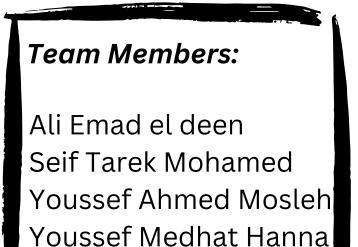
Supervised By: Dr.Ahmed Youssef Badawy Eng.Nour Eldeen Magdy Machine Learning 2024

Project Name Track: Medical Diagnosis

Skin Cancer Using Tensor Flow





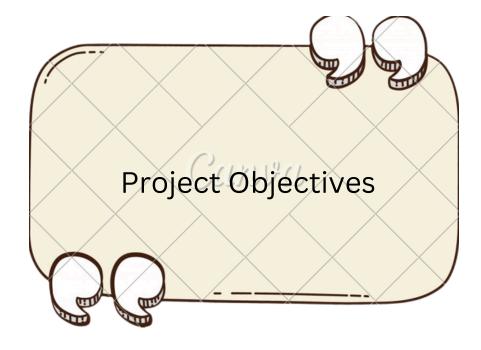
Skin cancer is among the most common types of cancer, and quick identification considerably enhances the odds of survival. The purpose of this work is to develop cutting-edge deep learning models that can classify images of skin cells and accurately **detect** cases of **skin cancer**.

Challenges and Problem Statements

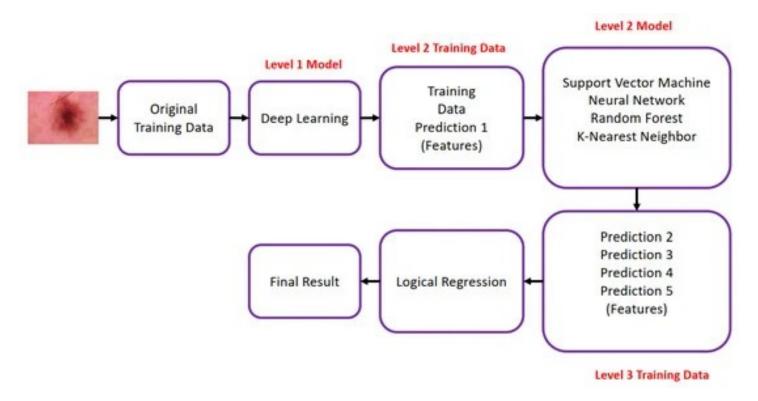
The principle barriers to skin cancer detection are that it is a low priority in primary care, that the majority of exams do not result in significant findings, and that many providers lack expertise to adequately identify high risk lesions. So The main goal of using machine learning/deep learning in skin cancer classification is to improve the diagnostic accuracy of skin cancers,

Project Overview

We will use a dataset that contains images for the two categories that are malignant or benign. We will use the transfer learning technique to achieve better results in less amount of training. We will use EfficientNet architecture as the backbone of our model along with the pre-trained weights of the same obtained by training it on the image net dataset.



- Deep learning models can recognize complex pictures, text, sounds, and other data patterns to produce accurate insights and predictions.
- Specify whether Given Data set Images is <u>benign</u> or <u>mallignant</u>
- Algorithm:



Importing Libraries

<u>Python</u> libraries make it very easy for us to handle the data and perform typical and complex tasks with a single line of code.

- **Pandas** This library helps to load the data frame in a 2D array format and has multiple functions to perform analysis tasks in one go.
- **Numpy**_– Numpy arrays are very fast and can perform large computations in a very short time.
- Matplotlib_ This library is used to draw visualizations.
- **Sklearn** This module contains multiple libraries having pre-implemented functions to perform tasks from data preprocessing to model development and evaluation.
- **Tensor Flow** This is an open-source library that is used for Machine Learning and Artificial intelligence and provides a range of functions to achieve complex functionalities with single lines of code.

```
[ ] import numpy as np
  import pandas as pd
  import seaborn as sb
  import matplotlib.pyplot as plt

from glob import glob
  from PIL import Image
  from sklearn.model_selection import train_test_split

import tensorflow as tf
  from tensorflow import keras
  from keras import layers
  from functools import partial

AUTO = tf.data.experimental.AUTOTUNE
  import warnings
  warnings.filterwarnings('ignore')
```

```
[ ] images = glob('train_cancer/*/*.jpg')
len(images)
```



