

cnn-assignment-vinodh

December 6, 2023

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.

0.0.1 Importing Skin Cancer Data

0.0.2 Importing all the important libraries

```
[1]: # !pip show tensorflow
```

```
[2]: 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
```

```
[3]: def visualizeClasses(dataset):
    plt.figure(figsize=(10, 10))
    for images, labels in dataset.take(1):
        for i in range(9):
            ax = plt.subplot(3, 3, i + 1)
            plt.imshow(images[i].numpy().astype(np.uint8))
            plt.title(class_names[i])
            plt.axis("off")
```

```
[4]: ## If you are using the data by mounting the google drive, use the following :
from google.colab import drive
drive.mount('/content/gdrive')

##Ref:https://towardsdatascience.com/
↳downloading-datasets-into-google-drive-via-google-colab-bcb1b30b0166
```

Mounted at /content/gdrive

This assignment uses 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.

```
[5]: # Defining the path for train and test images
## Todo: Update the paths of the train and test dataCset
data_dir_train = pathlib.Path('/content/gdrive/MyDrive/UpGrad/AI_ML/
                             ↪CNN_Melanoma_Dataset/Train')
data_dir_test = pathlib.Path('/content/gdrive/MyDrive/UpGrad/AI_ML/
                             ↪CNN_Melanoma_Dataset/Test')

# using to run locally
#data_dir_train = pathlib.Path("/Users/nagavi@F-Secure.com/Skills/Melanoma_CNN/
#                             ↪Dataset/Train")
#data_dir_test = pathlib.Path("/Users/nagavi@F-Secure.com/Skills/Melanoma_CNN/
#                             ↪Dataset/Test")
```

```
[6]: image_count_train = len(list(data_dir_train.glob('*/*.jpg')))
print(image_count_train)
image_count_test = len(list(data_dir_test.glob('*/*.jpg')))
print(image_count_test)
```

2239

118

0.0.3 Load using keras.preprocessing

Let's load these images off disk using the helpful image_dataset_from_directory utility.

0.0.4 Create a dataset

Define some parameters for the loader:

```
[7]: batch_size = 32
img_height = 180
img_width = 180
validation_split_value = 0.2
seed_value = 123
```

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

```
[8]: ## 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(
    data_dir_train,
    # labels="inferred",
```

```

#   label_mode="categorical",
batch_size=batch_size,
image_size=(img_height, img_width),
color_mode="rgb",
shuffle=True,
seed=seed_value,
validation_split=validation_split_value,
subset = "training",
interpolation='bilinear',
follow_links=False
)

```

Found 2239 files belonging to 9 classes.
Using 1792 files for training.

```
[9]: ## Write your validation 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
val_ds = tf.keras.preprocessing.image_dataset_from_directory(
    data_dir_train,
    labels="inferred",
    # label_mode="categorical",
    batch_size=batch_size,
    image_size=(img_height, img_width),
    color_mode="rgb",
    shuffle=True,
    seed=seed_value,
    validation_split=validation_split_value,
    subset = "validation",
    interpolation='bilinear',
    follow_links=False
)
```

Found 2239 files belonging to 9 classes.
Using 447 files for validation.

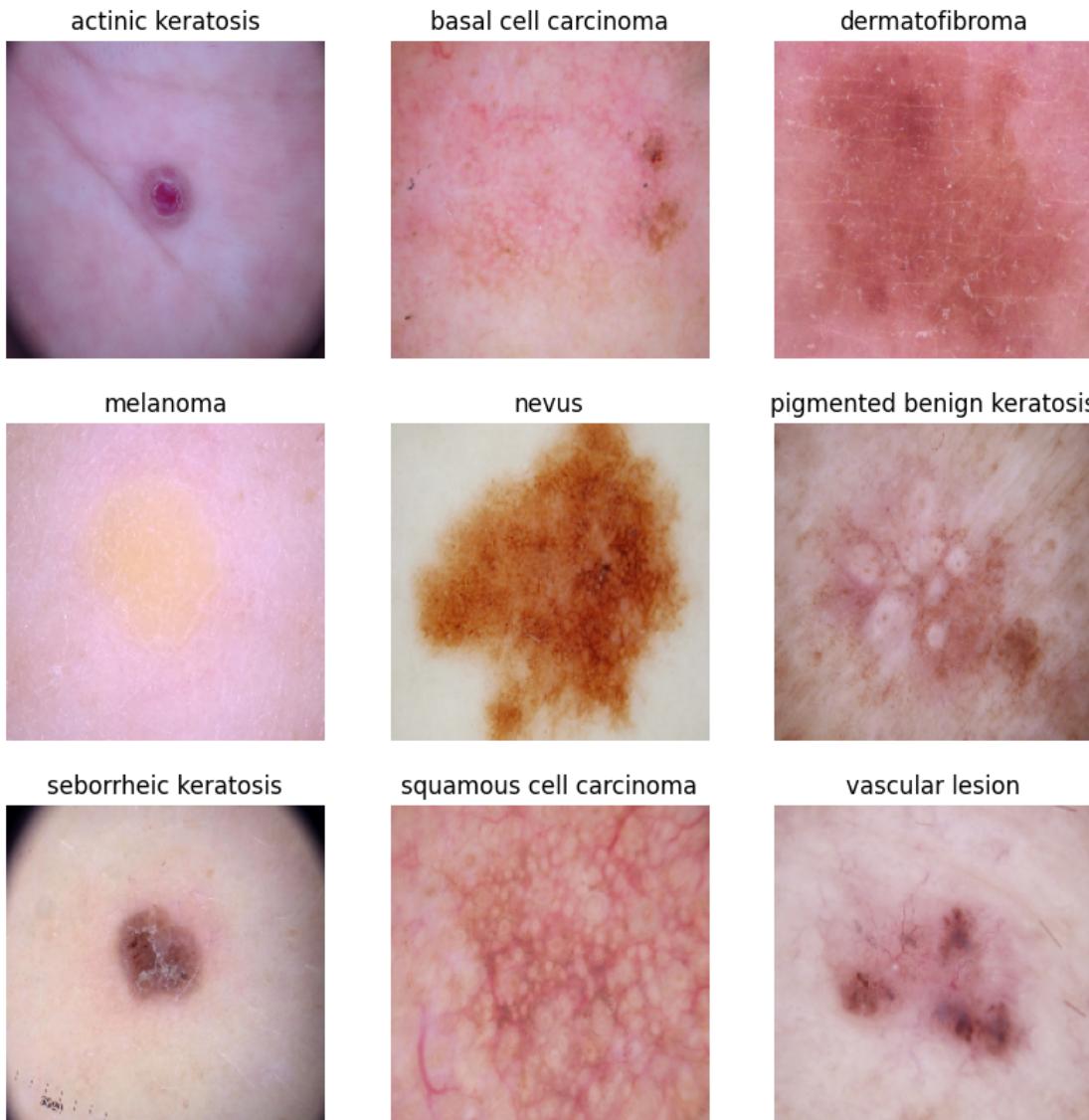
```
[10]: # List out all the classes of skin cancer and store them in a list.
# You can find the class names in the class_names attribute on these datasets.
# These correspond to the directory names in alphabetical order.
class_names = train_ds.class_names
print(class_names)
```

