

Project Development Phase Model Performance Test

Date	26 JUNE 2025
Team ID	LTVIP2025TMID45471
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.	Model Summary	Total params: 3,573,828 Trainable params: 3,177,284 Non-trainable params: 396,544	<table><tr><th>Layer (type)</th><th>Output Shape</th><th>Param #</th></tr><tr><td>mobilenetv2_1.00_224 (Functional)</td><td>(None, 7, 7, 1280)</td><td>2,257,984</td></tr><tr><td>global_average_pooling2d (GlobalAveragePooling2d)</td><td>(None, 1280)</td><td>0</td></tr><tr><td>dropout (Dropout)</td><td>(None, 1280)</td><td>0</td></tr><tr><td>dense (Dense)</td><td>(None, 1024)</td><td>1,311,744</td></tr><tr><td>dropout_1 (Dropout)</td><td>(None, 1024)</td><td>0</td></tr><tr><td>dense_1 (Dense)</td><td>(None, 4)</td><td>4,100</td></tr></table> <p>Total params: 3,573,828 (13.63 MB)</p> <p>Trainable params: 3,177,284 (12.12 MB)</p> <p>Non-trainable params: 396,544 (1.51 MB)</p>	Layer (type)	Output Shape	Param #	mobilenetv2_1.00_224 (Functional)	(None, 7, 7, 1280)	2,257,984	global_average_pooling2d (GlobalAveragePooling2d)	(None, 1280)	0	dropout (Dropout)	(None, 1280)	0	dense (Dense)	(None, 1024)	1,311,744	dropout_1 (Dropout)	(None, 1024)	0	dense_1 (Dense)	(None, 4)	4,100																			
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2.	Accuracy	Training Accuracy – 94.58 Validation Accuracy -97.5	<table><tr><th></th><th>precision</th><th>recall</th><th>f1-score</th><th>support</th></tr><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></table> <p>Accuracy of the model 96.5%</p>		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
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3.	Fine Tunning Result(if Done)	Validation Accuracy -97.5	<pre>1/697 ----- 5:49:19 30s/step - accuracy: 0.2500 - loss: 2.2116 [20000 00-00-1751000665.071249 90 device_compiler.h:100] Compiled cluster using XLA! This line is logged at most once for the lifetime of the process. 697/697 ----- 197s 240ms/step - accuracy: 0.5235 - loss: 1.1117 - val_accuracy: 0.6880 - val_loss: 1.1162 Epoch 2/5 697/697 ----- 90s 120ms/step - accuracy: 0.8617 - loss: 0.3655 - val_accuracy: 0.9319 - val_loss: 0.2177 Epoch 3/5 697/697 ----- 86s 124ms/step - accuracy: 0.9129 - loss: 0.2253 - val_accuracy: 0.9577 - val_loss: 0.1130 Epoch 4/5 697/697 ----- 86s 124ms/step - accuracy: 0.9375 - loss: 0.1696 - val_accuracy: 0.8924 - val_loss: 0.3352 Epoch 5/5 697/697 ----- 84s 120ms/step - accuracy: 0.9458 - loss: 0.1577 - val_accuracy: 0.9756 - val_loss: 0.0644</pre>																																								

