```
#importing all the requied modules
from mpl_toolkits.mplot3d import Axes3D
from sklearn.preprocessing import StandardScaler
import matplotlib.pyplot as plt # plotting
import numpy as np # linear algebra
import os # accessing directory structure
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
from PIL import Image
import glob
import cv2
%matplotlib inline
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import os
from glob import glob
import seaborn as sns
from PIL import Image
np.random.seed(123)
from sklearn.preprocessing import label_binarize
from sklearn.metrics import confusion_matrix
import itertools
import keras
from keras.utils.np_utils import to_categorical # used for converting labels to one-hot-encoding
from keras.models import Sequential
from keras.layers import Dense, Dropout, Flatten, Conv2D, MaxPool2D
from keras import backend as K
import itertools
from keras.utils.np_utils import to_categorical # convert to one-hot-encoding
```

```
#import all the images from the folder
import glob
full_set=glob.glob('../input/skin-images/ham_data_surnamesABCD/ham_data_surnamesABCD/*.*')
```

```
#appending every image

full_set=[]
path=("../input/skin-images/ham_data_surnamesABCD/ham_data_surnamesABCD/*.*")

for i in glob.glob(path):
    s1=cv2.imread(i)
    full_set.append(s1)
```

```
#loading the csv file

nRowsRead = None
full_csv = pd.read_csv('../input/skin-csv/filename_to_category_map_surnamesABCD.csv', delimiter=',', nrows = nRow
```

```
#loading the csv file

nRowsRead = None
full_csv = pd.read_csv('../input/skin-csv/filename_to_category_map_surnamesABCD.csv', delimiter=',', nrows = nRow
full_csv.dataframeName = 'filename_to_category_map_surnamesABCD.csv'
n_Row, n_Col = full_csv.shape
print(f'There are {n_Row} rows and {n_Col} columns')
```

There are 5372 rows and 4 columns

+ Markdown

Code

```
full_csv_rep = pd.read_csv('../input/skin-csv/filename_to_category_map_surnamesABCD.csv')
```

```
print(full_csv)
         image id
                                         cell_type is_benign localization
     ISIC 0027419
                    Benign keratosis-like lesions
                                                          1.0
0
                                                                     scalp
     ISIC 0026769
                   Benign keratosis-like lesions
                                                          1.0
                                                                     scalp
1
2
     ISIC 0031633
                   Benign keratosis-like lesions
                                                          1.0
                                                                       ear
3
     ISIC 0029176
                   Benign keratosis-like lesions
                                                          1.0
                                                                      face
     ISIC 0029068
                    Benign keratosis-like lesions
4
                                                          1.0
                                                                      face
                                                                       . . .
                    Benign keratosis-like lesions
5367 ISIC 0027265
                                                          1.0
                                                                       NaN
5368 ISIC 0025029
                                 Melanocytic nevi
                                                          1.0
                                                                       NaN
5369 ISIC 0029462
                                 Melanocytic nevi
                                                          1.0
                                                                       NaN
     ISIC 0030510
                                 Melanocytic nevi
5370
                                                          1.0
                                                                       NaN
     ISIC_0033125
                                          Melanoma
                                                          1.0
5371
                                                                       NaN
[5372 rows x 4 columns]
```

```
len_csv = full_csv["image_id"]
 print(len(len_csv))
 map_images = {}
 for i in len_csv:
     path = "../input/skin-images/ham_data_surnamesABCD/ham_data_surnamesABCD/" + i + ".jpg"
     if i not in map_images.keys():
         map_images[i] = path
5372
 full_csv['path'] = full_csv['image_id'].map(lambda x : map_images[x])
 full_csv['image'] = full_csv['path'].map(lambda x: np.asarray(Image.open(x).resize((100,75))))
 full_csv = full_csv.dropna()
             + Markdown
 + Code
 full_csv.head()
     image_id
                        cell_type is_benign localization
                                                                                                              image
                                                                                    path
```

```
full_csv.head()
```