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

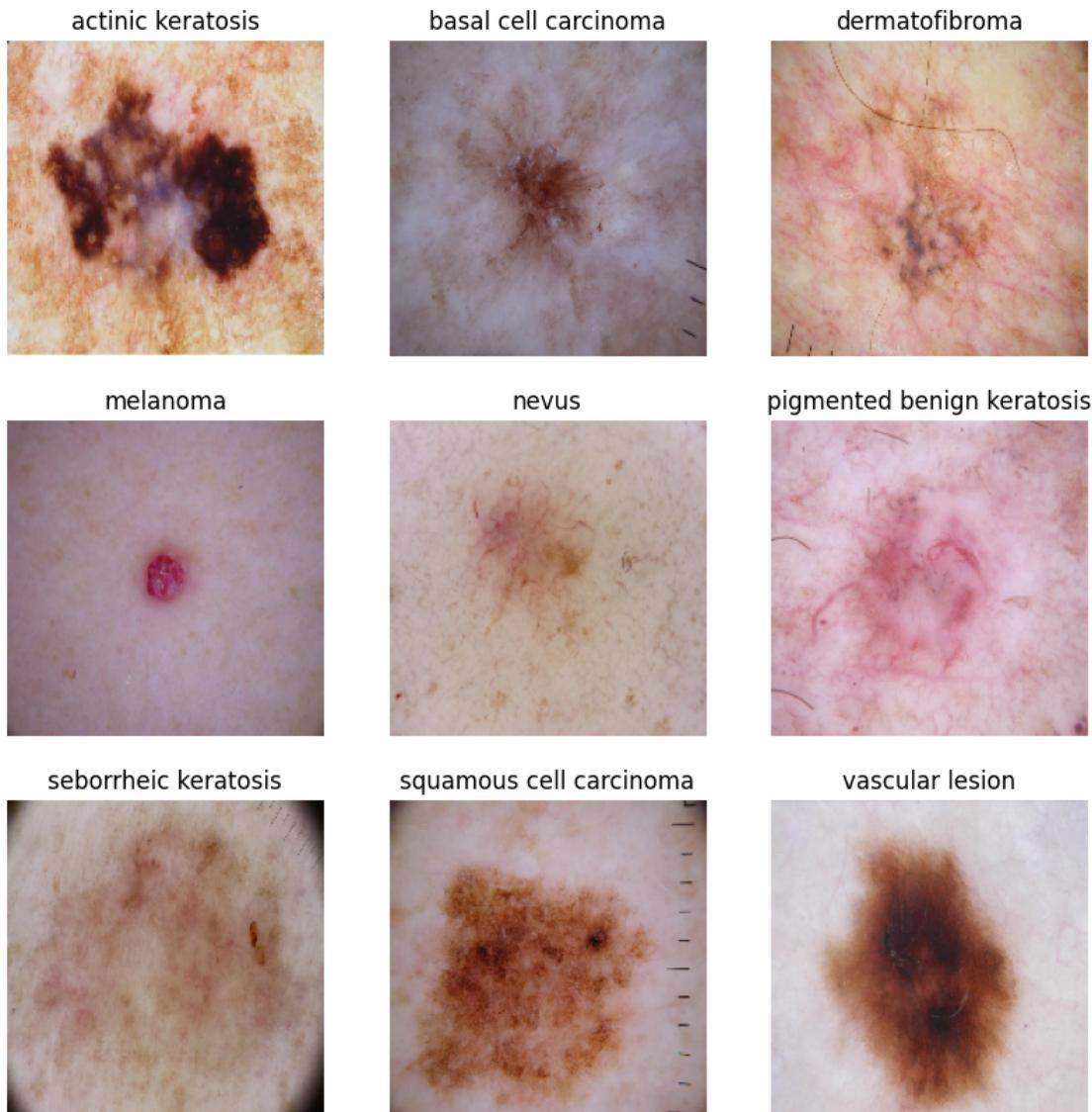
0.0.5 Visualize the data

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

```
[11]: # Visualize training dataset class instances  
visualizeClasses(train_ds)
```



```
[12]: # Visualize training dataset class instances  
visualizeClasses(val_ds)
```



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.

```
[13]: 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)
```

0.0.6 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]

0.0.7 Model 1: Vanilla Model

```
[14]: ### Your code goes here
num_classes = 9
padding_type = 'same'
activation_func = 'relu'

model = Sequential([
    layers.experimental.preprocessing.Rescaling(1./255, input_shape=(img_height, img_width, 3)),
    layers.Conv2D(filters = 16, kernel_size = 3, padding=padding_type, activation=activation_func),
    layers.MaxPooling2D(),
    layers.Conv2D(filters=32, kernel_size=3, padding=padding_type, activation=activation_func),
    layers.MaxPooling2D(),
    layers.Conv2D(filters=64, kernel_size=3, padding=padding_type, activation=activation_func),
    layers.MaxPooling2D(),
    layers.Flatten(),
    layers.Dense(units=128, activation=activation_func),
    layers.Dense(num_classes)
])
```

0.0.8 Compile the model

Choose an appropriate optimiser and loss function for model training

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

```
[16]: # View the summary of all layers
model.summary()
```

Model: "sequential"

Layer (type)	Output Shape	Param #
<hr/>		

rescaling (Rescaling)	(None, 180, 180, 3)	0
conv2d (Conv2D)	(None, 180, 180, 16)	448
max_pooling2d (MaxPooling2D)	(None, 90, 90, 16)	0
conv2d_1 (Conv2D)	(None, 90, 90, 32)	4640
max_pooling2d_1 (MaxPooling2D)	(None, 45, 45, 32)	0
conv2d_2 (Conv2D)	(None, 45, 45, 64)	18496
max_pooling2d_2 (MaxPooling2D)	(None, 22, 22, 64)	0
flatten (Flatten)	(None, 30976)	0
dense (Dense)	(None, 128)	3965056
dense_1 (Dense)	(None, 9)	1161
<hr/>		
Total params: 3989801 (15.22 MB)		
Trainable params: 3989801 (15.22 MB)		
Non-trainable params: 0 (0.00 Byte)		
<hr/>		

0.0.9 Train the model

```
[17]: epochs = 20
history = model.fit(
    train_ds,
    validation_data=val_ds,
    epochs=epochs
)
```

Epoch 1/20
56/56 [=====] - 592s 1s/step - loss: 1.8588 - accuracy: 0.3181 - val_loss: 1.6816 - val_accuracy: 0.4519
Epoch 2/20
56/56 [=====] - 1s 25ms/step - loss: 1.5978 - accuracy: 0.4414 - val_loss: 1.5276 - val_accuracy: 0.4765
Epoch 3/20
56/56 [=====] - 1s 22ms/step - loss: 1.4649 - accuracy: 0.4760 - val_loss: 1.4197 - val_accuracy: 0.5190
Epoch 4/20

```
56/56 [=====] - 1s 23ms/step - loss: 1.3822 - accuracy: 0.5151 - val_loss: 1.3873 - val_accuracy: 0.5257
Epoch 5/20
56/56 [=====] - 1s 21ms/step - loss: 1.2711 - accuracy: 0.5547 - val_loss: 1.5136 - val_accuracy: 0.4765
Epoch 6/20
56/56 [=====] - 1s 21ms/step - loss: 1.1746 - accuracy: 0.5859 - val_loss: 1.3641 - val_accuracy: 0.5123
Epoch 7/20
56/56 [=====] - 1s 21ms/step - loss: 1.1232 - accuracy: 0.6021 - val_loss: 1.7361 - val_accuracy: 0.4340
Epoch 8/20
56/56 [=====] - 1s 21ms/step - loss: 1.0232 - accuracy: 0.6367 - val_loss: 1.5063 - val_accuracy: 0.5481
Epoch 9/20
56/56 [=====] - 1s 21ms/step - loss: 0.9646 - accuracy: 0.6574 - val_loss: 1.4598 - val_accuracy: 0.5548
Epoch 10/20
56/56 [=====] - 1s 22ms/step - loss: 0.8744 - accuracy: 0.6914 - val_loss: 1.4202 - val_accuracy: 0.5347
Epoch 11/20
56/56 [=====] - 1s 21ms/step - loss: 0.7999 - accuracy: 0.7031 - val_loss: 1.5207 - val_accuracy: 0.5503
Epoch 12/20
56/56 [=====] - 1s 21ms/step - loss: 0.6862 - accuracy: 0.7411 - val_loss: 1.6025 - val_accuracy: 0.5727
Epoch 13/20
56/56 [=====] - 1s 22ms/step - loss: 0.6227 - accuracy: 0.7695 - val_loss: 1.5629 - val_accuracy: 0.5593
Epoch 14/20
56/56 [=====] - 1s 23ms/step - loss: 0.5576 - accuracy: 0.7874 - val_loss: 1.6278 - val_accuracy: 0.5503
Epoch 15/20
56/56 [=====] - 1s 23ms/step - loss: 0.5184 - accuracy: 0.8214 - val_loss: 1.9478 - val_accuracy: 0.4787
Epoch 16/20
56/56 [=====] - 1s 21ms/step - loss: 0.4588 - accuracy: 0.8343 - val_loss: 1.9199 - val_accuracy: 0.5168
Epoch 17/20
56/56 [=====] - 1s 21ms/step - loss: 0.4180 - accuracy: 0.8471 - val_loss: 1.8601 - val_accuracy: 0.5414
Epoch 18/20
56/56 [=====] - 1s 21ms/step - loss: 0.3700 - accuracy: 0.8594 - val_loss: 2.1036 - val_accuracy: 0.5369
Epoch 19/20
56/56 [=====] - 1s 21ms/step - loss: 0.3054 - accuracy: 0.8828 - val_loss: 2.0379 - val_accuracy: 0.5526
Epoch 20/20
```

```
56/56 [=====] - 1s 21ms/step - loss: 0.2963 - accuracy: 0.8929 - val_loss: 2.3513 - val_accuracy: 0.5481
```

0.0.10 Visualizing training results

```
[18]: 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=(8, 8))
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()
```



