White Blood Cell Image Classifier using Deep learning Techniques

A Report

submitted by

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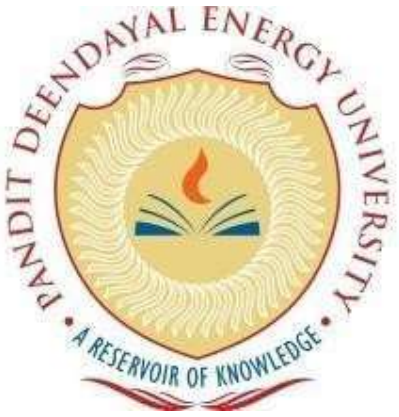
In fulfillment for the award of the degree

of

Masters of Technology

in

Data Science



Pandit Deendayal Energy University,
Gandhinagar

Academic Year

(2024-2025)

STUDENT DECLARATION

I, the undersigned, hereby declare that the work presented in this report is my own, and where ideas or words from other sources have been used, they have been appropriately cited and referenced. I affirm that I have complied with all academic integrity and honesty principles and have not misrepresented, falsified, or fabricated any data, facts, or sources in my submission.

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CERTIFICATE

It is to certify that the work contained in the thesis titled **"White Blood Cell Image Classifier using Deep learning Techniques"** by Dev Rajnikant Jethva has been carried out under our supervision & that has not been submitted elsewhere for a degree.

Institute Guide:

Dr. Yogesh Kumar

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ACKNOWLEDGEMENT

While a completed dissertation bears the single name of the student, the process that leads toits completion is always accomplished with the co-operation and guidance of many people around. This thesis is not the result of as individual but inputs from many individuals to whom I wish to acknowledge my appreciation.

The first and foremost, I owe my deepest sense of gratitude to my guide Dr. Yogesh Kumar, whose untiring guidance, constant encouragement and stimulating suggestions helpedme to fulfil this task. His faith in my abilities has led me to a path of confidence and determination. This report work would never be completed without his support, insightful suggestions, valuable time and facility at university campus to accomplish my task.

Last but far from least, I have no words to express the sense of gratitude for the support and understanding shown by my parents for their continuous inspiration, moral support and blessing.

Contents

Abstract

This study addresses the challenge of white blood cell (WBC) classification in blood images using advanced deep learning techniques. The primary objective is to develop a deep learning approach that enhances the accuracy and speed of WBC classification by employing state-of-the-art data preparation techniques such as augmentation and normalization. Various deep learning models, including Deep Neural Networks (DNNs), Convolutional Neural Networks (CNNs), VGG16, VGG19, and ResNet50, are evaluated to determine their effectiveness in classifying different types of WBCs. The study demonstrates that the VGG16 model outperforms other models with the highest training accuracy of 99.37% and validation accuracy of 94.62%, significantly surpassing ResNet50, which exhibited the lowest performance. The proposed CNN framework reduces computational complexity while maintaining high accuracy, addressing the limitations of more complex transfer learning models. Additionally, data augmentation techniques are utilized to balance the dataset and mitigate overfitting. The findings underscore the potential of advanced neural network architectures in medical image analysis, with implications for improving diagnostic accuracy and efficiency in clinical settings. Future work will focus on exploring additional models, optimizing existing ones, and extending their application to other medical imaging tasks to enhance clinical diagnostics further.

Objective

The main goal of this project is to develop an advanced deep learning approach for the accurate classification of various white blood cells (WBCs) in blood images. By leveraging state-of-the-art techniques in data preparation, including augmentation and normalization, alongside optimizing a range of deep learning models such as DNNs, CNNs, VGG16, VGG19, and ResNet50, the project aims to enhance both the accuracy and speed of WBC classification. This advancement promises significant improvements in medical diagnostics by providing a more efficient, reliable tool for identifying different types of WBCs, ultimately contributing to better patient outcomes and streamlined diagnostic processes. The project's success in achieving high classification accuracy and computational efficiency will represent a significant step forward in medical image analysis, paving the way for further innovations and practical applications in healthcare.

