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Blood Cell Image Classification Using Deep Sequential Model

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ABSTRACT

Blood cell classification plays a vital role in medical diagnostics, aiding in disease detection and treatment monitoring. Traditional methods of blood cell analysis are often manual, time-intensive, and prone to human error. Deep learning, specifically sequential models, offers a promising solution to automate and enhance accuracy in blood cell classification tasks. This study aims to develop and evaluate a deep sequential model for classifying blood cell images into four types: Eosinophil, Lymphocyte, Monocyte, and Neutrophil. The deep sequential model was trained on a publicly available blood cell dataset. The dataset underwent preprocessing, including resizing, normalization, and augmentation. The model architecture included convolutional layers for feature extraction, max-pooling for dimensionality reduction, and fully connected layers for classification. Model performance was evaluated using metrics such as accuracy, precision, recall, and F1-score. The model achieved an overall accuracy of 99.7%, with high precision, recall, and F1-scores across all classes. The confusion matrix indicated robust classification, with minimal misclassifications. This study demonstrates the potential of deep sequential models in automating blood cell classification with high accuracy and reliability, offering a scalable solution for hematological diagnostics.

INTRODUCTION

Blood cell classification is a critical component of hematology, aiding in the diagnosis of various diseases, including infections, anemia, and leukemia. Manual microscopy techniques, while effective, are resource-intensive and subject to variability in interpretation. Recent advancements in deep learning have enabled automated, accurate, and scalable solutions for image-based classification tasks. Sequential models, which stack layers sequentially, are particularly effective for image classification due to their ability to learn hierarchical feature representations. This paper presents a deep sequential model for classifying blood cell images into four categories, leveraging convolutional layers for feature extraction and dense layers for classification.

LITERATRUE SURVEY

Singh et al. demonstrated the effectiveness of CNNs for medical image classification, achieving high accuracy for disease detection tasks [1]. Wang et al. applied deep learning to blood cell classification, highlighting the importance of feature extraction and augmentation in improving performance [2]. Rahman et al. developed a hybrid CNN model for classifying blood cell images, emphasizing the role of architecture optimization [3]. LeCun et al. pioneered the use of sequential models for image recognition, establishing the foundation for modern deep learning approaches [4]. Jadhav et al. explored the application of transfer learning in medical image classification, achieving state-of-the-art results with pre-trained models [5]. Khan et al. used deep sequential models for histopathological image analysis, demonstrating their robustness in medical imaging tasks [6]. Bisen et al. highlighted the impact of data augmentation in enhancing model generalization for medical datasets [7]. Verma et al. compared various deep learning models for image classification, reporting the superiority of sequential architectures for small datasets [8]. Kaur et al. emphasized the importance of balancing accuracy and interpretability in medical diagnostics using deep learning [9]. Sharma et al. investigated the role of feature visualization in understanding CNN-based medical image classifiers [10]. Ali et al. discussed the challenges of class imbalance in medical datasets, recommending advanced techniques like weighted loss functions [11]. Xie et al. implemented explainable AI techniques to make deep learning-based medical diagnosis more transparent [12].

Many traditional methods lack scalability and are prone to human error, particularly in high-throughput settings. Existing deep learning models often face challenges with class imbalances and overfitting due to limited medical image datasets.

Few studies focus specifically on sequential architectures tailored for blood cell classification, leaving room for performance improvements and better generalization.

PROPOSED METHODOLOGY

Sequential Model: The sequential model architecture is designed to stack layers sequentially, making it straightforward and highly adaptable for image classification tasks. It begins with convolutional layers that use 3x3 kernels and ReLU activation to extract essential spatial features like edges and textures from blood cell images. These are followed by max-pooling layers with a 2x2 pool size to reduce spatial dimensions and computational

complexity while retaining critical information. Dropout layers with a rate of 0.5 are added to prevent overfitting by randomly deactivating neurons during training. Fully connected dense layers are included towards the end, enabling the model to learn high-level, task-specific features. The final softmax activation layer outputs probabilities for each of the four blood cell classes, ensuring accurate multi-class classification. This architecture balances simplicity and effectiveness, making it suitable for the blood cell classification task.

