

Model Development Phase Template

| | |
|---------------|--|
| Date | 20-06-2025 |
| Team ID | SWDTID1749906902 |
| Project Title | Early Stage Disease Diagnosis System Using Human Nail Image Processing |
| 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:

```

▶ from tensorflow.keras.layers import Dense, Flatten, Input
  from tensorflow.keras.models import Model
  from tensorflow.keras.preprocessing.image import ImageDataGenerator, load_img
  from tensorflow.keras.applications.vgg16 import VGG16, preprocess_input
  from glob import glob
  import numpy as np
  import matplotlib.pyplot as plt

[ ] imageSize = 224
    #adding preprocessing layer to the front of vgg
    vgg = VGG16(input_shape=(imageSize, imageSize, 3), weights='imagenet', include_top=False)

```

```
[ ] #don't train existing weights
    for layer in vgg.layers:
        layer.trainable = False
```

```
[ ] #our layers - you can add more if you want
    x = Flatten()(vgg.output)
```

```
[ ] prediction = Dense(17, activation='softmax')(x)
```

```
[ ] model = Model(inputs=vgg.input, outputs=prediction)
```

```
[ ] #viewing the structure of the model
    model.summary()
```

```
[ ] model.compile(
    loss='categorical_crossentropy',
    optimizer='adam',
    metrics=['accuracy']
)
```

```
[ ] from tensorflow.keras.preprocessing.image import ImageDataGenerator

train_datagen = ImageDataGenerator(rescale=1./255, shear_range=0.2, zoom_range=0.2, horizontal_flip=True)
test_datagen = ImageDataGenerator(rescale=1./255)
```

```
import os

# Assuming your training data is in a 'train' directory and testing data is in a 'test' directory
trainPath = '/content/drive/MyDrive/Early Stage Disease Diagnosis System/train'
testPath = '/content/drive/MyDrive/Early Stage Disease Diagnosis System/test'

# Define image size
imageSize = 224

training_set = train_datagen.flow_from_directory(trainPath,
                                                target_size = (imageSize, imageSize),
                                                batch_size = 32,
                                                class_mode = 'categorical')

test_set = test_datagen.flow_from_directory(testPath,
                                            target_size = (imageSize, imageSize),
                                            batch_size = 32,
                                            class_mode = 'categorical')
```

```
[ ] training_set.class_indices
```

```

▶ import sys
  # fit the model
  r = model.fit(
    training_set,
    validation_data=test_set,
    epochs=100,
    steps_per_epoch=len(training_set)//3,
    validation_steps=len(test_set)//3
  )

```

```

[ ] #saving the model
    model.save('vgg-16-nail-disease.h5')

```

```

▶ #import load_model class for loading h5 file
  from tensorflow.keras.models import load_model

  #import image class to process the images
  from tensorflow.keras.preprocessing import image
  from tensorflow.keras.applications.inception_v3 import preprocess_input
  import numpy as np

```

```

[ ] #loading saved model file
    model = load_model('vgg-16-nail-disease.h5')

```

```

[ ] #loading one random image
    img = image.load_img(r'content/drive/MyDrive/Early Stage Disease Diagnosis System/test/Darier\_s disease/45.PNG', target_size=(224, 224))

```

```

▶ #converting the image to array format
    x=image.img_to_array(img)
    x = np.expand_dims(x, axis=0)
    img_data = preprocess_input(x)

```

```

[ ] predictions = model.predict(img_data)

```

```

[ ] index = ['Darier_s disease', 'Muehrck-e_s lines', 'alopecia areata', 'beau_s lines', 'bluish nail',
             'clubbing', 'eczema', 'half and half nailes (Lindsay_s nails)', 'koilonychia', 'leukonychia',
             'onycholysis', 'pale nail', 'red lunula', 'splinter hemmorrhage', 'terry_s nail', 'white nail', 'yellow nail']

  # Get predicted class index and label
  output_index = np.argmax(predictions, axis=1)[0]
  result = index[output_index]

  print("Predicted Class:", result)

```

Model Validation and Evaluation Report:

| Model | Classification Report | F1 Score | Confusion Matrix |
|--------------------|-----------------------|----------|------------------|
| TensorFlow / Keras | - | 81% | - |

| | | | |
|---------------------|---|-----|---|
| VGG16 Model | - | 79% | - |
| Flask | - | 64% | - |
| flask_co rs.CORS | - | 78% | - |