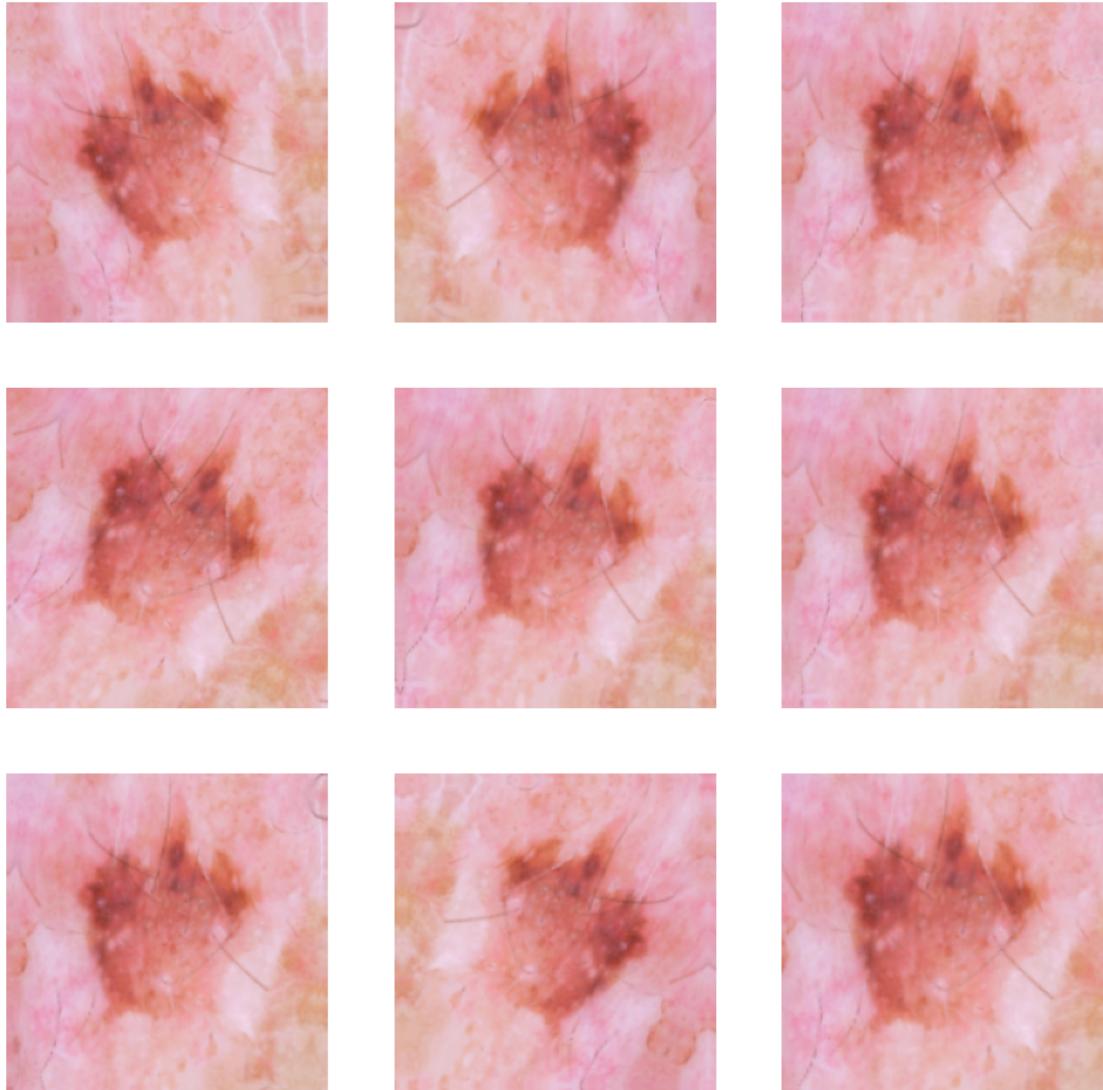
Todo: Write your findings after the model fit, see if there is an evidence of model overfit or underfit

- The training accuracy is around 89.29 and validation accuracy is around 54.81. This clearly shows that model is overfitting and thus will not be able to predict well on unseen data.
- Training accuracy of the model appears to increase linearly whereas validation accuracy remained stagnant between 47% to 53%.
- Such high training accuracy also points to the point that the model has learnt the noise in the data and low validation accuracy indicates that the model is not about to pick up general features among the dataset

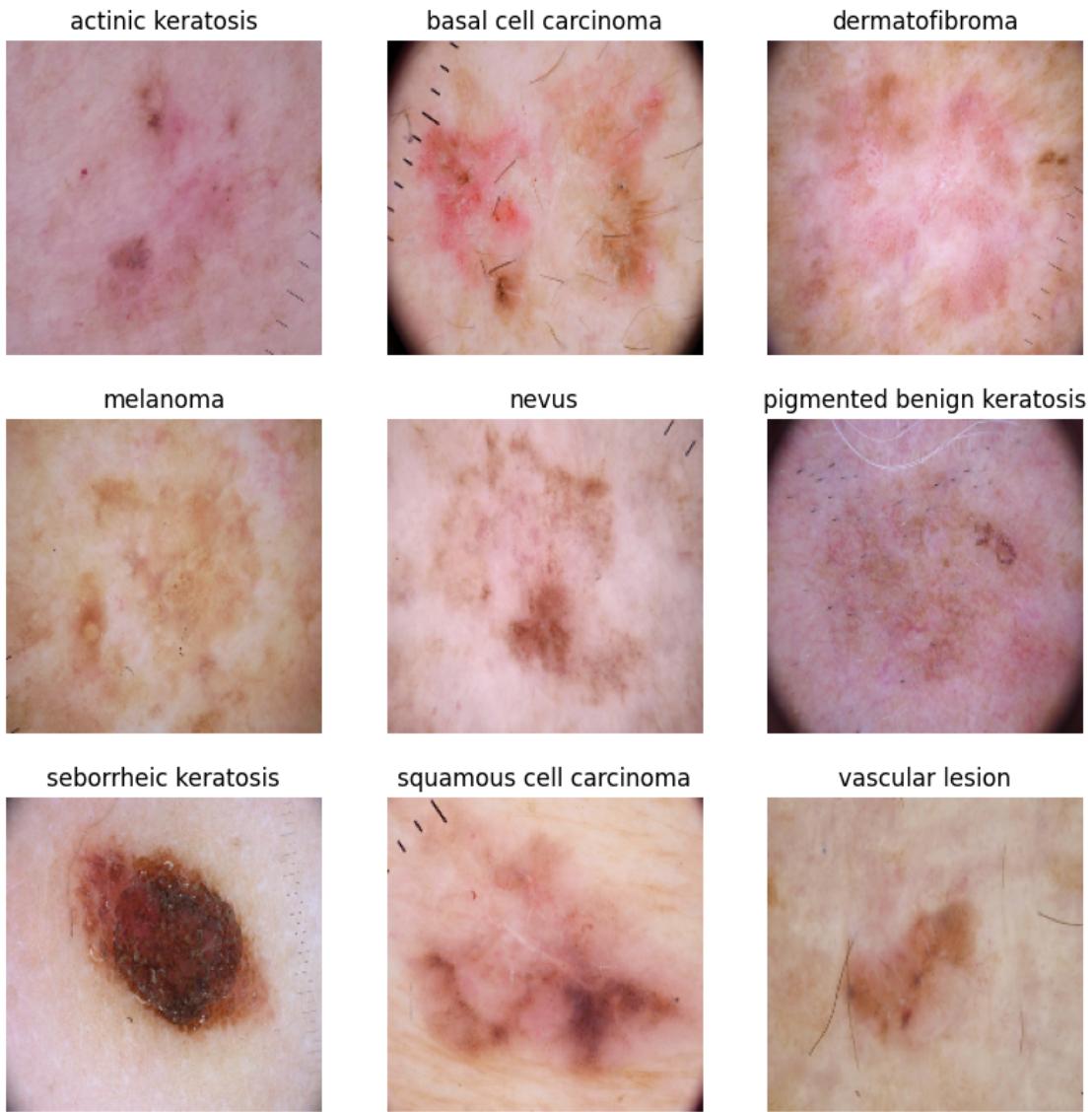
```
[19]: # augment the dataset by flipping the images
data_augmentation = keras.Sequential(
    [
        layers.experimental.preprocessing.RandomFlip("horizontal",
                                                     input_shape=(img_height,
                                                                 img_width,
                                                                 3)),
        layers.experimental.preprocessing.RandomRotation(0.1),
        layers.experimental.preprocessing.RandomZoom(0.1),
    ]
)
```

```
[20]: # visualize how your augmentation strategy works for one instance of training
       ↵image.

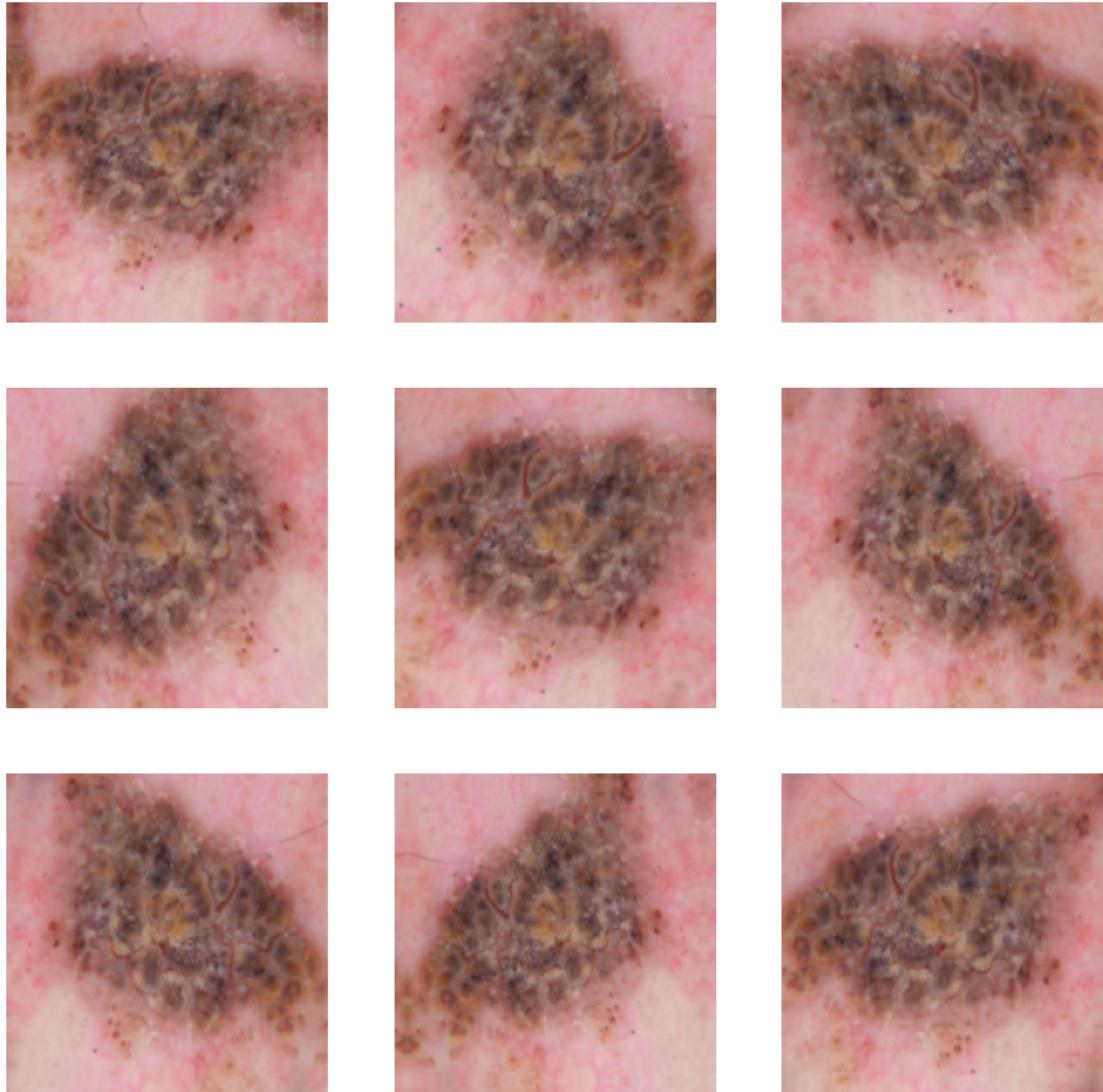
# visualize the augmented dataset - Training
plt.figure(figsize=(10, 10))
for images, _ in train_ds.take(1):
    for i in range(9):
        augmented_images = data_augmentation(images)
        ax = plt.subplot(3, 3, i + 1)
        plt.imshow(augmented_images[0].numpy().astype("uint8"))
        plt.axis("off")
```



```
[21]: # visualize one instance of each class after augmentation - Training dataset  
visualizeClasses(train_ds)
```



```
[22]: # visualize the augmented dataset - validation
class_names
plt.figure(figsize=(10, 10))
for images, _ in val_ds.take(1):
    for i in range(9):
        augmented_images = data_augmentation(images)
        ax = plt.subplot(3, 3, i + 1)
        plt.imshow(augmented_images[0].numpy().astype("uint8"))
        plt.axis("off")
```



```
[23]: # visualize one instance of each class after augmentation - Validation dataset  
visualizeClasses(val_ds)
```



