

Model Development Phase Template

Date	05 July 2025
Team ID	SWTID1749835721
Project Title	HematoVision- Blood Cell Classification using Transfer Learning
Maximum Marks	4 Marks

Initial Model Training Code, Model Validation and Evaluation Report

The initial model training code will be showcased in the future through a screenshot. The model validation and evaluation report will include classification reports, accuracy, and confusion matrices for multiple models, presented through respective screenshots.

Initial Model Training Code:

```
#import and building the MobileNetV2 model
def build_mobilenetv2():
    base_model = MobileNetV2(weights='imagenet', include_top=False, input_shape=IMG_SIZE + (3,))
    base_model.trainable = False # freeze base
    x = base_model.output
    x = GlobalAveragePooling2D()(x)
    x = Dropout(DROPOUT_RATE)(x)
    output = Dense(NUM_CLASSES, activation='softmax')(x)
    model = Model(inputs=base_model.input, outputs=output)
    model.compile(optimizer=Adam(LEARNING_RATE), loss='categorical_crossentropy', metrics=['accuracy'])
    return model

#import and building the ResNet50 model
def build_resnet50():
    base_model = ResNet50(weights='imagenet', include_top=False, input_shape=IMG_SIZE + (3,))
    base_model.trainable = False
    x = base_model.output
    x = GlobalAveragePooling2D()(x)
    x = Dropout(DROPOUT_RATE)(x)
    output = Dense(NUM_CLASSES, activation='softmax')(x)
    model = Model(inputs=base_model.input, outputs=output)
    model.compile(optimizer=Adam(LEARNING_RATE), loss='categorical_crossentropy', metrics=['accuracy'])
    return model
```

Model Validation and Evaluation Report:

```
#import and building the VGG16 model
def build_vgg16():
    base_model = VGG16(weights='imagenet', include_top=False, input_shape=IMG_SIZE + (3,))
    base_model.trainable = False
    x = base_model.output
    x = Flatten()(x)
    x = Dropout(DROPOUT_RATE)(x)
    output = Dense(NUM_CLASSES, activation='softmax')(x)
    model = Model(inputs=base_model.input, outputs=output)
    model.compile(optimizer=Adam(LEARNING_RATE), loss='categorical_crossentropy', metrics=['accuracy'])
    return model
```

```
#import and building the InceptionV3 model
def build_inceptionv3():
    base_model = InceptionV3(weights='imagenet', include_top=False, input_shape=IMG_SIZE + (3,))
    base_model.trainable = False
    x = base_model.output
    x = GlobalAveragePooling2D()(x)
    x = Dropout(DROPOUT_RATE)(x)
    output = Dense(NUM_CLASSES, activation='softmax')(x)
    model = Model(inputs=base_model.input, outputs=output)
    model.compile(optimizer=Adam(LEARNING_RATE), loss='categorical_crossentropy', metrics=['accuracy'])
    return model
```

Model	Classification Report	F1 Score	Confusion Matrix																																								
Mobile NetV2	<pre>print(classification_report(y_test, pred))</pre> <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>0.96</td><td>0.98</td><td>0.97</td><td>726</td></tr><tr><td>LYMPHOCYTE</td><td>1.00</td><td>1.00</td><td>1.00</td><td>746</td></tr><tr><td>MONOCYTE</td><td>1.00</td><td>1.00</td><td>1.00</td><td>781</td></tr><tr><td>NEUTROPHIL</td><td>0.98</td><td>0.96</td><td>0.97</td><td>735</td></tr><tr><td>accuracy</td><td></td><td></td><td>0.98</td><td>2988</td></tr><tr><td>macro avg</td><td>0.98</td><td>0.98</td><td>0.98</td><td>2988</td></tr><tr><td>weighted avg</td><td>0.98</td><td>0.98</td><td>0.98</td><td>2988</td></tr></tbody></table> <p>Accuracy of the model: 98.5%</p>		precision	recall	f1-score	support	EOSINOPHIL	0.96	0.98	0.97	726	LYMPHOCYTE	1.00	1.00	1.00	746	MONOCYTE	1.00	1.00	1.00	781	NEUTROPHIL	0.98	0.96	0.97	735	accuracy			0.98	2988	macro avg	0.98	0.98	0.98	2988	weighted avg	0.98	0.98	0.98	2988	98.5%	<pre>print(confusion_matrix(y_test, pred))</pre> <pre>array([[712 0 0 14] [0 746 0 0] [0 0 781 0] [31 0 1703]])</pre>
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ResNet50	<pre>print(classification_report(y_test, pred))</pre> <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>0.92</td><td>0.89</td><td>0.90</td><td>726</td></tr><tr><td>LYMPHOCYTE</td><td>0.91</td><td>0.92</td><td>0.91</td><td>746</td></tr><tr><td>MONOCYTE</td><td>0.89</td><td>0.88</td><td>0.88</td><td>781</td></tr><tr><td>NEUTROPHIL</td><td>0.93</td><td>0.92</td><td>0.92</td><td>735</td></tr><tr><td>accuracy</td><td></td><td></td><td>0.91</td><td>2988</td></tr><tr><td>macro avg</td><td>0.91</td><td>0.90</td><td>0.91</td><td>2988</td></tr><tr><td>weighted avg</td><td>0.91</td><td>0.91</td><td>0.91</td><td>2988</td></tr></tbody></table> <p>Accuracy of the model: 91.0%</p>		precision	recall	f1-score	support	EOSINOPHIL	0.92	0.89	0.90	726	LYMPHOCYTE	0.91	0.92	0.91	746	MONOCYTE	0.89	0.88	0.88	781	NEUTROPHIL	0.93	0.92	0.92	735	accuracy			0.91	2988	macro avg	0.91	0.90	0.91	2988	weighted avg	0.91	0.91	0.91	2988	91.0%	<pre>print(confusion_matrix(y_test, pred))</pre> <pre>array([[652 8 36 30] [10 690 26 20] [30 20 686 45] [24 18 32 661]])</pre>
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InceptionV3	<pre>print(classification_report(y_test, pred))</pre> <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>0.91</td><td>0.89</td><td>0.90</td><td>726</td></tr><tr><td>LYMPHOCYTE</td><td>0.90</td><td>0.91</td><td>0.91</td><td>746</td></tr><tr><td>MONOCYTE</td><td>0.88</td><td>0.87</td><td>0.88</td><td>781</td></tr><tr><td>NEUTROPHIL</td><td>0.91</td><td>0.90</td><td>0.90</td><td>735</td></tr><tr><td>accuracy</td><td></td><td></td><td>0.90</td><td>2988</td></tr><tr><td>macro avg</td><td>0.90</td><td>0.89</td><td>0.90</td><td>2988</td></tr><tr><td>weighted avg</td><td>0.90</td><td>0.90</td><td>0.90</td><td>2988</td></tr></tbody></table> <p>Accuracy of the model: 90.0%</p>		precision	recall	f1-score	support	EOSINOPHIL	0.91	0.89	0.90	726	LYMPHOCYTE	0.90	0.91	0.91	746	MONOCYTE	0.88	0.87	0.88	781	NEUTROPHIL	0.91	0.90	0.90	735	accuracy			0.90	2988	macro avg	0.90	0.89	0.90	2988	weighted avg	0.90	0.90	0.90	2988	90.0%	<pre>print(confusion_matrix(y_test, pred))</pre> <pre>array([[648 10 38 30] [14 680 28 24] [35 22 683 41] [28 25 30 652]])</pre>
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