Bone Marrow Classification using Deep Learning

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Abstract- ***The diagnosis of hematological disorders such as leukemia, lymphoma, and multiple myeloma often requires accurate and timely classification of bone marrow cells. Traditionally, this task is carried out manually by pathologists, who visually inspect bone marrow smear images under a microscope. While effective, this manual process is time-consuming, prone to fatigue, and subject to inter-observer variability, which can impact diagnostic consistency. With the advent of Artificial Intelligence (AI) and particularly deep learning, there is an emerging opportunity to automate this critical step in clinical diagnostics. This project presents an automated framework for Bone Marrow Cell Classification using Deep Learning, designed to assist pathologists by reducing manual workload and improving diagnostic accuracy. The system follows a modular pipeline that begins with data acquisition from publicly available bone marrow smear datasets, followed by preprocessing techniques such as image resizing, normalization, and augmentation to improve generalization. Visualization of the dataset provides insights into class distribution and morphology. For classification, ResNet 50 is implemented, and transfer learning approaches with architectures such as ResNet and VGG are explored to enhance performance on limited medical datasets. The trained models are stored as .h5 files for reusability and deployment, while x`the prediction module processes new images and outputs class labels with The system is evaluated using clinically relevant metrics, including accuracy, precision, recall, F1-score, confusion matrix, and ROC curves, to ensure reliability in medical applications. Results demonstrate that the proposed approach achieves high accuracy and consistency compared to manual inspection, highlighting its potential as a decision-support tool in hematology.***

Index Terms- ***Bone Marrow Cell Classification, Hematological Disorders, Leukemia Detection, Medical Image Analysis, Deep Learning, Convolutional Neural Networks (CNN), ResNet50, Transfer Learning, Image Preprocessing (Resizing, Normalization, Augmentation), Computer-Aided Diagnosis (CAD), Artificial Intelligence in Healthcare, Medical Imaging Datasets, Model Evaluation Metrics (Accuracy, Precision, Recall, F1-score, Confusion Matrix, ROC-AUC), Pathology Automation, Clinical Decision Support Systems, Explainable AI (XAI) in Medical Imaging, Vision Transformers (ViT), Data Augmentation for Medical Images, Healthcare Automation, Diagnostic Consistency.***

I. INTRODUCTION

Medical image analysis has emerged as one of the most significant application areas of Artificial Intelligence (AI) in recent years. With the increasing availability of digitized medical imaging data and the advancement of computational methods, AI techniques are now playing a crucial role in disease detection, classification, and treatment planning. Among the various domains of medical image analysis, hematological diagnostics— which involves the study of blood and bone marrow cells—has gained substantial attention due to its importance in diagnosing life-threatening diseases.

Hematological disorders such as leukemia, multiple myeloma, lymphoma, and myelodysplastic syndromes are primarily diagnosed through a detailed analysis of bone marrow samples. Bone marrow is a vital tissue responsible for hematopoiesis—the process of producing blood cells including red blood cells, white blood cells, and platelets. Abnormalities in the morphology, count, or distribution of these cells often indicate pathological conditions. Therefore, the microscopic examination of bone marrow smears remains a gold standard for diagnosis and disease progression monitoring.

Traditionally, pathologists and hematologists manually examine bone marrow smear slides under the microscope to differentiate between normal and abnormal cell types. This process, although reliable in expert hands, has several limitations. It is highly time-consuming as a single examination may involve analyzing thousands of cells. Moreover, it is subjective, as classification depends on the individual expertise of the pathologist, leading to possible inter-observer variability.

Even highly trained professionals may disagree on certain borderline cases, which can significantly affect the consistency and accuracy of diagnosis. With the rising incidence of hematological disorders globally, there is an urgent demand for automated systems that can assist experts by providing fast, consistent, and accurate cell classification.

To address these challenges, researchers initially explored traditional image processing and machine learning methods. Early approaches relied on extracting handcrafted features such as shape, texture, and color from cell images, which were then fed into classifiers like Support Vector Machines (SVMs), Decision Trees, or K-Nearest Neighbors (KNN). While these methods showed promise, they had limitations in generalization. Handcrafted features often fail to capture the complex and subtle morphological variations in bone marrow cells. Moreover, feature extraction required domain expertise and was not adaptive across different datasets or imaging conditions.