Introduction

Blood is composed of various components including different cell types and plasma. Blood performs the crucial function of transporting oxygen and nutrients to the body's tissues and organs. Additionally, it helps eliminate waste products like carbon dioxide and ammonia. Blood performs several biological functions like transport of gases to and from the body and exchanging them in the lungs, clotting of blood by making oxyhemoglobin, immune response, and body temperature regularization.

Blood serves several important biological functions including oxygen transport, cell regeneration, clotting, body temperature regulation, and immune response. It comprises four essential cellular components: red blood cells (RBCs), white blood cells (WBCs), platelets, and plasma. RBCs, which make up around 40% to 50% of total blood volume, are primarily responsible for the supply of oxygen throughout the body from the lungs where gaseous exchange takes place between the human body and its environment. WBCs are found in both the lymphatic nodes and the blood. Although WBCs constitute only 1% of the blood in a healthy individual, they play a critical role in the immune system's defense against foreign invaders. WBCs actively seek out, identify, and bind to bacterial, fungal, or viral proteins to eliminate them and provide a first-hand defense against intruders. Several types of WBCs are identified each performing its specific function in our body's immune response.

WBCs also known as leukocytes, have the crucial function of providing immunity and the first defense wall in the human body against intruders and diseases. These cells can be categorized into four primary types: neutrophils, eosinophils, lymphocytes, and monocytes. Each type possesses distinct physical and functional characteristics. Neutrophils are granulocytes equipped with enzymes that aid in the digestion of pathogens. Monocytes are classified into macrophages that eat up the damaged cells including RBC platelets and detrimental invaders. Eosinophils are the defense force against viral infections and also contribute to infection and tissue damage as observed in numerous diseases. Lymphocytes safeguard the body against tumor cells and cells infected by viruses.

Computer-aided diagnostic (CAD) methods and machine learning (ML) have extensively been used by several studies during the last two decades to address the limitations

of WBC diagnosis and subgroup determination in laboratory image analysis. Tiese studies have focused on analyzing blood smear images to diagnose, differentiate, and count various types of WBCs. ML, a prominent branch of artificial intelligence, encompasses algorithms and mathematical relationships that enable computers to learn from experience without explicit programming. The application of ML in medical data processing has yielded remarkable success, particularly in disease diagnosis. In medical image processing, ML methods have proven beneficial in complex medical decision-making processes by extracting and analyzing image features. As the availability of medical diagnostic tools increased and generated large volumes of high-quality data, there emerged a pressing need for more advanced data analysis methods. Traditional approaches are unable to effectively analyze such vast amounts of data or identify underlying data patterns. In this context, the present study contributes in the following ways

- This study presents a framework for accurate white blood cell classification using an optimized convolutional neural network (CNN). Contradictory to existing works which predominantly rely on more complex transfer learning-based models, the deep learning CNN model is adopted to reduce computational complexity without affecting the model accuracy.
- For the most part, existing studies perform experiments on imbalanced datasets which might lead to model overfit for the majority class. Data augmentation is employed to balance the number of samples for various classes thereby reducing the probability of model overfitting.
- The efficacy of the proposed model is analyzed in comparison to several transfer learning models like ResNet, VGG16, MobileNet, and InceptionV3. In addition, the performance of the proposed model is compared with state-of-the-art approaches from existing literature.

The study aims to achieve these objectives through a systematic approach encompassing data preprocessing, model architecture design, training and evaluation like:

1. **Data Preprocessing:**

- **Data Collection:** Gather a large, diverse set of white blood cell (WBC) images from different sources or generate synthetic data to improve generalization.
- **Data Augmentation:** Apply techniques like rotation, flipping, zooming, and contrast adjustments to enhance dataset variability and improve model robustness.

- **Normalization & Resizing:** Normalize pixel values (e.g., between 0 and 1) and resize images to standard dimensions for consistent input to the model.
- **Labeling:** Ensure that the images are properly labeled based on the type of WBCs (e.g., neutrophils, lymphocytes, monocytes, eosinophils, and basophils).

