## Assignment-3

# Al-based localization and classification of skin disease with erythema

#### **Build CNN Model for Classification Of Flowers**

## 1. Image Augmentation

```
In [4]: #Image Agumentation
from tensorflow.keras.preprocessing.image import ImageDataGenerator

In [5]: train_datagen = ImageDataGenerator(rescale=1./255,zoom_range=0.2,horizontal_flip=True,vertical_flip=True)

In [6]: test_datagen = ImageDataGenerator(rescale=1./255)

In [9]: xtrain = train_datagen.flow_from_directory("/content/flowers",target_size=(64,64),class_mode='categorical',batch_size=100)
Found 4317 images belonging to 5 classes.

In [10]: xtest = test_datagen.flow_from_directory("/content/flowers",target_size=(64,64),class_mode='categorical',batch_size=100)
Found 4317 images belonging to 5 classes.
```

#### 2. Create Model

```
#Create model
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Convolution2D,MaxPooling2D,Flatten,Dense

model = Sequential()
```

## 3. Layers

#### Convolution

```
#Convolution Layer
model.add(Convolution2D(32,(3,3),activation='relu',input_shape=(64,64,3)))
```

## Maxpooling

```
#maxpooling
model.add(MaxPooling2D(pool_size=(2,2)))
```

#### Flatten

```
#Flatten
model.add(Flatten())
```

#### **Dense Layer**

```
#Dense Layer
model.add(Dense(300,activation='relu')) #hiddenlayer 1
model.add(Dense(300,activation='relu')) #hiddenlayer 2
model.add(Dense(150,activation='relu')) #hiddenlayer 3
```

## **Output Layer**

```
#Output layer
model.add(Dense(5,activation='softmax'))
```

## 4,5. Compile & Fit the model

#### 6. Save the Model

```
#saving
model.save('Flowers.h5')
```

#### 7. Test the model

```
[ 45., 68., 50.],
          [ 43., 39., 30.],
          [ 55., 45., 36.]]], dtype=float32)
  x = np.expand_dims(x,axis=0)
: array([[[[199., 198., 214.],
            [201., 200., 216.],
           [201., 200., 216.],
           [187., 188., 208.],
           [186., 187., 207.],
           [184., 185., 205.]],
          [[197., 199., 214.],
           [199., 201., 216.],
           [201., 200., 216.],
           [186., 187., 207.],
           [185., 186., 206.],
           [184., 185., 205.]],
          [[200., 200., 224.],
           [200., 191., 218.],
           [197., 203., 217.],
           [188., 186., 207.],
           [188., 186., 207.],
           [187., 185., 206.]],
          [ 45., 68., 50.],
          [ 43., 39., 30.],
          [ 55., 45., 36.]]], dtype=float32)
   x = np.expand_dims(x,axis=0)
   X
: array([[[[199., 198., 214.],
           [201., 200., 216.],
           [201., 200., 216.],
           [187., 188., 208.],
           [186., 187., 207.],
           [184., 185., 205.]],
          [[197., 199., 214.],
           [199., 201., 216.],
           [201., 200., 216.],
           [186., 187., 207.],
           [185., 186., 206.],
           [184., 185., 205.]],
          [[200., 200., 224.],
           [200., 191., 218.],
           [197., 203., 217.],
           [188., 186., 207.],
           [188., 186., 207.],
           [187., 185., 206.]],
```

```
. . . ,
           [[ 64., 65., 47.],
            [106., 120., 95.],
            [116., 136., 109.],
            [109., 130., 97.],
[117., 133., 106.],
           [104., 108., 91.]],
          [[ 32., 40., 27.],
[116., 145., 114.],
[123., 141., 117.],
            [ 24., 54., 28.],
[ 92., 121., 90.],
            [ 54., 25., 21.]],
           [[129., 125., 18.],
           [147., 148., 143.],
[114., 132., 110.],
            [ 45., 68., 50.],
            [ 43., 39., 30.],
            [ 55., 45., 36.]]]], dtype=float32)
   model.predict(x)
  1/1 [======== ] - 0s 141ms/step
: array([[0., 0., 0., 1., 0.]], dtype=float32)
  model.predict(x)
 1/1 [======== ] - 0s 141ms/step
 array([[0., 0., 0., 1., 0.]], dtype=float32)
  xtrain.class_indices
 {'daisy': 0, 'dandelion': 1, 'rose': 2, 'sunflower': 3, 'tulip': 4}
  op = ['daisy','dandelion','rose','sunflower','tulip']
  pred = np.argmax(model.predict(x))
  op[pred]
 1/1 [======] - 0s 26ms/step
 'sunflower'
```

## Split the data into training and testing