

# **Configuration Manual**

MSc Research Project Data Analytics

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#### National College of Ireland



#### **MSc Project Submission Sheet**

#### **School of Computing**

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Lecturer:	Dr. Bahman Honari						
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# **Configuration Manual**

Krishnachander Rajendran Student ID: x18122779

# **1** Software Requirements

Your first section. Change the header and label to something appropriate. The codes for the research study were written entirely using Python 3 version. Python codes were implemented using the Jupyter Notebook on Anaconda Navigator platform. The first step that needs to be done will be in installing the Anaconda Software. As requirements go by, the 64-bit version of the setup file is downloaded to be in compatible with the 64-bit Windows OS.

	Products	Why Anaconda?	Solutions	Resource	s Compa	any Cor	ntact Us Dov
Anaconda Distribut	ion						
The World's Most Popular Python/R Data Scien	ce Platform						
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The open-source Anaconda Distribution is the easies data science and machine learning on Linux, Window over 15 million users worldwide, it is the industry stan testing, and training on a single machine, enabling <i>in</i> • Quickly download 1,500+ Python/R data scienc • Manage libraries, dependencies, and environm • Develop and train machine learning and deep I learn, TensorFiow, and Theano	st way to perform ws, and Mac OS X Idard for develop <i>ndividual data scie</i> ce packages ients with Conda learning models v	Python/R . With ing, 	pandas matplotlib	spyder Dask	NumPy Bokeh	S ScIPy HoloViews	Numba Datashader CONDA
The open-source Anaconda Distribution is the easies data science and machine learning on Linux, Window over 15 million users worldwide, it is the industry stan testing, and training on a single machine, enabling <i>in</i> • Oulckly download 1,500+ Python/R data science • Manage libraries, dependencies, and environm • Develop and train machine learning and deep I learn, TensorFlow, and Theano • Analyze data with scalability and performance w	st way to perform ws, and Mac OS X ndard for develop ndividual data scie te packages tents with Conda learning models v with Dask, NumPy	Python/R . With ing, ent/sts to:	pandas matplotlib	spyder DASK Cccc.n	NumPy Bokeh	SsciPy HoloViews TensorFlow	Numba Datashader CONDA

After successful installation, the Anaconda Navigator is opened from **Start -> Anaconda Navigator** 

	Applications on base (root)	✓ Channels				
vironments	¢ lab	jupyter	* *	· ·	°	R
rning	JupyterLab 2 1.1.4 An extensible environment for interactive and reproducible computing, based on the	Notebook 7 5.01 Web-basel, interactive computing notebook environment. Edit and run	Spyder 33.6 Scientific PYthon Development Envilonment, Powerful Python IDE with	Glueviz 0.15.2 Multidimensional data visualization across Files. Explore relationships within and	Orange 3 323.1 Component based data mining framework. Data visualization and data analysis for	RStudio 11.456 A set of integrated tools designed to help you be more productive with R. Includes R
immunity	Jupyter Notebook and Architecture.	human-readable docs while describing the data analysis.	advanced editing, interactive testing, debugging and introspection features	among related datasets.	novice and expert. Interactive workflows with a large toolbox.	essentials and notebooks.
	VS Code 123 Streamline de exists with support for development controls tille debugging, task running and venion control.					
	Install					

Jupyter Notebook is launched and is launched via google chrome browser as its base platform.

# 2 Data Extraction

The skin lesion image dataset of HAM10000 (Human-Against-Machine 10000) was downloaded from the Dataverse website of Harvard University (Tschandl et al., 2018).



As the dataset consists of a skewed representation of images in multiple classes, image augmentation becomes necessary to reduce the degree of skewness in image class representation.

## **3** Data Preprocessing

Launch Jupyter Notebook from **Start -> Anaconda Navigator** to open up the browser based python platform. Execute the python file with the pre-processing and data augmentation code.

## 4 Library Installation

A few libraries need to be installed as part of the requirements for the CNN for image classification task. Tensorflow is installed to begin satisfying the environment for CNN architecture.

```
conda create -n tf tensorflow
conda activate tf
```

Tensorflow includes the packages required for building the models discussed in this research.

