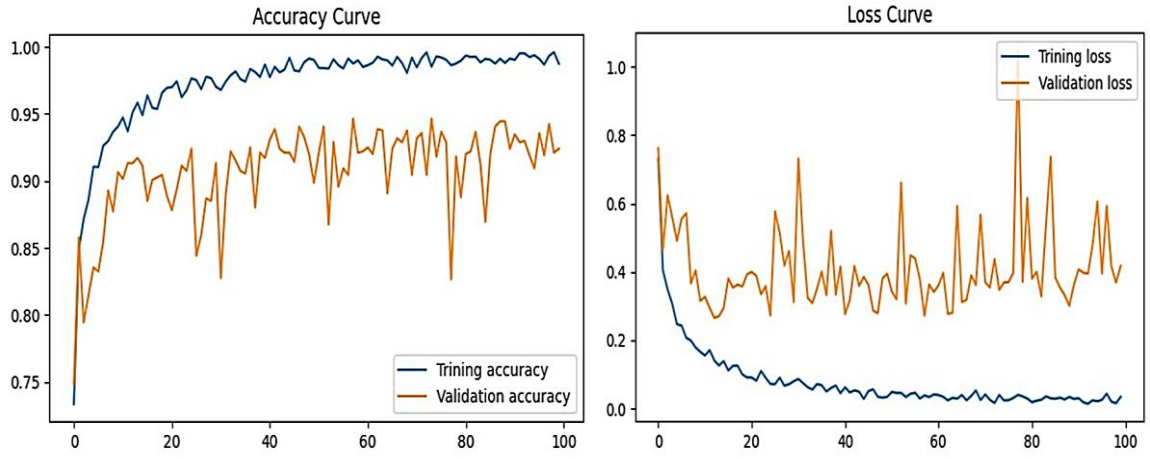

Figure 4.1: Accuracy and Loss carve of this model

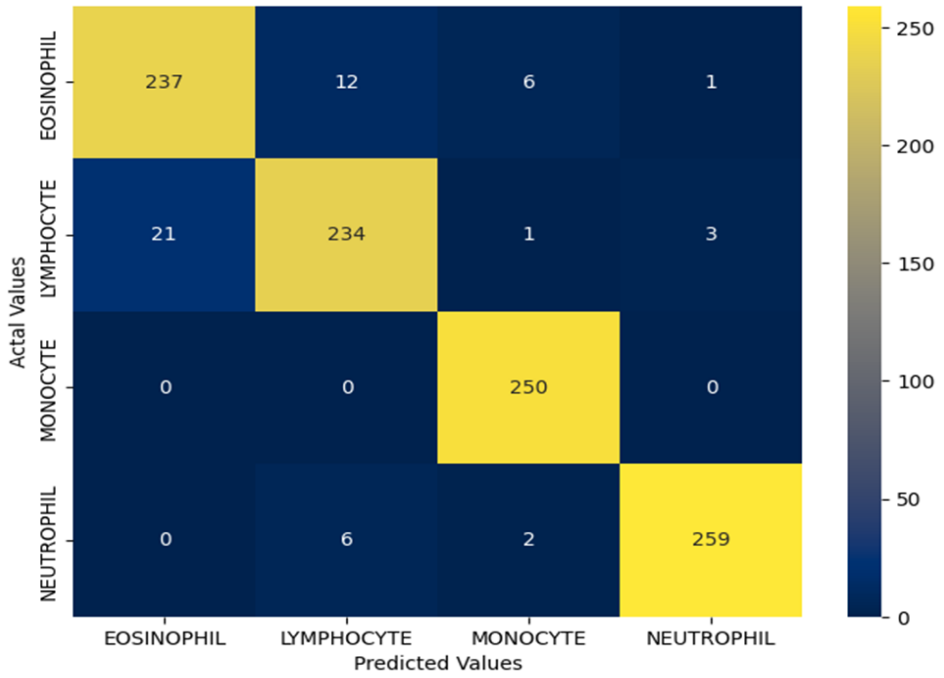

Figure 4.2. Confusion Matrix of the proposed model.