Now, let's check the number of images we have got here, You can download Images from here ## train_cancer - Google Drive

```
#replace backslash with forward slash to avoid unexpected errors
images = [path.replace('\\', '/') for path in images]

df = pd.DataFrame({'C:\Users\youss\OneDrive\Desktop\ML Project\DS.zip\train_cancer': images})

df['label'] = df['C:\Users\youss\OneDrive\Desktop\ML Project\DS.zip\train_cancer'].str.split('/', expand=True)[1]

filepath label

train_cancer/benign/30.jpg benign

train_cancer/benign/19.jpg benign

train_cancer/benign/14.jpg benign

train_cancer/benign/14.jpg benign

images = glob('train_cancer/*/*.jpg')
len(images)
```

Converting the labels to 0 and 1 will save our work of label encoding

```
df['label_bin'] = np.where(df['label'].values == 'malignant', 1, 0)
df.head()
```

```
x = df{'label'}.value_counts()
plt.ple(x.values,
    labels=x.index,
    autopet='%1.if%%')
plt.show()

malignant

88.9%

11.1%
benign
```

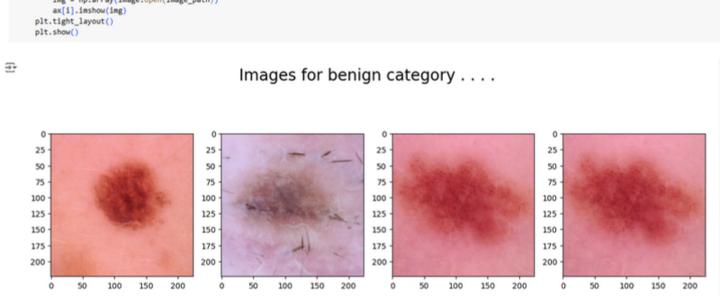
An approximately equal number of images have been given for each of the classes so, data imbalance is not a problem here.

```
for cat in df['label'].unique():
    temp = df[df['label'] == cat]

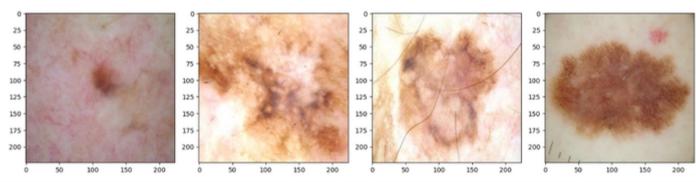
index_list = temp.index
    fig, ax = plt.subplots(1, 4, figsize=(15, 5))
    fig.suptitle(f'Images for (cat) category . . . .', fontsize=20)
    for i in range(4):
        index = np.random.randint(0, len(index_list))
        index = index_list[index]
        data = df.iloc[index]

    image_path = data[0]

    img = np.array(Image.open(image_path))
        ax[i].imshow(img)
    plt.tight_layout()
    plt.show()
```



Images for malignant category



Now, let's split the data into training and validation parts by using the train_test_split function.

```
features = df['C:\Users\youss\OneDrive\Desktop\ML Project\DS.zip\train_cancer']
    target = df['label_bin']
    X_train, X_val, Y_train, Y_val = train_test_split(features, target,
                      test_size=0.15,
                      random_state=10)
    X_train.shape, X_val.shape
₹ ((229,), (41,))
   def decode_image(C:\Users\youss\OneDrive\Desktop\ML Project\DS.zip\train_cancer, label=None):
      img = tf.io.read_file(filepath)
      img = tf.image.decode_jpeg(img)
      img = tf.image.resize(img, [224, 224])
      img = tf.cast(img, tf.float32) / 255.0
      if label == 0:
        Label = 0
      else:
        Label = 1
```

Image input pipelines have been implemented below so, that we can pass them without any need to load all the data beforehand.