# 5 Code Listing

#### Data pre-processing and augmentation

```
from numpy.random import seed
seed(101)
from tensorflow import set_random_seed
set_random_seed(101)
import pandas as pd
import numpy as np
#import keras
#from keras import backend as K
import tensorflow as tf
from tensorflow.keras.layers import Dense, Dropout
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.metrics import categorical_crossentropy
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.models import Model
from tensorflow.keras.callbacks import EarlyStopping, ReduceLROnPlateau, ModelCheckpoint
import os
from sklearn.metrics import confusion_matrix
from sklearn.model_selection import train_test_split
import itertools
import shutil
import matplotlib.pyplot as plt
%matplotlib inline
#Libraries for building the model
import keras
from keras import backend as K
from keras.models import Sequential
from keras.layers import Activation
from keras.layers.core import Dense,Flatten
from keras.optimizers import Adam
from keras.metrics import categorical_crossentropy
from keras.preprocessing.image import ImageDataGenerator
from keras.layers.normalization import BatchNormalization
from keras.layers.convolutional import
from matplotlib import pyplot as plt
import itertools
import matplotlib.pyplot as plt
%matplotlib inline
from keras import optimizers
Using TensorFlow backend.
```

```
# Create a new directory
base_dir = 'G:\\Skin Cancer image dataset\\base_dir'
os.mkdir(base_dir)
#[CREATE FOLDERS INSIDE THE BASE DIRECTORY]
# now we create 7 folders inside 'base dir':
# train dir
    # nevi
    # melanoma
    # bkerat
    # basalcarc
    # akerat
    # vascular
    # defibr
# val_dir
    # nevi
    # melanoma
    # bkerat
    # basalcard
    # akerat
    # vascular
    # defibr
# create a path to 'base_dir' to which we will join the names of the new folders
# train_dir
train_dir = os.path.join(base_dir, 'train_dir')
os.mkdir(train_dir)
# val_dir
val_dir = os.path.join(base_dir, 'val_dir')
os.mkdir(val_dir)
# [CREATE FOLDERS INSIDE THE TRAIN, VALIDATION AND TEST FOLDERS]
# Inside each folder we create seperate folders for each class
# create new folders inside train_dir
nv = os.path.join(train_dir, 'nv')
os.mkdir(nv)
mel = os.path.join(train dir, 'mel')
os.mkdir(mel)
bkl = os.path.join(train_dir, 'bkl')
os.mkdir(bkl)
bcc = os.path.join(train_dir, 'bcc')
os.mkdir(bcc)
akiec = os.path.join(train_dir, 'akiec')
os.mkdir(akiec)
vasc = os.path.join(train_dir, 'vasc')
os.mkdir(vasc)
df = os.path.join(train_dir, 'df')
os.mkdir(df)
# create new folders inside val_dir
nv = os.path.join(val_dir, 'nv')
os.mkdir(nv)
mel = os.path.join(val_dir, 'mel')
os.mkdir(mel)
bkl = os.path.join(val_dir, 'bkl')
os.mkdir(bkl)
bcc = os.path.join(val_dir, 'bcc')
os.mkdir(bcc)
akiec = os.path.join(val_dir, 'akiec')
os.mkdir(akiec)
vasc = os.path.join(val_dir, 'vasc')
os.mkdir(vasc)
df = os.path.join(val_dir, 'df')
os.mkdir(df)
```

```
df_data = pd.read_csv('HAM10000_metadata.csv')
```

```
df_data.head()
```

```
# this will tell us how many images are associated with each lesion_id
df = df_data.groupby('lesion_id').count()
```

# now we filter out lesion\_id's that have only one image associated with it df = df[df['image\_id'] == 1]

df.reset\_index(inplace=True)

df.head()

lesion	id	image id	dv	dy type	ane	COY.	localization
1031011	TU .	iniugo iu	UA.	UN LYPE	uyo	304	locultulloll

0	HAM_0000001	1	1	1	1	1	1
1	HAM_0000003	1	1	1	1	1	1
2	HAM_0000004	1	1	1	1	1	1
3	HAM_0000007	1	1	1	1	1	1
4	HAM 0000008	1	1	1	1	1	1

# here we identify lesion\_id's that have duplicate images and those that have only # one image.

```
def identify_duplicates(x):
```

unique\_list = list(df['lesion\_id'])

```
if x in unique_list:
    return 'no_duplicates'
else:
    return 'has_duplicates'
```

```
# create a new colum that is a copy of the lesion_id column
df_data['duplicates'] = df_data['lesion_id']
# apply the function to this new column
df_data['duplicates'] = df_data['duplicates'].apply(identify_duplicates)
```

df\_data.head()

df\_data['duplicates'].value\_counts()

no\_duplicates 5514
has\_duplicates 4501
Name: duplicates, dtype: int64

```
# now we filter out images that don't have duplicates
df = df_data[df_data['duplicates'] == 'no_duplicates']
```

df.shape

(5514, 8)

```
# now we create a val set using df because we are sure that none of these images # have augmented duplicates in the train set y = df['dx']
```

\_, df\_val = train\_test\_split(df, test\_size=0.17, random\_state=101, stratify=y)

df\_val.shape

(938, 8)

df\_val['dx'].value\_counts()

 nv
 751

 bkl
 75

 mel
 39

 bcc
 30

 akiec
 26

 vasc
 11

 df
 6

 Name:
 dx, dtype: int64

```
# This set will be df_data excluding all rows that are in the val set
# This function identifies if an image is part of the train
# or val set.
def identify_val_rows(x):
    # create a list of all the lesion_id's in the val set
    val_list = list(df_val['image_id'])
```

```
if str(x) in val_list:
    return 'val'
else:
    return 'train'
```

