```
import tensorflow as tf
import tensorflow_hub as hub
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import seaborn as sns
from tensorflow.keras.utils import get_file
from sklearn.metrics import roc_curve, auc, confusion_matrix
from imblearn.metrics import sensitivity_score, specificity_score

import os
import glob
import zipfile
import random

# to get consistent results after multiple runs
tf.random.set_seed(7)
np.random.seed(7)
random.seed(7)

# 0 for benign, 1 for malignant
class_names = ["benign", "malignant"]


def download_and_extract_dataset():
  # dataset from https://github.com/udacity/dermatologist-ai
  # 5.3GB
  train_url = "https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/train.zip"
  # 824.5MB
  valid_url = "https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/valid.zip"
  # 5.1GB
  test_url  = "https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/test.zip"
  for i, download_link in enumerate([valid_url, train_url, test_url]):
    temp_file = f"temp{i}.zip"
    data_dir = get_file(origin=download_link, fname=os.path.join(os.getcwd(), temp_file))
    print("Extracting", download_link)
    with zipfile.ZipFile(data_dir, "r") as z:
      z.extractall("data")
    # remove the temp file
    os.remove(temp_file)

# comment the below line if you already downloaded the dataset
download_and_extract_dataset()
```

```
Downloading data from https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/valid.zip
864538487/864538487 [==============================] - 56s 0us/step
Extracting https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/valid.zip
Downloading data from https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/train.zip
5736557430/5736557430 [==============================] - 489s 0us/step
Extracting https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/train.zip
Downloading data from https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/test.zip
5528640507/5528640507 [==============================] - 448s 0us/step
Extracting https://s3-us-west-1.amazonaws.com/udacity-dlnfd/datasets/skin-cancer/test.zip
```

```
# preparing data
# generate CSV metadata file to read img paths and labels from it
def generate_csv(folder, label2int):
    folder_name = os.path.basename(folder)
    labels = list(label2int)
    # generate CSV file
    df = pd.DataFrame(columns=["filepath", "label"])
    i = 0
    for label in labels:
        print("Reading", os.path.join(folder, label, "*"))
        for filepath in glob.glob(os.path.join(folder, label, "*")):
            df.loc[i] = [filepath, label2int[label]]
            i += 1
    output_file = f"{folder_name}.csv"
    print("Saving", output_file)
    df.to_csv(output_file)

# generate CSV files for all data portions, labeling nevus and seborrheic keratosis
# as 0 (benign), and melanoma as 1 (malignant)
# you should replace "data" path to your extracted dataset path
# don't replace if you used download_and_extract_dataset() function
generate_csv("data/train", {"nevus": 0, "seborrheic_keratosis": 0, "melanoma": 1})
generate_csv("data/valid", {"nevus": 0, "seborrheic_keratosis": 0, "melanoma": 1})
generate_csv("data/test", {"nevus": 0, "seborrheic_keratosis": 0, "melanoma": 1})
```

```
Reading data/train/nevus/*
Reading data/train/seborrheic_keratosis/*
```

```
Reading data/train/melanoma/*
Saving train.csv
Reading data/valid/nevus/*
Reading data/valid/seborrheic_keratosis/*
Reading data/valid/melanoma/*
Saving valid.csv
Reading data/test/nevus/*
Reading data/test/seborrheic_keratosis/*
Reading data/test/melanoma/*
Saving test.csv
```

```
# loading data
train_metadata_filename = "train.csv"
valid_metadata_filename = "valid.csv"
# load CSV files as DataFrames
df_train = pd.read_csv(train_metadata_filename)
df_valid = pd.read_csv(valid_metadata_filename)
n_training_samples = len(df_train)
n_validation_samples = len(df_valid)
print("Number of training samples:", n_training_samples)
print("Number of validation samples:", n_validation_samples)
train_ds = tf.data.Dataset.from_tensor_slices((df_train["filepath"], df_train["label"]))
valid_ds = tf.data.Dataset.from_tensor_slices((df_valid["filepath"], df_valid["label"]))
```

