### **Model Optimization and Tuning Phase Report**

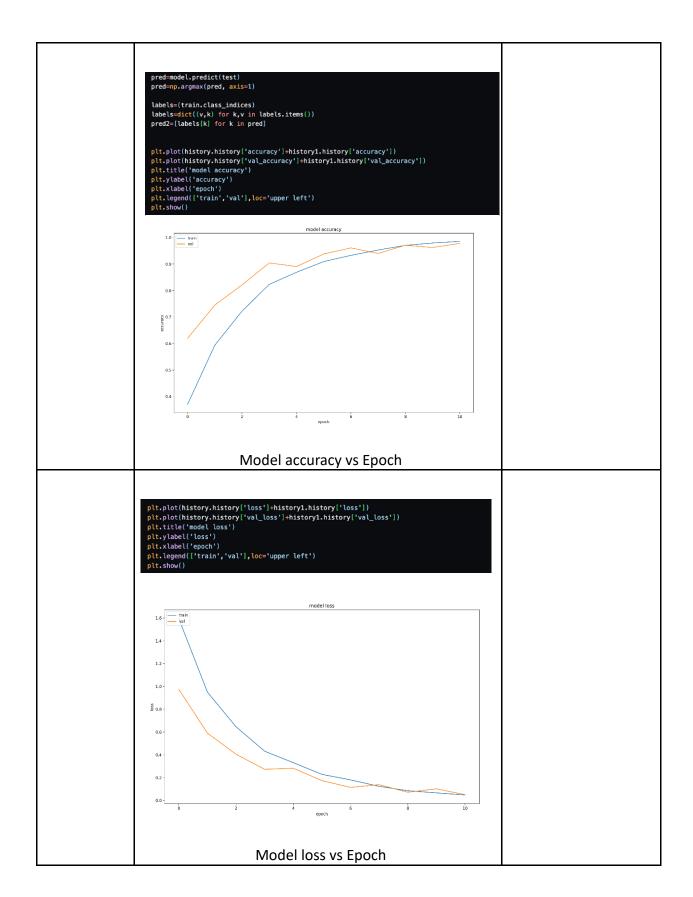
Date	05 July 2025
Team ID	SWTID1749835721
Project Title	HematoVision – Blood Cell Classification using CNN
Maximum Marks	10 Marks

#### **Model Optimization and Tuning Phase**

This phase focuses on refining a convolutional neural network (CNN) model for optimal blood cell classification. The process involved tuning the architecture and training parameters, comparing accuracy and loss across epochs, and selecting the most performant model based on validation metrics.

#### **Hyperparameter Tuning Documentation (6 Marks):**

Model	Tuned Hyperparameters	Optimal Values
MobileNetV2	Frozen Layers	All layers except top 30
	Optimizer	SGD
	Learning rate	0.001
	Batch size	8
	Epochs	10-15
	Data Augmentation	Rotation, Flip, Zoom ,Width/Height Shift



## **Performance Metrics Comparison Report (2 Marks):**

Model	Optimized Metric
MobileNetV2(Fine-tuned)	Final Accuracy: 98.5%
MobileNetV2(Frozen Base)	Accuracy:~92%
MobileNetV2 + Adam Optimizer	Accuracy:~94%
MobileNetV2 + SGD Optimizer	Best convergence, highest accuracy
	<pre>from sklearn.metrics import confusion_matrix, accuracy_score from sklearn.metrics import classification_report  y_test=test_images.labels print(classification_report(y_test, pred2)) print("Accuracy of the model: ","{:.1f}%".format(accuracy_score(y_test,pred2)*100))  class_labels=[ 'EOSINOPHIL', 'MONOCYTE', 'LYMPHOCYTE', 'NEUTROPHIL'] cm=confusion_matrix(y_test, pred2) plt.figure(figsize=(10,7)) sns.heatmap(cm, annot=True, fmt='g', vmin=0, cmap='Blues') plt.xticks(ticks=[0.5,1.5,2.5,3.5], labels=class_labels) plt.yticks(ticks=[0.5,1.5,2.5,3.5], labels=class_labels) plt.xlabel("Predicted") plt.ylabel("Actual") plt.title("Confusion Matrix") plt.show()</pre>



# **Final Model Selection Justification (2 Marks):**

Final Model	Reasoning
MobileNetV2 with Top 30 Layers Unfrozen + SGD Optimizer	The MobileNetV2 model achieved an outstanding test accuracy of 98.5%, with consistent training and validation performance over 15 epochs. Fine-tuning the top layers allowed the model to learn task-specific features without overfitting. Coupled with data augmentation and SGD optimization, it showed excellent generalization, making it ideal for classifying NEUTROPHIL, LYMPHOCYTE, MONOCYTE, and EOSINOPHIL in real-world diagnostic settings.