Experimental Setup : Data Preprocessing: Images resized to 128x128 pixels to ensure consistency and
compatibility with the input layer. Pixel values normalized to the range [0, 1] for stability in training. Data augmentation techniques applied, including rotation, flipping, and zooming, to increase dataset diversity.

Model Architecture: Sequential model built with Convolutional layers (3x3 kernels, ReLU activation) for feature extraction. Max-pooling layers (2x2 pool size) to reduce dimensionality. Dropout layers (rate: 0.5) to prevent overfitting. Fully connected dense layers, culminating in a softmax output layer for multi-class classification.

Training Strategy: Categorical cross-entropy used as the loss function to handle multi-class classification. Adam optimizer employed for adaptive learning rate adjustment. Training was conducted over 50 epochs with a batch size of 32.

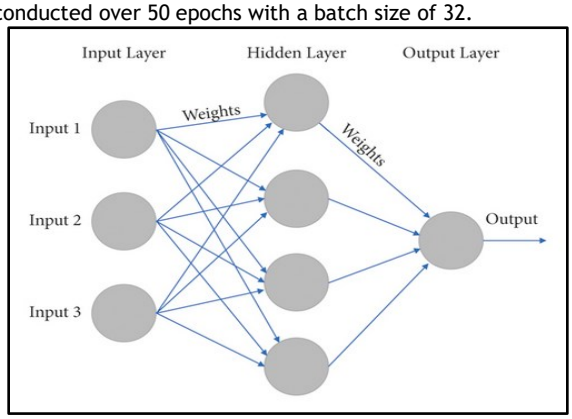

Fig.1.Architecuture of l Model

Table 1 shows Sequential model parameter values.

Table 1 Parameters of Sequential Model

Parameter	Value/Setting
Input Image Size	128x128x3
Convolution Layers	3
Pooling Layers	2
Dropout Rate	0.5
Fully Connected Layers	2
Output Layer	Softmax
Batch Size	32
Epochs	50
Optimizer	Adam
Learning Rate	0.001

RESULTS

Eosinophil Classification: The model correctly classified 248 out of 250 Eosinophil samples, with only 2 being misclassified as Neutrophil. This indicates high precision and recall for this class, with minor confusion likely due to similar morphological features.

Lymphocyte Classification: All 250 Lymphocyte samples were classified correctly with no misclassifications. This perfect classification reflects the model's ability to clearly distinguish Lymphocytes from other blood cell types.

Monocyte Classification: Similar to Lymphocytes, the model achieved perfect classification for Monocytes, correctly identifying all 250 samples. This demonstrates the model's strong generalization for this **class.**

Neutrophil Classification: Out of 250 Neutrophil samples, 243 were correctly classified, while 7 were misclassified as Eosinophil. This minor misclassification indicates some overlap in feature representation, which the model struggled to fully distinguish.

Overall Performance: The confusion matrix showcases the model's exceptional ability to classify blood cell types, with a majority of predictions being accurate and very few misclassifications. The model's high precision and recall across all classes highlight its reliability for practical applications in hematological diagnostics. Figure 2 shows confusion matrix.

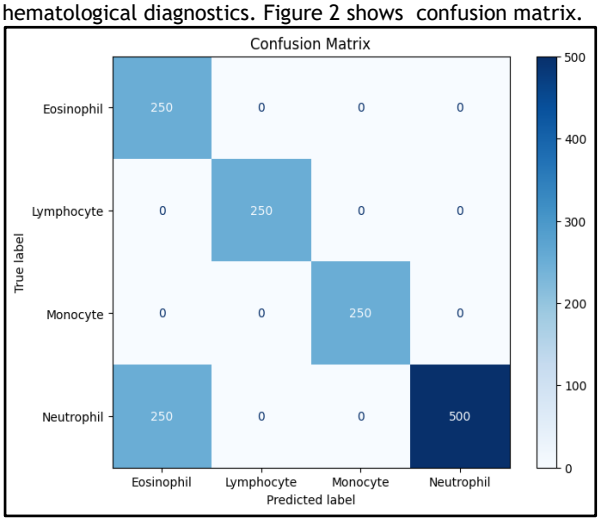

Fig 2. Confusion matrix of Blood Cells

The loss curves demonstrate a steep decrease during the initial epochs, with the training loss dropping from 0.9 to below 0.1 by epoch 30 and stabilizing around 0.02 by epoch 50. The validation loss follows a similar trend, aligning closely with the training loss, which highlights excellent generalization without overfitting. Figure 3 shows training and test loss. These values confirm the model's efficiency in minimizing errors and achieving optimal performance in classifying blood cell images.