	image_id	cell_type	is_benign	localization	path	image
0	ISIC_0027419	Benign keratosis-like lesions	1.0	scalp	/input/skin- images/ham_data_surnamesABCD/ham	[[[190, 153, 194], [192, 154, 196], [191, 153,
1	ISIC_0026769	Benign keratosis-like lesions	1.0	scalp	/input/skin- images/ham_data_surnamesABCD/ham	[[[185, 127, 137], [189, 133, 147], [194, 136,
2	ISIC_0031633	Benign keratosis-like lesions	1.0	ear	/input/skin- images/ham_data_surnamesABCD/ham	[[[134, 90, 113], [147, 102, 125], [159, 115,
3	ISIC_0029176	Benign keratosis-like lesions	1.0	face	/input/skin- images/ham_data_surnamesABCD/ham	[[[191, 146, 129], [192, 146, 133], [194, 145,
4	ISIC_0029068	Benign keratosis-like lesions	1.0	face	/input/skin- images/ham_data_surnamesABCD/ham	[[[149, 105, 85], [156, 114, 95], [163, 124, 1

```
X=full_csv["image"]
Y=full_csv["cell_type"]
```

```
lass_name = ['Benign keratosis-like lesions ','Dermatofibroma','Melanoma','Vascular lesions','Basal cell carcinoma'
lt.figure(figsize=(20,20))
pr i in range(0,16) :
   plt.subplot(10,3,i+1)
   plt.axis('off')
```

```
class_name = ['Benign keratosis-like lesions ','Dermatofibroma','Melanoma','Vascular lesions','Basal cell carcing
plt.figure(figsize=(20,20))
for i in range(0,16):
    plt.subplot(10,3,i+1)
    plt.axis('off')
    plt.imshow(full_set[i], cmap="gray_r")
```

```
X=full_csv["image"]
Y=full_csv["cell_type"]
```

```
print(X)
        [[[190, 153, 194], [192, 154, 196], [191, 153,...
1
        [[[185, 127, 137], [189, 133, 147], [194, 136,...
2
        [[[134, 90, 113], [147, 102, 125], [159, 115, ...
3
        [[[191, 146, 129], [192, 146, 133], [194, 145,...
4
        [[[149, 105, 85], [156, 114, 95], [163, 124, 1...
5253
        [[[211, 135, 148], [211, 135, 148], [210, 134,...
        [[[243, 161, 173], [243, 161, 173], [244, 162,...
5254
5255
        [[[175, 162, 180], [176, 163, 180], [176, 163,...
        [[[49, 11, 25], [53, 15, 28], [59, 21, 34], [7...]
5256
5257
        [[[213, 150, 167], [213, 150, 167], [213, 150,...
Name: image, Length: 5258, dtype: object
  x_{train_o}, x_{test_o}, y_{train_o}, y_{test_o} = train_{test_split}(X, Y, test_size=0.30, random_state=6969)
```

```
x_train = np.asarray(x_train_o.tolist())
x_test = np.asarray(x_test_o.tolist())

x_train_mean = np.mean(x_train)
x_train_std = np.std(x_train)
```

```
train, x_validate, y_train, y_validate = train_test_split(x_train, y_train, test_size = 0.30, random_state = 69)
```

```
input_shape = (75, 100, 3)
num_classes = 7

model = Sequential()
model.add(Conv2D(32, kernel_size=(3, 3), activation='relu', padding = 'Same', input_shape=input_shape))
model.add(Conv2D(32, kernel_size=(3, 3), activation='relu', padding = 'Same',))
model.add(MaxPool2D(pool_size = (2, 2)))
model.add(Dropout(0.25))

model.add(Conv2D(64, (3, 3), activation='relu', padding = 'Same'))
model.add(Conv2D(64, (3, 3), activation='relu', padding = 'Same'))
model.add(MaxPool2D(pool_size=(2, 2)))
model.add(Dropout(0.40))
```

```
model.add(Flatten())
model.add(Dense(128, activation='relu'))
model.add(Dropout(0.5))
model.add(Dense(num_classes, activation='softmax'))
model.summary()
```

Model: "sequential"

Layer (type)	Output	Shape	Param #
conv2d (Conv2D)	(None,	75, 100, 32)	896
conv2d_1 (Conv2D)	(None,	75, 100, 32)	9248
max_pooling2d (MaxPooling2D)	(None,	37, 50, 32)	0
dropout (Dropout)	(None,	37, 50, 32)	0
conv2d_2 (Conv2D)	(None,	37, 50, 64)	18496
conv2d_3 (Conv2D)	(None,	37, 50, 64)	36928
max_pooling2d_1 (MaxPooling2	(None,	18, 25, 64)	0
dropout_1 (Dropout)	(None,	18, 25, 64)	0
flatten (Flatten)	(None,	28800)	0
dense (Dense)	(None,	128)	3686528
dropout_2 (Dropout)	(None,	128)	0
dense_1 (Dense)	(None,	7)	903

Total params: 3,752,999 Trainable params: 3,752,999 Non-trainable params: 0

d, use `learning rate` instead.

"The `lr` argument is deprecated, use `learning rate` instead.")

```
epochs = 50
 batch size = 10
 history = model.fit_generator(datagen.flow(x_train,y_train, batch_size=batch_size),
                                epochs = epochs, validation_data = (x_validate,y_validate),
                                verbose = 1, steps_per_epoch=x_train.shape[0] // batch_size
                                 , callbacks=[learning_rate_reduction])
 plt.plot(history.history['accuracy'], label='accuracy')
 plt.plot(history.history['val_accuracy'], label = 'val_accuracy')
 plt.xlabel('Epoch')
 plt.ylabel('Accuracy')
 plt.legend(loc='lower right')
/opt/conda/lib/python3.7/site-packages/keras/engine/training.py:1972: UserWarning: `Model.fit generator` is deprecated and
will be removed in a future version. Please use `Model.fit`, which supports generators.
```

```
warnings.warn('`Model.fit_generator` is deprecated and '
2022-04-26 22:07:08.940893: I tensorflow/compiler/mlir/mlir graph optimization pass.cc:185] None of the MLIR Optimization
Passes are enabled (registered 2)
Epoch 1/50
acv: 0.6875
Epoch 2/50
acy: 0.6884
Epoch 3/50
acy: 0.6866
Epoch 4/50
acy: 0.6893
Epoch 5/50
acy: 0.6920
Epoch 6/50
acv: 0.7029
```