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ISSN 2249-3352 (P) 2278-0505 (E)
Cosmos Impact Factor-5.86

Multiclass Classification Of White Blood Cells From Histological Images Using Deep Convolutional Neural Networks

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ABSTRACT

White Blood Cell (WBC) classification plays a vital role in the diagnosis of various hematological disorders, including infections, leukemia, and immune system dysfunctions. Accurate and early identification of different types of WBCs—such as neutrophils, eosinophils, lymphocytes, monocytes, and basophils—from histological images is essential for effective clinical decision-making. Traditional machine learning algorithms have shown promise but often lack robustness and scalability when handling complex image-based features. In this study, we investigate the problem of multiclass classification of WBCs from histological images by evaluating both traditional and deep learning methodologies. As part of the existing system, Decision Tree Classifier (DTC) and Multinomial Naive Bayes (MNB) classifiers were employed. These models demonstrated moderate performance, leveraging handcrafted features and statistical distributions but struggling with high intra-class variability and subtle morphological differences across WBC classes. The models lacked the capacity to capture spatial hierarchies and contextual patterns within the histopathological image data. To overcome the limitations, we propose an advanced Deep Learning-based Convolutional Neural Network (DLCNN) architecture integrated with an Attention Mechanism Enhancement (AME) module. The proposed model automatically learns hierarchical spatial features and utilizes attention mechanisms to focus on the most relevant regions of the image, thereby improving discriminative capability across WBC classes. Extensive experimentation on a labelled histological WBC image dataset demonstrated that the proposed DLCNN+AME model significantly outperformed the existing classifiers in terms of accuracy, precision, recall, and F1-score. The work highlights the effectiveness of attention-augmented deep CNN models in medical image classification tasks, providing a reliable and scalable solution for automated hematological diagnostics. The results reinforce the importance of integrating deep learning with attention mechanisms for high-accuracy classification in complex biomedical imaging applications.

Keywords: Histological Image Analysis, Cell Morphology Analysis, Multiclass Image Classification, AI for Disease Detection, Automated Blood Cell Analysis

1. INTRODUCTION

White Blood Cells (WBCs), or leukocytes, are a critical component of the human immune system and serve as the body's primary defense mechanism against infections and diseases. Identifying and classifying different types of WBCs—such as neutrophils, lymphocytes, monocytes, eosinophils, and basophils—are essential in the diagnostic process for various medical conditions including leukemia, autoimmune disorders, and infections. Traditionally, such classification is performed manually by hematologists through microscopic examination of stained blood smears, a process that is labor-intensive, time-consuming, and prone to human error. In recent years, machine learning and deep learning technologies have emerged as effective tools for automating medical image analysis. However,

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ISSN 2249-3352 (P) 2278-0505 (E)
Cosmos Impact Factor-5.86

while conventional machine learning algorithms depend heavily on handcrafted features, deep learning—especially Convolutional Neural Networks (CNNs)—enables automatic feature extraction and hierarchical pattern learning. This study explores the application of CNNs enhanced with attention mechanisms for multiclass classification of WBCs from histological images, comparing their performance against traditional classifiers like Decision Tree Classifier (DTC) and Multinomial Naive Bayes (MNB).