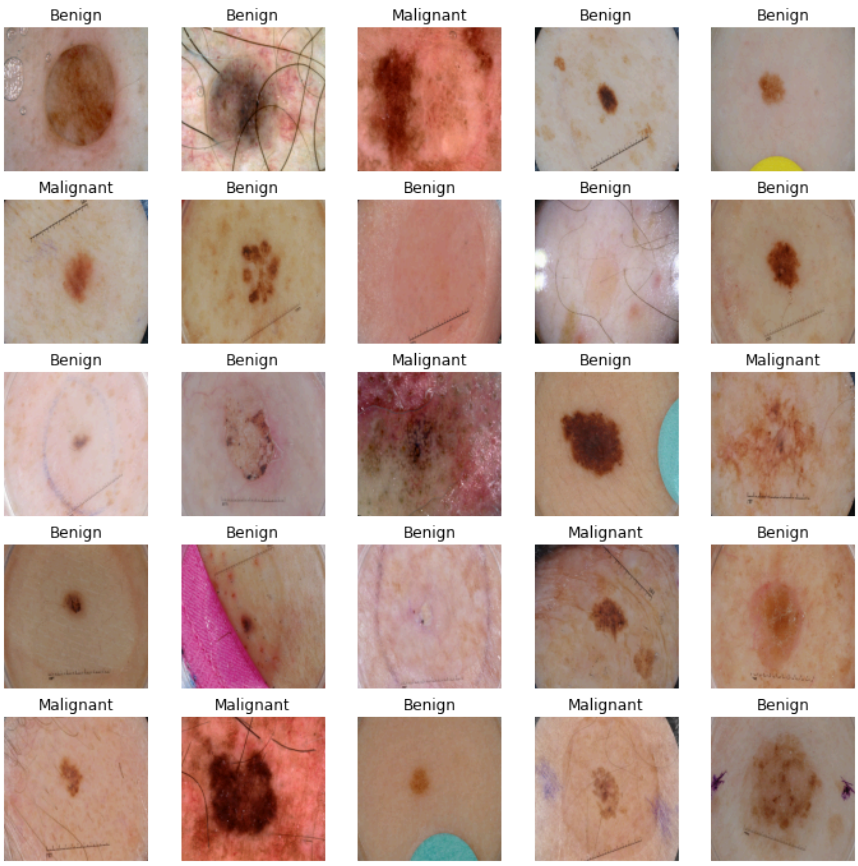
```
Number of training samples: 2000
Number of validation samples: 150
```

```
# preprocess data
def decode_img(img):
  # convert the compressed string to a 3D uint8 tensor
  img = tf.image.decode_jpeg(img, channels=3)
  # Use `convert_image_dtype` to convert to floats in the [0,1] range.
  img = tf.image.convert_image_dtype(img, tf.float32)
  # resize the image to the desired size.
  return tf.image.resize(img, [299, 299])


def process_path(filepath, label):
  # load the raw data from the file as a string
  img = tf.io.read_file(filepath)
  img = decode_img(img)
  return img, label


valid_ds = valid_ds.map(process_path)
train_ds = train_ds.map(process_path)
# test_ds = test_ds
for image, label in train_ds.take(1):
    print("Image shape:", image.shape)
    print("Label:", label.numpy())
```

```
Image shape: (299, 299, 3)
Label: 0
```

```
# training parameters
batch_size = 64
optimizer = "rmsprop"
```

```
def prepare_for_training(ds, cache=True, batch_size=64, shuffle_buffer_size=1000):
  if cache:
    if isinstance(cache, str):
      ds = ds.cache(cache)
    else:
      ds = ds.cache()
  # shuffle the dataset
  ds = ds.shuffle(buffer_size=shuffle_buffer_size)

  # Repeat forever
  ds = ds.repeat()
  # split to batches
  ds = ds.batch(batch_size)

  # `prefetch` lets the dataset fetch batches in the background while the model
  # is training.
  ds = ds.prefetch(buffer_size=tf.data.experimental.AUTOTUNE)

  return ds


valid_ds = prepare_for_training(valid_ds, batch_size=batch_size, cache="valid-cached-data")
train_ds = prepare_for_training(train_ds, batch_size=batch_size, cache="train-cached-data")


batch = next(iter(valid_ds))

def show_batch(batch):
  plt.figure(figsize=(12,12))
  for n in range(25):
      ax = plt.subplot(5,5,n+1)
      plt.imshow(batch[0][n])
      plt.title(class_names[batch[1][n].numpy()].title())
      plt.axis('off')

show_batch(batch)
```



```
# building the model
# InceptionV3 model & pre-trained weights
module_url = "https://tfhub.dev/google/tf2-preview/inception_v3/feature_vector/4"
m = tf.keras.Sequential([
    hub.KerasLayer(module_url, output_shape=[2048], trainable=False),
    tf.keras.layers.Dense(1, activation="sigmoid")
])

m.build([None, 299, 299, 3])
m.compile(loss="binary_crossentropy", optimizer=optimizer, metrics=["accuracy"])
m.summary()
```

