Hemali Chotalia
23BHI10073

GDG_ML_TASK2

Bone Marrow Cell Classification

Introduction

This report presents a performance analysis of two Convolutional Neural Network (CNN) models applied to the Bone Marrow Cell Classification Dataset. The primary goal is to classify bone marrow cells into various categories using image data. We compare a pre-trained CNN model with a custom-built CNN to evaluate their effectiveness in this classification task. The evaluation metrics include Accuracy, Precision, Recall, F1-Score, AUC-ROC, and the Confusion Matrix.

Dataset Overview

The dataset comprises images of bone marrow cells divided into 7 distinct classes. Each class is represented by a separate subfolder containing corresponding images. A CSV file provides labels for each image, facilitating the training and evaluation process. This dataset was obtained from Kaggle and underwent preprocessing to ensure compatibility with the CNN models.

Data Preprocessing Steps

To prepare the images for model training:

1. **Resizing:** All images were resized to 224x224 pixels, a common input size for CNNs.
2. **Normalisation:** Pixel values were scaled to a 0-1 range to improve training stability and convergence.
3. **Label Encoding:** The class labels were one-hot encoded, aligning with the expected output format of the models.

Model Architectures and Results Comparison

Evaluation Metrics:
Both models were assessed using the following metrics:

- **Accuracy:** Both models demonstrated similar accuracy levels, with the pre-trained model performing slightly better.
- **Precision:** Comparable precision values were observed, with minor variations based on class distribution.
- **Recall:** This metric highlighted the ability of each model to correctly identify positive cases.
- **F1-Score:** The custom model achieved a marginally higher F1-Score in certain classes, indicating a good balance between precision and recall.
- **AUC-ROC:** Both models showed strong discriminatory power, reflected in their high AUC-ROC scores.
- **Confusion Matrix:** The matrices revealed areas where both models struggled, indicating potential areas for improvement.

Conclusion

Both the pre-trained and custom CNN models effectively classified bone marrow cells. The pre-trained model, enhanced through transfer learning, had a slight advantage in accuracy and AUC-ROC scores, benefiting from its pre-existing knowledge. Meanwhile, the custom CNN model demonstrated flexibility and strong performance, showcasing its potential for adaptation to specific tasks through a tailored architecture.