2. **Model Architecture Design:**
    - **Model Selection:** Choose suitable architectures such as CNNs, VGG16, ResNet50, or newer models based on the complexity of your data and desired accuracy.
    - **Customization:** Fine-tune pre-trained models on your dataset using transfer learning to improve results while reducing training time.
    - **Layer Optimization:** Experiment with different layers (convolution, pooling, dropout) to balance complexity, overfitting, and computational efficiency.
3. **Model Training:**

- **Loss Function:** Use categorical cross-entropy for multi-class classification of WBCs.
- **Optimizer:** Choose appropriate optimizers like Adam or SGD, with tuning of learning rates for better convergence.
- **Batch Size and Epochs:** Experiment with batch sizes and the number of epochs to avoid underfitting/overfitting while achieving optimal performance.
- **Regularization:** Apply techniques like dropout, L2 regularization, and early stopping to prevent overfitting and enhance generalization.

4. **Model Evaluation:**
    - **Performance Metrics:** Track metrics like accuracy, precision, recall, F1-score, and AUC to evaluate model performance.
    - **Confusion Matrix:** Use confusion matrices to assess classification accuracy across different WBC types.
    - **Validation and Test Sets:** Use k-fold cross-validation and independent test sets to ensure the model generalizes well.

Problem Statement

Current methods for identifying and classifying different types of white blood cells are time-consuming and often lead to errors, which negatively affects the accuracy of medical diagnoses. Advances in deep learning have shown promise for improving the classification of white blood cells in images, but a more effective solution is needed to increase both the accuracy and speed of these methods for better diagnostics.

Methodology

Proposed Model Architecture:

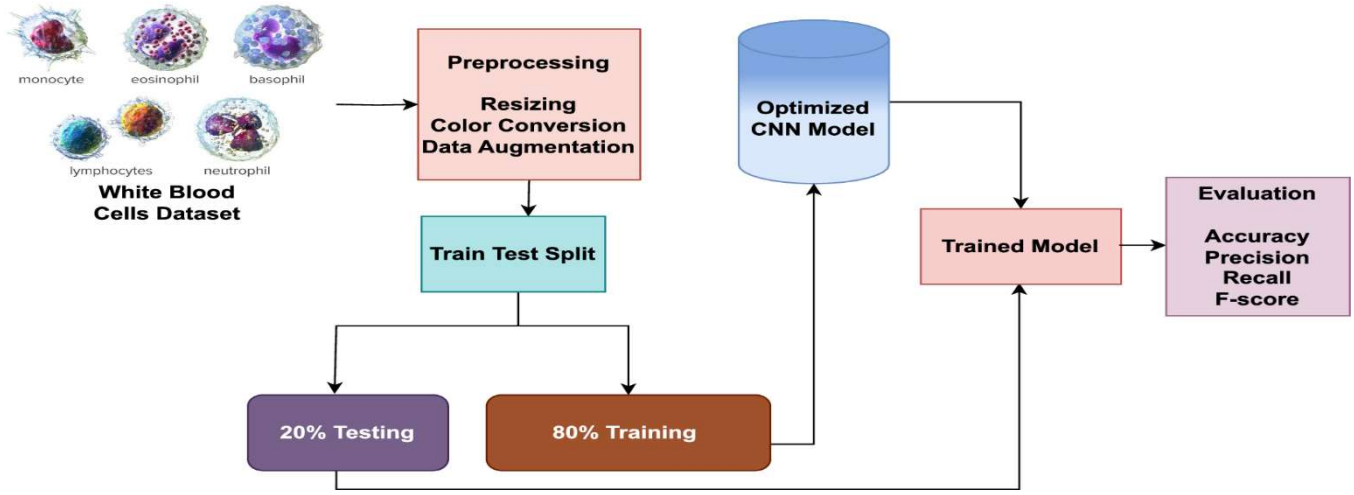

Fig 1. Proposed Model Architecture

The diagram illustrates the process flow for training and evaluating a **White Blood Cell (WBC) Image Classifier** using a Convolutional Neural Network (CNN). Here's a detailed description of each step involved:

1. **White Blood Cells Dataset:**
   - **Content**: The dataset consists of images of different types of white blood cells (WBCs), including monocytes, eosinophils, basophils, lymphocytes, and neutrophils.
2. **Preprocessing:**
   - **Resizing**: The images are resized to a standard dimension suitable for input into the CNN model.
   - **Color Conversion**: The images may be converted into a suitable color format (e.g., RGB or grayscale) based on the model requirements.
   - **Data Augmentation**: Techniques such as rotation, flipping, zooming, and contrast adjustments are applied to artificially increase the diversity of the dataset and prevent overfitting.

3. **Train-Test Split:**
    - The dataset is split into two parts: 80% for training and 20% for testing.
    - **Training Set (80%)**: This portion of the data is used to train the CNN model.
    - **Testing Set (20%)**: This portion is reserved for evaluating the model's performance after training.

4. **Training the Model:**
    - The model is trained on the training set using the optimized CNN architecture.
    - During training, the CNN model learns from the WBC images, adjusting its parameters through backpropagation and optimization to improve its accuracy in classifying different WBC types.
5. **Evaluation:**
    - After the model is trained, its performance is evaluated on the test set.
    - **Metrics**: Evaluation metrics include:
    - **Accuracy**: The percentage of correct predictions.
    - **Precision**: The proportion of positive identifications that were actually correct.
    - **Recall**: The proportion of actual positives that were correctly identified.
    - **F1-Score**: The harmonic mean of precision and recall, providing a balance between the two.

Data Collection and Preprocessing

The dataset contains a total of 17,092 images of individual normal cells, which were acquired using the analyzer CellaVision DM96 in the Core Laboratory at the Hospital Clinic of Barcelona. The dataset is organized in the following eight groups: neutrophils, eosinophils, basophils, lymphocytes, monocytes, immature granulocytes (promyelocytes, myelocytes, and metamyelocytes), erythroblasts and platelets or thrombocytes. The size of the images is 360 x 363 pixels, in format JPG, and they were annotated by expert clinical pathologists. The images were captured from individuals without infection, hematologic or oncologic disease and free of any pharmacologic treatment at the moment of blood collection.

This high-quality labelled dataset may be used to train and test machine learning and deep learning models to recognize different types of normal peripheral blood cells. To our knowledge, this is the first publicly available set with large numbers of normal peripheral blood cells, so that it is expected to be a canonical dataset for model benchmarking. Figure 2 shows the different types of white blood cell images.