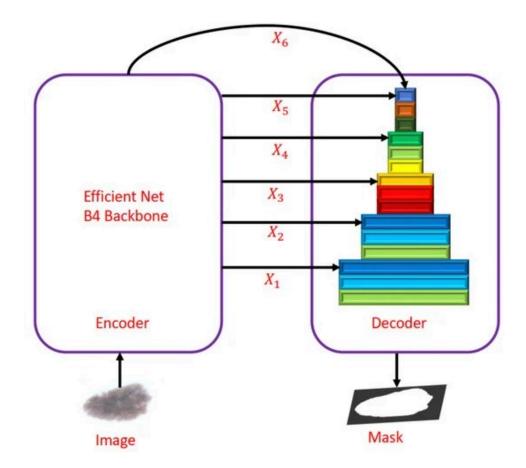
```
train_ds = (
     tf.data.Dataset
     .from_tensor_slices((X_train, Y_train))
     .map(decode_image, num_parallel_calls=AUTO)
     .batch(32)
     .prefetch(AUTO)
   val_ds = (
     tf.data.Dataset
     .from_tensor_slices((X_val, Y_val))
     .map(decode_image, num_parallel_calls=AUTO)
     .batch(32)
     .prefetch(AUTO)
[ ] from tensorflow.keras.applications.efficientnet import EfficientNetB7
   pre_trained_model = EfficientNetB7(
     input_shape=(224, 224, 3),
     weights='imagenet',
     include_top=False
    for layer in pre_trained_model.layers:
     layer.trainable = False
from tensorflow.keras import Model
   inputs = layers.Input(shape=(224, 224, 3))
   x = layers.Flatten()(inputs)
   x = layers.Dense(256, activation='relu')(x)
   x = layers.BatchNormalization()(x)
   x = layers.Dense(256, activation='relu')(x)
   x = layers.Dropout(0.3)(x)
   x = layers.BatchNormalization()(x)
   outputs = layers.Dense(1, activation='sigmoid')(x)
   model = Model(inputs, outputs)
[ ] model.compile(
     loss=tf.keras.losses.BinaryCrossentropy(from_logits=True),
     optimizer='adam',
     metrics=['AUC']
[ ] history = model.fit(train_ds,
          validation_data=val_ds,
          epochs=5.
          verbose=1)
 history = model.fit(train_ds,
           validation_data=val_ds,
           epochs=5,
           verbose=1)
 Epoch 1/5
               Epoch 2/5
               8/8 [=====
    Epoch 3/5
    8/8 [----
                  Epoch 4/5
    8/8 [====
                Epoch 5/5
    [ ] hist_df = pd.DataFrame(history.history)
    hist_df.head()
                auc val_loss val_auc
    0 0.884477 0.677150 2.470377 0.500000
     1 0.624001 0.858943 0.817437 0.476351
    2 0.519542 0.902520 1.200533 0.486486
    3 0.443939 0.958507 0.752024 0.513514
    4 0.377754 0.941076 0.621685 0.520270
```

```
hist_df['loss'].plot()
     hist_df['val_loss'].plot()
     plt.title('Loss v/s Validation Loss')
     plt.legend()
     plt.show()
3
                               Loss v/s Validation Loss
      2.5
                                                                      loss
                                                                     val_loss
      2.0
      1.5
      1.0
      0.5
            0.0
                    0.5
                           1.0
                                   1.5
                                           2.0
                                                   2.5
                                                          3.0
                                                                  3.5
                                                                          4.0
      hist_df['auc'].plot()
      hist_df['val_auc'].plot()
plt.title('AUC v/s Validation AUC')
       plt.legend()
       plt.show()
 =
                                   AUC v/s Validation AUC
                    auc
                    val_auc
        0.9
        0.8
        0.5
```

Model Development:

For this task, we will use the EfficientNet architecture and leverage the benefit of pre-trained weights of such large networks.