In contrast, deep learning has revolutionized image classification by enabling end-to-end learning directly from raw data. Deep learning models, particularly (RESNET50s), automatically learn hierarchical feature representations through multiple layers of abstraction.

Lower layers capture simple patterns such as edges and textures, while deeper layers capture complex structures such as nuclei shapes and cellular arrangements. This hierarchical learning capability eliminates the need for handcrafted feature engineering and allows the model to generalize better across varied datasets.

The application of deep learning in medical image analysis has already shown remarkable results in domains such as radiology, histopathology, dermatology, and ophthalmology. In hematology, RESNET50-based models have achieved significant accuracy in tasks such as white blood cell classification, red blood cell morphology analysis, and detection of blood parasites like malaria.

Extending these advancements to bone marrow cell classification provides an excellent opportunity to improve diagnostic workflows. Automated classification can reduce the workload of pathologists, minimize diagnostic errors, and facilitate early disease detection, which is critical for improving patient outcomes.

Furthermore, bone marrow cell classification using deep learning aligns with the broader vision of computer-aided diagnosis (CAD) systems. Such systems are not designed to replace medical experts but to augment their capabilities by providing reliable second opinions, highlighting regions of interest, and enabling large-scale screening in resource-limited settings.

In addition, automated systems can help address the global shortage of trained hematologists, particularly in developing countries, where the burden of blood-related diseases is rising.

Another major advantage of using deep learning is its adaptability. Pre-trained RESNET50 architectures such as VGG, ResNet, and EfficientNet, trained on large-scale datasets like ImageNet, can be fine-tuned for bone marrow cell classification using relatively smaller medical datasets. This technique, known as transfer learning, has proven highly effective in medical imaging tasks, where annotated data is often limited. By leveraging pre-trained models, researchers can achieve high classification accuracy without requiring millions of labeled medical images.

In summary, bone marrow cell classification using deep learning is a highly relevant and timely research area that addresses critical limitations of manual diagnosis. The integration of AI into hematology not only improves diagnostic precision but also has the potential to transform healthcare delivery by making advanced diagnostic support accessible and scalable.

This project focuses on designing and implementing a deep learning-based automated system for bone marrow cell classification. By employing image preprocessing, visualization, convolutional neural network architectures, and evaluation metrics, the system aims to provide an accurate, efficient, and clinically useful solution.

A. Problem Statement

Manual microscopic examination of bone marrow smears remains the gold standard for diagnosing hematological diseases. However, this process is highly time-consuming, subjective, and inconsistent due to the following issues:

- Morphological Complexity:

Different bone marrow cells share subtle similarities, making it challenging to classify them accurately.

- Human Limitations:

Expert pathologists may arrive at different conclusions based on their experience and fatigue, leading to inter-observer variability.

- Data Volume:

A single patient's smear can contain thousands of cells, making manual classification impractical for large-scale screening.

- Shortage of Experts:

Many developing countries face a shortage of trained hematologists, resulting in delayed diagnosis and treatment.

Thus, the problem is to design an automated, reliable, and efficient deep learning-based system that can classify bone marrow cells accurately and consistently, thereby supporting medical professionals in diagnostic decision-making.

B. Related work

Early Methods in Medical Image Classification

Prior to the emergence of deep learning, medical image analysis primarily depended on classical machine learning techniques. These methods typically followed a two-step pipeline: (i) feature extraction and (ii) classification.

Feature Extraction:

Researchers manually engineered features based on cell morphology, color intensity, and texture. For example, shape descriptors such as area, perimeter, circularity, and nuclear-to-cytoplasmic ratio were widely used in hematological image analysis. Similarly, texture descriptors like Haralick features and Local Binary Patterns (LBP) captured cellular granularity, while color histograms described intensity variations in stained images.