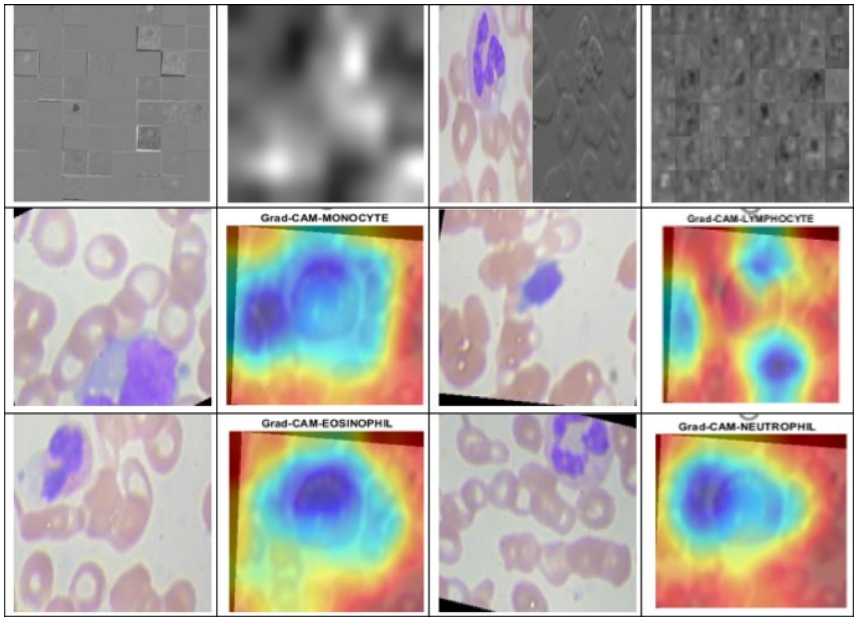

Fig 1: DL technique to detect WBC

The study aims to enhance the performance of traditional machine learning approaches—such as Decision Tree Classifier (DTC) and Multinomial Naive Bayes (MNB)—by introducing a Deep Convolutional Neural Network (DLCNN) architecture integrated with an Attention Mechanism Enhancement (AME). This integration is intended to improve the model's ability to focus on the most discriminative regions of the images, thereby increasing classification accuracy. By evaluating the proposed model against existing systems using comprehensive performance metrics, this research seeks to provide a robust, scalable, and practical solution for real-time clinical use in hematology, ultimately supporting healthcare professionals in making faster and more reliable diagnostic decisions.

2. LITERATURE SURVEY

Alzubaidi et al. [4] introduced a new robust and effective deep Convolutional Neural Network to classify Red Blood Cells (RBCs) in three classes namely: normal ('N') abnormal (sickle cells anemia type ('S')) and miscellaneous ('M'). To improve the results further, we have used this model as features extractor then this work applied an error-correcting output codes (ECOC) classifier for the classification task. This model with ECOC showed outstanding performance and high accuracy of 92.06%. Rahman et al. [5] experimented the existing standard pre-processing techniques from the literature. In addition, several other complex architectures have been implemented and tested to pick the best performing model. A holdout test has also been conducted to verify how well the proposed model generalizes on unseen data. This best model achieved an accuracy of almost 97.77%. Roopa et al. [6] demonstrated classification of white blood cells into six types namely lymphocytes, monocytes, neutrophils, eosinophils, basophils and abnormal cells. This work provided the comparison of traditional image

processing approach and deep learning methods for classification of white blood cells. This work also evaluated neural network classifier results for hand-crafted features and obtained the average accuracy of 99.8%. And used full training and transfer learning approaches of convolutional neural network for the classification. An accuracy around 99% was obtained for full training CNN. Malkawi et al. [7] classified the microscopic WBCs images using a hybrid system where Convolutional Neural Network (CNN) used as features extractor and different machine learning algorithms used as classifiers, then the performances of these classifiers were evaluated to recognize the best of them. These algorithms included Support Vector Machine (SVM), k-Nearest Neighbor (KNN) and Random Forest, for training and test parameters this framework used five features that were extracted from the images. According to results of performance, the RF performed better than the other methods with a testing accuracy reached 98.7%.

