Problem Statement

To build a CNN based model which can accurately detect melanoma. Melanoma is a type of cancer that can be deadly if not detected early. It accounts for 75% of skin cancer deaths. A solution which can evaluate images and alert the dermatologists about the presence of melanoma has the potential to reduce a lot of manual effort needed in diagnosis.

Importing Skin Cancer Data

Importing all the important libraries

```
import pathlib
import tensorflow as tf
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import os
import PIL
from tensorflow import keras
from tensorflow.keras import layers
from tensorflow.keras.models import Sequential
```

train_ds have total 2239, test_ds have total 118 files, total =2357 files, there are 9 classes

In this assignment, I use a dataset of about 2357 images of skin cancer types. The dataset contains 9 sub-directories in each train and test subdirectories. The 9 sub-directories contains the images of 9 skin cancer types respectively.

Create a dataset

Define some parameters for the loader:

```
```

```
batch_size = 32
img_height = 180
img_width = 180
channels = 3
```

Use 80% of the images for training, and 20% for validation.

```
## Write your train dataset here
## Note use seed=123 while creating your dataset using tf.keras.preprocessing.image_dataset_from_directory
## Note, make sure your resize your images to the size img_height*img_width, while writting the dataset
train_ds = tf.keras.preprocessing.image_dataset_from_directory(
    r'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging Collaboration\\Train',
    shuffle =True ,
    image_size =(img_height,img_width)  , # image_size =(180,180,3)
    batch_size = batch_size             # 32
)
```

```
Found 2239 files belonging to 9 classes.
```

```
len(train_ds)
```

```
70
```

The totle files is 2239 and btach_size is 32

totole_batch = (2239/32) ~ 70

its mean 70 iteration

```
# train dataset belong classe name
train_ds.class_names
```

```
['actinic keratosis',
 'basal cell carcinoma',
 'dermatofibroma',
 'melanoma',
 'nevus',
 'pigmented benign keratosis',
 'seborrheic keratosis',
 'squamous cell carcinoma',
 'vascular lesion']
```

```
# test_data
val_ds = tf.keras.preprocessing.image_dataset_from_directory(
    r'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging Collaboration\\Test',
    shuffle =True ,
    image_size =(img_height,img_width)  , # image_size = (180,180,3)
    batch_size = batch_size             # 32
)
```

```
Found 118 files belonging to 9 classes.
```

The totle files is 118 and btach_size is 32

totole_batch = (118/32) ~ 4

its mean 4 iteration

```
len(val_ds)
```

```
4
```

```
# test dataset belong classe name
val_ds.class_names
```

```
['actinic keratosis',
 'basal cell carcinoma',
 'dermatofibroma',
 'melanoma',
 'nevus',
 'pigmented benign keratosis',
 'seborrheic keratosis',
 'squamous cell carcinoma',
 'vascular lesion']
```

```
# this is tensore form because multidimension data
val_ds
```

```
<_BatchDataset element_spec=(TensorSpec(shape=(None, 180, 180, 3), dtype=tf.float32, name=None), TensorSpec(shape=(None,),
dtype=tf.int32, name=None))>
```

```
# convert simple form
# fetch 1 batch , 1 batch have 32 files
```

```
for image_batch , lable_batch in val_ds.take(1) :
    print('this is one batch shape :',image_batch.shape)  # (batch_size,img_height,img_width,chanells)
    print('this is lable shape :',lable_batch.shape)
```

```
this is one batch shape : (32, 180, 180, 3)
this is lable shape : (32,)
```

```
# normal formn
for image_batch , label_batch in train_ds.take(1):
    print(image_batch.numpy())
    print('\n')
    print('convergt the lable in numeric : ',label_batch.numpy())
```

```
[[[[192.       170.       157.      ]
   [192.       170.       157.      ]
   [192.05556  170.05556  157.05556 ]
   ...
   [195.       171.       159.      ]
   [197.       173.       163.      ]
   [197.       173.       163.      ]]

  [[192.       170.       157.      ]
   [192.       170.       157.      ]
   [192.05556  170.05556  157.05556 ]
   ...
   [195.       171.       159.      ]
   [197.       173.       163.      ]
   [197.       173.       163.      ]]

  [[191.       169.       156.      ]
   [193.       171.       158.      ]
   [191.       169.       156.      ]
   ...
   [195.       171.       159.      ]
   [195.       171.       161.      ]
   [194.275    170.275    160.275   ]]

  ...

  [[191.38351  171.38351  160.38351 ]
   [194.18842  174.18842  163.18842 ]
   [193.       173.       162.      ]
   ...
   [181.94446  157.94446  145.94446 ]
   [187.       159.       148.      ]
   [187.       159.       148.      ]]
```

```
 [[191.       171.       160.      ]
  [191.       171.       160.      ]
  [191.56386  171.56386  160.56386 ]
  ...
  [189.       165.       153.      ]
  [191.36664  163.36664  152.36664 ]
  [189.       161.       150.      ]]

 [[191.       171.       160.      ]
  [191.       171.       160.      ]
  [194.9165   174.9165   163.9165  ]
  ...
  [189.       165.       153.      ]
  [191.36664  163.36664  152.36664 ]
  [189.       161.       150.      ]]]


[[[128.96666  120.066666  77.46667 ]
  [136.92     123.9       89.21    ]
  [140.75     130.95      94.85    ]
  ...
  [127.49971  127.49971   93.49971 ]
  [130.1      126.9       94.      ]
  [124.333206 121.333206  90.333206]]
```

```
# List out all the classes of skin cancer and store them in a list.
# You can find the class names in the class_names attribute on these datasets.
# These class_names = orrespond to the directory names in alphabetical order.
class_names = train_ds.class_names
print(class_names)
n_classes = len(class_names)
print(n_classes)
```

```
['actinic keratosis', 'basal cell carcinoma', 'dermatofibroma', 'melanoma', 'nevus', 'pigmented benign keratosis', 'seborrheic keratosis'
9
```