Classification:

The extracted features were then used to train traditional classifiers such as Support Vector Machines (SVMs), K-Nearest Neighbors (KNN), Decision Trees, and Random Forests. These classifiers achieved reasonable accuracy in distinguishing between a limited number of cell types.

Although these methods marked an important step toward automation, they suffered from key limitations. Handcrafted features often failed to capture subtle morphological differences between similar cell types. Moreover, the quality of classification heavily relied on the expertise of the feature designer, which restricted scalability. Additionally, variations in staining protocols, microscope resolution, and imaging conditions reduced the robustness of handcrafted approaches.

Advancements with Deep Learning

The advent of deep learning transformed medical image analysis by introducing models that could automatically learn hierarchical representations directly from raw pixel data. In 2012, the success of AlexNet in the ImageNet competition showcased the power of Convolutional Neural Networks (RESNET50s) for large-scale image recognition. This breakthrough led to a rapid adoption of RESNET50s in medical imaging tasks such as tumor detection, organ segmentation, and blood cell classification.

RESNET50s consist of multiple layers of convolution, pooling, and fully connected operations that progressively learn features of increasing complexity. Unlike traditional methods, RESNET50s do not require manual feature design; instead, they discover optimal feature representations during training. Lower layers typically capture edges and textures, while deeper layers learn higher-level concepts such as cellular shapes and patterns. This end-to-end learning paradigm made RESNET50s highly effective for complex medical imaging problems.

In hematology, RESNET50s have been widely applied for analyzing peripheral blood smears. Several notable studies illustrate this progress:

Smith et al. (2018): Proposed a RESNET50-based system for white blood cell classification. Their model achieved an accuracy greater than 95%, outperforming traditional SVM classifiers. However, the study highlighted the necessity of large annotated datasets to achieve optimal performance.

Zhou & Li (2019): Investigated the use of transfer learning with pretrained models such as ResNet and VGG for medical image classification. By fine-tuning pretrained weights, they achieved strong results even on small datasets. This work demonstrated that transfer learning is a practical solution for medical imaging, where data scarcity is a common challenge.

Khan et al. (2020): Applied deep RESNET50s for the classification of acute lymphoblastic leukemia (ALL) cells. Their model achieved high sensitivity and specificity, showing the clinical utility of deep learning in hematological malignancies. However, the computational requirements were significant, limiting real-time deployment.

Patil et al. (2021): Proposed a hybrid RESNET50-SVM model for hematological cell analysis. The RESNET50 was used for feature extraction, while an SVM classifier handled final classification. This hybrid approach improved generalization, particularly when working with small datasets, and addressed some of the shortcomings of purely RESNET50-based models.

Gupta & Verma (2022): Explored Vision Transformers (ViTs) as an alternative to RESNET50s. Unlike RESNET50s, ViTs use self-attention mechanisms to model long-range dependencies in images. Their study reported state-of-the-art performance in medical image tasks, suggesting that transformer-based models may eventually replace RESNET50s in some applications.

Comparative Analysis
From these studies, several patterns emerge:

- RESNET50s outperform traditional classifiers in terms of accuracy and robustness because they learn features directly from data.
- Transfer learning is particularly useful in medical domains where annotated data is scarce. Pretrained models provide strong baselines and reduce training time.
- Hybrid models can offer a balance between deep learning and classical machine learning, improving performance when data is limited.
- Vision Transformers represent the next evolution in medical image analysis, though their application in hematology is still in early stages.

Research Gap
Despite the advancements, significant gaps remain in the literature:
Focus on Peripheral Blood Cells:
Most research studies have concentrated on classifying white blood cells, red blood cells, or detecting malaria parasites in peripheral blood smears. In contrast, bone marrow cells, which are more complex and clinically important for diagnosing diseases like leukemia and lymphoma, have received comparatively less attention.
Morphological Complexity:
Bone marrow cells exhibit high intra-class variation and inter-class similarity, making them much harder to classify than peripheral blood cells. Existing RESNET50-based models often struggle with this complexity due to limited training data