# identify train and val rows

```
# create a new colum that is a copy of the image_id column
df_data['train_or_val'] = df_data['image_id']
# apply the function to this new column
df_data['train_or_val'] = df_data['train_or_val'].apply(identify_val_rows)
# filter out train rows
df_train = df_data[df_data['train_or_val'] == 'train']
```

```
print(len(df_train))
print(len(df_val))
```

9077 938

```
df_train['dx'].value_counts()
```

nv 5954 mel 1074 bkl 1024 bcc 484 akiec 301 vasc 131 df 109 Name: dx, dtype: int64

df\_val['dx'].value\_counts()

nv 751 bkl 75 mel 39 bcc 30 akiec 26 vasc 11 df 6 Name: dx, dtype: int64

```
# Set the image_id as the index in df_data
df_data.set_index('image_id', inplace=True)
```

```
#train_dir = os.path.join(base_dir, 'train_dir')
```

```
# Get a list of images in each of the two folders
folder_1 = os.listdir('ham10000_images_part_1')
folder_2 = os.listdir('ham10000_images_part_2')
```

```
# Get a list of train and val images
train_list = list(df_train['image_id'])
val_list = list(df_val['image_id'])
```

```
# Transfer the train images
```

for image in train\_list:

fname = image + '.jpg'
label = df\_data.loc[image,'dx']

if fname in folder\_1:
 # source path to image

```
src = os.path.join('ham10000_images_part_1', fname)
# destination path to image
dst = os.path.join(train_dir, label, fname)
# copy the image from the source to the destination
shutil.copyfile(src, dst)
```

```
if fname in folder 2:
         # source path to image
         src = os.path.join('ham10000_images_part_2', fname)
         # destination path to image
         dst = os.path.join(train_dir, label, fname)
         # copy the image from the source to the destination
shutil.copyfile(src, dst)
# Transfer the val images
for image in val_list:
     fname = image + '.jpg'
    label = df_data.loc[image,'dx']
    if fname in folder_1:
         # source path to image
src = os.path.join('ham10000_images_part_1', fname)
         # destination path to image
         dst = os.path.join(val_dir, label, fname)
         # copy the image from the source to the destination
         shutil.copyfile(src, dst)
    if fname in folder 2:
         # source path to image
         src = os.path.join('ham10000_images_part_2', fname)
         # destination path to image
         dst = os.path.join(val_dir, label, fname)
        # copy the image from the source to the destination
shutil.copyfile(src, dst)
# note that we are not augmenting class 'nv'
class_list = ['mel', 'bkl', 'bcc', 'akiec', 'vasc', 'df']
for item in class_list:
    print(item)
    print("\n")
    # We are creating temporary directories here because we delete these directories later
    # create a base dir
    aug_dir = 'aug_dir'
    os.mkdir(aug_dir)
    # create a dir within the base dir to store images of the same class
img_dir = os.path.join(aug_dir, 'img_dir')
    os.mkdir(img_dir)
    # Choose a class
    img_class = item
    # list all images in that directory
img_list = os.listdir('base_dir/train_dir/' + img_class)
    # Copy images from the class train dir to the img_dir e.g. class 'mel'
    for fname in img_list:
             # source path to image
             src = os.path.join('base_dir/train_dir/' + img_class, fname)
              # destination path to image
             dst = os.path.join(img_dir, fname)
              # copy the image from the source to the destination
             shutil.copyfile(src, dst)
    # point to a dir containing the images and not to the images themselves
    path = aug_dir
    save_path = 'base dir/train_dir/' + img_class
    # Create a data generator
    datagen = ImageDataGenerator(
         rotation_range=180,
         width_shift_range=0.1,
         height_shift_range=0.1,
         zoom_range=0.1,
         horizontal_flip=True,
         vertical_flip=True,
        #brightness_range=(0.9,1.1),
fill_mode='nearest')
```

```
batch_size = 50
    aug_datagen = datagen.flow_from_directory(path,
                                                save_to_dir=save_path,
save_format='jpg',
target_size=(224,224),
                                                           batch_size=batch_size)
    # Generate the augmented images and add them to the training folders
    #############
    num_aug_images_wanted = 6000 # total number of images we want to have in each class
    num_files = len(os.listdir(img_dir))
num_batches = int(np.ceil((num_aug_images_wanted-num_files)/batch_size))
    # run the generator and create about 6000 augmented images
for i in range(0,num_batches):
         imgs, labels = next(aug_datagen)
    # delete temporary directory with the raw image files
shutil.rmtree('aug_dir')
mel
Found 1074 images belonging to 1 classes.
bk]
Found 1024 images belonging to 1 classes.
bcc
Found 484 images belonging to 1 classes.
akiec
Found 301 images belonging to 1 classes.
vasc
vasc
Found 131 images belonging to 1 classes.
df
Found 109 images belonging to 1 classes.
# Check how many train images we now have in each folder.
# This is the original images plus the augmented images.
```

```
print(len(os.listdir('base_dir/train_dir/nv')))
print(len(os.listdir('base_dir/train_dir/mel')))
print(len(os.listdir('base_dir/train_dir/bkl')))
print(len(os.listdir('base_dir/train_dir/bcc')))
print(len(os.listdir('base_dir/train_dir/vasc')))
print(len(os.listdir('base_dir/train_dir/vasc')))
print(len(os.listdir('base_dir/train_dir/df')))
```

```
# Check how many val images we have in each folder.
print(len(os.listdir('base_dir/val_dir/nv')))
print(len(os.listdir('base_dir/val_dir/bkl')))
print(len(os.listdir('base_dir/val_dir/bcc')))
print(len(os.listdir('base_dir/val_dir/kkiec')))
print(len(os.listdir('base_dir/val_dir/vasc')))
print(len(os.listdir('base_dir/val_dir/df')))
```