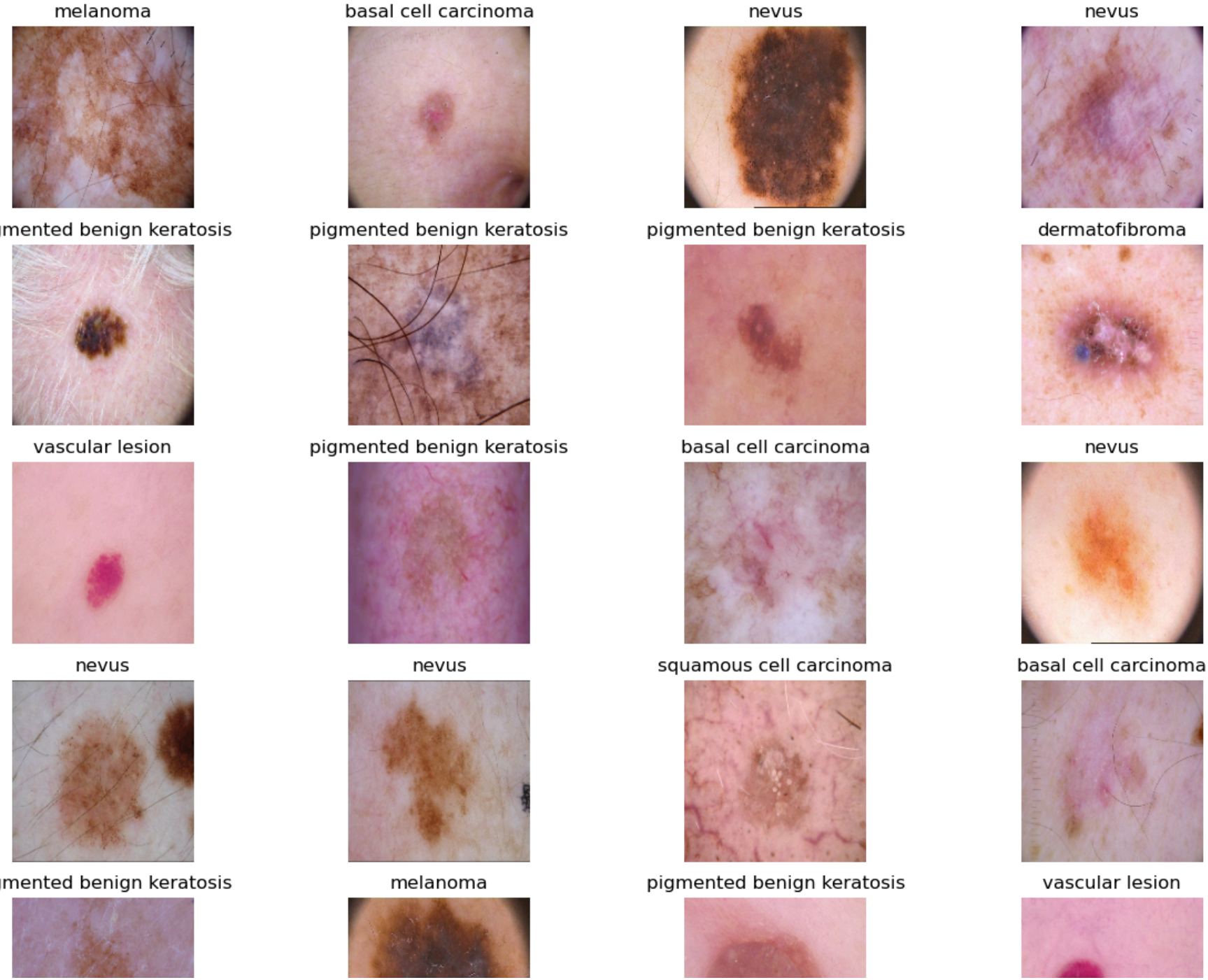
Visualize the data

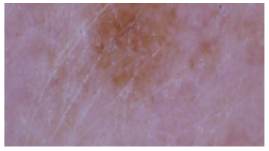
Todo, create a code to visualize one instance of all the nine classes present in the dataset

```
import matplotlib.pyplot as plt
```

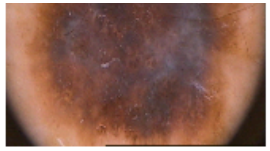
```
### your code goes here, you can use training or validation data to visualize

plt.figure(figsize=(15,20))
for image_batch , labels_batch in train_ds.take(1):
  print(image_batch.shape)
  print(labels_batch.numpy())
  for i in range(32):
    plt.subplot(8,4,i+1)
    plt.imshow(image_batch[i].numpy().astype('uint8'))
    plt.title(class_names[labels_batch[i]])
    plt.axis('off')
```

```
(32, 180, 180, 3)
[3 1 4 4 5 5 5 2 8 5 1 4 4 4 7 1 5 3 5 8 7 5 7 5 1 4 1 6 7 5 7 4]
```

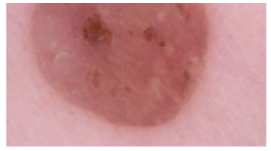




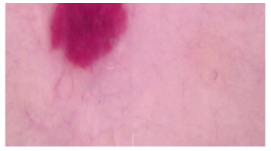
squamous cell carcinoma



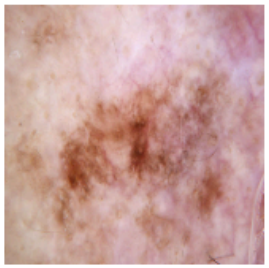
pigmented benign keratosis



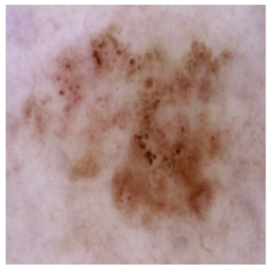
squamous cell carcinoma



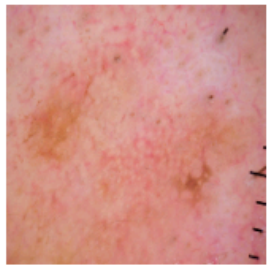
pigmented benign keratosis



basal cell carcinoma

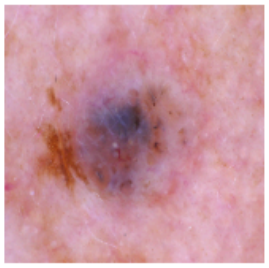


nevus



basal cell carcinoma

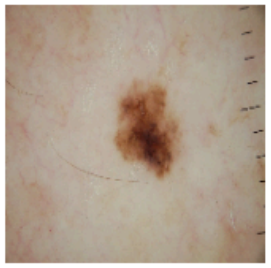
seborrheic keratosis



squamous cell carcinoma

pigmented benign keratosis

squamous cell carcinoma



nevus

The `image_batch` is a tensor of the shape `(32, 180, 180, 3)`. This is a batch of 32 images of shape `180x180x3` (the last dimension refers to color channels RGB). The `label_batch` is a tensor of the shape `(32,)`, these are corresponding labels to the 32 images.

`Dataset.cache()` keeps the images in memory after they're loaded off disk during the first epoch.