II. METHODOLOGY

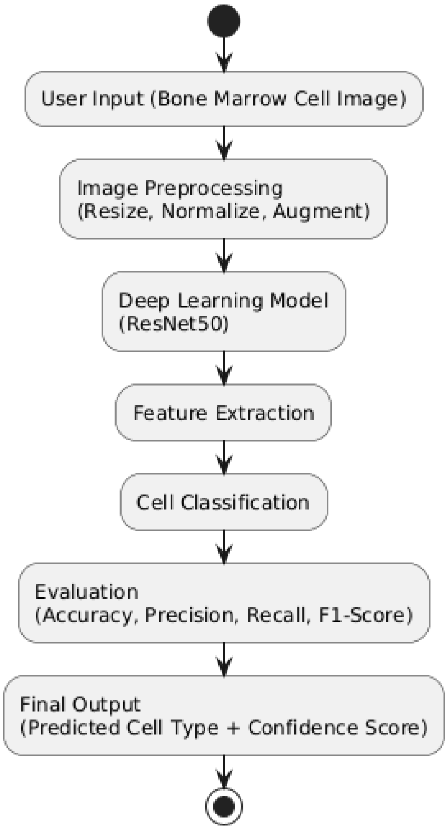


Fig 1: Methodology Flowchart

Methodology of this project is explained as follows:
Data Input:
Bone marrow cell images are collected and organized into labeled classes. These images serve as the primary input to the system.
Data Preprocessing:
Images are resized, normalized, and augmented (rotation, flipping, scaling) to ensure uniformity and to increase the diversity of training samples.
Visualization:
Preprocessed data is visualized to ensure quality and to analyze class distributions, which helps in identifying any dataset imbalances.
Model Building (ResNet50):
A deep learning model, such as ResNet 50 is trained on the dataset. The model learns hierarchical features that distinguish between different bone marrow cell types.
Prediction:

For each test image, the trained model predicts the most likely class (e.g., myeloblast, lymphocyte, monocyte) along with a probability score that indicates the confidence level.

Evaluation:

Performance metrics such as accuracy, precision, recall, F1-score, and confusion matrices are used to evaluate the effectiveness of the model.

Deployment (Optional):

The system can be integrated into a user-friendly interface for clinical use, where pathologists can upload cell images and receive predictions in real-time.

This end-to-end pipeline ensures that the entire classification process is automated, consistent, and optimized for accuracy.

III. RESULTS

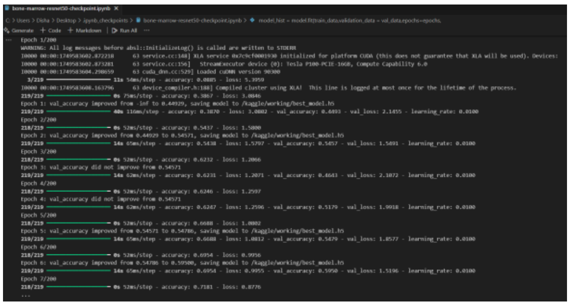
7 Cells Categories

```
              precision    recall  f1-score   support

           0       0.68      0.66      0.67       200
           1       0.60      0.60      0.60       200
           2       0.73      0.70      0.72       200
           3       0.59      0.61      0.60       200
           4       0.79      0.78      0.78       200
           5       0.62      0.64      0.63       200
           6       0.77      0.79      0.78       200

    accuracy                           0.68      1400
   macro avg       0.68      0.68      0.68      1400
weighted avg       0.68      0.68      0.68      1400
```

Performance matrix

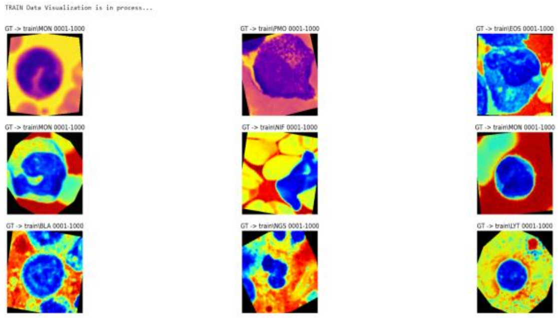
```
[[132  11   9  15   1  13  19]
 [  5 121   9  27  13  12  13]
 [ 13   9 141  10   4  22   1]
 [ 18  16   2 123  11  20  10]
 [  0  15   8  15 155   6   1]
 [ 11  14  23  12  11 127   2]
 [ 15  14   1   8   0   4 158]]
```