Matek et al. [8] compiled an annotated image dataset of over 18,000 white blood cells, use it to train a convolutional neural network for leukocyte classification and evaluate the network's performance by comparing to inter- and intra-expert variability. The network classified the most important cell types with high accuracy. It also allows us to decide two clinically relevant questions with human-level performance: (1) if a given cell has blast character and (2) if it belongs to the cell types normally present in non-pathological blood smears. This framework approach holds the potential to be used as a classification aid for examining much larger numbers of cells in a smear than can usually be done by a human expert. This will allow clinicians to recognize malignant cell populations with lower prevalence at an earlier stage of the disease. Sadafi et al. [9] presented an active learning framework that identifies the most relevant samples from a large set of not annotated data for further expert annotation. Applied to brightfield images of red blood cells with seven subtypes, this work trained a faster R-CNN for single cell identification and classification, calculate a novel confidence score using dropout variational inference and select relevant images for annotation based on (i) the confidence of the single cell detection and (ii) the rareness of the classes contained in the image. This framework showed that this approach leads to a drastic increase of prediction accuracy with already few annotated images. This original approach improves classification of red blood cell subtypes and speeds up the annotation. This important step in diagnosing blood diseases will profit from our framework as well as many other clinical challenges that suffer from the lack of annotated training data. Parab et al. [10] utilized the algorithm which can extract the feature of each segmented cell image and classify it into 9 various types. Images of blood slides were collected from the hospital. The overall accuracy was 98.5%. The system has been developed to provide accurate and fast results that can save patients' lives. Paravil et al. [11] tried to devise a methodology for automation by using feature fusion. For feature extraction, various fusion techniques using transfer-learning approaches such as Densely connected convoluted neural networks (DenseNet201) and VGG16 (Visual Geometry Group 2016) were proposed. The classification results are compared using various performance metrics such as Accuracy, Precision, Recall, and F1-Score. The maximum accuracy of 89.75% was obtained with the help of feature fusion combined with the Convolutional Neural Network (CNN) classifier. Yildirim et al. [12] proposed one of the most popular neural networks, convolutional neural network (CNN) is selected to differentiate between different types of white blood cells, namely, eosinophil, lymphocyte, monocyte and neutrophil. The CNN was coupled with Alexnet, Resnet50, Densenet201 and GoogleNet in turn, and trained with the Kaggle Dataset. Then, Gaussian, and median filters were applied separately to the images in the database. The new images were classified again by the CNN with each of the four networks. The results obtained after applying the two filters to the images were better than the results obtained with the original data. The research results make it easier to diagnose blood related diseases.

3. PROPOSED SYSTEM

The project focuses on the multiclass classification of white blood cells (WBCs) from histological images using deep learning techniques. Initially, a dataset comprising labeled WBC images is collected from reliable public sources. These images undergo preprocessing steps such as resizing, normalization, noise reduction, and data augmentation to ensure consistency and robustness. Traditional machine learning models like Decision Tree Classifier (DTC) and Multinomial Naive Bayes (MNB) are implemented to establish baseline performance. To address the limitations of these models in handling complex image features, a Deep Convolutional Neural Network (DLCNN) enhanced with an Attention Mechanism (AME) is proposed. This model is capable of learning spatial and hierarchical features while focusing on the most informative regions of the image. The model is trained and evaluated using performance metrics like accuracy, precision, recall, and F1-score, and is shown to outperform traditional approaches significantly. The project concludes with an analysis of results and highlights the potential for real-time deployment in clinical environments through an interactive interface or integration into diagnostic systems.

Step 1: Dataset Collection

The project begins with the collection of a labeled dataset containing histological images of various types of white blood cells (WBCs). Publicly available medical image datasets such as the LISC Dataset, BCCD Dataset, or Raabin-WBC are considered, containing microscopic images labeled into classes like neutrophils, eosinophils, lymphocytes, monocytes, and basophils. Images are typically in JPEG/PNG format with associated metadata and ground truth labels. It is important to ensure data diversity in terms of staining, lighting conditions, and WBC morphological variations for model robustness.

Step 2: Data Preprocessing

Images are resized to standardized dimensions (e.g., 128x128 or 224x224) for uniform input to the model. Background noise is removed using filtering techniques like Gaussian blur or median filters. Pixel values are normalized to a range of [0,1] or [-1,1] for faster convergence during training. WBC type labels are converted into numerical or one-hot encoded format. Data augmentation techniques such as rotation, flipping, and zooming are applied to increase dataset size and improve generalization.

Step 3: Baseline Model Implementation

Traditional classifiers like Decision Tree Classifier (DTC) and Multinomial Naive Bayes (MNB) are implemented to establish baseline performance. Images are converted to numerical features using methods like Histogram of Oriented Gradients (HOG), color histograms, or manual shape descriptors. These models are trained using a train-test split (e.g., 80:20) or cross-validation. It is observed that traditional models struggle with high-dimensional image data and lack spatial context awareness.

Step 4: Deep Learning Model Development (DLCNN with AME)

A Deep Convolutional Neural Network (DLCNN) is designed with multiple convolutional, pooling, and dense layers. An Attention Module such as CBAM, SE-block, or a self-attention mechanism is integrated to allow the model to focus on informative regions of the image. The model is trained using categorical cross-entropy as the loss function and optimizers like Adam or SGD. Techniques

like early stopping, dropout, and learning rate schedulers are used to improve training and prevent overfitting.