`Dataset.prefetch()` overlaps data preprocessing and model execution while training.

```
# incress the perfomance
AUTOTUNE = tf.data.experimental.AUTOTUNE
train_ds = train_ds.cache().shuffle(1000).prefetch(buffer_size=AUTOTUNE)
val_ds = val_ds.cache().shuffle(1000).prefetch(buffer_size=AUTOTUNE)
```

```
# resize and rescale the value
resize_and_rescale = tf.keras.Sequential([
    tf.keras.layers.experimental.preprocessing.Resizing(img_height,img_width),
    tf.keras.layers.experimental.preprocessing.Rescaling(1.0/255)
])
```

```
# data augmentation

data_augmentation = tf.keras.Sequential([
    tf.keras.layers.experimental.preprocessing.RandomFlip('horizontal_and_vertical'),
    tf.keras.layers.experimental.preprocessing.RandomRotation(0.3)
])
```

Create the model

Todo: Create a CNN model, which can accurately detect 9 classes present in the dataset. Use `layers.experimental.preprocessing.Rescaling` to normalize pixel values between (0,1). The RGB channel values are in the `[0, 255]` range. This is not ideal for a neural network. Here, it is good to standardize values to be in the `[0, 1]`

```
from tensorflow.keras.layers import Dense, Dropout, Activation, Flatten, Conv2D, MaxPooling2D ,BatchNormalization
```

```
input_shape = (batch_size , img_height , img_width , channels)
```

```
# create CNN model

model = Sequential()


model.add(resize_and_rescale)

model.add(data_augmentation)

model.add(Conv2D(32,kernel_size=(3,3),padding='same',activation='relu',input_shape=input_shape))

model.add(Conv2D(64,kernel_size=(3,3),padding='same',activation='relu'))

model.add(MaxPooling2D(2,2))

model.add(Conv2D(64,kernel_size=(3,3),padding='same',activation='relu'))

model.add(MaxPooling2D(2,2))

model.add(Flatten())

model.add(Dense(32,activation='relu'))

model.add(Dense(64,activation='relu'))

model.add(Dropout(0.10))

model.add(Dense(n_classes))
```

Compile the model

Choose an appropirate optimiser and loss function for model training

```
### Todo, choose an appropirate optimiser and loss function
model.compile(optimizer='adam',
              loss=tf.keras.losses.SparseCategoricalCrossentropy(from_logits=True),
              metrics=['accuracy'])
```

```
model.build(input_shape)
```

```
# View the summary of all layers
model.summary()
```

```
Model: "sequential_4"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 sequential (Sequential)     (None, 180, 180, 3)       0

 sequential_1 (Sequential)   (None, 180, 180, 3)       0

 conv2d_3 (Conv2D)           (32, 180, 180, 32)        896

 conv2d_4 (Conv2D)           (32, 180, 180, 64)        18496

 max_pooling2d_2 (MaxPooling  (32, 90, 90, 64)         0
 2D)

 conv2d_5 (Conv2D)           (32, 90, 90, 64)          36928

 max_pooling2d_3 (MaxPooling  (32, 45, 45, 64)         0
 2D)

 flatten_1 (Flatten)         (32, 129600)              0

 dense_3 (Dense)             (32, 32)                  4147232

 dense_4 (Dense)             (32, 64)                  2112

 dropout_1 (Dropout)         (32, 64)                  0

 dense_5 (Dense)             (32, 9)                   585

=================================================================
Total params: 4,206,249
Trainable params: 4,206,249
Non-trainable params: 0
_________________________________________________________________
```

Train the model

```
```

```
epochs = 5

history = model.fit(
  train_ds,
  validation_data=val_ds,
  epochs=epochs
)
```

```
Epoch 1/5
70/70 [==============================] - 170s 2s/step - loss: 2.0418 - accuracy: 0.2099 - val_loss: 2.1368 - val_accuracy: 0.2203
Epoch 2/5
70/70 [==============================] - 163s 2s/step - loss: 1.7312 - accuracy: 0.3671 - val_loss: 2.0937 - val_accuracy: 0.2373
Epoch 3/5
70/70 [==============================] - 165s 2s/step - loss: 1.6390 - accuracy: 0.4015 - val_loss: 2.1337 - val_accuracy: 0.3305
Epoch 4/5
70/70 [==============================] - 162s 2s/step - loss: 1.5440 - accuracy: 0.4573 - val_loss: 1.9169 - val_accuracy: 0.3475
Epoch 5/5
70/70 [==============================] - 165s 2s/step - loss: 1.4787 - accuracy: 0.4833 - val_loss: 2.0865 - val_accuracy: 0.3729
```

```
# accuracy of model each epochs
history.history['accuracy']
```

```
[0.2099151462316513,
 0.3671281933784485,
 0.4015185236930847,
 0.45734703540802,
 0.4832514524459839]
```

```
# validation accuracy of model each epochs
history.history['val_accuracy']
```

```
[0.22033898532390594,
 0.23728813230991364,
 0.3305084705352783,
 0.347457617521286,
 0.37288135290145874]
```