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 keras_layer (KerasLayer)    (None, 2048)              21802784

 dense (Dense)               (None, 1)                 2049

=================================================================
Total params: 21,804,833
Trainable params: 2,049
Non-trainable params: 21,802,784
_________________________________________________________________
```

```
model_name = f"benign-vs-malignant_{batch_size}_{optimizer}"
tensorboard = tf.keras.callbacks.TensorBoard(log_dir=os.path.join("logs", model_name))
# saves model checkpoint whenever we reach better weights
modelcheckpoint = tf.keras.callbacks.ModelCheckpoint(model_name + "_{val_loss:.3f}.h5", save_best_only=True, verbose=1)

history = m.fit(train_ds, validation_data=valid_ds,
                steps_per_epoch=n_training_samples // batch_size,
                validation_steps=n_validation_samples // batch_size, verbose=1, epochs=100,
                callbacks=[tensorboard, modelcheckpoint])
```

```
Epoch 1/100
31/31 [==============================] - ETA: 0s - loss: 0.4572 - accuracy: 0.7772
Epoch 1: val_loss improved from inf to 0.55681, saving model to benign-vs-malignant_64_rmsprop_0.557.h5
31/31 [==============================] - 178s 3s/step - loss: 0.4572 - accuracy: 0.7772 - val_loss: 0.5568 - val_accuracy: 0.789
Epoch 2/100
31/31 [==============================] - ETA: 0s - loss: 0.4020 - accuracy: 0.8130
Epoch 2: val_loss improved from 0.55681 to 0.48952, saving model to benign-vs-malignant_64_rmsprop_0.490.h5
31/31 [==============================] - 9s 286ms/step - loss: 0.4020 - accuracy: 0.8130 - val_loss: 0.4895 - val_accuracy: 0.81
Epoch 3/100
31/31 [==============================] - ETA: 0s - loss: 0.3823 - accuracy: 0.8266
Epoch 3: val_loss improved from 0.48952 to 0.47676, saving model to benign-vs-malignant_64_rmsprop_0.477.h5
31/31 [==============================] - 8s 267ms/step - loss: 0.3823 - accuracy: 0.8266 - val_loss: 0.4768 - val_accuracy: 0.80
Epoch 4/100
31/31 [==============================] - ETA: 0s - loss: 0.3637 - accuracy: 0.8251
Epoch 4: val_loss did not improve from 0.47676
31/31 [==============================] - 8s 254ms/step - loss: 0.3637 - accuracy: 0.8251 - val_loss: 0.5025 - val_accuracy: 0.78
Epoch 5/100
31/31 [==============================] - ETA: 0s - loss: 0.3633 - accuracy: 0.8387
Epoch 5: val_loss improved from 0.47676 to 0.45733, saving model to benign-vs-malignant_64_rmsprop_0.457.h5
31/31 [==============================] - 9s 289ms/step - loss: 0.3633 - accuracy: 0.8387 - val_loss: 0.4573 - val_accuracy: 0.78
Epoch 6/100
31/31 [==============================] - ETA: 0s - loss: 0.3477 - accuracy: 0.8432
Epoch 6: val_loss did not improve from 0.45733
31/31 [==============================] - 8s 266ms/step - loss: 0.3477 - accuracy: 0.8432 - val_loss: 0.4644 - val_accuracy: 0.77
Epoch 7/100
31/31 [==============================] - ETA: 0s - loss: 0.3419 - accuracy: 0.8463
Epoch 7: val_loss did not improve from 0.45733
31/31 [==============================] - 9s 279ms/step - loss: 0.3419 - accuracy: 0.8463 - val_loss: 0.4624 - val_accuracy: 0.78
Epoch 8/100
31/31 [==============================] - ETA: 0s - loss: 0.3402 - accuracy: 0.8493
Epoch 8: val_loss improved from 0.45733 to 0.42326, saving model to benign-vs-malignant_64_rmsprop_0.423.h5
31/31 [==============================] - 9s 292ms/step - loss: 0.3402 - accuracy: 0.8493 - val_loss: 0.4233 - val_accuracy: 0.79
Epoch 9/100
31/31 [==============================] - ETA: 0s - loss: 0.3494 - accuracy: 0.8438
Epoch 9: val_loss improved from 0.42326 to 0.40612, saving model to benign-vs-malignant_64_rmsprop_0.406.h5
31/31 [==============================] - 9s 279ms/step - loss: 0.3494 - accuracy: 0.8438 - val_loss: 0.4061 - val_accuracy: 0.82
Epoch 10/100
31/31 [==============================] - ETA: 0s - loss: 0.3237 - accuracy: 0.8564
Epoch 10: val_loss did not improve from 0.40612
31/31 [==============================] - 8s 260ms/step - loss: 0.3237 - accuracy: 0.8564 - val_loss: 0.4904 - val_accuracy: 0.75
Epoch 11/100
31/31 [==============================] - ETA: 0s - loss: 0.3242 - accuracy: 0.8543
Epoch 11: val_loss did not improve from 0.40612
31/31 [==============================] - 9s 278ms/step - loss: 0.3242 - accuracy: 0.8543 - val_loss: 0.4568 - val_accuracy: 0.78
Epoch 12/100
31/31 [==============================] - ETA: 0s - loss: 0.3337 - accuracy: 0.8473
Epoch 12: val_loss did not improve from 0.40612
31/31 [==============================] - 8s 258ms/step - loss: 0.3337 - accuracy: 0.8473 - val_loss: 0.4702 - val_accuracy: 0.81
Epoch 13/100
31/31 [==============================] - ETA: 0s - loss: 0.3350 - accuracy: 0.8453
Epoch 13: val_loss did not improve from 0.40612
```

