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Automated Bone Marrow Cell Classification for Haematological Disease using Machine Learning

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***Abstract*— Accurate classification of bone marrow cells is essential for diagnosing hematological disorders. However, manual classification is labor-intensive and susceptible to human error. Previous approaches, including CNN combined with SVM, CNN with XGBoost, and Siamese networks, faced challenges related to limited accuracy and poor generalization. This study utilizes transfer learning to automate and enhance the classification process. A dataset containing 170,000 expertly annotated bone marrow cell images was used to evaluate the performance of four pretrained deep learning models—VGG16, ResNet50, InceptionV3, and EfficientNetB5. These models were enhanced with additional layers and trained using data augmentation techniques. Among them, EfficientNetB5 achieved the highest performance, attaining a training accuracy of 98.47% and a validation accuracy of 89.39%, outperforming the other models. The results indicate that transfer learning models can significantly improve diagnostic accuracy and efficiency. This study provides a robust solution for real-time, automated hematological analysis, addressing limitations in current diagnostic practices.**

***Index Terms*— Hematological disorders, Bone marrow cell classification, deep learning, EfficientNetB5, VGG16, ResNet50, InceptionV3, automated diagnosis, medical image analysis.**

I. INTRODUCTION

Classification of bone marrow cells is essential for the diagnosis of hematological conditions such anemia and leukemia. The recognition and classification of Bone marrow smears containing various cell types are necessary for precise medical diagnosis and planning for therapy. Traditionally, pathologists carry out this work by hand, which is prone to human error and takes a lot of time. Factors such as inter-observer variability and fatigue can significantly affect the accuracy of these diagnoses. With the growing prevalence of hematological disorders globally, there is an urgent need for reliable and efficient diagnostic tools to support clinical decision-making. Automated solutions can alleviate these challenges by offering consistent and rapid analysis, thereby enhancing diagnosis precision and lessening the workload for medical personnel.

Several machine learning and deep learning techniques have been investigated in the past for automating the classification of bone marrow cells. Siamese models neural networks have been applied, but these methods exhibit significant limitations. For example, CNN+SVM and CNN+XGBoost demonstrated low accuracy (32% and 28%, respectively), rendering them impractical for clinical use. Although Siamese neural networks achieved 91% accuracy, the model required significant computational resources and was prone to overfitting when generalized to larger datasets.

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Additionally, these methods often lacked scalability and robustness, which are crucial for real-world applications. Such limitations highlight the need for improved models that can provide higher accuracy, generalizability, and computational efficiency, particularly for datasets containing diverse and complex images of bone marrow cells.

The primary objective of this study is to develop an effective, automated framework for bone marrow cell classification using transfer learning. Four state-of-the-art architectures—VGG16, ResNet50, InceptionV3, and EfficientNetB5—are evaluated based on computational efficiency, training accuracy, and validation accuracy. The study aims to identify the optimal architecture by fine-tuning and optimizing each model. To improve generalization and handle intra-class variability, data augmentation techniques are incorporated throughout the training process.

The framework is designed with scalability and clinical applicability in mind, and its performance is benchmarked against existing methods. This study seeks to bridge the gap between theoretical advancements in deep learning and real-world applications in hematological diagnostics.This work contributes several key advancements to the field of automated medical image analysis

II. Related Work

Recent progress in automated bone marrow cell classification has been driven by innovative applications of deep learning (DL) and machine learning (ML) methodologies. One approach employed ResNeXt-50 alongside XGBoost, forgoing traditional feature extraction in favor of modeling inter-image similarities and differences. This was accomplished through a Siamese neural network, which achieved 91% accuracy on training data and 84% on validation data, demonstrating strong generalization capabilities [2]. To enhance localization and tackle class imbalance, the use of YOLO integrated with Grad-CAM was proposed, alongside data augmentation techniques [3].

To further address class imbalance challenges, Guo et al. (2022) applied advanced signal processing techniques, leading to marked improvements in classification performance [4]. Meanwhile, Chandradevan et al. (2020) utilized ML techniques for analyzing bone marrow aspirates, specifically focusing on nonneoplastic cell classification, a crucial area in diagnostic hematology [5].

Early work in the field includes Theera-Umpon (2005), who introduced a segmentation and classification system for white blood cells using fuzzy logic—a significant milestone in automated hematologic analysis [7]. More recently, Wang et al. (2022) demonstrated the effectiveness of CNNs in processing whole-slide bone marrow images, emphasizing the scalability of DL techniques in clinical imaging [8][9]. Similarly, Dorini et al. (2007) contributed to white blood cell segmentation through morphological operations and scale-space methods, laying the groundwork for contemporary automation approaches [10].