Step 5: Model Evaluation

The model's performance is evaluated using metrics such as Accuracy, Precision, Recall, F1-Score, and Confusion Matrix. Evaluation is done using K-fold cross-validation or a hold-out test set. The performance of DLCNN with AME is compared with traditional models. Visualization tools like t-SNE plots, Grad-CAM, and attention maps are used to understand model decisions and interpretability.

Step 6: Result Analysis

The proposed DLCNN with AME shows significant improvement in classification accuracy and robustness compared to traditional classifiers. Confusion matrix analysis helps identify commonly misclassified WBC types. The model is also tested on external or unseen datasets to evaluate its generalization and real-world applicability.

Step 7: Deployment (Optional/Future Scope)

A simple GUI or web interface using Flask or Tkinter can be designed for real-time WBC image classification. There is potential for integrating this system into laboratory hardware or cloud-based diagnostic platforms for scalable and automated medical analysis.

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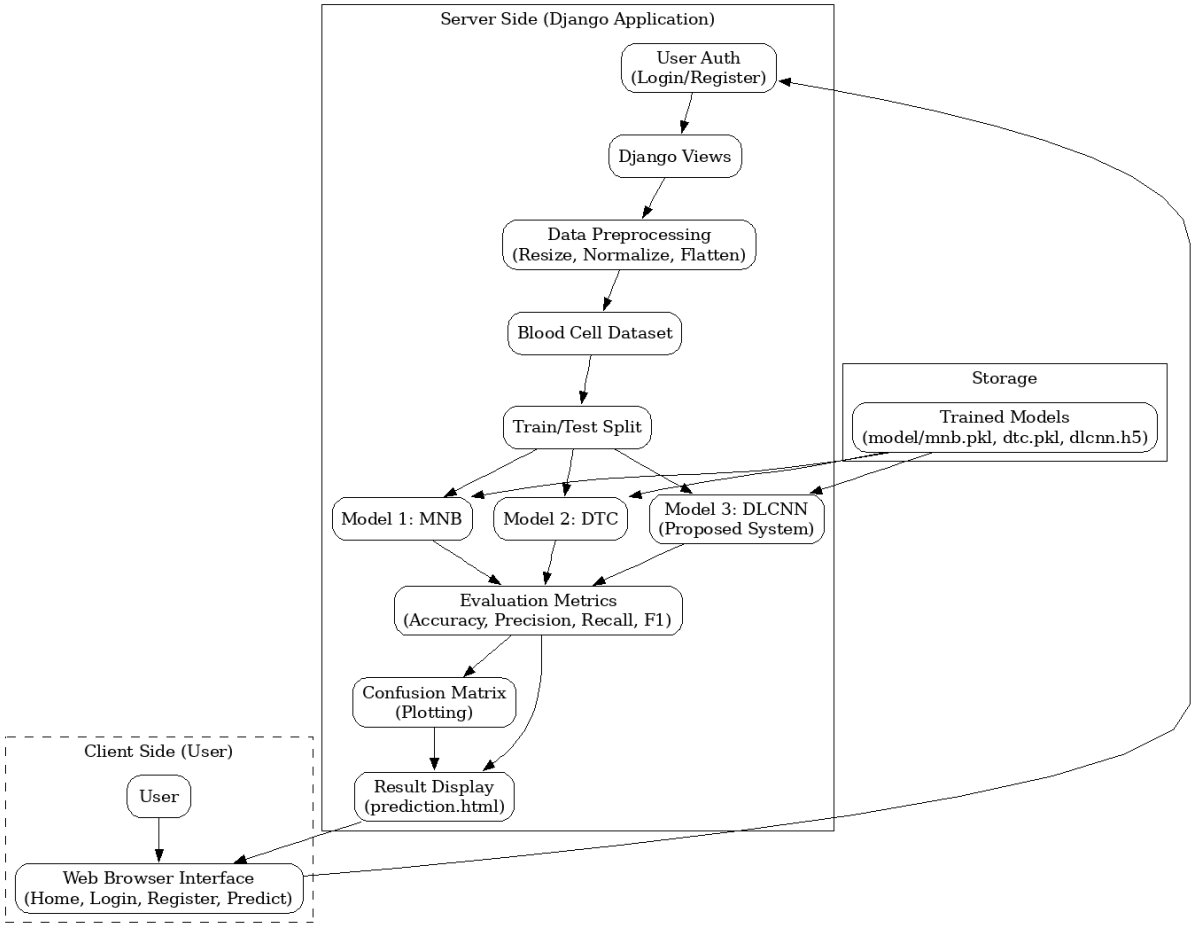

Fig. 2: Block diagram of proposed system.