0.0.11 Create the model, compile and train the model

0.0.12 Model 2: Vanilla Model + Dropout Layer + Data Augmentation (to counter overfitting)

```
[24]: ## You can use Dropout layer if there is an evidence of overfitting in your
     ↵ findings
# Add dropout layer
num_classes = 9
padding_type = 'same'
activation_func = 'relu'
```

```

model = Sequential([
    layers.experimental.preprocessing.Rescaling(1./255, input_shape=(img_height, img_width, 3)),
    layers.Conv2D(filters = 16, kernel_size = 3, padding=padding_type, activation=activation_func),
    layers.MaxPooling2D(),
    layers.Conv2D(filters=32, kernel_size=3, padding=padding_type, activation=activation_func),
    layers.MaxPooling2D(),
    layers.Conv2D(filters=64, kernel_size=3, padding=padding_type, activation=activation_func),
    layers.MaxPooling2D(),
    layers.Dropout(0.2),
    layers.Flatten(),
    layers.Dense(units=128, activation=activation_func),
    layers.Dense(num_classes)
])

```

0.0.13 Compiling the model

[25]: *## Compile code - with dropout layer*

```

model.compile(optimizer='adam',
              loss=tf.keras.losses.
              SparseCategoricalCrossentropy(from_logits=True),
              metrics=['accuracy'])

```

[26]: `model.summary()`

```

Model: "sequential_2"
-----
Layer (type)          Output Shape         Param #
=====
rescaling_1 (Rescaling)    (None, 180, 180, 3)      0
conv2d_3 (Conv2D)        (None, 180, 180, 16)     448
max_pooling2d_3 (MaxPooling2D) (None, 90, 90, 16)      0
conv2d_4 (Conv2D)        (None, 90, 90, 32)     4640
max_pooling2d_4 (MaxPooling2D) (None, 45, 45, 32)      0
conv2d_5 (Conv2D)        (None, 45, 45, 64)    18496
max_pooling2d_5 (MaxPooling2D) (None, 22, 22, 64)      0

```

```

g2D)

dropout (Dropout)           (None, 22, 22, 64)      0
flatten_1 (Flatten)         (None, 30976)          0
dense_2 (Dense)             (None, 128)            3965056
dense_3 (Dense)             (None, 9)               1161
=====
Total params: 3989801 (15.22 MB)
Trainable params: 3989801 (15.22 MB)
Non-trainable params: 0 (0.00 Byte)
-----

```

0.0.14 Training the model

```
[27]: ## Your code goes here, note: train your model for 20 epochs
epochs = 20
history = model.fit(
    train_ds,
    validation_data=val_ds,
    epochs=epochs
)
```

```

Epoch 1/20
56/56 [=====] - 6s 32ms/step - loss: 2.0173 - accuracy: 0.2656 - val_loss: 1.7965 - val_accuracy: 0.3289
Epoch 2/20
56/56 [=====] - 2s 27ms/step - loss: 1.6494 - accuracy: 0.4129 - val_loss: 1.4758 - val_accuracy: 0.5101
Epoch 3/20
56/56 [=====] - 2s 28ms/step - loss: 1.4877 - accuracy: 0.4732 - val_loss: 1.4541 - val_accuracy: 0.5213
Epoch 4/20
56/56 [=====] - 1s 27ms/step - loss: 1.3960 - accuracy: 0.5061 - val_loss: 1.4847 - val_accuracy: 0.4631
Epoch 5/20
56/56 [=====] - 2s 27ms/step - loss: 1.3321 - accuracy: 0.5318 - val_loss: 1.4163 - val_accuracy: 0.5034
Epoch 6/20
56/56 [=====] - 2s 28ms/step - loss: 1.2435 - accuracy: 0.5619 - val_loss: 1.4394 - val_accuracy: 0.5034
Epoch 7/20
56/56 [=====] - 2s 29ms/step - loss: 1.2634 - accuracy: 0.5642 - val_loss: 1.3853 - val_accuracy: 0.5324
Epoch 8/20

```

```
56/56 [=====] - 2s 30ms/step - loss: 1.1188 - accuracy: 0.6094 - val_loss: 1.3873 - val_accuracy: 0.5548
Epoch 9/20
56/56 [=====] - 2s 28ms/step - loss: 1.0558 - accuracy: 0.6211 - val_loss: 1.3649 - val_accuracy: 0.5526
Epoch 10/20
56/56 [=====] - 1s 27ms/step - loss: 1.0017 - accuracy: 0.6401 - val_loss: 1.6966 - val_accuracy: 0.5011
Epoch 11/20
56/56 [=====] - 2s 27ms/step - loss: 1.0120 - accuracy: 0.6440 - val_loss: 1.5230 - val_accuracy: 0.5481
Epoch 12/20
56/56 [=====] - 2s 27ms/step - loss: 0.9539 - accuracy: 0.6496 - val_loss: 1.6477 - val_accuracy: 0.5414
Epoch 13/20
56/56 [=====] - 2s 28ms/step - loss: 0.9028 - accuracy: 0.6674 - val_loss: 1.5861 - val_accuracy: 0.5123
Epoch 14/20
56/56 [=====] - 2s 28ms/step - loss: 0.8021 - accuracy: 0.7087 - val_loss: 1.5832 - val_accuracy: 0.5414
Epoch 15/20
56/56 [=====] - 2s 28ms/step - loss: 0.7133 - accuracy: 0.7405 - val_loss: 1.5965 - val_accuracy: 0.5414
Epoch 16/20
56/56 [=====] - 2s 30ms/step - loss: 0.6944 - accuracy: 0.7489 - val_loss: 1.7004 - val_accuracy: 0.4855
Epoch 17/20
56/56 [=====] - 2s 29ms/step - loss: 0.6071 - accuracy: 0.7751 - val_loss: 2.0114 - val_accuracy: 0.5190
Epoch 18/20
56/56 [=====] - 2s 29ms/step - loss: 0.5300 - accuracy: 0.8069 - val_loss: 2.1887 - val_accuracy: 0.5570
Epoch 19/20
56/56 [=====] - 2s 28ms/step - loss: 0.4715 - accuracy: 0.8125 - val_loss: 2.0039 - val_accuracy: 0.5034
Epoch 20/20
56/56 [=====] - 2s 28ms/step - loss: 0.4330 - accuracy: 0.8292 - val_loss: 2.2661 - val_accuracy: 0.5324
```

0.0.15 Visualizing the results

```
[28]: 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=(8, 8))
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?

- The training accuracy is reduced compared to the previous model. The accuracy is around 82.92
- The validation accuracy is around 53.24
- The difference between training accuracy & validation accuracy is reduced but we have to increase both accuracies by adding more dataset

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.