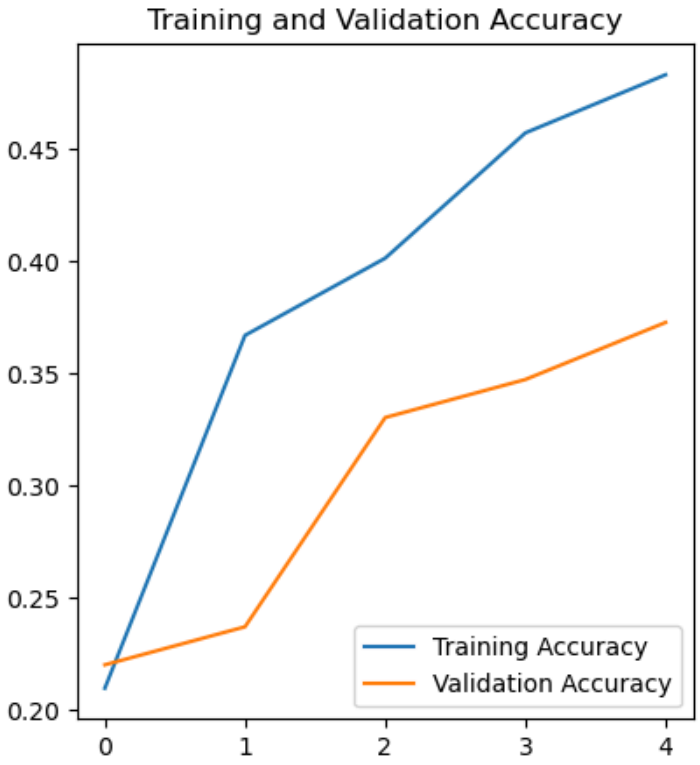
```
# lost
history.history['loss']
```

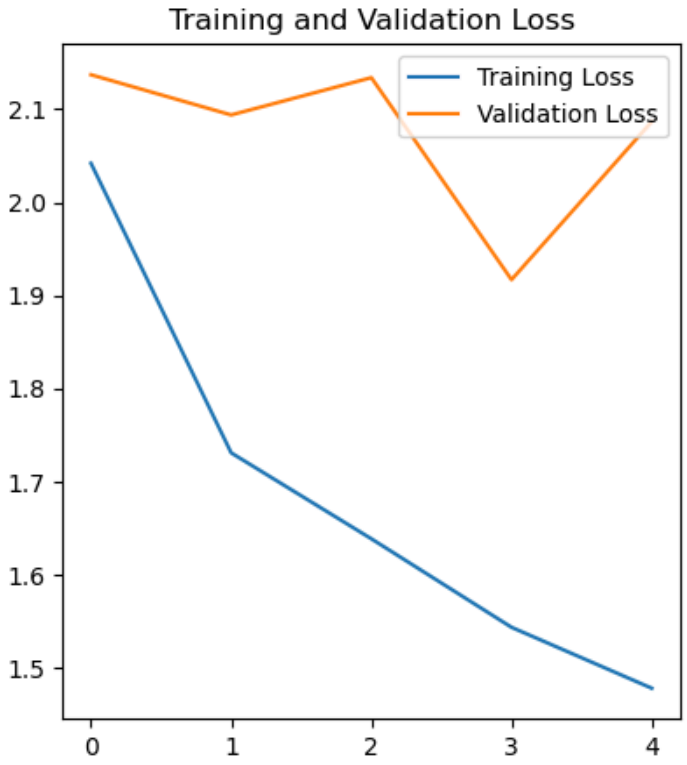
```
[2.0418248176574707,
 1.7312301397323608,
 1.6389880180358887,
```

```
        1.5440226793289185,
        1.478682041168213]
```

Visualizing training results

```
acc = history.history['accuracy']
val_acc = history.history['val_accuracy']

loss = history.history['loss']
val_loss = history.history['val_loss']

epochs_range = range(epochs)

plt.figure(figsize=(10, 5))
plt.subplot(1, 2, 1)
plt.plot(epochs_range, acc, label='Training Accuracy')
plt.plot(epochs_range, val_acc, label='Validation Accuracy')
plt.legend(loc='lower right')
plt.title('Training and Validation Accuracy')

plt.subplot(1, 2, 2)
plt.plot(epochs_range, loss, label='Training Loss')
plt.plot(epochs_range, val_loss, label='Validation Loss')
plt.legend(loc='upper right')
plt.title('Training and Validation Loss')
plt.show()
```





Todo: Write your findings after the model fit, see if there is an evidence of model overfit or underfit

`Traning-accuracy = 48` and

`validation-accuracy = 37`

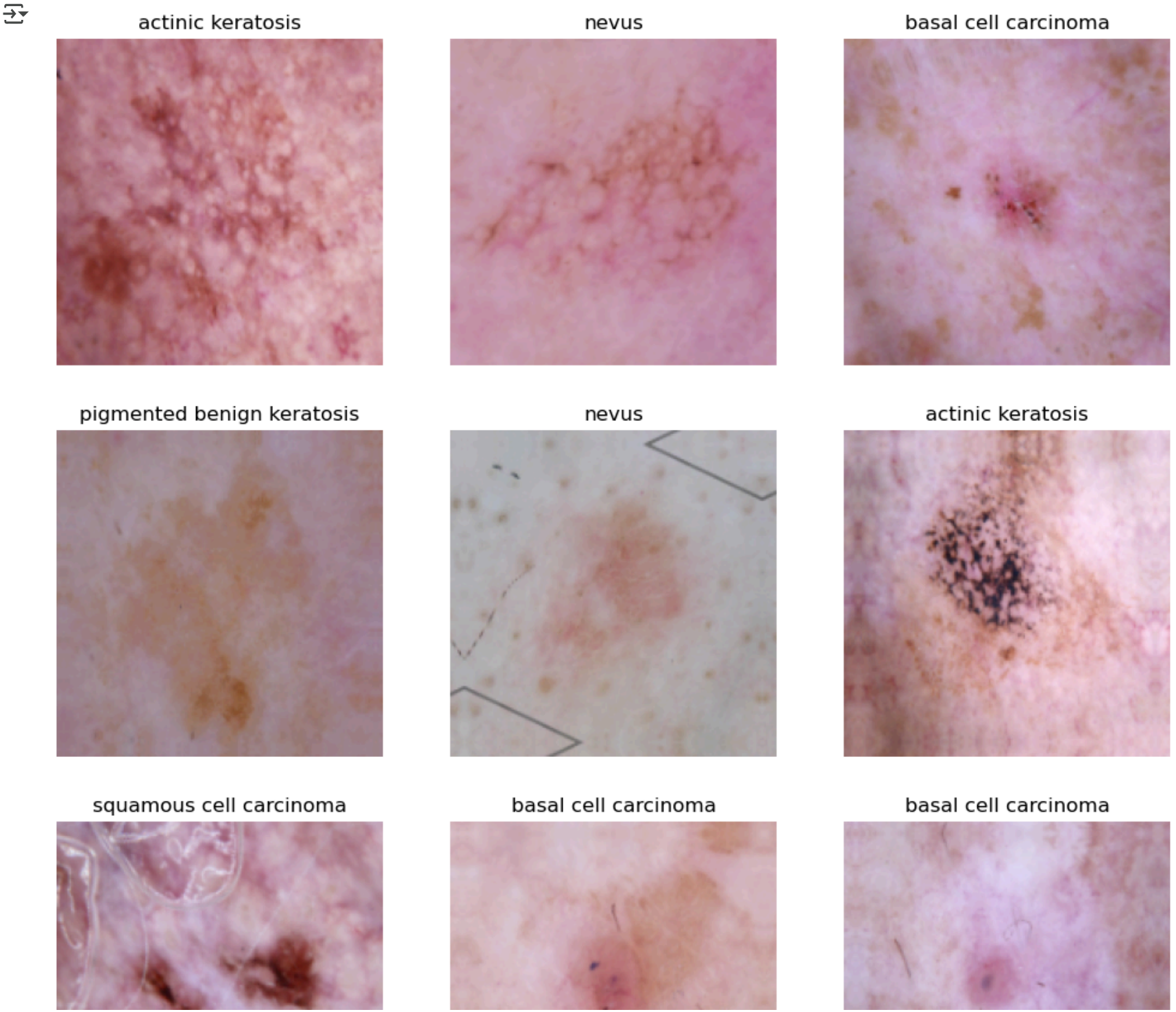
this is underfit model not good acurracy of traning and validation dataset