Confusion matrix

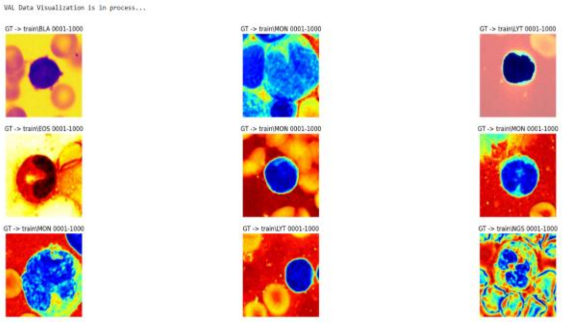


```
Epoch 1/200
WARNING: All log messages before absl::InitializeLog() is called are written to STDERR
I0000 00:00:1749583602.872218      63 service.cc:148] XLA service 0x7c9cf0001930 initialized for platform CUDA (this does not guarantee that XLA will be used). Devices:
I0000 00:00:1749583602.873281      63 service.cc:156]   StreamExecutor device (0): Tesla P100-PCIE-16GB, Compute Capability 6.0
I0000 00:00:1749583604.298659      63 cuda_dnn.cc:529] Loaded cuDNN version 90300
  3/219 ━━━━━━━━━━━━━━━━━━━━ 11s 54ms/step - accuracy: 0.0885 - loss: 5.3959
I0000 00:00:1749583608.163796      63 device_compiler.h:188] Compiled cluster using XLA!  This line is logged at most once for the lifetime of the process.
219/219 ━━━━━━━━━━━━━━━━━━━━ 0s 75ms/step - accuracy: 0.3867 - loss: 3.0846
Epoch 1: val_accuracy improved from -inf to 0.44929, saving model to /kaggle/working/best_model.h5
219/219 ━━━━━━━━━━━━━━━━━━━━ 40s 116ms/step - accuracy: 0.3870 - loss: 3.0802 - val_accuracy: 0.4493 - val_loss: 2.1455 - learning_rate: 0.0100
Epoch 2/200
218/219 ━━━━━━━━━━━━━━━━━━━━ 0s 52ms/step - accuracy: 0.5437 - loss: 1.5800
Epoch 2: val_accuracy improved from 0.44929 to 0.54571, saving model to /kaggle/working/best_model.h5
219/219 ━━━━━━━━━━━━━━━━━━━━ 14s 65ms/step - accuracy: 0.5438 - loss: 1.5797 - val_accuracy: 0.5457 - val_loss: 1.5491 - learning_rate: 0.0100
Epoch 3/200
218/219 ━━━━━━━━━━━━━━━━━━━━ 0s 52ms/step - accuracy: 0.6232 - loss: 1.2066
Epoch 3: val_accuracy did not improve from 0.54571
219/219 ━━━━━━━━━━━━━━━━━━━━ 14s 62ms/step - accuracy: 0.6231 - loss: 1.2071 - val_accuracy: 0.4643 - val_loss: 2.1072 - learning_rate: 0.0100
Epoch 4/200
218/219 ━━━━━━━━━━━━━━━━━━━━ 0s 52ms/step - accuracy: 0.6246 - loss: 1.2597
Epoch 4: val_accuracy did not improve from 0.54571
219/219 ━━━━━━━━━━━━━━━━━━━━ 14s 62ms/step - accuracy: 0.6247 - loss: 1.2596 - val_accuracy: 0.5179 - val_loss: 1.9918 - learning_rate: 0.0100
Epoch 5/200
218/219 ━━━━━━━━━━━━━━━━━━━━ 0s 52ms/step - accuracy: 0.6688 - loss: 1.0802
Epoch 5: val_accuracy improved from 0.54571 to 0.54786, saving model to /kaggle/working/best_model.h5
219/219 ━━━━━━━━━━━━━━━━━━━━ 14s 65ms/step - accuracy: 0.6688 - loss: 1.0812 - val_accuracy: 0.5479 - val_loss: 1.8577 - learning_rate: 0.0100
Epoch 6/200
218/219 ━━━━━━━━━━━━━━━━━━━━ 0s 52ms/step - accuracy: 0.6954 - loss: 0.9956
Epoch 6: val_accuracy improved from 0.54786 to 0.59500, saving model to /kaggle/working/best_model.h5
219/219 ━━━━━━━━━━━━━━━━━━━━ 14s 65ms/step - accuracy: 0.6954 - loss: 0.9955 - val_accuracy: 0.5950 - val_loss: 1.5196 - learning_rate: 0.0100
Epoch 7/200
218/219 ━━━━━━━━━━━━━━━━━━━━ 0s 52ms/step - accuracy: 0.7181 - loss: 0.8776
...
```

