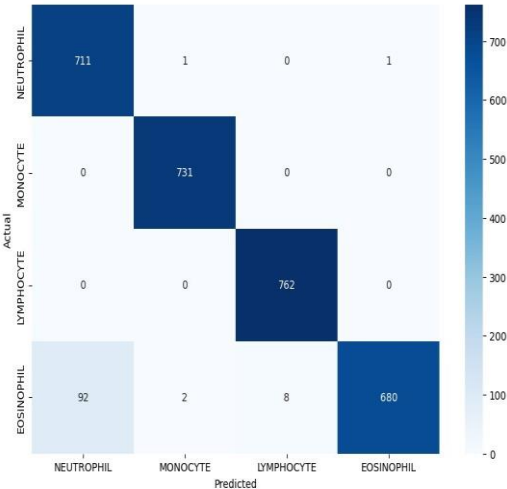


Project Development Phase Model Performance Test

Date	26 JUNE 2025
Team ID	LTVIP2025TMID39901
Project Name	Hematovision – Advanced Blood Cell Classification using Transfer Learning
Maximum Marks	10 Marks

Model Performance Testing:

Project team shall fill the following information in model performance testing template.

S.No.	Parameter	Values	Screenshot																																																																	
1.	Metrics	<div>CLASSIFICATION MODEL: CONFUSION MATRIX 4-class matrix (Eosinophil,neutrophil,monocyte, lympocyte) Accuracy Score-96.5%& Classification ReportPrecision=0.97 Recall=0.97 F1-score=0.96 Total Samples:2988</div>	<div><table><thead><tr><th></th><th>precision</th><th>recall</th><th>f1-score</th><th>support</th></tr></thead><tbody><tr><td>EOSINOPHIL</td><td>0.89</td><td>1.00</td><td>0.94</td><td>713</td></tr><tr><td>LYMPHOCYTE</td><td>1.00</td><td>1.00</td><td>1.00</td><td>731</td></tr><tr><td>MONOCYTE</td><td>0.99</td><td>1.00</td><td>0.99</td><td>762</td></tr><tr><td>NEUTROPHIL</td><td>1.00</td><td>0.87</td><td>0.93</td><td>782</td></tr><tr><td>accuracy</td><td></td><td></td><td>0.97</td><td>2988</td></tr><tr><td>macro avg</td><td>0.97</td><td>0.97</td><td>0.97</td><td>2988</td></tr><tr><td>weighted avg</td><td>0.97</td><td>0.97</td><td>0.96</td><td>2988</td></tr></tbody></table><p>Accuracy of the model 96.5%</p><p>Confusion Matrix</p><table><thead><tr><th></th><th>NEUTROPHIL</th><th>MONOCYTE</th><th>LYMPHOCYTE</th><th>EOSINOPHIL</th></tr></thead><tbody><tr><th>NEUTROPHIL</th><td>711</td><td>1</td><td>0</td><td>1</td></tr><tr><th>MONOCYTE</th><td>0</td><td>731</td><td>0</td><td>0</td></tr><tr><th>LYMPHOCYTE</th><td>0</td><td>0</td><td>762</td><td>0</td></tr><tr><th>EOSINOPHIL</th><td>92</td><td>2</td><td>8</td><td>680</td></tr></tbody></table></div>		precision	recall	f1-score	support	EOSINOPHIL	0.89	1.00	0.94	713	LYMPHOCYTE	1.00	1.00	1.00	731	MONOCYTE	0.99	1.00	0.99	762	NEUTROPHIL	1.00	0.87	0.93	782	accuracy			0.97	2988	macro avg	0.97	0.97	0.97	2988	weighted avg	0.97	0.97	0.96	2988		NEUTROPHIL	MONOCYTE	LYMPHOCYTE	EOSINOPHIL	NEUTROPHIL	711	1	0	1	MONOCYTE	0	731	0	0	LYMPHOCYTE	0	0	762	0	EOSINOPHIL	92	2	8	680
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2.	Tune the Model	Hyperparameter Tuning - Validation Method -	<div><div>1/697 ————— 5:49:19 38s/step - accuracy: 0.2500 - loss: 2.2116</div><div>10000 00:00:1751080605.071249 98 device_compiler.h:188] Compiled cluster using XLA! This line is logged at most once for the lifetime of the process.</div><div>697/697 ————— 197s 240ms/step - accuracy: 0.5235 - loss: 1.1117 - val_accuracy: 0.6800 - val_loss: 1.1162</div><div>Epoch 2/5</div><div>697/697 ————— 90s 129ms/step - accuracy: 0.8617 - loss: 0.3655 - val_accuracy: 0.9319 - val_loss: 0.2177</div><div>Epoch 3/5</div><div>697/697 ————— 86s 124ms/step - accuracy: 0.9129 - loss: 0.2253 - val_accuracy: 0.9577 - val_loss: 0.1130</div><div>Epoch 4/5</div><div>697/697 ————— 86s 124ms/step - accuracy: 0.9375 - loss: 0.1696 - val_accuracy: 0.8924 - val_loss: 0.3352</div><div>Epoch 5/5</div><div>697/697 ————— 84s 120ms/step - accuracy: 0.9458 - loss: 0.1577 - val_accuracy: 0.9756 - val_loss: 0.0644</div></div>
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