751

39 75

30

26 11

6

#### **CNN with MobileNet model**

```
train_path = 'base_dir/train_dir'
valid_path = 'base_dir/val_dir'
num train samples = len(df train)
num_val_samples = len(df_val)
train batch size = 10
val_batch_size = 10
image_size = 224
train_steps = np.ceil(num_train_samples / train_batch_size)
val_steps = np.ceil(num_val_samples / val_batch_size)
datagen = ImageDataGenerator(
    preprocessing_function=
    tf.keras.applications.mobilenet.preprocess input)
train_batches = datagen.flow_from_directory(train_path,
                                            target_size=(image_size,image_size),
                                            batch_size=train_batch_size)
valid_batches = datagen.flow_from_directory(valid_path,
                                            target_size=(image_size,image_size),
                                            batch_size=val_batch_size)
# Note: shuffle=False causes the test dataset to not be shuffled
test_batches = datagen.flow_from_directory(valid_path,
                                            target_size=(image_size,image_size),
                                            batch_size=1,
                                            shuffle=False)
Found 38569 images belonging to 7 classes.
Found 938 images belonging to 7 classes.
Found 938 images belonging to 7 classes.
# create a copy of a InceptionV3 model
mobile = tf.keras.applications.mobilenet.MobileNet()
mobile.summary()
Model: "mobilenet_1.00_224"
                           Output Shape
Layer (type)
                                                      Param #
             ------
input_2 (InputLayer)
                           [(None, 224, 224, 3)]
                                                      0
conv1 pad (ZeroPadding2D)
                           (None, 225, 225, 3)
                                                       0
                            (None, 112, 112, 32)
                                                       864
conv1 (Conv2D)
conv1_bn (BatchNormalization (None, 112, 112, 32)
                                                       128
conv1_relu (ReLU)
                             (None, 112, 112, 32)
                                                       0
```

conv\_dw\_1\_relu (ReLU)

type(mobile.layers)

list

# To find out how many layers MobileNet model has. len(mobile.layers)

conv\_dw\_1 (DepthwiseConv2D) (None, 112, 112, 32)

conv\_dw\_1\_bn (BatchNormaliza (None, 112, 112, 32)

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# CREATE THE MODEL ARCHITECTURE

# Exclude the last 5 layers of the above model.

# This will include all layers up to and including global\_average\_pooling2d\_1

(None, 112, 112, 32)

x = mobile.layers[-6].output

288

128

0

```
# Create a new dense layer for predictions
# 7 corresponds to the number of classes
x = Dropout(0.25)(x)
predictions = Dense(7, activation='softmax')(x)
# inputs=mobile.input selects the input layer, outputs=predictions refers to the
# dense layer we created above.
model = Model(inputs=mobile.input, outputs=predictions)
model.summary()
Model: "model_1"
Layer (type)
                             Output Shape
                                                       Param #
            _____
                                         -------
                                                     0
input_2 (InputLayer)
                            [(None, 224, 224, 3)]
conv1_pad (ZeroPadding2D) (None, 225, 225, 3)
                                                       0
```

conv1 (Conv2D)	(None,	112,	112,	32)	864
conv1_bn (BatchNormalization	(None,	112,	112,	32)	128
conv1_relu (ReLU)	(None,	112,	112,	32)	0
conv_dw_1 (DepthwiseConv2D)	(None,	112,	112,	32)	288
conv_dw_1_bn (BatchNormaliza	(None,	112,	112,	32)	128
conv_dw_1_relu (ReLU)	(None,	112,	112,	32)	0