```
31/31 [==============================] - 8s 258ms/step - loss: 0.3350 - accuracy: 0.8453 - val_loss: 0.4289 - val_accuracy: 0.82
Epoch 14/100
31/31 [==============================] - ETA: 0s - loss: 0.3050 - accuracy: 0.8649
Epoch 14: val_loss did not improve from 0.40612
31/31 [==============================] - 8s 258ms/step - loss: 0.3050 - accuracy: 0.8649 - val_loss: 0.4649 - val_accuracy: 0.78
```

```
# evaluation

# load testing set
test_metadata_filename = "test.csv"
df_test = pd.read_csv(test_metadata_filename)
n_testing_samples = len(df_test)
print("Number of testing samples:", n_testing_samples)
test_ds = tf.data.Dataset.from_tensor_slices((df_test["filepath"], df_test["label"]))

def prepare_for_testing(ds, cache=True, shuffle_buffer_size=1000):
  # This is a small dataset, only load it once, and keep it in memory.
  # use `.cache(filename)` to cache preprocessing work for datasets that don't
  # fit in memory.
  if cache:
    if isinstance(cache, str):
      ds = ds.cache(cache)
    else:
      ds = ds.cache()

  ds = ds.shuffle(buffer_size=shuffle_buffer_size)

  return ds


test_ds = test_ds.map(process_path)
test_ds = prepare_for_testing(test_ds, cache="test-cached-data")
```

```
Number of testing samples: 600
```

```
# convert testing set to numpy array to fit in memory (don't do that when testing
# set is too large)
y_test = np.zeros((n_testing_samples,))
X_test = np.zeros((n_testing_samples, 299, 299, 3))
for i, (img, label) in enumerate(test_ds.take(n_testing_samples)):
  # print(img.shape, label.shape)
  X_test[i] = img
  y_test[i] = label.numpy()

print("y_test.shape:", y_test.shape)
```

```
y_test.shape: (600,)
```

```
# load the weights with the least loss
m.load_weights("benign-vs-malignant_64_rmsprop_0.399.h5")
```

```
print("Evaluating the model...")
loss, accuracy = m.evaluate(X_test, y_test, verbose=0)
print("Loss:", loss, "  Accuracy:", accuracy)
```

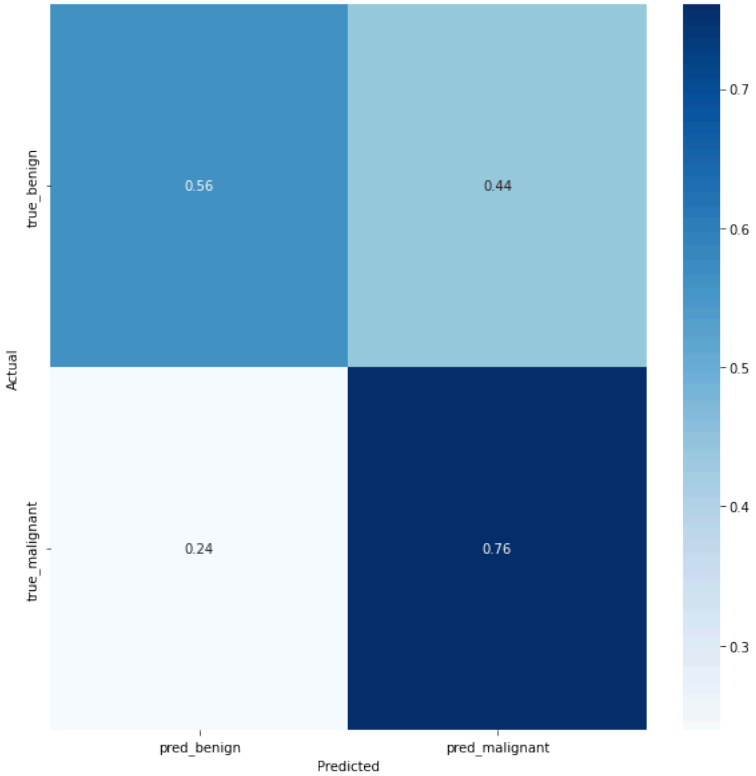
```
Evaluating the model...
Loss: 0.4762299060821533   Accuracy: 0.7883333563804626
```