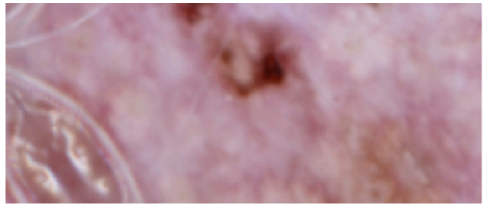
Write your findings here

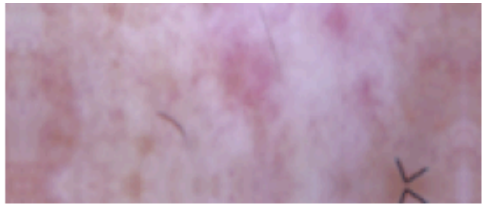
```
# Todo, after you have analysed the model fit history for presence of underfit or overfit, choose an appropriate data augumentation strategy.
# Your code goes here

# data augmentation
```

```
data_augmentation = keras.Sequential(
  [
    layers.experimental.preprocessing.RandomFlip("horizontal",
                                                 input_shape=(img_height,
                                                              img_width,
                                                              3)),
    layers.experimental.preprocessing.RandomRotation(0.1),
    layers.experimental.preprocessing.RandomZoom(0.1)
  ]
)
```

```
# Todo, visualize how your augmentation strategy works for one instance of training image.
# Your code goes here
plt.figure(figsize=(12, 12))
for images, labels in train_ds.take(1):
  for i in range(9):
    augmented_images = data_augmentation(images)
    ax = plt.subplot(3, 3, i + 1)
    plt.imshow(augmented_images[i].numpy().astype("uint8"))
    plt.title(class_names[labels[i]])
    plt.axis("off")
```


actinic keratosis
nevus
basal cell carcinoma
pigmented benign keratosis
nevus
actinic keratosis
squamous cell carcinoma
basal cell carcinoma
basal cell carcinoma





Todo:

Create the model, compile and train the model

```
## You can use Dropout layer if there is an evidence of overfitting in your findings

## Your code goes here

model = Sequential()

model.add(data_augmentation)

model.add(resize_and_rescale)

model.add(Conv2D(16,kernel_size=(3,3),padding='same',activation='relu'))

model.add(MaxPooling2D(2,2))

model.add(Conv2D(32,kernel_size=(3,3),padding='same',activation='relu'))

model.add(MaxPooling2D(2,2))


model.add(Conv2D(64,kernel_size=(3,3),padding='same',activation='relu'))


model.add(MaxPooling2D(2,2))

model.add(Dropout(0.2))


model.add(Flatten())

model.add(Dense(128,activation='relu'))
```

```
model.add(Dense(n_classes))
```

Compiling the model

```
## Your code goes here
model.compile(optimizer='adam',
              loss=tf.keras.losses.SparseCategoricalCrossentropy(from_logits=True),
              metrics=['accuracy'])
```

Training the model

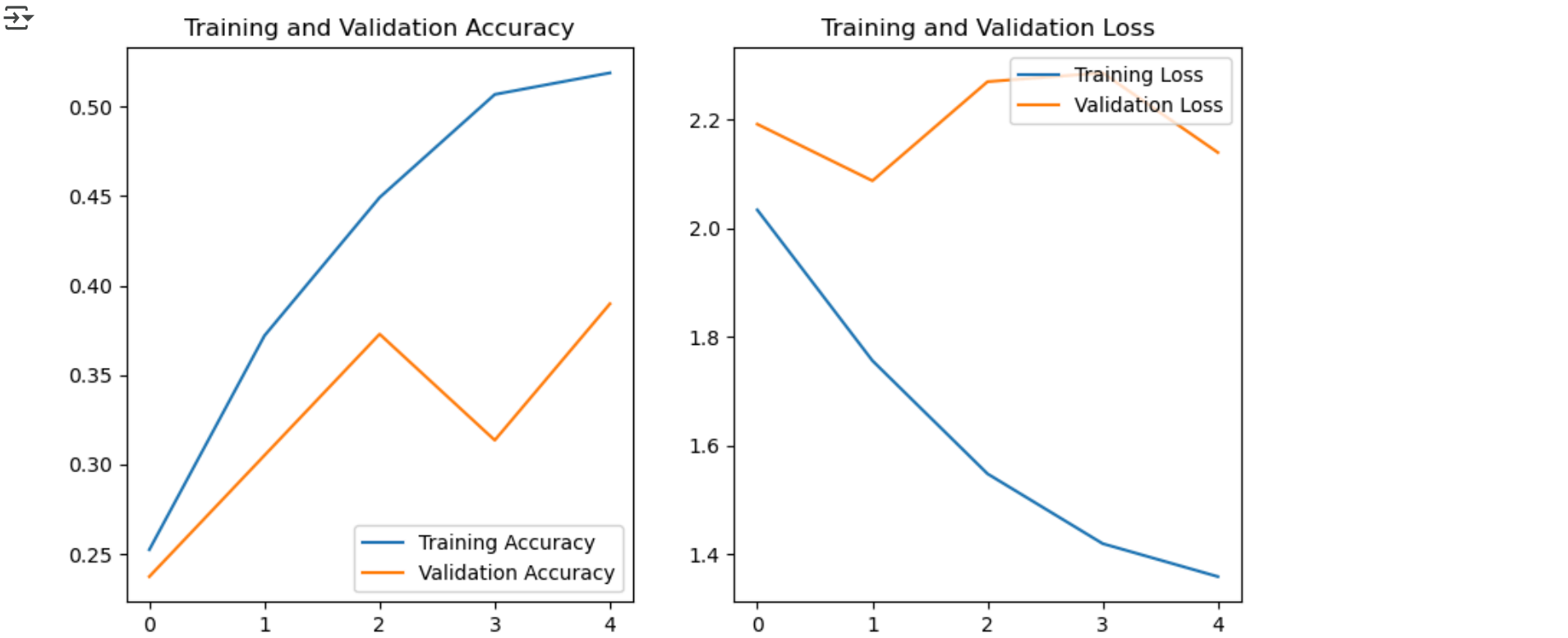
```
## Your code goes here, note: train your model for 20 epochs
epochs = 5

history = model.fit(
  train_ds,
  validation_data=val_ds,
  epochs=epochs
)
```

```
Epoch 1/5
70/70 [==============================] - 38s 509ms/step - loss: 2.0340 - accuracy: 0.2523 - val_loss: 2.1918 - val_accuracy: 0.2373
Epoch 2/5
70/70 [==============================] - 35s 495ms/step - loss: 1.7566 - accuracy: 0.3720 - val_loss: 2.0876 - val_accuracy: 0.3051
Epoch 3/5
70/70 [==============================] - 35s 502ms/step - loss: 1.5484 - accuracy: 0.4493 - val_loss: 2.2700 - val_accuracy: 0.3729
Epoch 4/5
70/70 [==============================] - 35s 500ms/step - loss: 1.4199 - accuracy: 0.5069 - val_loss: 2.2862 - val_accuracy: 0.3136
Epoch 5/5
70/70 [==============================] - 35s 500ms/step - loss: 1.3593 - accuracy: 0.5190 - val_loss: 2.1396 - val_accuracy: 0.3898
```

Visualizing the results

```
acc = history.history['accuracy']
val_acc = history.history['val_accuracy']

loss = history.history['loss']
```

```
val_loss = history.history['val_loss']

epochs_range = range(epochs)

plt.figure(figsize=(10, 5))
plt.subplot(1, 2, 1)
plt.plot(epochs_range, acc, label='Training Accuracy')
plt.plot(epochs_range, val_acc, label='Validation Accuracy')
plt.legend(loc='lower right')
plt.title('Training and Validation Accuracy')

plt.subplot(1, 2, 2)
plt.plot(epochs_range, loss, label='Training Loss')
plt.plot(epochs_range, val_loss, label='Validation Loss')
plt.legend(loc='upper right')
plt.title('Training and Validation Loss')
plt.show()
```



Todo: Write your findings after the model fit, see if there is an evidence of model overfit or underfit. Do you think there is some improvement now as compared to the previous model run?