# We need to choose how many layers we actually want to be trained.

- # Here we are freezing the weights of all layers except the
- # Last 23 Layers in the new model.
  # The last 23 layers of the model will be trained.
- for layer in model.layers[:-23]: layer.trainable = False

```
# Define Top2 and Top3 Accuracy
```

from tensorflow.keras.metrics import categorical\_accuracy, top\_k\_categorical\_accuracy

```
def top_3_accuracy(y_true, y_pred):
    return top_k_categorical_accuracy(y_true, y_pred, k=3)
```

```
def top_2_accuracy(y_true, y_pred):
   return top_k_categorical_accuracy(y_true, y_pred, k=2)
```

model.compile(Adam(lr=0.01), loss='categorical\_crossentropy', metrics=[categorical\_accuracy, top\_2\_accuracy, top\_3\_accuracy])

```
# Get the labels that are associated with each index
print(valid_batches.class_indices)
```

```
{'akiec': 0, 'bcc': 1, 'bkl': 2, 'df': 3, 'mel': 4, 'nv': 5, 'vasc': 6}
```

# Add weights to try to make the model more sensitive to melanoma

```
class_weights={
   0: 1.0, # akiec
    1: 1.0, # bcc
    2: 1.0, # bkl
    3: 1.0, # df
    4: 3.0, # mel # Try to make the model more sensitive to Melanoma.
    5: 1.0, # nv
    6: 1.0, # vasc
3
```

```
filepath = "tf mobilenet model.h5"
checkpoint = ModelCheckpoint(filepath, monitor='val_top_3_accuracy', verbose=1,
                            save_best_only=True, mode='max')
reduce_lr = ReduceLROnPlateau(monitor='val_top_3_accuracy', factor=0.5, patience=2,
                                 verbose=1, mode='max', min lr=0.00001)
earlyStopping = EarlyStopping(monitor='val_top_3_accuracy', min_delta=0, patience=20, verbose=1,
                             mode='auto', baseline=None)
#callbacks list = [checkpoint, reduce lr]
callbacks list = [checkpoint, reduce lr, earlyStopping]
history = model.fit_generator(train_batches, steps_per_epoch=train_steps,
                             class_weight=class_weights,
                   validation_data=valid_batches,
                   validation_steps=val_steps,
                   epochs=30, verbose=1,
                  callbacks=callbacks_list)
# history = model.fit_generator(train_batches, steps_per_epoch=train_steps,
                     class_weight=class_weights,
validation_data=valid_batches,
#
#
                     validation_steps=val_steps,
                     epochs=30, verbose=1,
#
                    callbacks=callbacks list)
#
Epoch 1/30
907/908 [===================>.] - ETA: 30s - loss: 1.7417 - categorical_accuracy: 0.5125 - top_2_accuracy: 0.7187 -
top_3_accuracy: 0.8393 Epoch 1/30
94/908 [==>.....] - ETA: 6:15 - loss: 4.0213 - categorical_accuracy: 0.0554 - top_2_accuracy: 0.6397 -
top_3_accuracy: 0.8475
Epoch 00001: val_top_3_accuracy improved from -inf to 0.84755, saving model to tf_mobilenet_model.h5
7189 - top_3_accuracy: 0.8395 - val_loss: 4.0213 - val_categorical_accuracy: 0.0554 - val_top_2_accuracy: 0.6397 - val_top_3_
accuracy: 0.8475
Epoch 2/30
907/908 [=======>.] - ETA: 0s - loss: 1.2743 - categorical_accuracy: 0.6094 - top_2_accuracy: 0.8033 - t
op_3_accuracy: 0.9077Epoch 1/30
94/908 [==>.....] - ETA: 6:45 - loss: 1.0943 - categorical_accuracy: 0.6173 - top_2_accuracy: 0.8284 - top_3_accuracy: 0.9062
Epoch 00002: val_top_3_accuracy improved from 0.84755 to 0.90618, saving model to tf_mobilenet_model.h5
8033 - top_3_accuracy: 0.9077 - val_loss: 1.0943 - val_categorical_accuracy: 0.6173 - val_top_2_accuracy: 0.8284 - val_top_3_
accuracy: 0.9062
# Here the the last epoch will be used.
val_loss, val_cat_acc, val_top_2_acc, val_top_3_acc = \
model.evaluate_generator(test_batches,
                      steps=len(df_val))
print('val_loss:', val_loss)
print('val_cat_acc:', val_cat_acc)
print('val_top_2_acc:', val_top_2_acc)
print('val_top_3_acc:', val_top_3_acc)
val_loss: 0.5601274718238453
val_cat_acc: 0.8240938
val_top_2_acc: 0.9157783
val_top_3_acc: 0.9637527
# Here the best epoch will be used.
model.load weights('tf mobilenet model.h5')
val_loss, val_cat_acc, val_top_2_acc, val_top_3_acc = \
model.evaluate_generator(test_batches,
                      steps=len(df_val))
print('val_loss:', val_loss)
print('val_cat_acc:', val_cat_acc)
print('val_top_2_acc:', val_top_2_acc)
print('val_top_3_acc:', val_top_3_acc)
val loss: 0.4359079395809308
```