Model Architecture:



We will implement a model using the Functional API of Keras which will contain the following parts:

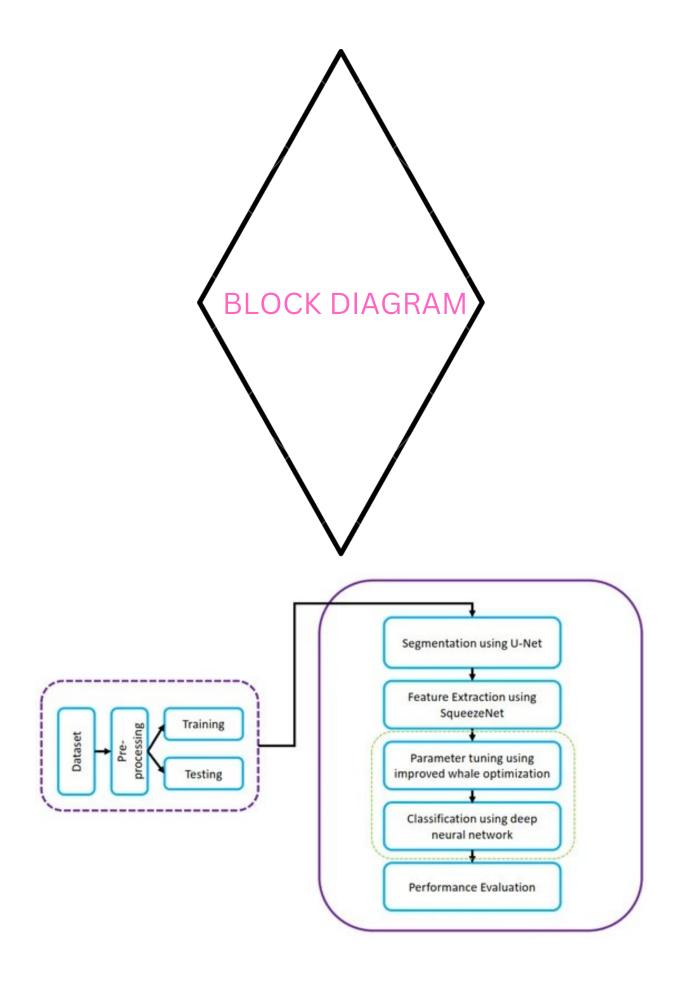
- The base model is the EfficientNet model in this case.
- The Flatten layer flattens the output of the base model's output.
- Then we will have two fully connected layers followed by the output of the flattened layer.
- We have included some Batch Normalization layers to enable stable and fast training and a Dropout layer before the final layer to avoid any possibility of overfitting.
- The final layer is the output layer which outputs soft probabilities for the three classes.

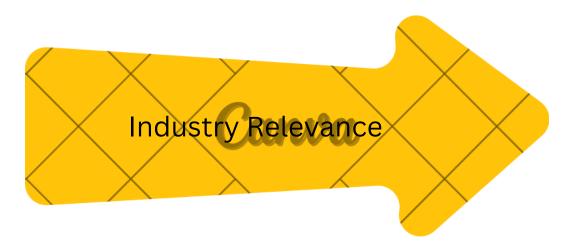
Output:

While compiling a model we provide these three essential parameters:

- <u>optimizer</u> This is the method that helps to optimize the cost function by using gradient descent.
- <u>loss</u> The loss function by which we monitor whether the model is improving with training or not.

 metrics – This helps to evaluate the model by predicting the training and the validation data.





To facilitate the development of computer-aided diagnosis systems in the segmentation and classification of melanoma. To build and evaluate the MED-NODE system for detecting skin cancer with dermoscopic images. To address the small size and insufficient diversity of images in the skin-disease dataset.



Busineess & Entrepreneurship Potential

TensorFlow Optimizations from Intel:

Intel collaborates with Google* to upstream most optimizations into the stock distribution of TensorFlow with the newest optimizations and features being released earlier as Intel® Extension for TensorFlow*. These optimizations can be enabled with a few lines of code and will accelerate TensorFlow-based training and inference performance on Intel CPU and GPU hardware.

Intel Neural Compressor:

Intel Neural Compressor is an open-source Python library that runs on CPUs or GPUs that performs model quantization to reduce the model size and increase the speed of deep learning inference for deployment. Intel Neural Compressor is a part of the Intel AI Analytics Toolkit. This library automates popular methods such as quantization, compression, pruning, and knowledge distillation across multiple deep learning frameworks.

References

- 1.Research Gate.com
- 2.MDPI

3.geeks for greeks.com

For Dataset: ## train cancer