```
from sklearn.metrics import accuracy_score

def get_predictions(threshold=None):
  """
  Returns predictions for binary classification given `threshold`
  For instance, if threshold is 0.3, then it'll output 1 (malignant) for that sample if
  the probability of 1 is 30% or more (instead of 50%)
  """
  y_pred = m.predict(X_test)
  if not threshold:
    threshold = 0.5
  result = np.zeros((n_testing_samples,))
  for i in range(n_testing_samples):
    # test melanoma probability
    if y_pred[i][0] >= threshold:
      result[i] = 1
    # else, it's 0 (benign)
  return result

threshold = 0.23
# get predictions with 23% threshold
# which means if the model is 23% sure or more that is malignant,
# it's assigned as malignant, otherwise it's benign
y_pred = get_predictions(threshold)
accuracy_after = accuracy_score(y_test, y_pred)
print("Accuracy after setting the threshold:", accuracy_after)
```

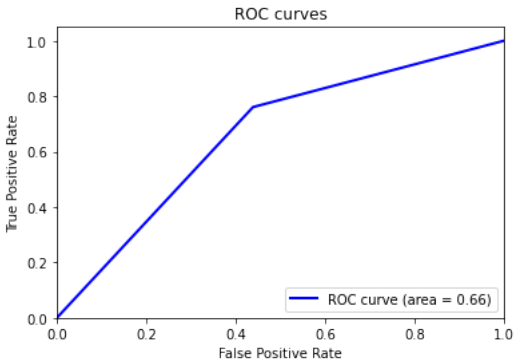
```
19/19 [==============================] - 2s 123ms/step
Accuracy after setting the threshold: 0.7883333333333333
```

```
import seaborn as sns
from sklearn.metrics import roc_curve, auc, confusion_matrix

def plot_confusion_matrix(y_test, y_pred):
  cmn = confusion_matrix(y_test, y_pred)
  # Normalise
  cmn = cmn.astype('float') / cmn.sum(axis=1)[:, np.newaxis]
  # print it
  print(cmn)
  fig, ax = plt.subplots(figsize=(10,10))
  sns.heatmap(cmn, annot=True, fmt='.2f',
              xticklabels=[f"pred_{c}" for c in class_names],
              yticklabels=[f"true_{c}" for c in class_names],
              cmap="Blues"
              )
  plt.ylabel('Actual')
  plt.xlabel('Predicted')
  # plot the resulting confusion matrix
  plt.show()


def plot_roc_auc(y_true, y_pred):
    """
    This function plots the ROC curves and provides the scores.
    """
    # prepare for figure
    plt.figure()
    fpr, tpr, _ = roc_curve(y_true, y_pred)
    # obtain ROC AUC
    roc_auc = auc(fpr, tpr)
    # print score
    print(f"ROC AUC: {roc_auc:.3f}")
    # plot ROC curve
    plt.plot(fpr, tpr, color="blue", lw=2,
                label='ROC curve (area = {f:.2f})'.format(d=1, f=roc_auc))
    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.05])
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('ROC curves')
    plt.legend(loc="lower right")
    plt.show()

plot_confusion_matrix(y_test, y_pred)
plot_roc_auc(y_test, y_pred)
sensitivity = sensitivity_score(y_test, y_pred)
specificity = specificity_score(y_test, y_pred)

print("Melanoma Sensitivity:", sensitivity)
print("Melanoma Specificity:", specificity)
```