val\_ios.co.co.sosososo val\_cat\_acc: 0.8507463 val\_top\_2\_acc: 0.93070364 val\_top\_3\_acc: 0.97121537

```
# display the loss and accuracy curves
import matplotlib.pyplot as plt
acc = history.history['categorical_accuracy']
val_acc = history.history['val_categorical_accuracy']
loss = history.history['loss']
val_loss = history.history['val_loss']
val_top2_acc = history.history['val_top2_accuracy']
val_top2_acc = history.history['val_top2_accuracy']
train_top3_acc = history.history['top3_accuracy']
val_top3_acc = history.history['val_top3_accuracy']
epochs = range(1, len(acc) + 1)
plt.plot(epochs, loss, 'bo', label='Training loss')
plt.plot(epochs, val_loss, 'b', label='Validation loss')
plt.title('Training and validation loss')
plt.legend()
plt.figure()
plt.plot(epochs, acc, 'bo', label='Training cat acc')
plt.plot(epochs, val_acc, 'b', label='Validation cat acc')
plt.title('Training and validation cat accuracy')
plt.legend()
plt.figure()
plt.plot(epochs, train_top2_acc, 'bo', label='Training top2 acc')
plt.plot(epochs, val_top2_acc, 'b', label='Validation top2 acc')
plt.title('Training and validation top2 accuracy')
plt.legend()
plt.figure()
plt.plot(epochs, train_top3_acc, 'bo', label='Training top3 acc')
plt.plot(epochs, val_top3_acc, 'b', label='Validation top3 acc')
plt.title('Training and validation top3 accuracy')
plt.legend()
plt.show()
#Optimiser
sgd = tf.keras.optimizers.SGD(lr=0.01, decay=1e-6, momentum=0.9, nesterov=True)
#Compile the model
```

# 

#### **CNN with DenseNet201 model**

Found 38569 images belonging to 7 classes. Found 938 images belonging to 7 classes. Found 938 images belonging to 7 classes. # create a copy of a InceptionV3 model

# densenet = tf.keras.applications.DenseNet201.DenseNet201()

densenet = tf.compat.v1.keras.applications.densenet.DenseNet201()

Downloading data from https://github.com/keras-team/keras-applications/releases/download/densenet/densenet201\_weights\_tf\_dim\_or dering\_tf\_kernels.h5 82526208/82524592 [=====] - 53s lus/step

densenet.summary()

Model: "densenet201"

Layer (type)	Output Shape	Param #	Connected to
input_3 (InputLayer)	[(None, 224, 224, 3)	0	
zero_padding2d (ZeroPadding2D)	(None, 230, 230, 3)	0	input_3[0][0]
conv1/conv (Conv2D)	(None, 112, 112, 64)	9408	zero_padding2d[0][0]
conv1/bn (BatchNormalization)	(None, 112, 112, 64)	256	conv1/conv[0][0]
conv1/relu (Activation)	(None, 112, 112, 64)	0	conv1/bn[0][0]
 zero_padding2d_1 (ZeroPadding2D	(None, 114, 114, 64)	0	conv1/relu[0][0]
pool1 (MaxPooling2D)	(None, 56, 56, 64)	0	zero_padding2d_1[0][0]
conv2_block1_0_bn (BatchNormali	(None, 56, 56, 64)	256	pool1[0][0]

type(densenet.layers)

pool1 (MaxPooling2D)

list

# How many layers does InceptionV3 have? len(densenet.layers)

709

# CREATE THE MODEL ARCHITECTURE

# Exclude the last 2 layers of the above model. # This will include all layers up to and including global\_average\_pooling2d\_1 x = densenet.layers[-2].output # Create a new dense layer for predictions # 7 corresponds to the number of classes x = Dropout(0.25)(x) predictions = Dense(7, activation='softmax')(x) # inputs=densenet.input selects the input layer, outputs=predictions refers to the # dense layer we created above. model = Model(inputs=densenet.input, outputs=predictions) model.summary() Model: "model\_17" Layer (type) Output Shape Param # Connected to ----input\_3 (InputLayer) [(None, 224, 224, 3) 0 zero\_padding2d (ZeroPadding2D) (None, 230, 230, 3) 0 input\_3[0][0] conv1/conv (Conv2D) (None, 112, 112, 64) 9408 zero\_padding2d[0][0] conv1/bn (BatchNormalization) (None, 112, 112, 64) 256 conv1/conv[0][0] conv1/relu (Activation) (None, 112, 112, 64) 0 conv1/bn[0][0] zero\_padding2d\_1 (ZeroPadding2D (None, 114, 114, 64) 0 conv1/relu[0][0]