In tackling the challenge of overlapping cells, Wang and Song (2007) utilized form analysis for segmenting cell clusters, enhancing interpretability in complex image regions [11]. Ma et al. (2020) presented a hybrid model combining DC-GAN and ResNet, showcasing the potential of generative models to enrich datasets and improve feature representation [12].

Vyshnav et al. (2020) introduced a deep learning model targeting multiple myeloma detection, reinforcing CNNs as reliable tools in hematologic cancer diagnosis [13].

Liu et al. investigated the interactions between bone marrow mesenchymal stem cells and cancer cells, highlighting their roles in therapy resistance and disease progression [14]. Integration of CNNs with SVMs by Truong et al. further improved white blood cell classification accuracy [15]. In another significant effort, Matek et al. leveraged expert-annotated cytology data to train deep neural networks for high-precision differentiation of various bone marrow cell morphologies [16].

The advancement of such technologies has been greatly facilitated by publicly available resources like the Cancer Imaging Archive (TCIA), which supports algorithm development and validation through extensive repositories of annotated medical images [17][21]. The availability of curated cytology datasets [18][19][20] has also standardized the training and evaluation process, promoting reproducible research and accelerating progress in automated diagnostic systems.

III. Methods and Materials

A. Dataset

The dataset used in this study comprises 170,000 expertly annotated bone marrow cell images, derived from bone marrow smears of 945 patients with various hematological disorders. It includes multiple cell types such as

neutrophils, eosinophils, lymphocytes, and others, each labeled by specialists. Due to significant class imbalance, data augmentation was employed to achieve balanced representation across classes.
To align with pre-trained transfer learning models, all images were resized to 224×224 pixels. Stratified sampling was used to split the dataset into training and validation sets in a 90:10 ratio, preserving class distributions.

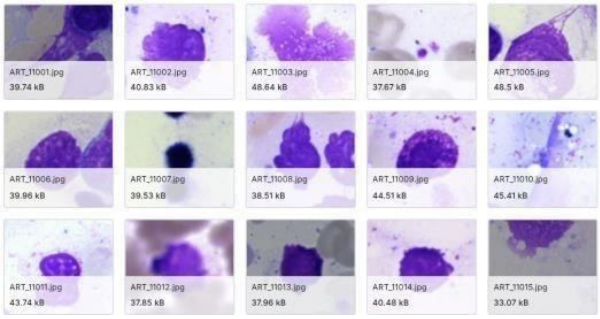

Fig 1: Sample dataset Preprocessing

To enhance generalization and address data imbalance, various augmentation techniques were applied, including horizontal flipping, rotation, zooming, and brightness adjustment. All images were resized to 224×224×3 and normalized to a [0, 1] pixel value range. Real-time augmentation was performed using TensorFlow's Keras ImageDataGenerator class, introducing variability and helping to reduce overfitting.

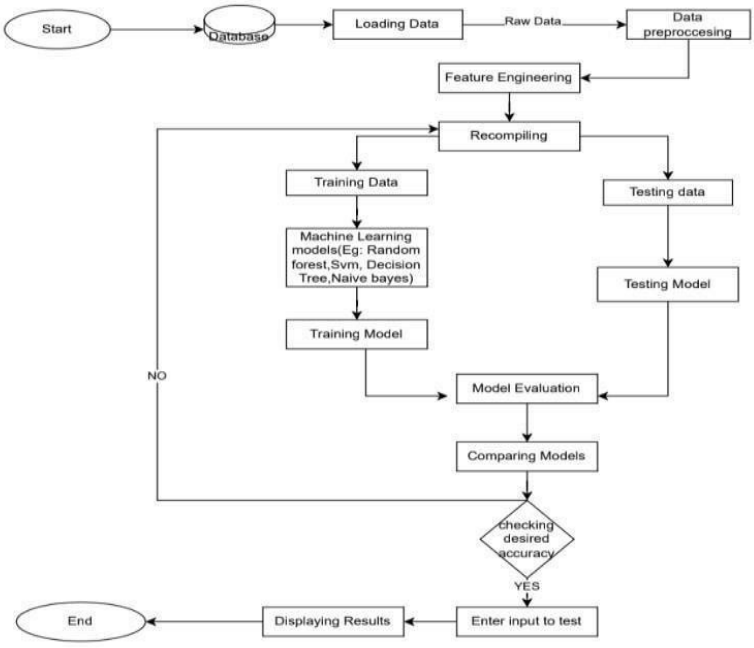

Fig 2: Flow diagram

B. Transfer Learning Models

Four pre-trained models—EfficientNetB5, ResNet50, InceptionV3, and VGG16—were fine-tuned using ImageNet weights. Custom layers were added, including Batch Normalization, a Dense layer (256 units, ReLU, L1/L2 regularization), Dropout (50%), and a final Dense layer with softmax activation. These models acted as feature extractors tailored for bone marrow cell classification