```
[30]: temp_train_ds = tf.keras.preprocessing.image_dataset_from_directory(  
        data_dir_train,  
        labels="inferred",  
        label_mode="categorical",  
        batch_size=2239,  
        image_size=(180, 180),  
        shuffle=True,  
        seed=123  
)
```

Found 2239 files belonging to 9 classes.

```
[31]: for images, labels in temp_train_ds:  
    temp = labels.numpy()
```

```
[32]: data = pd.DataFrame(temp,columns=class_names)
```

```
[33]: # display the data  
data
```

```
[33]: actinic keratosis  basal cell carcinoma  dermatofibroma  melanoma  \  
0          0.0            0.0            0.0            0.0  
1          0.0            0.0            0.0            1.0  
2          0.0            0.0            0.0            0.0  
3          0.0            0.0            0.0            0.0  
4          0.0            0.0            0.0            1.0  
...          ...            ...            ...            ...  
2234         0.0            0.0            0.0            0.0            0.0
```

```

2235          0.0          0.0          0.0          0.0
2236          0.0          0.0          0.0          1.0
2237          0.0          0.0          0.0          0.0
2238          0.0          0.0          0.0          1.0

      nevus  pigmented benign keratosis  seborrheic keratosis \
0        1.0              0.0            0.0
1        0.0              0.0            0.0
2        0.0              1.0            0.0
3        0.0              1.0            0.0
4        0.0              0.0            0.0
...
2234    ...          ...          ...
2235    0.0              1.0            0.0
2236    0.0              0.0            0.0
2237    0.0              0.0            0.0
2238    0.0              0.0            0.0

      squamous cell carcinoma  vascular lesion
0                  0.0            0.0
1                  0.0            0.0
2                  0.0            0.0
3                  0.0            0.0
4                  0.0            0.0
...
2234    ...          ...          ...
2235    0.0              0.0            0.0
2236    0.0              0.0            0.0
2237    1.0              0.0            0.0
2238    0.0              0.0            0.0

[2239 rows x 9 columns]

```

```
[34]: # display the details for each class
for col in data.columns:
    print(f'{col}\n', data[col].value_counts(ascending=True))
    print('-----')
```

```

actinic keratosis
1.0    114
0.0    2125
Name: actinic keratosis, dtype: int64
-----
basal cell carcinoma
1.0    376
0.0    1863
Name: basal cell carcinoma, dtype: int64

```

```
-----  
dermatofibroma  
1.0      95  
0.0    2144  
Name: dermatofibroma, dtype: int64  
-----  
melanoma  
1.0      438  
0.0    1801  
Name: melanoma, dtype: int64  
-----  
nevus  
1.0      357  
0.0    1882  
Name: nevus, dtype: int64  
-----  
pigmented benign keratosis  
1.0      462  
0.0    1777  
Name: pigmented benign keratosis, dtype: int64  
-----  
seborrheic keratosis  
1.0      77  
0.0    2162  
Name: seborrheic keratosis, dtype: int64  
-----  
squamous cell carcinoma  
1.0      181  
0.0    2058  
Name: squamous cell carcinoma, dtype: int64  
-----  
vascular lesion  
1.0      139  
0.0    2100  
Name: vascular lesion, dtype: int64  
-----
```

```
[35]: # display the different class names  
class_names
```

```
[35]: ['actinic keratosis',  
       'basal cell carcinoma',  
       'dermatofibroma',  
       'melanoma',  
       'nevus',  
       'pigmented benign keratosis',  
       'seborrheic keratosis',
```

```
'squamous cell carcinoma',
'vascular lesion']
```

```
[36]: # display the details for each class
for col in data.columns:
    print(f'{col}\n', data[col].value_counts(ascending=True))
    print('-----')
```

```
actinic keratosis
 1.0      114
 0.0     2125
Name: actinic keratosis, dtype: int64
-----
basal cell carcinoma
 1.0      376
 0.0     1863
Name: basal cell carcinoma, dtype: int64
-----
dermatofibroma
 1.0      95
 0.0    2144
Name: dermatofibroma, dtype: int64
-----
melanoma
 1.0      438
 0.0     1801
Name: melanoma, dtype: int64
-----
nevus
 1.0      357
 0.0     1882
Name: nevus, dtype: int64
-----
pigmented benign keratosis
 1.0      462
 0.0    1777
Name: pigmented benign keratosis, dtype: int64
-----
seborrheic keratosis
 1.0      77
 0.0    2162
Name: seborrheic keratosis, dtype: int64
-----
squamous cell carcinoma
 1.0      181
 0.0     2058
Name: squamous cell carcinoma, dtype: int64
```

```
-----  
vascular lesion  
1.0      139  
0.0     2100  
Name: vascular lesion, dtype: int64  
-----
```

Todo: Write your findings here:

- Which class has the least number of samples?

- Class with lowest Data is “seborrheic keratosis” with 77 images ##### - Which classes dominate the data in terms proportionate number of samples?
- Pigmented Benign Keratosis with sample size of 462.

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.

```
[37]: !pip install Augmentor
```

```
Collecting Augmentor  
  Downloading Augmentor-0.2.12-py2.py3-none-any.whl (38 kB)  
Requirement already satisfied: Pillow>=5.2.0 in /usr/local/lib/python3.10/dist-  
packages (from Augmentor) (9.4.0)  
Requirement already satisfied: tqdm>=4.9.0 in /usr/local/lib/python3.10/dist-  
packages (from Augmentor) (4.66.1)  
Requirement already satisfied: numpy>=1.11.0 in /usr/local/lib/python3.10/dist-  
packages (from Augmentor) (1.23.5)  
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.

```
[38]: path_to_training_dataset=data_dir_train  
import Augmentor  
for i in class_names:  
    p = Augmentor.Pipeline(str(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
```

```
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/actinic  
keratosis/output.  
  
Processing <PIL.JpegImagePlugin.JpegImageFile image mode=RGB size=600x450 at  
0x7B4A48F28250>: 100% | 500/500 [00:20<00:00, 23.85 Samples/s]  
  
Initialised with 376 image(s) found.  
Output directory set to  
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/basal cell  
carcinoma/output.  
  
Processing <PIL.Image.Image image mode=RGB size=600x450 at 0x7B4A8B94C760>:  
100% | 500/500 [00:22<00:00, 22.15 Samples/s]  
  
Initialised with 95 image(s) found.  
Output directory set to /content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Database/Train/dermatofibroma/output.  
  
Processing <PIL.Image.Image image mode=RGB size=600x450 at 0x7B4AC1D21420>:  
100% | 500/500 [00:26<00:00, 18.68 Samples/s]  
  
Initialised with 438 image(s) found.  
Output directory set to  
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/melanoma/output.  
  
Processing <PIL.Image.Image image mode=RGB size=3872x2592 at 0x7B4A48FAB490>:  
100% | 500/500 [01:37<00:00, 5.14 Samples/s]  
  
Initialised with 357 image(s) found.  
Output directory set to  
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/nevus/output.  
  
Processing <PIL.Image.Image image mode=RGB size=767x576 at 0x7B4A8B9D5900>:  
100% | 500/500 [01:23<00:00, 5.96 Samples/s]  
  
Initialised with 462 image(s) found.  
Output directory set to  
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/pigmented benign  
keratosis/output.  
  
Processing <PIL.JpegImagePlugin.JpegImageFile image mode=RGB size=600x450 at  
0x7B4AC0110E20>: 100% | 500/500 [00:19<00:00, 25.32 Samples/s]  
  
Initialised with 77 image(s) found.  
Output directory set to  
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic  
keratosis/output.  
  
Processing <PIL.Image.Image image mode=RGB size=1024x768 at 0x7B4A6850B640>:  
100% | 500/500 [00:42<00:00, 11.89 Samples/s]  
  
Initialised with 181 image(s) found.  
Output directory set to  
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/squamous cell  
carcinoma/output.
```

```
Processing <PIL.Image.Image image mode=RGB size=600x450 at 0x7B4A8B9D6860>:  
100%|      | 500/500 [00:18<00:00, 27.64 Samples/s]
```

```
Initialised with 139 image(s) found.
```

```
Output directory set to
```

```
/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/vascular  
lesion/output.
```

```
Processing <PIL.Image.Image image mode=RGB size=600x450 at 0x7B4A8B9039A0>:  
100%|      | 500/500 [00:18<00:00, 26.99 Samples/s]
```

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.