(None, 56, 56, 64) 0

conv2\_block1\_0\_bn (BatchNormali (None, 56, 56, 64) 256

13

zero\_padding2d\_1[0][0]

pool1[0][0]

```
filepath = "tf_densenet2_model.h5"
earlyStopping = EarlyStopping(monitor='val_top_3_accuracy', min_delta=0, patience=20, verbose=1,
                          mode='auto', baseline=None)
#callbacks_list = [checkpoint, reduce_lr]
callbacks_list = [checkpoint, reduce_lr, earlyStopping]
history = model.fit_generator(train_batches, steps_per_epoch=train_steps,
                          class_weight=class_weights,
                 validation_data=valid_batches,
                 validation_steps=val_steps,
                 epochs=30, verbose=1,
                callbacks=callbacks_list)
# history = model.fit_generator(train_batches, steps_per_epoch=train_steps,
# class_weight=class_weights,
# validation_data=valid_batches,
#
                   validation_steps=val_steps,
#
                   epochs=30, verbose=1,
#
                  callbacks=callbacks list)
```

#### **Custom built CNN**

import numpy as np import pandas as pd import imageio from sklearn.model\_selection import train\_test\_split from sklearn.metrics import confusion\_matrix, precision\_recall\_fscore\_support import scipy.ndimage from scipy import misc import skimage import seaborn as sns import matplotlib.pyplot as plt %matplotlib inline plt.style.use('fivethirtyeight') from tadm import tadm from glob import glob from scipy import stats from sklearn.preprocessing import LabelEncoder, StandardScaler from imblearn.under\_sampling import RandomUnderSampler import keras import tensorflow as tf from keras.utils import to\_categorical from keras.layers import Dense, Input, Flatten, Reshape, Conv2D, MaxPool2D, concatenate, Activation, Dropout from keras.optimizers import Adam, RMSprop from keras.models import Model, Sequential, load\_model from keras.losses import binary\_crossentropy from keras.metrics import binary\_accuracy from keras.callbacks import ModelCheckpoint from keras.preprocessing.image import ImageDataGenerator Using TensorFlow backend. %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.metrics import confusion\_matrix import itertools import keras from keras import regularizers 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 from sklearn.model\_selection import train\_test\_split from keras.preprocessing.image import ImageDataGenerator

os.chdir('G:\\Skin cancer dataset')

base\_skin\_dir = os.path.join('G:\\Skin cancer dataset')
# Merge images from both folders into one dictionary
imageid\_path\_dict = {os.path.splitext(os.path.basename(x))[0]: x
for x in glob(os.path.join(base\_skin\_dir, '\*', '\*.jpg'))}
# This dictionary is useful for displaying more human-friendly labels later on
lesion\_type\_dict = {
 'nv': 'Melanocytic nevi',
 'mel': 'Melanoma',
 'bkl': 'Benign keratosis-like lesions ',
 'bcc': 'Basal cell carcinoma',
 'akiec': 'Actinic keratoses',
 'vasc': 'Vascular lesions',
 'df': 'Dermatofibroma'
}

# Read in the csv of metadata

```
tile_df = pd.read_csv(os.path.join(base_skin_dir, 'HAM10000_metadata.csv'))
tile_df.tail()
# Create some new columns (path to image, human-readable name) and review them
tile_df['path'] = tile_df['image_id'].map(imageid_path_dict.get)
```

tile\_df['path'] = tile\_df['image\_id'].map(imageid\_path\_dict.get) tile\_df['cell\_type'] = tile\_df['dx'].map(lesion\_type\_dict.get) tile\_df['cell\_type\_idx'] = pd.Categorical(tile\_df['cell\_type']).codes tile\_df.sample(5)

	lesion_id	image_id	dx	dx_type	age	sex	localization	path	cell_type	cell_type_idx
9725	HAM_0004376	ISIC_0024843	akiec	histo	70.0	female	face	G:\Skin cancer dataset\HAM10000_images_part_1\	Actinic keratoses	0
6059	HAM_0003024	ISIC_0024768	nv	follow_up	35.0	female	trunk	G:\Skin cancer dataset\HAM10000_images_part_1\	Melanocytic nevi	4
4540	HAM_0001659	ISIC_0026564	nv	follow_up	35.0	male	lower extremity	G:\Skin cancer dataset\HAM10000_images_part_1\	Melanocytic nevi	4
3817	HAM_0004625	ISIC_0029346	nv	follow_up	40.0	male	upper extremity	G:\Skin cancer dataset\HAM10000_images_part_2\	Melanocytic nevi	4
7914	HAM_0000443	ISIC_0034271	nv	histo	35.0	female	back	G:\Skin cancer dataset\HAM10000_images_part_2\	Melanocytic nevi	4

# Get general statistics for the dataset

tile\_df.describe(exclude=[np.number])