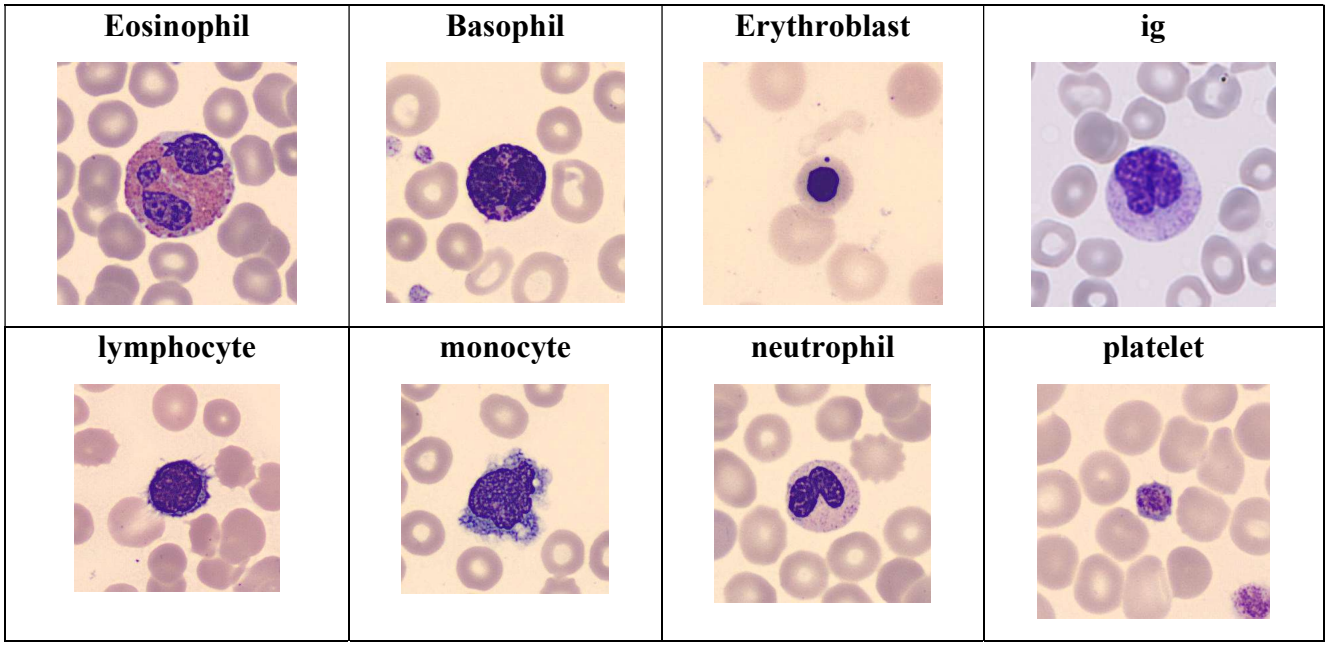

Figure 2. Different types of white blood cell images

Models

Here's a detailed breakdown of each model I have used for **White Blood Cell (WBC) Image Classification**:

1. **Deep Neural Network:**

   A Deep Neural Network (DNN) is a fully connected feed-forward neural network comprising multiple hidden layers between the input and output layers. In the context of white blood cell (WBC) image classification, the DNN takes the flattened image data as input, transforming the 2D image into a 1D vector. The hidden layers consist of several dense layers, where each neuron is fully connected to all neurons in both the preceding and following layers. Activation functions such as ReLU (Rectified Linear Unit) are typically used in hidden layers for efficient learning, while SoftMax is applied in the output layer for multi-class classification. Although DNNs have a simpler architecture and train faster compared to more complex models like CNNs, they often struggle with image data because they lack convolutional layers, which are essential for capturing spatial features. As a result, DNNs may not perform as well on intricate image recognition tasks and are more prone to overfitting.

2. **Convolutional Neural Network:**

   Convolutional Neural Networks (CNNs) are highly effective for image classification tasks due to their ability to learn spatial hierarchies from image data. Their architecture typically includes convolutional layers that automatically extract features such as edges and textures by sliding filters over the input image. Pooling layers then down sample the feature maps to reduce their spatial dimensions while retaining crucial information, with max pooling being a common technique. After feature extraction, the data is flattened and passed through fully connected layers for classification. To mitigate overfitting, dropout is often employed after these layers. CNNs excel in learning spatial patterns and are particularly well-suited for large image datasets, though they can be computationally intensive and require substantial data to generalize effectively.

3. **VGG16:**

   VGG16 is a widely used deep convolutional neural network renowned for its simplicity and effectiveness in image classification. Its architecture comprises 16 layers, including 13

convolutional layers and 3 fully connected layers. The convolutional layers utilize 3x3 filters with stride 1 and padding to capture fine-grained spatial details, while max pooling layers, applied after every two or three convolutional layers, reduce the spatial dimensions. The network ends with three dense layers for classification, using ReLU activation functions throughout except for the final layer, which employs SoftMax. Despite its effectiveness and suitability for transfer learning—enabling faster adaptation to new tasks such as white blood cell classification—VGG16 is computationally intensive, with around 138 million parameters, requiring significant memory and computing resources.

4. **VGG19:**

   VGG19 builds upon the VGG16 architecture by adding three additional convolutional layers, resulting in a total of 19 layers (16 convolutional and 3 fully connected). This increased depth enhances the network's ability to extract more complex features from images, making it particularly effective for datasets with intricate patterns. Like VGG16, VGG19 benefits from pre-trained models that facilitate transfer learning, enabling faster adaptation to specific tasks such as white blood cell classification. However, the added layers also make VGG19 more computationally demanding, requiring greater memory and processing power. Additionally, its complexity can lead to overfitting on smaller datasets if not properly fine-tuned.