C. Training Setup

Models were trained for 25 epochs using the Adamax optimizer (learning rate = 0.001) and categorical crossentropy loss. Training used a batch size of 32, with early stopping and model checkpoints to prevent overfitting. Performance was monitored using accuracy and validation accuracy

D. Evaluation Metrics

Model performance was assessed using accuracy, validation accuracy, loss, confusion matrix, precision, recall, and F1-score. These metrics provided insights into both overall and class-wise performance. Accuracy/loss curves were plotted for visualization, and the best model was selected based on comprehensive evaluation results.

IV. Results and Analysis

A. Model Performance Comparison

In this study, four state-of-the-art transfer learning models—VGG16, ResNet50, InceptionV3, and EfficientNetB5—were trained and evaluated on a curated bone marrow cell image dataset to assess their classification capabilities. The models were fine-tuned using consistent training protocols, and their performance was assessed based on training accuracy (TA), training loss (TL), validation accuracy (VA), and validation loss (VL).

The performance metrics are summarized in Table 1 below:

TABLE I: COMPARISON OF OUR MODELS

Model	TA	TL	VA	VL
VGG16	55.79%	2.6029	40.91%	2.9810
ResNet50	99.66%	2.9730	87.88%	3.1348
InceptionV3	98.04%	3.6510	87.88%	3.8751
EfficientNetB5	98.47%	3.1167	89.39%	3.2196

Table 1: Performance comparison of the proposed transfer learning models on the bone marrow cell dataset.

EfficientNetB5 outperformed all models with a validation accuracy of 89.39% and strong generalization, while VGG16 showed the weakest performance (40.91% validation accuracy) due to its shallow architecture. ResNet50 and InceptionV3 achieved high training accuracy but showed signs of overfitting, with validation accuracies of 87.88%.

B. Accuracy and Loss Trends

Training and validation curves revealed that VGG16 severely underfit, with low accuracy and high loss. ResNet50 and InceptionV3 showed strong training performance but moderate overfitting. EfficientNetB5 achieved the best balance, with 98.47% training and 89.39% validation accuracy, indicating strong generalization and robustness.