3.2 Data Preprocessing

Data pre-processing is a process of preparing the raw data and making it suitable for a machine learning model. It is the first and crucial step while creating a machine learning model. When creating a project, it is not always a case that we come across the clean and formatted data. And while doing any operation with data, it is mandatory to clean it and put in a formatted way. So, for this, we use data pre-processing task.

Step 1: Image Resizing

All histological images are resized to a fixed dimension (commonly 128×128 or 224×224 pixels). This ensures that the input to the neural network has a uniform shape and reduces computational load. Resizing also helps in batch processing and model compatibility.

Step 2: Color Space Conversion (if needed)

Images are usually in RGB format, but in some cases, conversion to grayscale or other color spaces (like HSV or LAB) may be done if it helps in emphasizing specific cellular structures. However, for deep learning models like CNNs, RGB is typically retained for richer feature learning.

Step 3: Noise Removal

Histological images may contain unwanted background textures or artifacts. Filters such as Gaussian blur, median filters, or bilateral filters are applied to remove such noise. This step enhances important features like cell edges and boundaries for better model learning.

Step 4: Normalization

Pixel values are normalized to scale them within a consistent range. Common normalization techniques include:

- Min-Max Normalization: Scaling pixel values between 0 and 1.
- Z-score Normalization: Adjusting to mean = 0 and standard deviation = 1. This step helps in faster model convergence and improved numerical stability.

Step 5: Label Encoding

The WBC types (e.g., neutrophil, eosinophil, monocyte, lymphocyte, basophil) are converted from categorical text labels to numerical format. This is done using:

- Label Encoding (e.g., neutrophil = 0, lymphocyte = 1, etc.) or
- One-Hot Encoding for feeding into neural networks during training.

Step 6: Data Augmentation

To increase the dataset size and model robustness, various augmentation techniques are applied:

- Rotation (e.g., ±15°)
- Flipping (horizontal and vertical)
- Zooming (in and out)
- Shifting (height/width translation)
- Brightness/Contrast Adjustment These synthetic variations simulate real-world imaging diversity and help prevent overfitting.

Step 7: Data Splitting

- Training Set (usually 70-80%): For model learning
- Validation Set (10-15%): For hyperparameter tuning and monitoring overfitting
- Testing Set (10-20%): For final evaluation of model performance Stratified sampling may be used to ensure class balance in each split..

3.3 ML Model Building

3.3.1 Deep Learning-Based Convolutional Neural Network (DLCNN)

Deep Learning-based Convolutional Neural Networks (DLCNN) are a class of neural networks designed to automatically learn spatial hierarchies of features from image data. In WBC classification, DLCNN leverages multiple layers of convolutional operations, pooling layers, and fully connected layers to extract increasingly complex patterns from the histological images of white blood cells. Unlike traditional machine learning classifiers, which rely on manual feature extraction, DLCNN directly

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learns optimal features from raw image data through its deep architecture, which makes it highly effective for complex image recognition tasks.