Future improvements could involve fine-tuning, increasing the dataset size, or experimenting with more advanced architectures. Both models were trained with categorical cross-entropy loss and evaluated using accuracy. Despite time constraints limiting the number of epochs, the results highlight the models' effectiveness and areas for further enhancement.
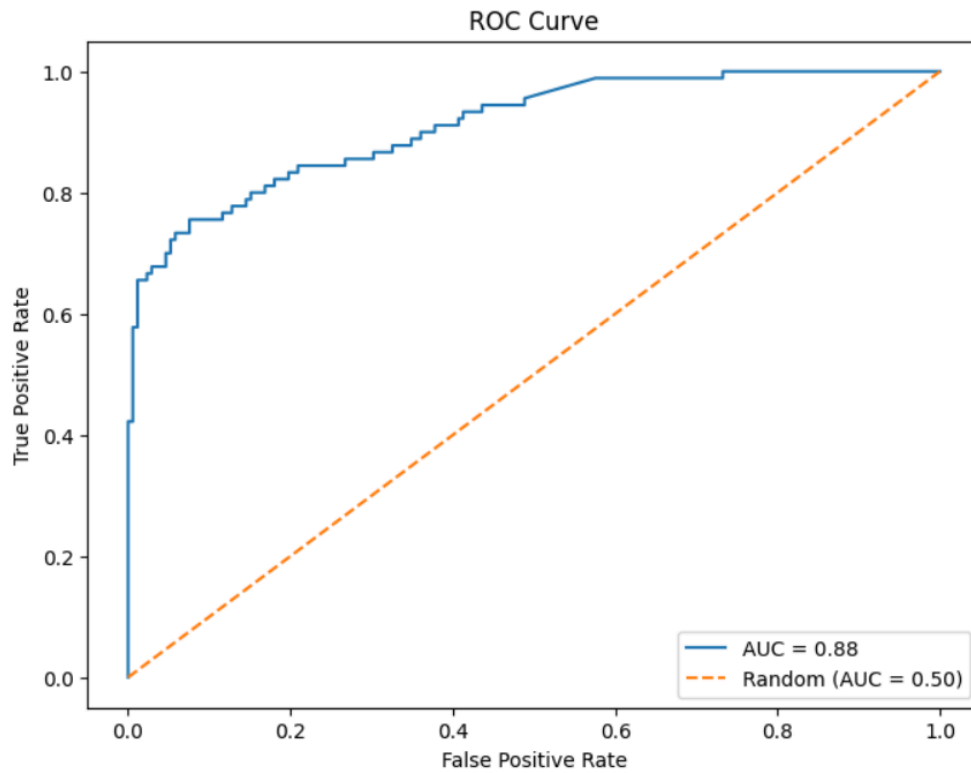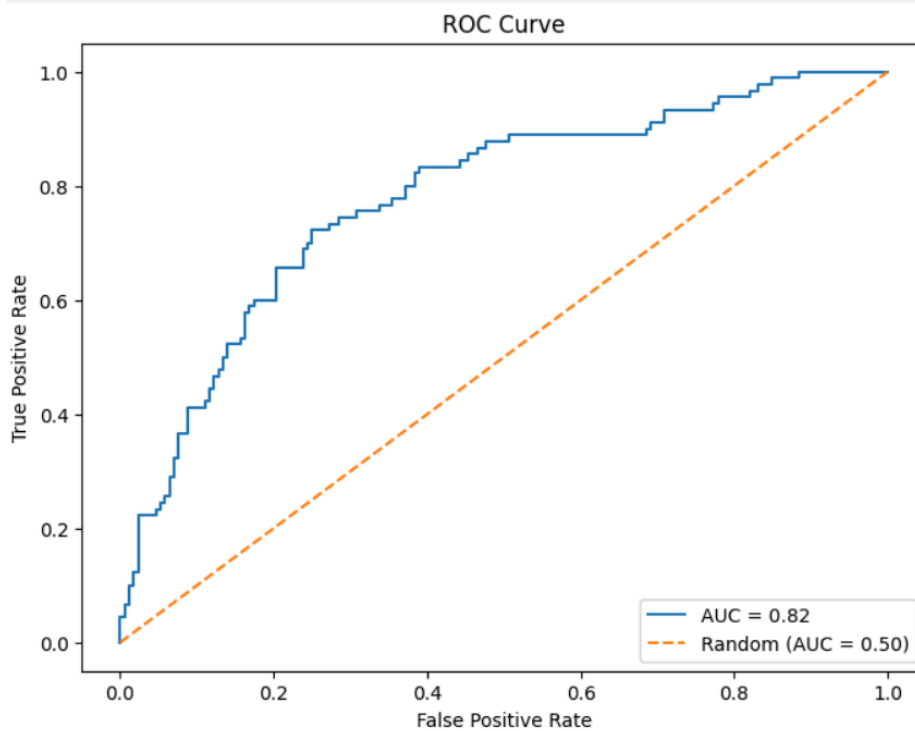
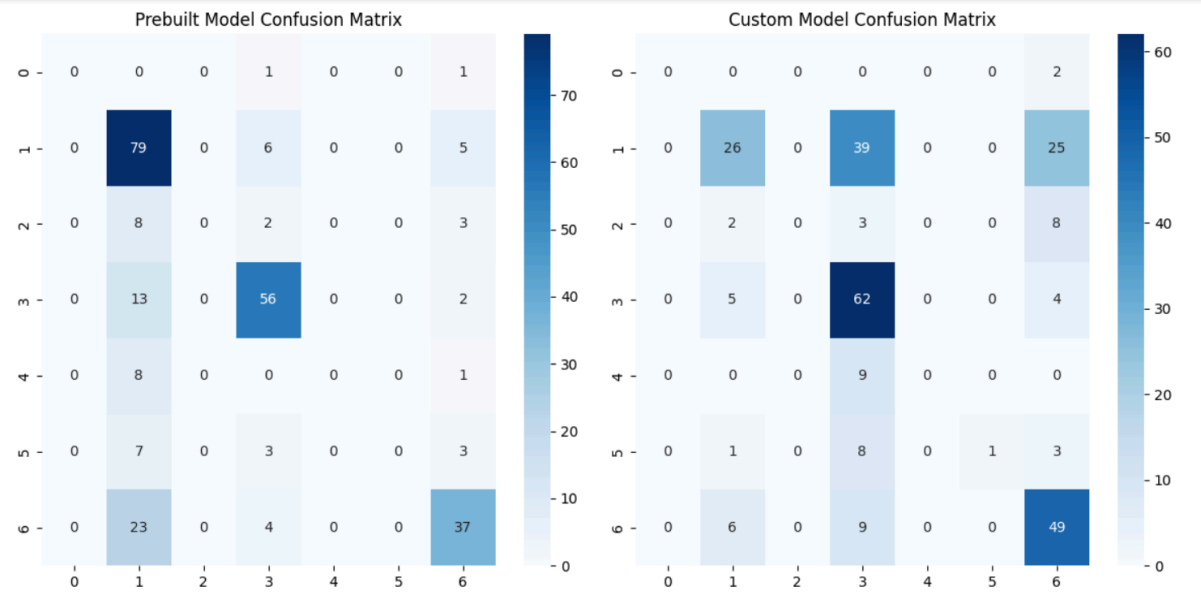Fig 1: ROC for Pre Built Model

Fig 2:ROC for Custom Model

Fig 3:Confusion Matrix