```
[[0.5610766  0.4389234 ]
 [0.23931624 0.76068376]]
```

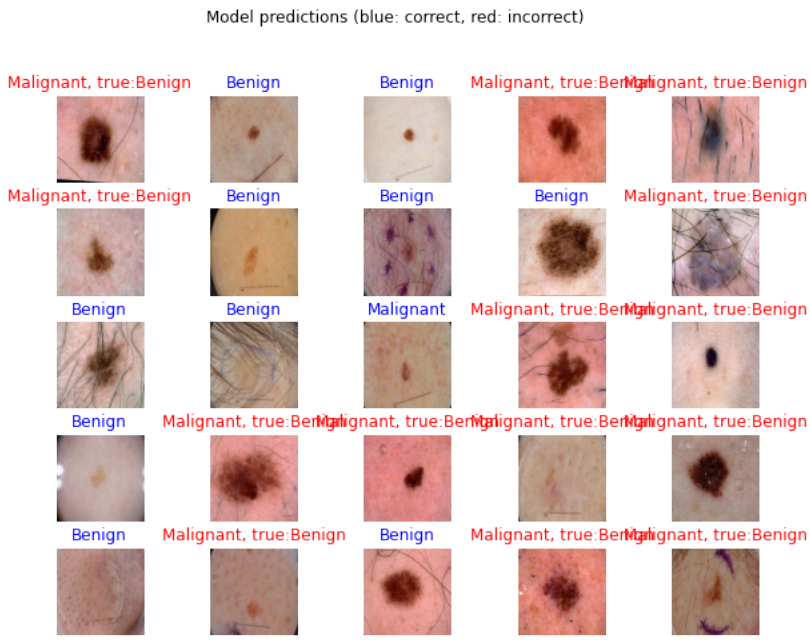



```
ROC AUC: 0.661
```




```
Melanoma Sensitivity: 0.7606837606837606
Melanoma Specificity: 0.5610766045548654
```

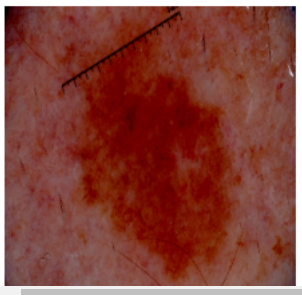
```
def plot_images(X_test, y_pred, y_test):
  predicted_class_names = np.array([class_names[int(round(id))] for id in y_pred])
  # some nice plotting
  plt.figure(figsize=(10,9))
  for n in range(30, 60):
      plt.subplot(6,5,n-30+1)
      plt.subplots_adjust(hspace = 0.3)
      plt.imshow(X_test[n])
      # get the predicted label
      predicted_label = predicted_class_names[n]
      # get the actual true label
      true_label = class_names[int(round(y_test[n]))]
      if predicted_label == true_label:
          color = "blue"
          title = predicted_label.title()
      else:
          color = "red"
          title = f"{predicted_label.title()}, true:{true_label.title()}"
      plt.title(title, color=color)
      plt.axis('off')
  _ = plt.suptitle("Model predictions (blue: correct, red: incorrect)")
  plt.show()

plot_images(X_test, y_pred, y_test)
```




```
# a function given a function, it predicts the class of the image
def predict_image_class(img_path, model, threshold=0.5):
  img = tf.keras.preprocessing.image.load_img(img_path, target_size=(299, 299))
  img = tf.keras.preprocessing.image.img_to_array(img)
  img = tf.expand_dims(img, 0) # Create a batch
  img = tf.keras.applications.inception_v3.preprocess_input(img)
  img = tf.image.convert_image_dtype(img, tf.float32)
  predictions = model.predict(img)
  score = predictions.squeeze()
  if score >= threshold:
    print(f"This image is {100 * score:.2f}% malignant.")
  else:
    print(f"This image is {100 * (1 - score):.2f}% benign.")

  plt.imshow(img[0])
  plt.axis('off')
  plt.show()
```

```
predict_image_class("data/test/melanoma/ISIC_0013767.jpg", m)
```

```
1/1 [==============================] - 0s 27ms/step
WARNING:matplotlib.image:Clipping input data to the valid range for imshow with RGB d
[[0.6803772]]
0.6803772
This image is 68.04% malignant.
```



```
predict_image_class("data/test/nevus/ISIC_0012092.jpg", m)
```

```
1/1 [==============================] - 0s 50ms/step
WARNING:matplotlib.image:Clipping input data to the valid range for imshow with RGB d
[[0.21590327]]
0.21590327
This image is 78.41% benign.
```