5. **ResNet50:**

   ResNet50, or Residual Network with 50 layers, is a robust deep convolutional neural network designed to address the vanishing gradient problem in very deep architectures through the use of residual connections. These shortcut connections bypass one or more layers, facilitating more effective gradient flow during backpropagation. The network employs deeper convolutional layers with a bottleneck design—using 1x1 convolutions—to reduce the number of parameters compared to models like VGG. Instead of traditional fully connected layers, ResNet50 utilizes global average pooling to compress the feature map into a single value per feature map, followed by a SoftMax layer for classification. While ResNet50 is more parameter-efficient and performs exceptionally well in transfer learning, achieving state-of-the-art results with about 25 million parameters, it remains computationally intensive and may require fine-tuning of its residual block configurations.

Results

Table 1. compares the performance of five different machine learning models: DNN, CNN, VGG16, VGG19, and ResNet50. The CNN model demonstrated excellent performance with a high training accuracy of 98.18% and a validation accuracy of 88.60%, coupled with a low training loss of 8.81%. VGG16 outperformed the other models, achieving the highest training accuracy of 99.37% and a validation accuracy of 94.62%, with a minimal training loss of 1.85%. VGG19 also performed well, with a training accuracy of 90.67% and a validation accuracy of 87.66%, though it had a higher training loss of 28.77%. The DNN model showed moderate performance, with training and validation accuracies around 68%, but a high training loss of 78.67%. In contrast, ResNet50 struggled significantly, with low training and validation accuracies of 37.77% and 39.37%, respectively, and a very high training loss of 188%. Overall, VGG16 emerged as the best-performing model, while ResNet50 had the most difficulty in this comparison.

Model Name	Train Accuracy	Training loss	Validation Accuracy
DNN	68.43%	78.67%	68.53%
CNN	98.19%	8.81%	88.60%
VGG16	99.87%	1.85%	94.62%
VGG19	90.67%	28.77%	87.76%
ResNet50	37.77%	188%	39.37%

Table 1. show the result of different models

Figure 3. shows a line graph titled **"Model Accuracy Comparison,"** which compares the accuracy percentages of different models: DNN, CNN, VGG16, VGG19, and ResNet50. The graph includes three lines representing Train Accuracy (blue), Validation Accuracy (green), and Test Accuracy (orange). The y-axis represents accuracy percentages ranging from 0 to 100%, while the x-axis lists the model names.