This model like underfiting beacuse

`Traning accuracy = 51` and

`Validation accuracy = 38`

Todo: Find the distribution of classes in the training dataset.

Context: Many times real life datasets can have class imbalance, one class can have proportionately higher number of samples compared to the others. Class imbalance can have a detrimental effect on the final model quality. Hence as a sanity check it becomes important to check what is the distribution of classes in the data.

```
class_names
```

```
['actinic keratosis',
 'basal cell carcinoma',
 'dermatofibroma',
 'melanoma',
 'nevus',
 'pigmented benign keratosis',
 'seborrheic keratosis',
 'squamous cell carcinoma',
 'vascular lesion']
```

```
data_dir_train = pathlib.Path(r"C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collabor
```

```
image_count_train = len(list(data_dir_train.glob('*/*.jpg')))
print(image_count_train)
```

```
2239
```

```
#plot number of images in each Class
count=[]
for name in class_names:
```

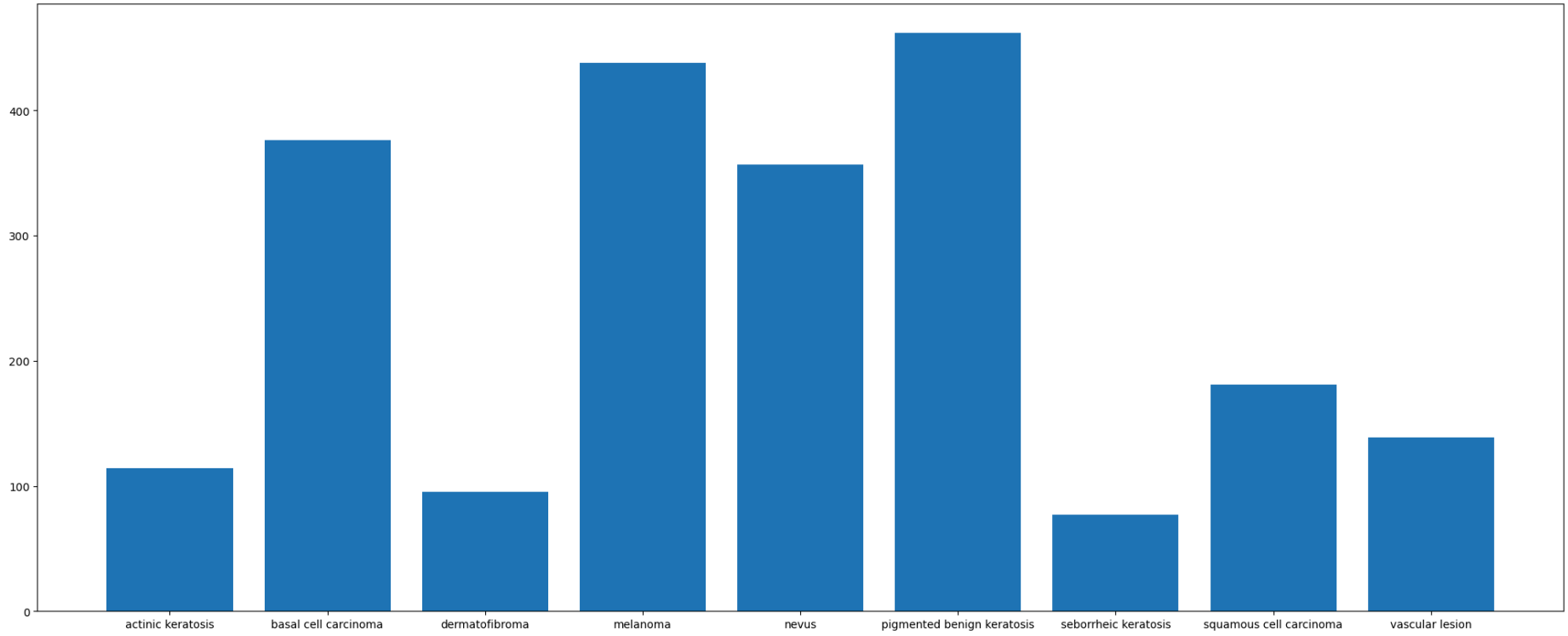
```
    count.append(len(list(data_dir_train.glob(name+'/*.jpg'))))
```

```
count
```

```
[114, 376, 95, 438, 357, 462, 77, 181, 139]
```

```
#plot number of images in each Class
count=[]
for name in class_names:
    count.append(len(list(data_dir_train.glob(name+'/*.jpg'))))
plt.figure(figsize=(25,10))
plt.bar(class_names,count)
```

```
<BarContainer object of 9 artists>
```



Todo: Write your findings here:

- Which class has the least number of samples?

- Which classes dominate the data in terms proportionate number of samples?

Todo: Rectify the class imbalance

Context: You can use a python package known as `Augmentor` (https://augmentor.readthedocs.io/en/master/) to add more samples across all classes so that none of the classes have very few samples.

```
!pip install Augmentor
```

```
Defaulting to user installation because normal site-packages is not writeable
Collecting Augmentor
  Downloading Augmentor-0.2.12-py2.py3-none-any.whl (38 kB)
Requirement already satisfied: tqdm>=4.9.0 in c:\programdata\anaconda3\lib\site-packages (from Augmentor) (4.64.1)
Requirement already satisfied: numpy>=1.11.0 in c:\users\user\appdata\roaming\python\python39\site-packages (from Augmentor) (1.23.5)
Requirement already satisfied: Pillow>=5.2.0 in c:\programdata\anaconda3\lib\site-packages (from Augmentor) (9.2.0)
Requirement already satisfied: colorama in c:\programdata\anaconda3\lib\site-packages (from tqdm>=4.9.0->Augmentor) (0.4.5)
Installing collected packages: Augmentor
Successfully installed Augmentor-0.2.12
```

To use `Augmentor`, the following general procedure is followed:

1. Instantiate a `Pipeline` object pointing to a directory containing your initial image data set.
2. Define a number of operations to perform on this data set using your `Pipeline` object.
3. Execute these operations by calling the `Pipeline's` `sample()` method.

```
path_to_training_dataset=str(data_dir_train)+'/'
import Augmentor
for i in class_names:
    p = Augmentor.Pipeline(path_to_training_dataset + i)
    p.rotate(probability=0.7, max_left_rotation=10, max_right_rotation=10)
    p.sample(500) ## We are adding 500 samples per class to make sure that none of the classes are sparse.
```

```
Initialised with 114 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
```

```
Initialised with 376 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
Initialised with 95 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
Initialised with 438 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
Initialised with 357 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
Initialised with 462 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
Initialised with 77 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
Initialised with 181 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
Initialised with 139 image(s) found.
Output directory set to C:\Users\user\OneDrive\Desktop\Deep Learning\Project\Skin cancer ISIC The International Skin Imaging Collaboratio
```

Augmentor has stored the augmented images in the output sub-directory of each of the sub-directories of skin cancer types.. Lets take a look at total count of augmented images.