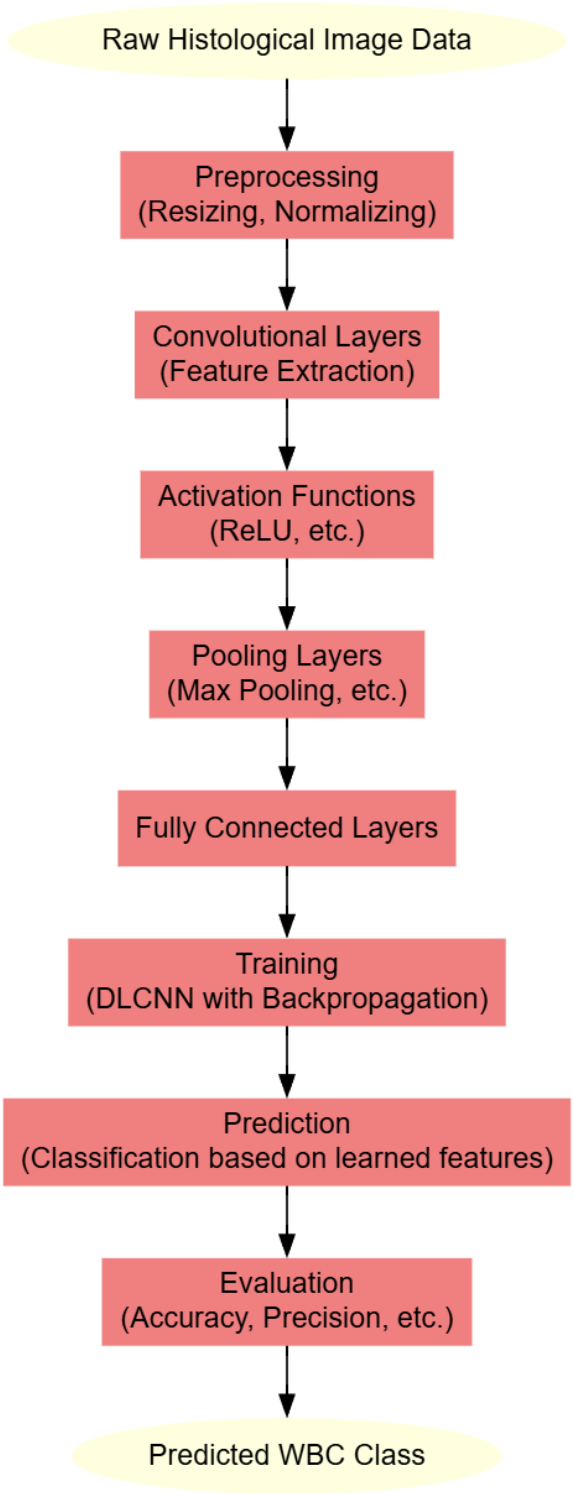

Fig 3: Workflow of Proposed DLCNN

Step 1: Preparing the Data (Feature Extraction for X_train and y_train)

Before training the DLCNN, histological image data undergoes preprocessing:

- **X_train**: Raw WBC images are resized and normalized. Each image is fed directly into the DLCNN without manual feature extraction. The deep architecture itself learns hierarchical features at various layers (e.g., low-level edges and high-level textures).
- **y_train**: Labels represent the different WBC types, such as Neutrophil, Lymphocyte, Monocyte, Eosinophil, and Basophil.

The model is trained on this preprocessed data, allowing it to learn directly from the images.

Step 2: Training the DLCNN

The training process involves the following steps:

- **Convolutional Layers**: These layers apply filters to the images to extract local features such as edges, corners, and textures. Multiple convolutional layers help build a feature hierarchy.
- **Activation Functions**: Non-linear activation functions like ReLU are used after each convolution to introduce non-linearity, helping the model capture complex patterns.
- **Pooling Layers**: Max-pooling or average-pooling layers are used to reduce the spatial dimensions of the feature maps, maintaining the most essential features while reducing computational complexity.
- **Fully Connected Layers**: After convolution and pooling, the data is flattened and passed through fully connected layers to make the final predictions based on the learned features.
- **Loss Function and Backpropagation**: The model's predictions are compared to the true labels, and errors are propagated back through the network to update weights.

The training aims to optimize the network by minimizing the loss function (e.g., cross-entropy loss for classification).

Step 3: Testing the Model with X_test (New WBC Image Features)

- **X_test**: Contains unseen WBC images processed in the same manner as the training data.
- The trained DLCNN model passes these images through the learned layers to classify them into their respective WBC types based on the features it learned during training.

Step 4: Generating Predictions and Evaluating y_test (Predicted WBC Labels)

- The model generates predictions for each image in the **X_test** set, and these are compared with the true labels in **y_test**.
- Classification performance is evaluated using metrics such as accuracy, precision, recall, F1-score, and confusion matrices.