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

```
4500
```

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

```
[40]: !pip install glob2  
import glob
```

```
Requirement already satisfied: glob2 in /usr/local/lib/python3.10/dist-packages  
(0.7)
```

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

```
[41]: ['/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0029967.jpg_3d791616-5d1d-47d8-b2f1-9db2dfb  
b8965.jpg',  
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0029578.jpg_411665b6-1711-4ce1-be46-cdba74a  
df03a.jpg',  
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0026629.jpg_5fe608ba-8cff-4a0e-8d5b-b56ebf2  
616a8.jpg',  
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0027598.jpg_9d840e48-a969-4358-94e0-74c8238  
d2753.jpg',  
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0031735.jpg_8caf3eaf-5d2d-431d-bb4f-20e7579  
6a5d8.jpg',  
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0033675.jpg_00e6ea0d-e349-413f-8acb-56d9315
```

```
fe134.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0033891.jpg_ce2f1a90-0df7-4834-93bb-97b2db6
 56d01.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0031457.jpg_47691cc1-8f60-4872-8813-f33f32c
 f7d77.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0031344.jpg_5e87aea7-2200-4cb7-a528-b03f3e9
 b9f1a.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0029297.jpg_a7ed1f76-da67-4775-9511-0d332df
 8e752.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0028790.jpg_516fc44-8807-4df0-a9d1-4b39358
 b3e42.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0027745.jpg_e8eac50f-f586-4dd8-8c02-de77255
 ab606.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0031443.jpg_ea30838a-b75f-42c0-a165-630adda
 d7772.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0027008.jpg_75c56e25-3452-4f6e-b26e-a6c8b4c
 4d29b.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0025954.jpg_7489a677-79a3-4dd7-b8d7-b8ac847
 64f32.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0028651.jpg_5e7f65d9-9669-4091-89ab-536121b
 ea409.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0025594.jpg_c8de4fd0-6443-41f1-9aa6-d56e3d6
 d66c8.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0030015.jpg_c1eac19b-644c-4501-9d71-4761ce1
 e57a5.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0025504.jpg_26430aee-499c-42d2-bd24-1d34b23
 cd6eb.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0033780.jpg_98bb33bb-c355-4ae8-8902-1f4190b
 c7541.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0028346.jpg_cc1647c4-33e8-4f3e-b401-3bc2108
 8524e.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
```

```
/output/dermatofibroma_original_ISIC_0029039.jpg_61248f14-f3ac-4496-8deb-  
dddc56bd14af.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0031271.jpg_6bba5d6f-d18d-4474-83bd-a101c00  
b9072.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0026473.jpg_1836e914-f98d-40b2-b1ee-7b7700d  
be288.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0033847.jpg_287deebd-6e91-4f50-b30b-5d88b60  
cdf99.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0031429.jpg_ed21c72f-7e4d-4f2f-b55b-217e225  
69120.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0027141.jpg_1d0decccd-5d53-419c-a5da-86c6613  
c01e1.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0026789.jpg_27a10496-a5f4-46c3-a232-073c460  
c7c0c.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0028926.jpg_3fde52fb-f6d8-4037-b243-6b30974  
232a5.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0029248.jpg_c3f579ff-d208-4f57-bbbe-49d5266  
4fce8.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0029891.jpg_e5b3baf0-e473-41c5-89e6-ff14a6e  
7353b.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0030665.jpg_a3e70542-182f-4393-8b28-2344fdb  
9c56c.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0033695.jpg_710af86c-48c3-480c-b946-3a0f210  
17e4a.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0025911.jpg_be7dfc1d-d7b1-465a-bedc-80c79f1  
27af7.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0030427.jpg_3799d108-bf93-41e9-aa0d-095708e  
2399e.jpg',  
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma  
/output/dermatofibroma_original_ISIC_0031344.jpg_3ee8805b-09a3-4342-a3fe-c8dc7c0  
885bf.jpg',
```

```
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0031827.jpg_fb92b92d-d3d3-45e7-8a37-eb1ae76
59ce0.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0032941.jpg_1a8af4ba-2ac8-4e95-985f-016a473
2b474.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0032114.jpg_b654a357-7a0c-49c0-a5f6-7908d91
e16fe.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0030427.jpg_71e5bbb6-4a86-4ca2-8cc1-1e7d294
985a7.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0033554.jpg_72eadee4-6434-43c7-bb47-6848445
45c6d.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0029783.jpg_453ae4dc-
ee85-4f54-b0e3-1e80feb6295f.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0033005.jpg_cede2746-aa55-4c21-ac20-a82b4f4
390c8.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0026473.jpg_16b89ff6-ab1c-4282-b816-fb2b065
f5ac4.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0029177.jpg_902af6c7-e276-4970-a1cd-f201a02
11829.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0031443.jpg_806b86a5-467f-4c47-8a4a-9a773ce
4152d.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0030757.jpg_31ee7629-1a47-47b3-822b-f790734
fa280.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0031271.jpg_df5af44f-0530-4c81-8ab5-78b1599
93c95.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0029783.jpg_58fc5b8e-8fa4-4faf-921b-fdebb59
5f7f7.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0030011.jpg_c2d6d1c8-a59f-47b0-8577-a5610eb
b4448.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0027141.jpg_1f95ff45-c95e-4031-ace0-3264eaf
5f1c0.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
/output/dermatofibroma_original_ISIC_0029962.jpg_9e5cd502-7889-4ad5-9f43-3f78368
```

```
82e82.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0025903.jpg_8d2feb80-f82b-4a8b-ad8f-b3b5ad2
 3e58d.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0025911.jpg_8b4ff973-4908-4652-9647-817da47
 38887.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0031429.jpg_d08e1259-3e6a-4f6f-b207-fdfeee0
 d696f.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0026254.jpg_b8c920ed-a7b8-4e83-87bc-58d7973
 c8b0a.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0034135.jpg_6a19256c-626f-4974-9e73-e98e319
 88203.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0025504.jpg_5e993f83-a131-4a53-8a93-396cbc4
 4cedf.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0030757.jpg_1ed9c6e8-3fa2-4d41-85f4-e3a9cf
 bd482.jpg',
 '/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/dermatofibroma
 /output/dermatofibroma_original_ISIC_0025504.jpg_4791fad5-34ba-4bbc-b02d-25866e0
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```

```

keratosis_original_ISIC_0011135.jpg_4cb192dc-2864-44b9-815a-03018ff9d686.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic
keratosis/output/seborrheic
keratosis_original_ISIC_0011056.jpg_3a309da5-97f0-4470-8b85-adf193cb60fd.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic
keratosis/output/seborrheic
keratosis_original_ISIC_0011185.jpg_499bb9f9-d0ad-4580-a7ba-304ebdecabaa.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic
keratosis/output/seborrheic
keratosis_original_ISIC_0011045.jpg_2cc246fb-50d9-4642-867f-f9816c5e3c44.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic
keratosis/output/seborrheic
keratosis_original_ISIC_0010917.jpg_79a496a3-71b1-4c01-9637-af55ad7d5deb.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic
keratosis/output/seborrheic
keratosis_original_ISIC_0011112.jpg_70c63f60-4033-4f47-b74d-1c840d35e0ac.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic
keratosis/output/seborrheic
keratosis_original_ISIC_0010982.jpg_132ff321-64cd-48b3-9240-590865ea76d0.jpg',
'/content/gdrive/MyDrive/UpGrad/AI_ML/CNN_Melanoma_Dataset/Train/seborrheic
keratosis/output/seborrheic
keratosis_original_ISIC_0011132.jpg_c82ba4cb-2a33-4745-aabe-ea909be2210a.jpg',
...]

```

```
[42]: # lesion_list = [os.path.basename(os.path.dirname(os.path.dirname(y))) for y in glob.glob(os.path.join(data_dir_train, '*', 'output', '*.jpg'))]
# lesion_list[1:5]

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

```
[42]: ['dermatofibroma',
'dermatofibroma',
'dermatofibroma']
```



```
[43]: dataframe_dict_new = dict(zip(path_list, lesion_list_new))
original_df = pd.DataFrame(list(dataframe_dict_new.items()), columns = ['Path', 'Label'])

[44]: df2 = pd.DataFrame(list(dataframe_dict_new.items()), columns = ['Path', 'Label'])
#new_df = pd.concat([original_df, df2], ignore_index=True)
new_df = original_df.append(df2)
```

