Python Coding

pip3 install tensorflow tensorflow_hub matplotlib seaborn numpy pandas sklearn imblearn

```
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"]
```

Preparing the Dataset

```
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()
# 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})
# 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"]))
```

Output:

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):
```

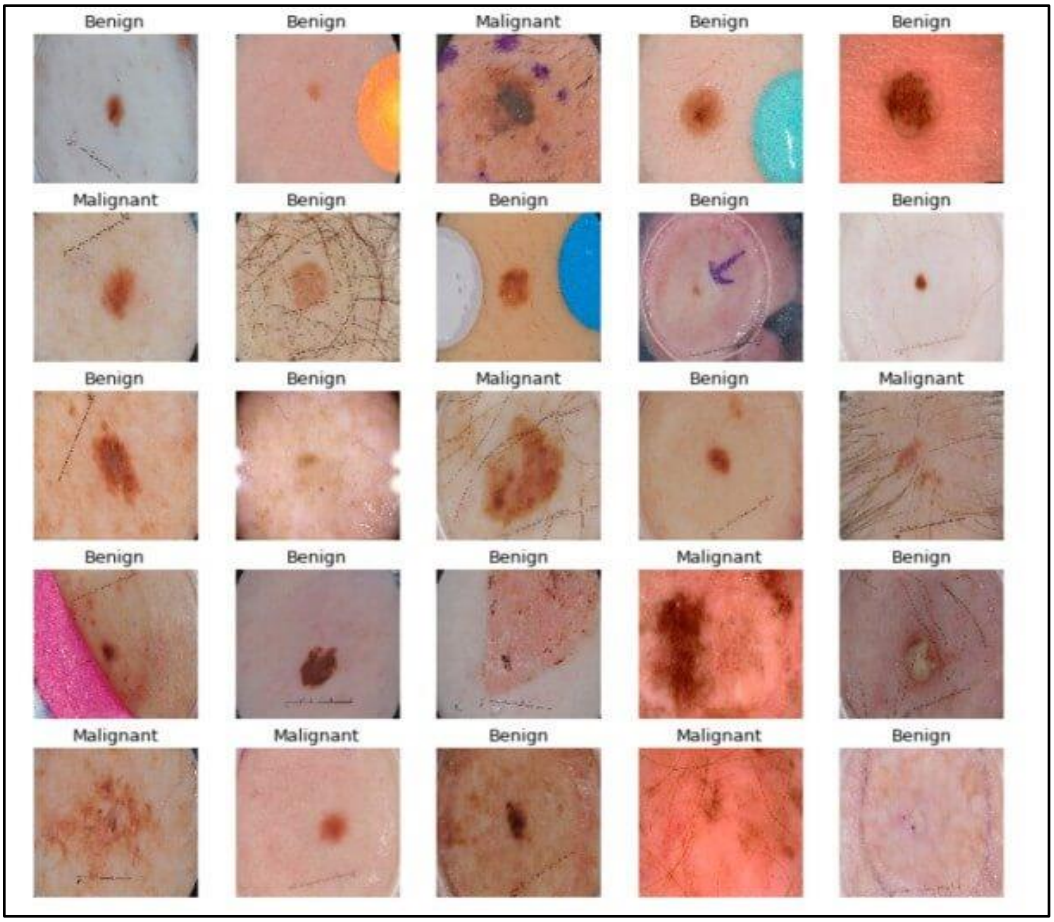
```
  if cache:
    if isinstance(cache, str):
      ds = ds.cache(cache)
    else:
      ds = ds.cache()
  # shuffle the dataset
  ds = ds.shuffle(buffer_size=shuffle_buffer_size)
  # Repeat forever
  ds = ds.repeat()
  # split to batches
  ds = ds.batch(batch_size)
  # `prefetch` lets the dataset fetch 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)
```

Output:




```
# 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()
```

Output:

Model: "sequential"

_____

Layer (type) Output Shape Param #

==========

keras_layer (KerasLayer) multiple 21802784

_____

dense (Dense) multiple 2049

==========

Total params: 21,804,833

Trainable params: 2,049

Non-trainable params: 21,802,784

_____

Training the Model