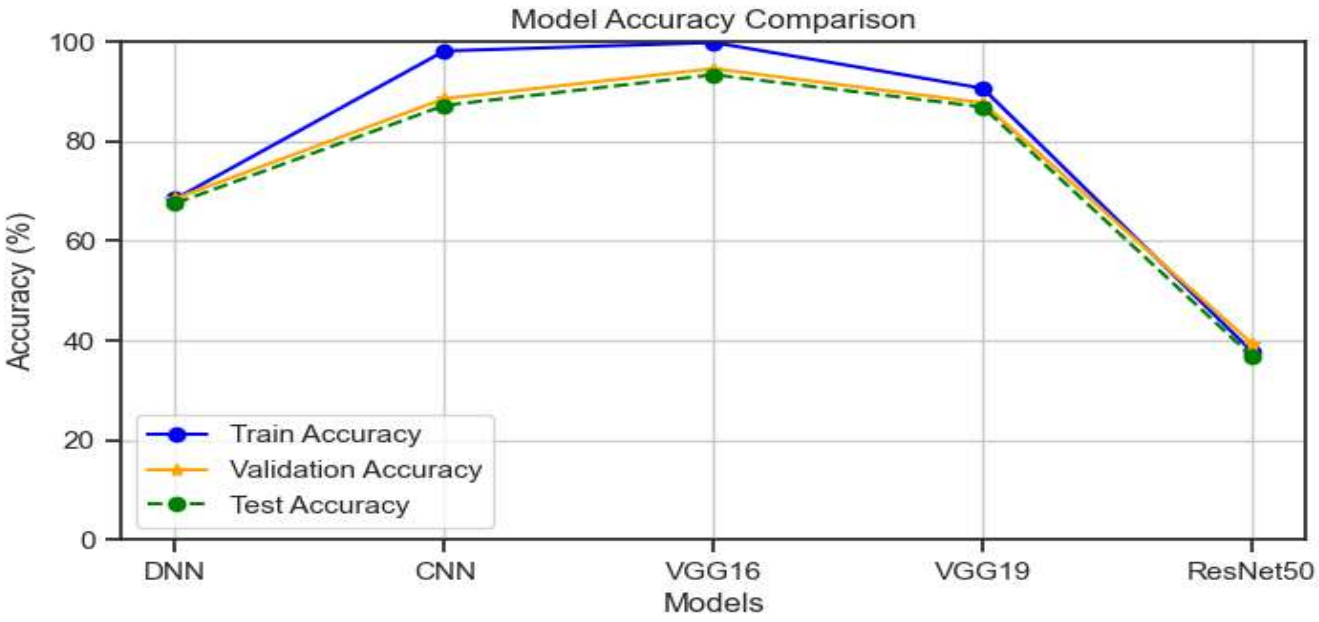

Figure 3. Model Accuracy Comparison

- **DNN**: Moderate performance with accuracies around 68%.
- **CNN**: Excellent performance with high accuracies, especially in training (98.18%) and validation (88.60%).
- **VGG16**: Outstanding performance with the highest accuracies, particularly in training (99.37%) and validation (94.62%).
- **VGG19**: Good performance with high accuracies, though slightly lower than VGG16.
- **ResNet50**: Poor performance with low accuracies and high training loss.

The graph visually represents the effectiveness of each model, highlighting VGG16 as the best performer and ResNet50 as the least effective in this comparison.

- **Classification reports and the number of instances for each class of VGG16 model:**

Class Name	Precision	Recall	F1-Score	Support
Basophil	0.91	0.95	0.93	237
Eosinophil	0.95	0.98	0.97	596
Erythroblast	0.91	0.96	0.94	294
Ig	0.89	0.88	0.88	602
Lymphocyte	0.96	0.88	0.92	241
Monocyte	0.89	0.84	0.86	307
Neutrophil	0.94	0.95	0.94	679
Platelet	0.99	1.00	0.99	462
Accuracy			0.93	3418
Macro Avg	0.93	0.93	0.93	3418
Weighted Avg	0.93	0.93	0.93	3418

Future Scope

- **Model Exploration:** Investigate additional models and architectures to further enhance classification performance.
- **Optimization:** Refine and optimize existing models to improve accuracy and reduce computational complexity.
- **Extended Applications:** Apply the developed models to other medical imaging tasks to explore their broader utility in clinical diagnostics.
- **Deployment:** Consider practical deployment strategies for integrating these models into clinical workflows to assist with real-time diagnostics.

Conclusion

This study successfully demonstrates that deep learning models can significantly enhance the accuracy of white blood cell (WBC) classification from images. Among the models evaluated, VGG16 emerged as the most effective, achieving the highest training and validation accuracies, while ResNet50 performed the weakest. The findings underscore the potential of using advanced neural network architectures for medical image analysis, specifically in improving the diagnosis of blood-related conditions.

The study highlights several key contributions:

1. **Optimized Model Framework:** The proposed CNN model framework reduces computational complexity while maintaining high accuracy, in contrast to more complex transfer learning models.
2. **Balanced Datasets:** Data augmentation techniques were employed to address dataset imbalance, thus mitigating overfitting risks and enhancing model performance.
3. **Comparative Analysis:** The effectiveness of the proposed model was rigorously compared against several established models and state-of-the-art approaches, demonstrating the superiority of VGG16 in this context.

These findings will be presented at a conference, contributing valuable insights to the field of medical image analysis and potentially improving clinical diagnostic practice.

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