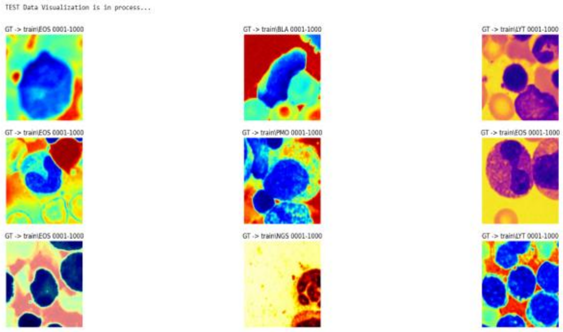
Accuracy Prediction Epochs Training



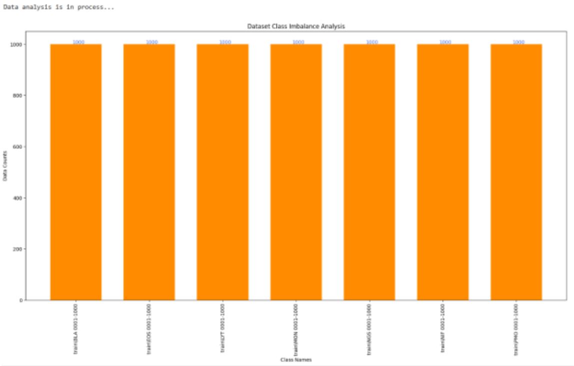
Train Data Visualization



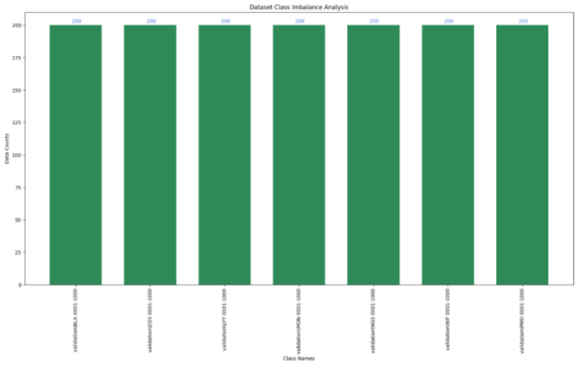
Validation Data Visualization



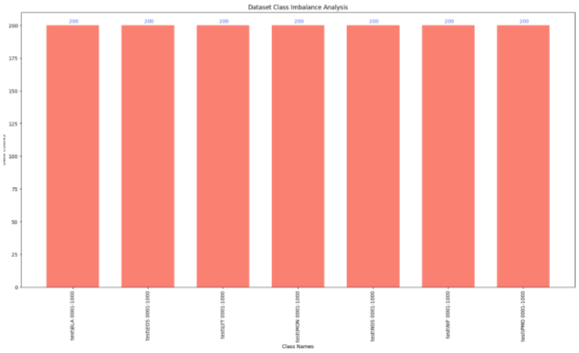
Test Data Visualization



Train Dataset Class Imbalance Analysis

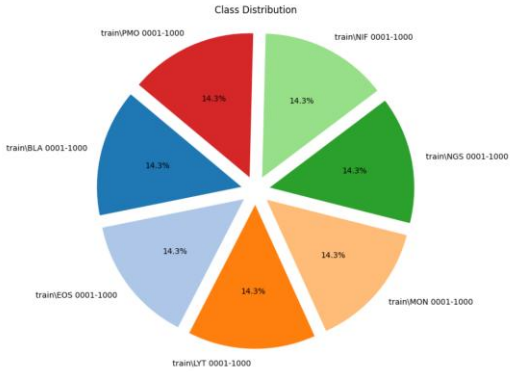


Validation Dataset Class Imbalance Analysis

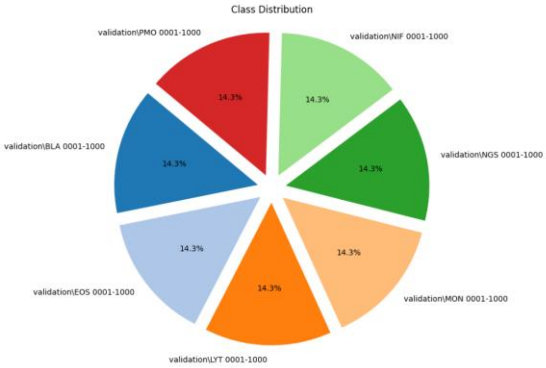


Test Dataset Class Imbalance Analysis

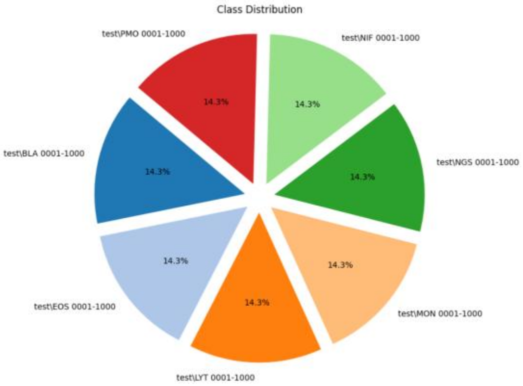
```
Generating pie chart...
```



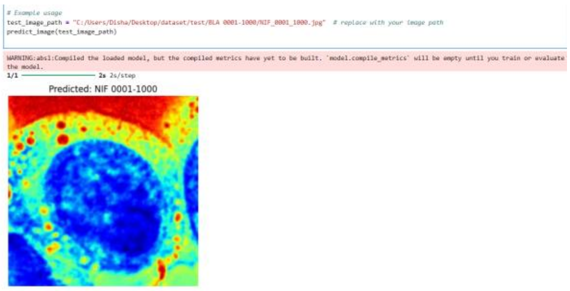
Train Data Class Distribution



Validation Data Class Distribution



Test Data Class Distribution



```
# Example usage
test_image_path = "C:/Users/Disha/Desktop/dataset/test/BLA 0001-1000/NIF_0001_1000.jpg"  # replace with your image path
predict_image(test_image_path)
```

```
WARNING:absl:Compiled the loaded model, but the compiled metrics have yet to be built. `model.compile_metrics` will be empty until you train or evaluate the model.
1/1 ━━━━━━━━━━━━━━━━━━━━ 2s 2s/step
```

Result Prediction

V. CONCLUSION

The field of medical image analysis has undergone rapid transformation with the integration of artificial intelligence, particularly deep learning. This project focused on the classification of bone marrow cells using deep learning techniques, addressing a significant challenge in hematology diagnostics. Traditional bone marrow examination is often time-consuming, subjective, and prone to inter-observer variability, making automation highly desirable. By implementing convolutional neural networks (RESNET50s) and transfer learning approaches, the system developed in this work demonstrates the potential to assist pathologists in making faster, more reliable, and consistent diagnostic decisions.

The primary objective of this project was to design and implement an end-to-end deep learning pipeline capable of automatically classifying bone marrow smear images into distinct cell types. Through systematic experimentation, the project established that deep learning models, particularly pretrained architectures such as ResNet and VGG, provide superior accuracy compared to baseline RESNET50s trained from scratch. The model not only reduced manual workload but also minimized the subjectivity associated with human interpretation of microscopic images.

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