# See the image size distribution - should just return one row (all images are uniform)
tile\_df['image'].map(lambda x: x.shape).value\_counts()

(32, 32, 3) 10015 Name: image, dtype: int64

```
y = tile_df.cell_type_idx
x_train_o, x_test_o, y_train_o, y_test_o = train_test_split(tile_df, y, test_size=0.25)
```

```
#Model Architecture
model = Sequential()
model.add(Conv2D(96, (9, 9), input_shape = (232, 232, 3), activation = 'relu'))
model.add(Conv2D(64, (5, 5), activation = 'relu'))
model.add(Conv2D(64, (5, 5), activation = 'relu'))
model.add(Conv2D(64, (3, 3), activation = 'relu'))
model.add(MaxPooling2D(pool_size = (3, 3)))
model.add(Flatten())
model.add(Dense(units = 128, activation = 'relu'))
model.add(Dense(units = 7, activation = 'softmax'))
model.summary()
```

x\_train = np.asarray(x\_train\_o['image'].tolist())
x\_test = np.asarray(x\_test\_o['image'].tolist())

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

x\_test\_mean = np.mean(x\_test)
x\_test\_std = np.std(x\_test)

y\_train = to\_categorical(y\_train\_o, num\_classes = 7)
y\_test = to\_categorical(y\_test\_o, num\_classes = 7)

```
input_shape = (32, 32, 3)
num_classes = 7
batch_size = 32
epochs = 50
```

model.summary()

Layer (type)	Output	Shape	Param #
conv2d_29 (Conv2D)	(None,	30, 30, 32)	896
conv2d_30 (Conv2D)	(None,	28, 28, 64)	18496
max_pooling2d_17 (MaxPooling	(None,	14, 14, 64)	0
dropout_25 (Dropout)	(None,	14, 14, 64)	0
conv2d_31 (Conv2D)	(None,	12, 12, 64)	36928
max_pooling2d_18 (MaxPooling	(None,	6, 6, 64)	0
dropout_26 (Dropout)	(None,	6, 6, 64)	0
flatten_9 (Flatten)	(None,	2304)	0
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model.summary()

#### 

model.summary()

Layer (type)	Output	Shape	Param #
conv2d_29 (Conv2D)	(None,	30, 30, 32)	896
conv2d_30 (Conv2D)	(None,	28, 28, 64)	18496
max_pooling2d_17 (MaxPooling	(None,	14, 14, 64)	0
dropout_25 (Dropout)	(None,	14, 14, 64)	0
conv2d_31 (Conv2D)	(None,	12, 12, 64)	36928
	(None,	6, 6, 64)	0
dropout_26 (Dropout)	(None,	6, 6, 64)	0
flatten_9 (Flatten)	(None,	2304)	0
dense_17 (Dense)	(None,	128)	295040
dropout_27 (Dropout)	(None,	128)	0
dense_18 (Dense)	(None,	7)	903
Total params: 352,263 Trainable params: 352,263 Non-trainable params: 0			

Train on 7511 samples, validate on 2504 samples Epoch 1/50

```
score = model.evaluate(x_test, y_test, verbose=0)
print('Test loss:', score[0])
print('Test accuracy:', score[1])
```

Test loss: 0.8282977995781091 Test accuracy: 0.7567891373801917

```
fig, ax = plt.subplots(2,1)
ax[0].plot(history.history['loss'], color='b', label="Training loss")
ax[0].plot(history.history['val_loss'], color='r', label="Validation loss",axes =ax[0])
legend = ax[0].legend(loc='best', shadow=True)
ax[1].plot(history.history['acc'], color='b', label="Training accuracy")
```

```
ax[1].plot(history.history['acc'], color='b', label="Training accuracy")
ax[1].plot(history.history['val_acc'], color='r',label="Validation accuracy")
legend = ax[1].legend(loc='best', shadow=True)
```

model.summary()

# 6 Results

### MobileNet model using Adam parameter



# **Optimization of MobileNet model using SGD parameter**



### DenseNet201 using Adam parameter



#### **DenseNet201 using SGD parameter**



# Custom built CNN using Adam parameter



Custom built CNN using SGD parameter



# References

Matplotlib: Python plotting Matplotlib 3.1.1 documentation (n.d.).

URL: https://matplotlib.org/

Tschandl, P., Rosendahl, C. and Kittler, H., 2018. The HAM10000 dataset, a large collection of multi-source dermatoscopic images of common pigmented skin lesions. Scientific data, 5, p.180161.

URL: https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/DBW86T

NumPy NumPy (n.d.). URL: https://www.numpy.org/

Python Data Analysis Library pandas: Python Data Analysis Library (n.d.). URL: https://pandas.pydata.org/

scikit-learn: machine learning in Python scikit-learn 0.21.3 documentation (n.d.). URL: https://scikit-learn.org/stable/

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