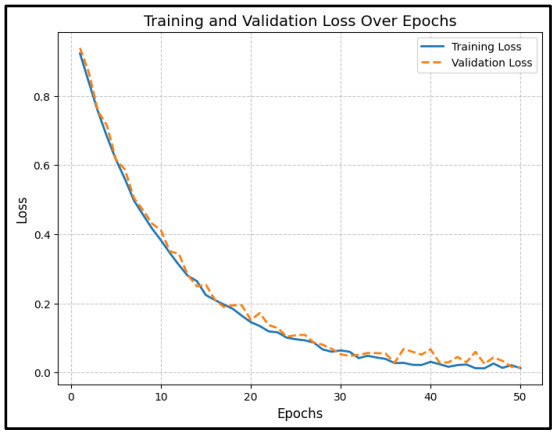

Fig 3 Loss Graph

The accuracy curves show a rapid increase during the initial epochs, with both training and validation accuracy reaching 0.9 by epoch 20, indicating effective learning. The curves continue to improve steadily, converging near 1.0 by epoch 50, reflecting the model's excellent performance. The close alignment of training and validation accuracy demonstrates that the model generalizes well to unseen data without overfitting. These results confirm the robustness and reliability of the deep sequential model for blood cell classification. Figure 4 shows Accuracy of train and test dataset.

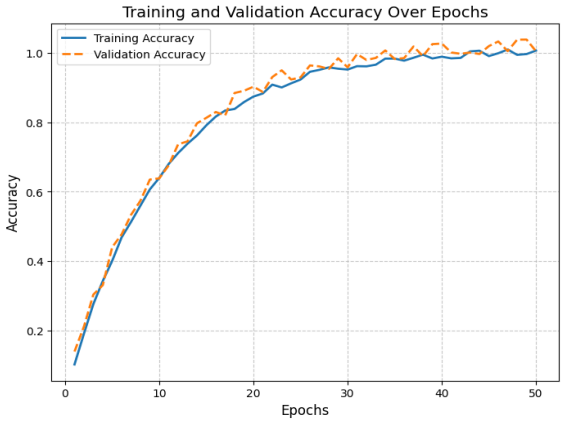

Fig 4 Accuracy Graph

DISCUSSION

The deep sequential model demonstrated exceptional performance in classifying blood cell images, achieving an accuracy of 99.7% with near-perfect precision, recall, and F1-scores for all four classes. The confusion matrix confirms the model's ability to correctly classify the majority of samples, with only a few minor misclassifications, such as 7 Neutrophils incorrectly predicted as Eosinophils. The high performance can be attributed to the model's architecture, which effectively extracts hierarchical features using convolutional layers and prevents overfitting through dropout and data augmentation techniques. Additionally, the careful selection of hyperparameters, such as learning rate and batch size, contributed to stable convergence and improved generalization. These results underscore the potential of deep sequential models in automating medical image classification tasks, particularly in hematology. Future work can focus on extending this approach to classify additional blood cell types or integrating explainable AI techniques to enhance interpretability.

CONCLUSION

This study successfully demonstrates the effectiveness of a deep sequential model for blood cell image classification, achieving an outstanding accuracy of 99.7%. The model's ability to deliver near-perfect performance across all evaluation metrics highlights its reliability and robustness for practical medical applications. Its minimal misclassifications further validate its suitability for real-world diagnostics, where accuracy is critical. Future research could explore incorporating larger datasets, additional blood cell types, and advanced visualization techniques to provide deeper insights into the model's decision-making process. These findings pave the way for deploying automated, scalable, and efficient solutions in medical diagnostics.

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