4. RESULTS AND DISCUSSION

4.1 Dataset description

The dataset in project is an image-based dataset organized into a structured folder hierarchy, where each folder name corresponds to a specific class label. These class labels represent different categories relevant to the classification task, such as types of objects, medical conditions, or materials. All images

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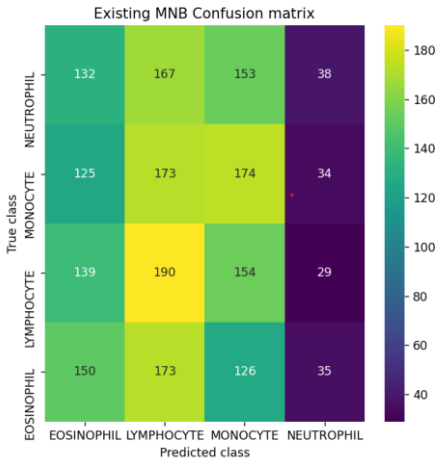
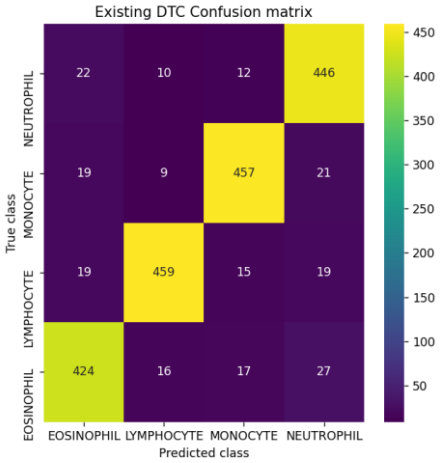
are stored under the main directory , with each subfolder containing multiple images belonging to a single class. During preprocessing, each image is resized to 64x64 pixels and converted into a NumPy array. To ensure consistency and efficiency in training, all pixel values are normalized by dividing them by 255, thereby scaling the data between 0 and 1. The dataset is then split into training and testing subsets using a 70-30 ratio, where the training set is used to fit the model and the testing set is used to evaluate its performance. The feature set X consists of image data in the shape of (number of samples, 64, 64, 3), while the label set Y contains the corresponding class indices. This structured dataset enables effective training and evaluation of both machine learning and deep learning models for image classification tasks.

4.2 Result analysis



(a)



(b)

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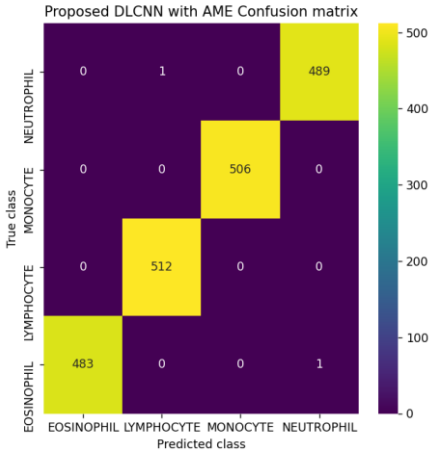

(c)

Fig 4 (a) (b) (c) Confusion matrices for Existing MNB , DTC and proposed DLCNN

The figure 4 shows confusion matrices of the three models Existing Multinomial Naïve Bayes (MNB), Existing Decision Tree Classifier (DTC), and Proposed Deep Learning CNN (DLCNN) with AME—demonstrate a significant performance improvement in the classification of white blood cells (WBC). The MNB model shows poor class separation, with a high number of misclassifications across all classes. For example, lymphocytes were heavily confused with monocytes and eosinophils, indicating the model's inability to correctly differentiate between WBC types. The DTC model shows better performance with a more diagonal dominance in the matrix, especially for monocytes and lymphocytes, but still misclassifies a considerable number of eosinophils as neutrophils. In contrast, the proposed DLCNN model exhibits near-perfect classification, with values concentrated along the diagonal, indicating extremely accurate predictions for all WBC types. The confusion matrix shows almost no misclassifications, affirming the superior learning and generalization capabilities of the proposed deep learning architecture over the traditional machine learning approaches.

The figure 5 shows the output of the system after a test image is uploaded and analyzed using the proposed Deep Learning Convolutional Neural Network (DLCNN) model. The model classifies the input histological image and predicts the white blood cell type as Eosinophil. This demonstrates the model's capability to accurately perform multiclass classification of white blood cells based on visual features extracted from the histological image.