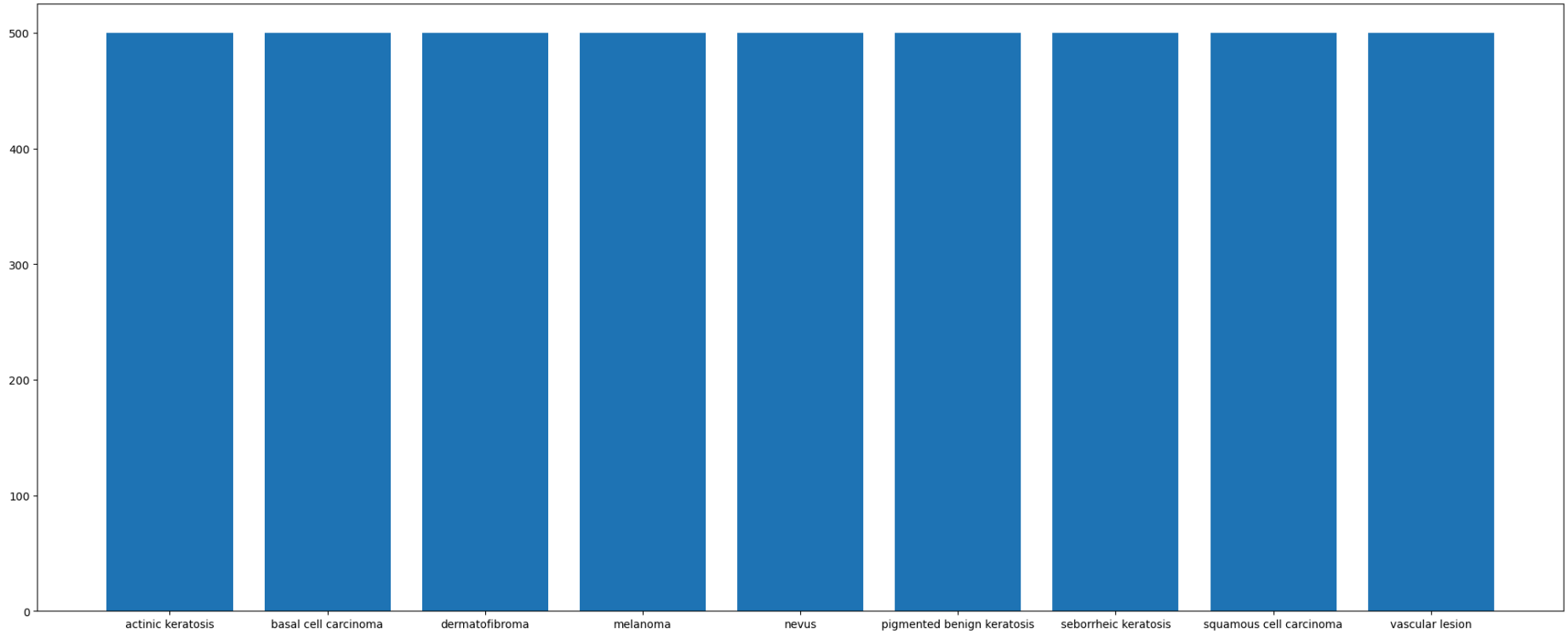
```
#Augmentor has stored the augmented images in the output sub-directory of each of the sub-directories of skin cancer types..
#Lets take a look at total count of augmented images.

image_count_train = len(list(data_dir_train.glob('*/output/*.jpg')))
print(image_count_train)
```

```
4500
```

Lets see the distribution of augmented data after adding new images to the original training data.

```
# Check the distribution of data again.
count=[]
for name in class_names:
    count.append(len(list(data_dir_train.glob(name+'*/output/*.jpg'))))
plt.figure(figsize=(25,10))
plt.bar(class_names,count)
```

```
<BarContainer object of 9 artists>
```



Lets see the distribution of augmented data after adding new images to the original training data.

```
import os
from glob import glob
```

```
path_list_new = [x for x in glob(os.path.join(data_dir_train, '*','output', '*.jpg'))]
path_list
```

```
['C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025780.jpg_0182fce3-efd0-45a5-b6a5-
307413ce243e.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025780.jpg_21419686-7e06-4279-a219-
edf80e606605.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025780.jpg_2d6963fc-8fd1-4066-a4d7-
```

```
ef8f599df354.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025780.jpg_4332bcc6-b75b-4d4a-9ef1-
4bffedea2d6b.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025780.jpg_98db07fa-1890-41d7-8d13-
bae13a45ea07.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025780.jpg_bc94f74c-540c-4a2c-81ea-
988a59216113.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025803.jpg_35b2af0d-21b8-4134-9fc4-
4a2d4145ddbb.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025803.jpg_40e438e8-ce2b-4594-8e57-
6a7f3b913797.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025803.jpg_4401c832-7c6b-491a-b913-
676e962daf7d.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025803.jpg_899989d2-de82-4e37-ac7f-
146536d4b391.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025803.jpg_c736a533-418d-4009-958b-
ea57df1d1bde.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025825.jpg_32750e3f-84ad-47f8-a3f9-
82ed168ed006.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025825.jpg_610657a2-82c3-4415-8194-
b1bb7abca48e.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025825.jpg_7979c79c-d035-4d8e-9d70-
d5496c3c83e9.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025825.jpg_c7edab9a-7412-4c95-8898-
0a9b8d77cae6.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025953.jpg_06249c9c-180f-4499-85ec-
9f9c063b6592.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025953.jpg_0b74dfbc-2083-469c-af3b-
66b72b4d8d4a.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025953.jpg_1f4861b5-fde1-4138-87d0-
c3fb09e194c1.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
Collaboration\\Train\\actinic keratosis\\output\\actinic keratosis_original_ISIC_0025953.jpg_2f9126e4-e320-48fe-8572-
```

```
 9cb0fe6042ff.jpg',
 'C:\\Users\\user\\OneDrive\\Desktop\\Deep Learning\\Project\\Skin cancer ISIC The International Skin Imaging
```

```
lesion_list_new = [os.path.basename(os.path.dirname(os.path.dirname(y))) for y in glob(os.path.join(data_dir_train, '*','output', '*.jpg'))]
lesion_list_new
```

```
['actinic keratosis',
 'actinic keratosis',
 'actinic keratosis',
 'actinic keratosis',
 'actinic keratosis',
 'actinic keratosis',
 'actinic keratosis',
 'actinic keratosis',
 'actinic keratosis',
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```