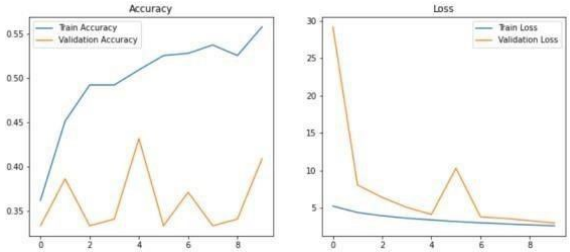

Fig 3: VGG16 Graph

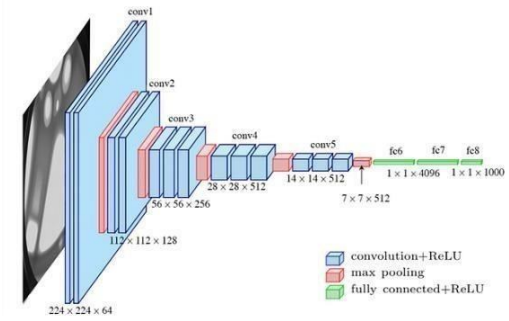

Fig4: VGGNet Architecture

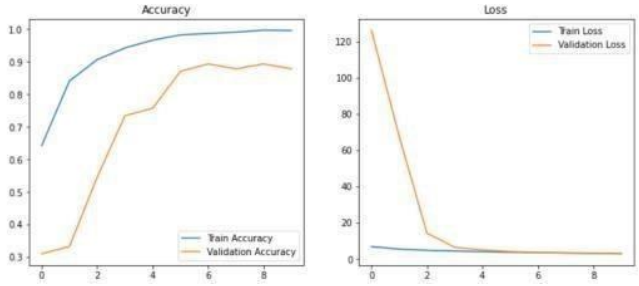

Fig5: RESNET 50 line plot

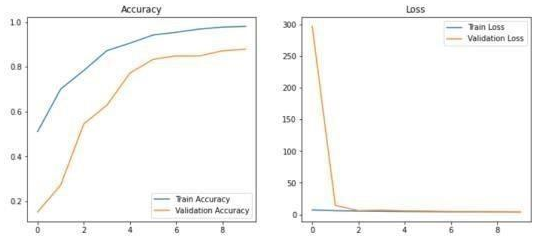

Fig6: Inception V3

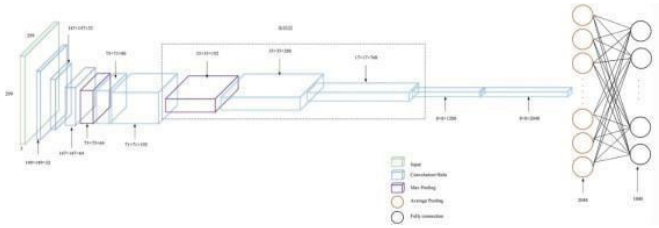

Fig6: Inception v3 architecture

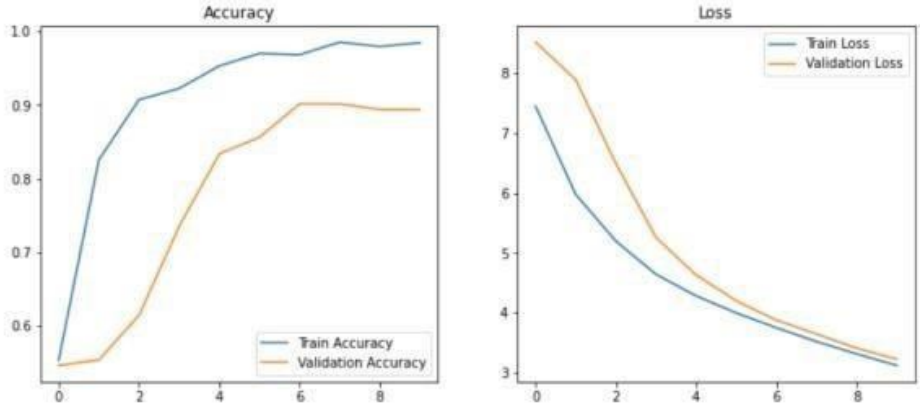

Fig7: Efficientnetb5

C. Comparison with Existing Work

This study significantly improves upon previous research that used CNN in additon with SVM and CNN in addition with XGBoost, which achieved only 32% and 28% accuracy, respectively. Even a Siamese network, which was previously considered optimal, reached 91% accuracy but had computational inefficiencies. In contrast, EfficientNetB5 provides a strong alternative with comparable accuracy and better computational efficiency.

V. CONCLUSION

This study's main goal was to use deep learning models to improve bone marrow cell classification in order to increase the efficiency and diagnostic accuracy of hematological analysis. This method seeks to lessen the need for manual assessment by automating the classification process, which will reduce errors and improve diagnosis uniformity. The study used sophisticated deep learning architectures to reliably classify bone marrow cell pictures. This automated system provides a dependable and effective way to distinguish between various types of bone marrow cells, which not only expedites diagnostic procedures but also advances hematological analysis. four state-of-the-art transfer learning models: EfficientNetB5, ResNet50, InceptionV3, and VGG16. 170,000 expert-annotated photos made up the dataset, which was preprocessed, enhanced, and used to train and assess .
Compared to previous studies, which employed CNN+SVM and CNN+XGBoost (32% and 28% accuracy, respectively) and the Siamese network (91% accuracy), our findings indicate that EfficientNetB5 provides a more balanced and computationally efficient solution for automated bone marrow cell classification.

DISCUSSION AND FUTURE WORK

A. Discussion

Model performance varied significantly by architecture. VGG16 underperformed due to its shallow design, while EfficientNetB5 achieved the highest validation accuracy (89.39%) and best generalization. ResNet50 and InceptionV3 showed signs of overfitting, underscoring the need for careful architecture selection in medical imaging tasks.

B. Future Work

Future efforts will focus on enhancing generalization through advanced regularization, improved data augmentation, and addressing class imbalance using GANs, SMOTE, or class-weighted losses. Exploration of

Vision Transformers, Siamese Networks, GradCAM for interpretability, YOLO for ROI detection, and deployment via TensorFlow Lite or ONNX is planned to build a robust and deployable diagnostic tool.

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