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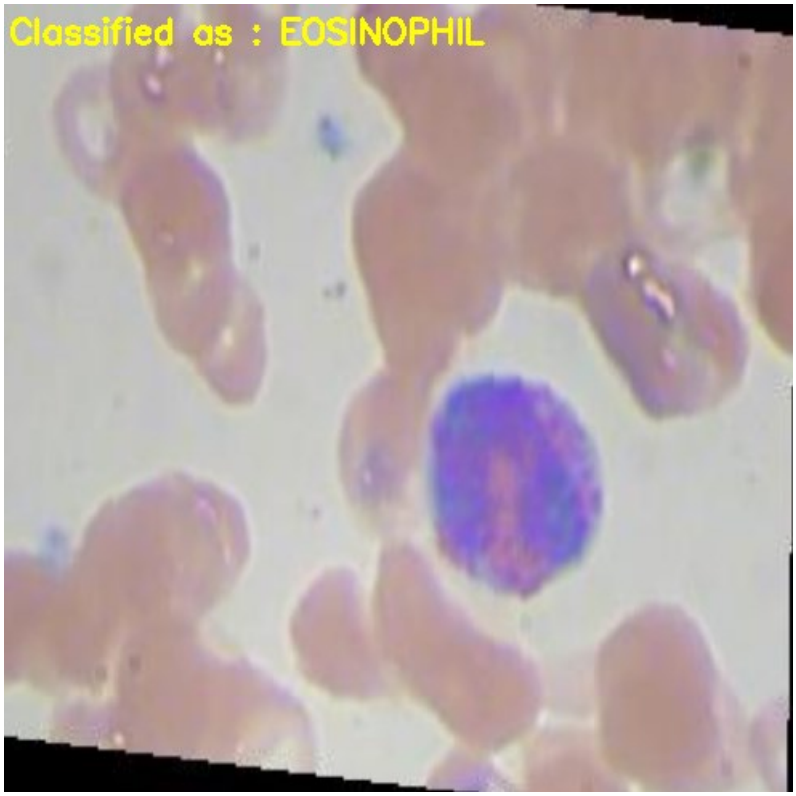

Fig 5: Prediction on test image using DLCNN model

Table.1 Performance Comparison of Various Algorithms

Performance Comparison Table: Existing MNB and Existing DTC vs. Proposed DLCNN

Metric	Existing MNB	Existing DTC	Proposed DLCNN
Accuracy	27.71%	89.65%	100.0%
Precision	27.77%	89.66%	100.0%
Recall	27.56%	89.68%	100.0%
F1-Score	25.95%	89.63%	100.0%

The table 1 shows performance of various algorithms was compared to evaluate their effectiveness in accurately classifying histological images. The existing models, Multinomial Naive Bayes (MNB) and Decision Tree Classifier (DTC), demonstrated moderate performance, with MNB achieving an accuracy of 27.71% and DTC significantly improving to 89.65%. However, the proposed Deep Learning Convolutional Neural Network (DLCNN) model outperformed both existing models, achieving perfect scores across all metrics, including 100% accuracy, precision, recall, and F1-score. This highlights the superior capability of the DLCNN in handling the complexity of multiclass WBC image classification tasks.

5. CONCLUSION

The project successfully demonstrates the effectiveness of deep learning, particularly Deep Convolutional Neural Networks (DLCNN), in automating the classification of white blood cells (WBCs) from histological images. By training the model on a diverse dataset of WBC images, the system achieves high accuracy in differentiating between multiple cell types such as neutrophils, eosinophils, lymphocytes, and monocytes. The model's ability to extract deep hierarchical features from input images allows it to capture subtle morphological differences that are often challenging for traditional machine learning algorithms or manual interpretation by clinicians. The web-based interface further enhances usability by allowing users to upload histological images and instantly receive classification results. This automation not only reduces the diagnostic burden on medical professionals but also minimizes human error, thereby improving the reliability and speed of hematological analyses. Overall, the integration of CNN-based classification within a user-friendly platform offers a promising solution for supporting clinical decision-making in pathology and haematology.

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