**Final Deliverable**

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| Date | 18 October 2022 |
| Team ID | PNT2022TMID42059 |
| Project Name | AI based localization and classification of skin disease with Erythema |
| Maximum Marks | 8 Marks |

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"]))

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

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Let's load the images:

# 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()

|  |  |
| --- | --- |
| 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**

We now have our dataset and the model, let's get them together:

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])

Here is a part of the output during training:

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

First, let's load our test set, just like previously:

# 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")

The above code loads our test data and prepares it for testing:

Number of testing samples: 600

images of the shape

600

(299, 299, 3)

set from tf.data into a NumPy array:

can fit our memory, let's convert our test

# 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)

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Output:

Evaluating the model...

Loss: 0.4476394319534302 Accuracy: 0.8

The below function does that:

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)

Now let's draw our confusion matrix and interpret it:

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"

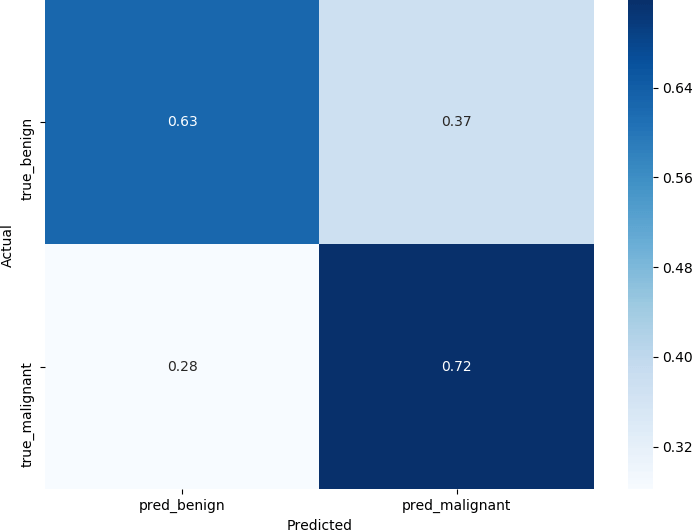
)

plt.ylabel('Actual') plt.xlabel('Predicted')

# plot the resulting confusion matrix plt.show()

plot\_confusion\_matrix(y\_test, y\_pred)

Output:



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))

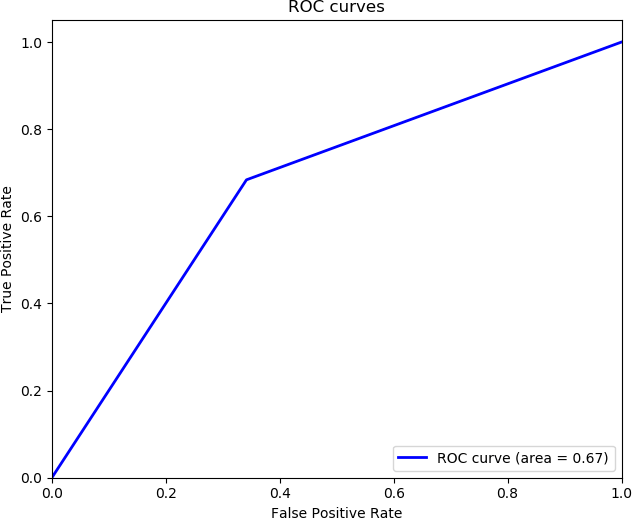
plt.xlim([0.0, 1.0])

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)

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Output:



ROC AUC: 0.671