```
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])
```

Output:

Train for 31 steps, validate for 2 steps

Epoch 1/100

30/31 [==============================>.] - ETA: 9s - loss: 0.4609 - accuracy: 0.7760

Epoch 00001: val_loss improved from inf to 0.49703, saving model to benign-vs-malignant_64_rmsprop_0.497.h5

31/31 [==============================] - 282s 9s/step - loss: 0.4646 - accuracy: 0.7722 - val_loss: 0.4970 - val_accuracy: 0.8125

<..SNIPED..>

Epoch 27/100

30/31 [==============================>.] - ETA: 0s - loss: 0.2982 - accuracy: 0.8708

Epoch 00027: val_loss improved from 0.40253 to 0.38991, saving model to benign-vs-malignant_64_rmsprop_0.390.h5

31/31 [==============================] - 21s 691ms/step - loss: 0.3025 - accuracy: 0.8684 - val_loss: 0.3899 - val_accuracy: 0.8359

<..SNIPED..>

Epoch 41/100

30/31 [==============================>.] - ETA: 0s - loss: 0.2800 - accuracy: 0.8802

Epoch 00041: val_loss did not improve from 0.38991

31/31 [==============================] - 21s 690ms/step - loss: 0.2829 - accuracy: 0.8790 - val_loss: 0.3948 - val_accuracy: 0.8281

Epoch 42/100

30/31 [==============================>.] - ETA: 0s - loss: 0.2680 - accuracy: 0.8859

Epoch 00042: val_loss did not improve from 0.38991

31/31 [==============================] - 21s 693ms/step - loss: 0.2722 - accuracy: 0.8831 - val_loss: 0.4572 - val_accuracy: 0.8047

Model Evaluation:

```
# 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):
  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)
# load the weights with the least loss
m.load_weights("benign-vs-malignant_64_rmsprop_0.390.h5")
print("Evaluating the model...")
loss, accuracy = m.evaluate(X_test, y_test, verbose=0)
print("Loss:", loss, "  Accuracy:", accuracy)
```

Output:

Evaluating the model...

Loss: 0.4476394319534302 Accuracy: 0.8

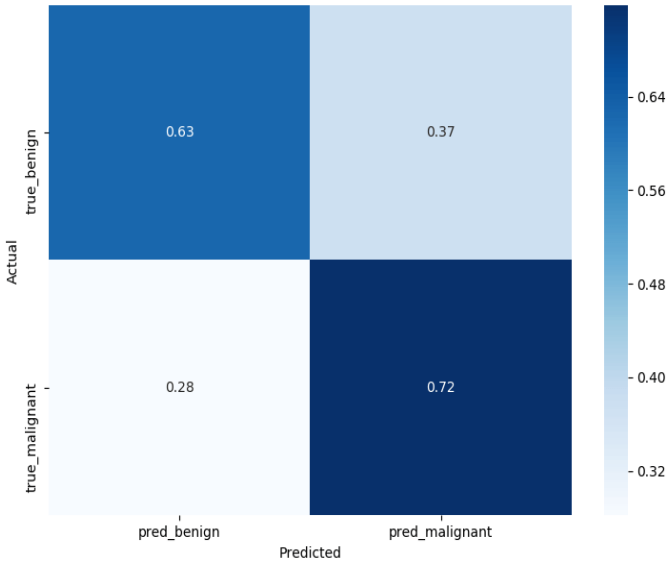
```
def get_predictions(threshold=None):
  """
  Returns predictions for binary classification given `threshold`
  For instance, if threshold is 0.3, then it'll output 1 (malignant) for that sample if
  the probability of 1 is 30% or more (instead of 50%)
  """
  y_pred = m.predict(X_test)
  if not threshold:
    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)
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()

plot_confusion_matrix(y_test, y_pred)
```

Output:




```
sensitivity = sensitivity_score(y_test, y_pred)
specificity = specificity_score(y_test, y_pred)

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

Output:

Melanoma Sensitivity: 0.717948717948718

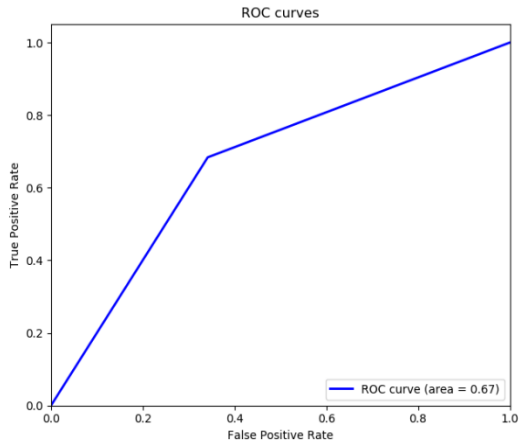
Melanoma Specificity: 0.6252587991718427

```
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_roc_auc(y_test, y_pred)
```

Output:



ROC AUC: 0.671