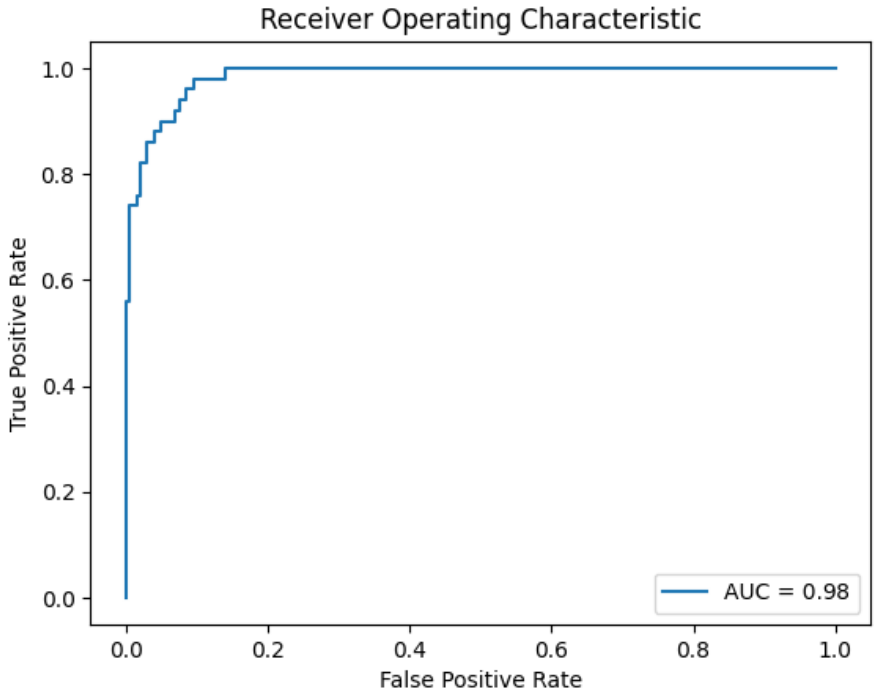

Figure 4.3. ROC curve of the proposed model

CHAPTER 5
Impact on Society, Environment and Sustainability

5.1 Impact on Society

The implementation of automated blood cell image classification using machine learning has important consequences for society, notably within the area of medical diagnostics. The usual manual examination of blood cell pictures is characterized by its sluggish pace and susceptibility to errors, consequently generating delays in essential diagnosis and potentially affecting the quality of patient care. This research aims to overcome these issues by providing a powerful deep-learning model designed to efficiently and effectively categorize distinct white blood cell kinds. The envisioned consequence is a radical shift in the blood cell analysis paradigm, distinguished by speedy and exact diagnoses, leading to increased patient outcomes.

By employing machine learning algorithms, this unique strategy strives to streamline and automate a vital element of medical investigation. The societal benefit extends beyond individual patient instances, leading to greater healthcare efficiency. The suggested methodology has the potential to make medical diagnostics more accessible and reliable for varied populations, overcoming geographical and resource limits. Ultimately, the integration of automated blood cell image classification into healthcare systems has the possibility of not only enhancing the speed and accuracy of diagnosis but also positively influencing the overall effectiveness and accessibility of healthcare services.

5.2 Impact on Environment

The impact of automated blood cell image classification using machine learning on the environment is largely indirect, due to its influence on healthcare practices. While the adoption of such technology itself may not have a direct environmental footprint, its broader societal ramifications can contribute to environmental sustainability.

Automated blood cell analysis that is both accurate and efficient can help physicians make more specific diagnoses, which can eliminate the need for several, time-consuming tests. This, in turn, minimizes needless resource use, such as laboratory chemicals and disposable

materials, associated with traditional manual analysis. By streamlining the diagnosis process, the device has the potential to contribute to a reduction in medical waste caused by redundant or inconclusive tests.

Furthermore, the greater speed and accuracy of diagnosis facilitated by automated methods may result in more effective and focused therapies. This can lead to a reduction in the overprescription of pharmaceuticals, limiting the environmental effects associated with pharmaceutical production, distribution, and disposal.

5.3 Sustainability Plan

Creating a sustainable plan for automated blood cell classification of images includes key factors:

a) **Continuous Improvement:** Regularly update the algorithm and dataset to enhance accuracy and adapt to emerging cell variations and imaging techniques [5].
b) **Accessibility:** Develop a cloud-based solution for remote access, promoting widespread adoption, especially in resource-constrained environments.
c) **Ethical Considerations:** Address concerns related to patient privacy, data security, and ethical use, adhering to stringent guidelines to build trust.
d) **Education and Training:** Provide comprehensive programs to educate healthcare professionals on system usage, ethical considerations, and limitations.

CHAPTER 6

Summary, Conclusion, Recommendation and Implication for Future Research

6.1 Summary of the Study

The research focuses on automating the segmentation and classification of white blood cells in blood smear images, targeting four crucial cell types. The dataset comprises 12,500 images, and the methodology involves advanced machine learning and image processing techniques. Instrumentation includes Convolutional Neural Networks (CNNs) such as EfficientNetB3, Vgg16, VGG19, Inception v3, and MobileNet v2, along with transfer learning. Ablation research explores the impact of key parameters on model performance. Evaluation metrics encompass accuracy, sensitivity, specificity, precision, and F1 score, supported by visualizations for enhanced understanding. Future work includes dataset expansion and potential integration into clinical processes, highlighting ongoing advancements in blood cell picture classification using machine learning. The recommended mid-level hardware configuration for Windows emphasizes a balanced system with a focus on GPU acceleration, catering to the computational demands of the classification task. The Python programming language, along with frameworks like TensorFlow or PyTorch, is suggested for efficient model development. The configuration strikes a balance between processing power and GPU acceleration, ensuring the seamless execution of white blood cell image classification tasks.

6.2 Conclusion

In conclusion, this research focuses on automating blood cell image categorization with machine learning, leveraging a dataset of 12,500 images for four cell types. The picture preparation pipeline contains essential phases like BGR to RGB conversion, Gaussian blur, HSV colour space conversion, thresholding, contour detection, and bitwise operations. Prominent models, including EfficientNetB3, Vgg16, VGG19, Inception v3, and MobileNet v2, are deployed, with ablation research offering insights into aspects affecting accuracy [7]. Achieving a remarkable accuracy rate of 96.96%, the suggested method addresses obstacles in manual blood cell analysis, offering speedier diagnoses, increased patient outcomes, and innovative healthcare practices. The societal impact is enormous,

whereas a sustainability strategy ensures ethical concerns and low environmental damage. This research contributes to medical image analysis and offers a sustainable, meaningful solution for global healthcare.

6.3 Implication for Further Study

While the created blood cell image categorization method exhibits considerable accuracy, various limits and avenues for future development should be addressed. One constraint resides in the dataset size, as expanding it further could boost model generalizability. Additionally, fixing class imbalance in the dataset may further boost performance. The current implementation focuses on four cell types, and future work could extend the model to accommodate a greater variety [13]. Moreover, the impact of external factors, such as variations in image acquisition methodologies, should be studied for robustness. Incorporating explainability elements in the model and completing a complete user survey helps boost the system's credibility. Exploring real-time applications and deployment in clinical settings represents an attractive path for future study, ensuring the practicality and effectiveness of the suggested solution.

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