```
        'actinic keratosis',
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        'actinic keratosis',
        'actinic keratosis',
        'actinic keratosis',
        'actinic keratosis',
        'actinic keratosis',
```

```
dataframe_dict_new = dict(zip(path_list_new, lesion_list_new))
```

```
# Get Existing images in Dataframe
path_list=[]
lesion_list=[]
for name in class_names:
  for file in data_dir_train.glob(name+'/*.jpg'):
    path_list.append(str(file))
    lesion_list.append(name)

dataframe_dict_original=dict(zip(path_list,lesion_list))
original_df=pd.DataFrame(list(dataframe_dict_original.items()),columns=['Path','Label'])
```

```
df2 = pd.DataFrame(list(dataframe_dict_new.items()),columns = ['Path','Label'])
new_df = original_df.append(df2)
```

```
C:\Users\user\AppData\Local\Temp\ipykernel_8560\390629722.py:2: FutureWarning: The frame.append method is deprecated and will be removed
  new_df = original_df.append(df2)
```

```
new_df['Label'].value_counts()
```

```
pigmented benign keratosis    962
melanoma                      938
basal cell carcinoma          876
nevus                         857
squamous cell carcinoma       681
vascular lesion               639
```

```
actinic keratosis            614
dermatofibroma               595
seborrheic keratosis         577
Name: Label, dtype: int64
```

So, now we have added 500 images to all the classes to maintain some class balance. We can add more images as we want to improve training process.

Todo: Train the model on the data created using Augmentor

```
batch_size = 32
img_height = 180
img_width = 180
```

Todo: Create a training dataset

```
train_ds = tf.keras.preprocessing.image_dataset_from_directory(
  data_dir_train,
  seed=123,
  validation_split = 0.2,
  subset = 'training',
  image_size=(img_height, img_width),
  batch_size=batch_size)
```

```
Found 6739 files belonging to 9 classes.
Using 5392 files for training.
```

Todo: Create a validation dataset

```
val_ds = tf.keras.preprocessing.image_dataset_from_directory(
  data_dir_train,
  seed=123,
  validation_split = 0.2,
  subset = 'validation',
  image_size=(img_height, img_width),
  batch_size=batch_size)
```

```
Found 6739 files belonging to 9 classes.
Using 1347 files for validation.
```

Todo: Create your model (make sure to include normalization)

```
## your code goes here
AUTOTUNE = tf.data.experimental.AUTOTUNE

train_ds = train_ds.cache().shuffle(1000).prefetch(buffer_size=AUTOTUNE)
val_ds = val_ds.cache().prefetch(buffer_size=AUTOTUNE)

model = Sequential([
  layers.experimental.preprocessing.Rescaling(1./255),
  layers.Conv2D(16, 3, padding='same', activation='relu'),
  layers.MaxPooling2D(),
  layers.Conv2D(32, 3, padding='same', activation='relu'),
  layers.MaxPooling2D(),
  layers.Conv2D(64, 3, padding='same', activation='relu'),
  layers.MaxPooling2D(),
  layers.Dropout(0.2),
  layers.Flatten(),
  layers.Dense(128, activation='relu'),
  layers.Dense(n_classes)
])
```

Todo: Compile your model (Choose optimizer and loss function appropriately)

```
## your code goes here
model.compile(optimizer='adam',
              loss=tf.keras.losses.SparseCategoricalCrossentropy(from_logits=True),
              metrics=['accuracy'])
```

Todo: Train your model

```
epochs = 15

history = model.fit(
  train_ds,
```

```
  validation_data=val_ds,
  epochs=epochs
)
```

```
Epoch 1/15
169/169 [==============================] - 85s 392ms/step - loss: 1.7765 - accuracy: 0.3253 - val_loss: 1.4211 - val_accuracy: 0.4640
Epoch 2/15
169/169 [==============================] - 60s 354ms/step - loss: 1.3658 - accuracy: 0.4974 - val_loss: 1.2279 - val_accuracy: 0.5405
Epoch 3/15
169/169 [==============================] - 56s 332ms/step - loss: 1.1204 - accuracy: 0.5864 - val_loss: 1.1006 - val_accuracy: 0.6192
Epoch 4/15
169/169 [==============================] - 60s 355ms/step - loss: 0.9075 - accuracy: 0.6786 - val_loss: 0.9068 - val_accuracy: 0.6867
Epoch 5/15
169/169 [==============================] - 57s 337ms/step - loss: 0.7345 - accuracy: 0.7409 - val_loss: 0.8675 - val_accuracy: 0.7120
Epoch 6/15
169/169 [==============================] - 58s 343ms/step - loss: 0.5584 - accuracy: 0.8103 - val_loss: 0.8806 - val_accuracy: 0.7023
Epoch 7/15
169/169 [==============================] - 61s 364ms/step - loss: 0.4537 - accuracy: 0.8399 - val_loss: 0.8229 - val_accuracy: 0.7402
Epoch 8/15
169/169 [==============================] - 68s 400ms/step - loss: 0.3895 - accuracy: 0.8626 - val_loss: 0.7161 - val_accuracy: 0.7669
Epoch 9/15
169/169 [==============================] - 62s 365ms/step - loss: 0.3276 - accuracy: 0.8798 - val_loss: 0.7766 - val_accuracy: 0.7803
Epoch 10/15
169/169 [==============================] - 61s 362ms/step - loss: 0.2586 - accuracy: 0.9052 - val_loss: 0.6599 - val_accuracy: 0.7854
Epoch 11/15
169/169 [==============================] - 61s 359ms/step - loss: 0.2360 - accuracy: 0.9136 - val_loss: 0.7659 - val_accuracy: 0.7832
Epoch 12/15
169/169 [==============================] - 63s 375ms/step - loss: 0.2102 - accuracy: 0.9221 - val_loss: 0.7580 - val_accuracy: 0.8010
Epoch 13/15
169/169 [==============================] - 68s 402ms/step - loss: 0.1886 - accuracy: 0.9290 - val_loss: 0.7340 - val_accuracy: 0.8010
Epoch 14/15
169/169 [==============================] - 63s 376ms/step - loss: 0.1923 - accuracy: 0.9295 - val_loss: 1.0826 - val_accuracy: 0.7661
Epoch 15/15
169/169 [==============================] - 60s 356ms/step - loss: 0.1964 - accuracy: 0.9269 - val_loss: 0.8915 - val_accuracy: 0.8048
```