<ipython-input-44-527460b6cb46>:3: FutureWarning: The frame.append method is deprecated and will be removed from pandas in a future version. Use pandas.concat instead.

```
    new_df = original_df.append(df2)
```

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

```
[45]: dermatofibroma          1000
      seborrheic keratosis    1000
      actinic keratosis      1000
      nevus                  1000
      melanoma               1000
      squamous cell carcinoma 1000
      vascular lesion         1000
      pigmented benign keratosis 1000
      basal cell carcinoma    1000
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

```
[48]: batch_size = 32
      img_height = 180
      img_width = 180
```

Todo: Create a training dataset

```
[49]: data_dir_train= data_dir_train ##"path to directory with training data + data
      ↪created using augmentor"
train_ds = tf.keras.preprocessing.image_dataset_from_directory(
      data_dir_train,
      seed=123,
      validation_split = 0.2,
      subset = 'training', ## Todo choose the correct parameter value, so that only
      ↪training data is referred to.,
      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

```
[50]: val_ds = tf.keras.preprocessing.image_dataset_from_directory(  
        data_dir_train,  
        seed=123,  
        validation_split = 0.2,  
        subset = 'validation', ## Todo choose the correct parameter value, so that  
        ↪only validation data is refered to,  
        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)

0.0.17 Model 3: Vanilla Model + Dropout Layer + Data Augmentation (to counter overfitting) + Class Balanced Dataset

```
[51]: ## your code goes here  
num_classes = 9  
  
model = Sequential([  
    layers.experimental.preprocessing.Rescaling(1./255, input_shape=(img_height, img_width, 3)),  
    layers.Conv2D(16, 3, padding='same', activation=activation_func),  
    layers.MaxPooling2D(),  
    layers.Conv2D(32, 3, padding='same', activation=activation_func),  
    layers.MaxPooling2D(),  
    layers.Conv2D(64, 3, padding='same', activation=activation_func),  
    layers.MaxPooling2D(),  
    layers.Flatten(),  
    layers.Dense(128, activation=activation_func),  
    layers.Dense(num_classes)  
])
```

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

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

```
[53]: model.summary()
```

Model: "sequential_3"

Layer (type)	Output Shape	Param #
<hr/>		
rescaling_2 (Rescaling)	(None, 180, 180, 3)	0
conv2d_6 (Conv2D)	(None, 180, 180, 16)	448
max_pooling2d_6 (MaxPooling2D)	(None, 90, 90, 16)	0
conv2d_7 (Conv2D)	(None, 90, 90, 32)	4640
max_pooling2d_7 (MaxPooling2D)	(None, 45, 45, 32)	0
conv2d_8 (Conv2D)	(None, 45, 45, 64)	18496
max_pooling2d_8 (MaxPooling2D)	(None, 22, 22, 64)	0
flatten_2 (Flatten)	(None, 30976)	0
dense_4 (Dense)	(None, 128)	3965056
dense_5 (Dense)	(None, 9)	1161
<hr/>		
Total params: 3989801 (15.22 MB)		
Trainable params: 3989801 (15.22 MB)		
Non-trainable params: 0 (0.00 Byte)		

Todo: Train your model

```
[54]: epochs = 50
# train the model using 50 epochs
history = model.fit(
    train_ds,
    validation_data=val_ds,
    epochs=epochs
)
```

```
Epoch 1/50
169/169 [=====] - 41s 222ms/step - loss: 1.7336 - 
accuracy: 0.3453 - val_loss: 1.3819 - val_accuracy: 0.4729
Epoch 2/50
169/169 [=====] - 43s 250ms/step - loss: 1.2981 -
```

```
accuracy: 0.5134 - val_loss: 1.2346 - val_accuracy: 0.5323
Epoch 3/50
169/169 [=====] - 48s 277ms/step - loss: 1.0503 -
accuracy: 0.6139 - val_loss: 1.0502 - val_accuracy: 0.6132
Epoch 4/50
169/169 [=====] - 39s 223ms/step - loss: 0.8844 -
accuracy: 0.6754 - val_loss: 1.0106 - val_accuracy: 0.6340
Epoch 5/50
169/169 [=====] - 36s 206ms/step - loss: 0.7150 -
accuracy: 0.7422 - val_loss: 1.1473 - val_accuracy: 0.5999
Epoch 6/50
169/169 [=====] - 36s 207ms/step - loss: 0.5747 -
accuracy: 0.7914 - val_loss: 0.8219 - val_accuracy: 0.7231
Epoch 7/50
169/169 [=====] - 43s 244ms/step - loss: 0.4394 -
accuracy: 0.8429 - val_loss: 0.7501 - val_accuracy: 0.7654
Epoch 8/50
169/169 [=====] - 38s 218ms/step - loss: 0.3628 -
accuracy: 0.8715 - val_loss: 0.7910 - val_accuracy: 0.7454
Epoch 9/50
169/169 [=====] - 40s 232ms/step - loss: 0.2989 -
accuracy: 0.8911 - val_loss: 0.7128 - val_accuracy: 0.7758
Epoch 10/50
169/169 [=====] - 39s 225ms/step - loss: 0.2481 -
accuracy: 0.9082 - val_loss: 0.7794 - val_accuracy: 0.7713
Epoch 11/50
169/169 [=====] - 35s 201ms/step - loss: 0.2160 -
accuracy: 0.9230 - val_loss: 0.8058 - val_accuracy: 0.7773
Epoch 12/50
169/169 [=====] - 40s 231ms/step - loss: 0.2691 -
accuracy: 0.9043 - val_loss: 0.7405 - val_accuracy: 0.7862
Epoch 13/50
169/169 [=====] - 38s 216ms/step - loss: 0.2003 -
accuracy: 0.9314 - val_loss: 0.7309 - val_accuracy: 0.7899
Epoch 14/50
169/169 [=====] - 34s 199ms/step - loss: 0.1691 -
accuracy: 0.9338 - val_loss: 0.8171 - val_accuracy: 0.7669
Epoch 15/50
169/169 [=====] - 35s 200ms/step - loss: 0.1613 -
accuracy: 0.9323 - val_loss: 0.8650 - val_accuracy: 0.7840
Epoch 16/50
169/169 [=====] - 44s 258ms/step - loss: 0.1492 -
accuracy: 0.9432 - val_loss: 0.7028 - val_accuracy: 0.8174
Epoch 17/50
169/169 [=====] - 38s 218ms/step - loss: 0.1332 -
accuracy: 0.9457 - val_loss: 0.8521 - val_accuracy: 0.7706
Epoch 18/50
169/169 [=====] - 35s 202ms/step - loss: 0.2076 -
```

```
accuracy: 0.9247 - val_loss: 0.8170 - val_accuracy: 0.7884
Epoch 19/50
169/169 [=====] - 39s 226ms/step - loss: 0.1394 -
accuracy: 0.9462 - val_loss: 0.9203 - val_accuracy: 0.7884
Epoch 20/50
169/169 [=====] - 34s 199ms/step - loss: 0.1302 -
accuracy: 0.9473 - val_loss: 0.8078 - val_accuracy: 0.8159
Epoch 21/50
169/169 [=====] - 35s 201ms/step - loss: 0.1393 -
accuracy: 0.9436 - val_loss: 0.8757 - val_accuracy: 0.7936
Epoch 22/50
169/169 [=====] - 35s 201ms/step - loss: 0.1498 -
accuracy: 0.9421 - val_loss: 0.9897 - val_accuracy: 0.7869
Epoch 23/50
169/169 [=====] - 35s 201ms/step - loss: 0.1834 -
accuracy: 0.9336 - val_loss: 0.9019 - val_accuracy: 0.7803
Epoch 24/50
169/169 [=====] - 35s 200ms/step - loss: 0.1384 -
accuracy: 0.9442 - val_loss: 0.9934 - val_accuracy: 0.7862
Epoch 25/50
169/169 [=====] - 35s 202ms/step - loss: 0.1148 -
accuracy: 0.9523 - val_loss: 0.9847 - val_accuracy: 0.7825
Epoch 26/50
169/169 [=====] - 39s 224ms/step - loss: 0.1678 -
accuracy: 0.9382 - val_loss: 0.9656 - val_accuracy: 0.7810
Epoch 27/50
169/169 [=====] - 38s 218ms/step - loss: 0.1087 -
accuracy: 0.9553 - val_loss: 0.8411 - val_accuracy: 0.8107
Epoch 28/50
169/169 [=====] - 35s 204ms/step - loss: 0.0969 -
accuracy: 0.9624 - val_loss: 0.9293 - val_accuracy: 0.8048
Epoch 29/50
169/169 [=====] - 35s 200ms/step - loss: 0.0984 -
accuracy: 0.9612 - val_loss: 1.0272 - val_accuracy: 0.7929
Epoch 30/50
169/169 [=====] - 35s 201ms/step - loss: 0.0915 -
accuracy: 0.9640 - val_loss: 1.2160 - val_accuracy: 0.7565
Epoch 31/50
169/169 [=====] - 35s 201ms/step - loss: 0.1146 -
accuracy: 0.9553 - val_loss: 1.1453 - val_accuracy: 0.7832
Epoch 32/50
169/169 [=====] - 35s 201ms/step - loss: 0.0968 -
accuracy: 0.9603 - val_loss: 1.0145 - val_accuracy: 0.7951
Epoch 33/50
169/169 [=====] - 35s 200ms/step - loss: 0.1419 -
accuracy: 0.9442 - val_loss: 1.1812 - val_accuracy: 0.7379
Epoch 34/50
169/169 [=====] - 39s 228ms/step - loss: 0.1191 -
```

