HematoVision: Blood Cell Subtype Classification Using Deep Learning

1. Introduction

Blood-based disease diagnosis relies heavily on microscopic analysis of blood cell morphology. Manual analysis is not only time-consuming but also prone to human error. Automating this task with computer vision significantly improves diagnostic workflows in hematology.

2. Objective

This project aims to build an intelligent classification system that can accurately identify four major subtypes of white blood cells: Eosinophils, Lymphocytes, Monocytes, and Neutrophils. The model is expected to provide high accuracy, fast inference, and model interpretability.

3. Dataset Description

Dataset sourced from Kaggle: ~12,500 labeled blood cell images categorized into four classes. Images are pre-augmented using rotation, zoom, and flipping, and structured in separate folders. Original set includes 410 labeled images with XML annotations.

4. Tools & Technologies

Python, TensorFlow, Keras, NumPy, Pandas, OpenCV, PIL, Matplotlib, Seaborn, Scikit-learn, Grad-CAM.

5. Preprocessing Pipeline

Image paths and labels were converted into structured DataFrames. Images were resized to 224x224 and normalized. Augmentations such as rotation, flipping, and zooming were applied using ImageDataGenerator.

6. Model Architecture

Used EfficientNetB0 for transfer learning due to its accuracy and efficiency. The custom head includes GlobalAveragePooling, Dropout, Dense layers with ReLU, and a final softmax output for 4 classes.

7. Evaluation Strategy

Accuracy, Precision, Recall, F1-Score, and Confusion Matrix were used. Model achieved an average F1-Score of 91%. Class-wise metrics showed consistent performance across all types.

8. Visual Interpretability (Grad-CAM)

Grad-CAM was used to highlight regions in the image contributing most to the classification, aiding in transparency and trust in the model's decisions.

9. Prediction Pipeline

After training, images are preprocessed and passed into the model to obtain predictions. Labels are mapped from numerical to categorical outputs.

10. Key Observations

Stable training and validation performance. Grad-CAM revealed model focused correctly on cell nuclei. Data augmentation helped overcome class imbalance.

11. Challenges

Addressed class imbalance through augmentation, overfitting with dropout and early stopping, and performance limitations using lightweight EfficientNet.

12. Future Enhancements

Include abnormal cells, deploy as API/web app, expand to red blood cell classification, and integrate SHAP or LIME for interpretability.

13. Conclusion

HematoVision is a high-performing, scalable, and interpretable model for blood cell subtype classification. It shows promise for integration into clinical diagnostic workflows.

14. References

1. https://www.kaggle.com/datasets/paultimothymooney/blood-cells
2. Tan & Le (2019) - EfficientNet
3. TensorFlow and Keras Documentation