```
accuracy: 0.9505 - val_loss: 1.0853 - val_accuracy: 0.7817
Epoch 35/50
169/169 [=====] - 35s 201ms/step - loss: 0.1517 -
accuracy: 0.9445 - val_loss: 0.8992 - val_accuracy: 0.7973
Epoch 36/50
169/169 [=====] - 37s 217ms/step - loss: 0.1009 -
accuracy: 0.9590 - val_loss: 1.0313 - val_accuracy: 0.7854
Epoch 37/50
169/169 [=====] - 35s 204ms/step - loss: 0.0962 -
accuracy: 0.9616 - val_loss: 1.1349 - val_accuracy: 0.8003
Epoch 38/50
169/169 [=====] - 35s 200ms/step - loss: 0.1193 -
accuracy: 0.9551 - val_loss: 1.0931 - val_accuracy: 0.7751
Epoch 39/50
169/169 [=====] - 35s 199ms/step - loss: 0.1207 -
accuracy: 0.9533 - val_loss: 1.0477 - val_accuracy: 0.7966
Epoch 40/50
169/169 [=====] - 35s 199ms/step - loss: 0.0865 -
accuracy: 0.9629 - val_loss: 1.0520 - val_accuracy: 0.8040
Epoch 41/50
169/169 [=====] - 35s 202ms/step - loss: 0.0915 -
accuracy: 0.9609 - val_loss: 1.0498 - val_accuracy: 0.7973
Epoch 42/50
169/169 [=====] - 37s 215ms/step - loss: 0.0874 -
accuracy: 0.9627 - val_loss: 1.2173 - val_accuracy: 0.7951
Epoch 43/50
169/169 [=====] - 39s 229ms/step - loss: 0.0971 -
accuracy: 0.9605 - val_loss: 1.3376 - val_accuracy: 0.7728
Epoch 44/50
169/169 [=====] - 35s 202ms/step - loss: 0.1353 -
accuracy: 0.9486 - val_loss: 1.1204 - val_accuracy: 0.7869
Epoch 45/50
169/169 [=====] - 40s 230ms/step - loss: 0.1242 -
accuracy: 0.9510 - val_loss: 1.3240 - val_accuracy: 0.7535
Epoch 46/50
169/169 [=====] - 38s 217ms/step - loss: 0.1144 -
accuracy: 0.9564 - val_loss: 1.3584 - val_accuracy: 0.7513
Epoch 47/50
169/169 [=====] - 35s 200ms/step - loss: 0.1061 -
accuracy: 0.9596 - val_loss: 1.3025 - val_accuracy: 0.7795
Epoch 48/50
169/169 [=====] - 35s 199ms/step - loss: 0.1199 -
accuracy: 0.9551 - val_loss: 1.5288 - val_accuracy: 0.7142
Epoch 49/50
169/169 [=====] - 34s 199ms/step - loss: 0.0964 -
accuracy: 0.9616 - val_loss: 1.4079 - val_accuracy: 0.7535
Epoch 50/50
169/169 [=====] - 34s 198ms/step - loss: 0.0810 -
```

```
accuracy: 0.9657 - val_loss: 1.2880 - val_accuracy: 0.7706
```

Todo: Visualize the model results

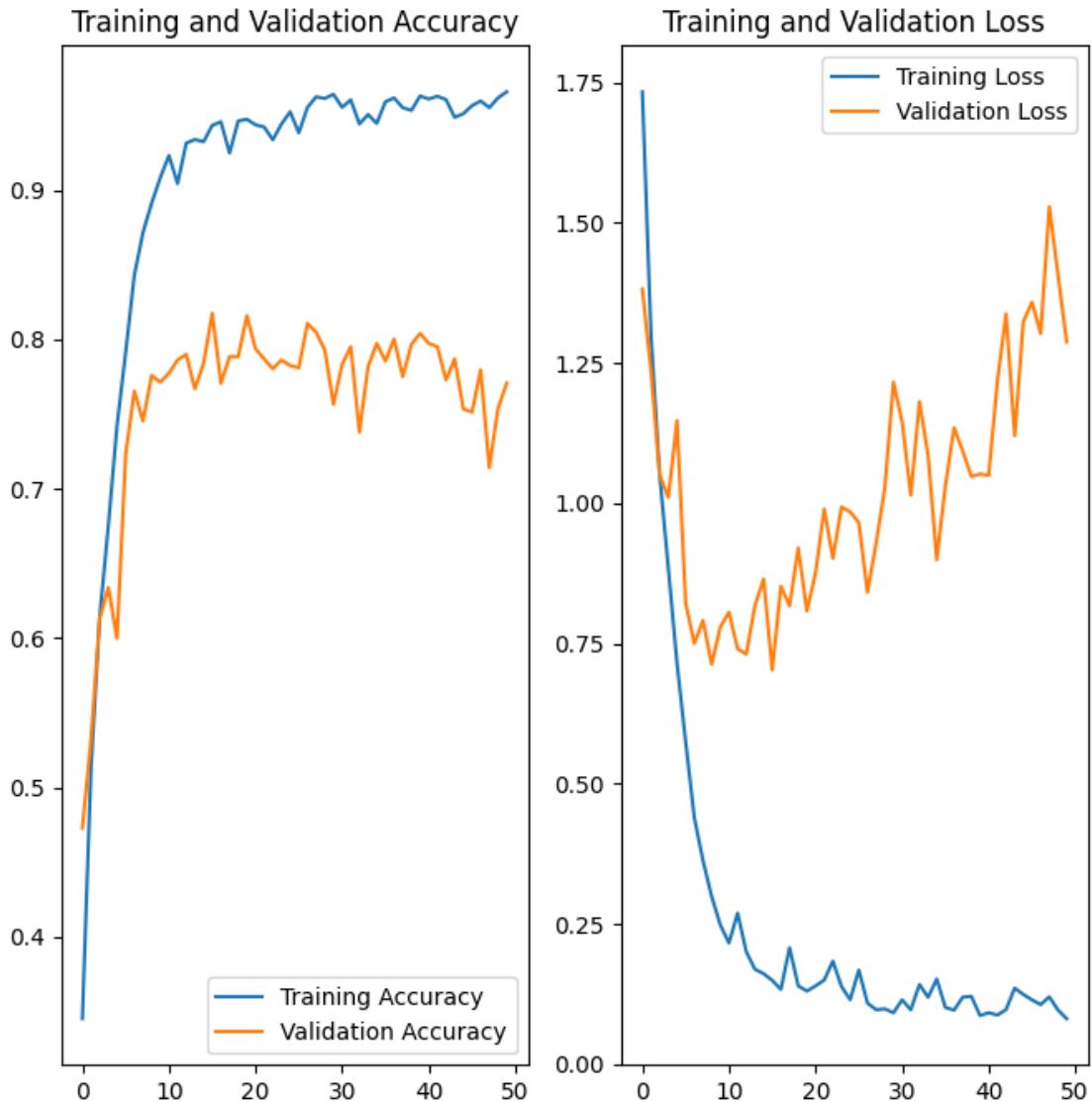
```
[55]: acc = history.history['accuracy']
val_acc = history.history['val_accuracy']

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

epochs_range = range(epochs)

plt.figure(figsize=(8, 8))
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: Analyze your results here. Did you get rid of underfitting/overfitting? Did class rebalance help?

0.0.18 Findings:

- The training accuracy has improved from the 2nd model. It is now 96.57
- Validation accuracy also improved from 2nd model. It is now 77.06
- After rebalancing using Augmentation the classes are balanced & we are getting better results.
- If more dataset is added we would certainly get better training & validation results.

Model 1: Vanilla Model * No Dropout Layers * List item * Small Dataset and No Augmentation
 * Model Training yeilded Non Accurate Model - Training accuracy 89% and Validation Accuracy 55% * Model was Overfitting - This was due to no dropout layers and no data augmentation

Model 2: Model 1 + Dropout Layers + Data Augmentation * Dropout Layers Added * Data Augmentation was added * Gap between Training Accuracy and Validation Accuracy decreased * Accuracy is still low - Training Accuracy 83% and Validation Accuracy 53%

Model 3: Model 2 + Class balanced Dataset * Dataset Added using Augmentor (500 images added per class) to counter class imbalance * Same Model 2 was used. * Model yeilded in 96% Training and 77% Validation Accuracy * This model can be improved further by including more dataset for training sot hat it further learns the generalizable features and performs better