https://github.com/wmadisonf/CNN-Dermoscopic-Image-Classification_HAM10000

```
In [1]: import tensorflow as tf
    print('Default GPU Device: {}'.format(tf.test.gpu_device_name()))
    print('TensorFlow Version: {}'.format(tf.__version__))
Default GPU Device: /device:GPU:0
```

This notebook was run on a laptop with a GTX 1070 GPU

TensorFlow Version: 2.0.0

GPU:0 with 6372 MB memory) -> physical GPU (device: 0, name: GeForce GTX 1070, compute capability: 6.1)

Table of Contents

- 1. Load Libraries
- 2. Read & Process Data
 - 2.1 Look inside HAM1000 directory
 - 2.2 Read metadata and encode lables
- 3. Merge image folders and create lesion type dictionary
- 4. Add New Columns
- 5. Clean Data
 - 5.2 Check for missing values indicated in ham_df.info()
 - 5.3 Use mean of age to fill age missing values
- 6. Exploratory Data Analysis (EDA)
 - 6.1 Cell Type Count
- 7. Resize Images
 - 7.1 Compare image size characteristics
 - 7.2 Resize Images for Model Input
 - 7.3 A sample of skin lesion images
- 8. Preprocess
 - 8.1 Train Test Validate
 - 8.1.1 Split: train / test = 80 / 20
 - 8.1.2 Change to a Numpy array
 - 8.1.3 Standardize
 - 8.1.4 One-hot encoding: Convert output to categorical crossentropy
 - 8.1.5 Split: train / validation = 0.87 / 0.13
 - 8.1.6 Reshape images to 3 dimensions
- 9. Test Model (modelT)
 - 9.1 Test Model Architecture
 - 9.2 Set the learning rate reduction and add data augumentation to the Test M
 - 9.2.1 Train modelT with Augmentation
 - 9.2.2 Evaluate Test Model Test Accuracy and Loss
 - 9.2.3 Test Model Accuracy and Loss Plots after Augumentation
- 10. Final Model
 - 10.1 Table 1 (Scores all runs)
 - 10.2 CNN Model Architecture
 - 10.3 Set Learning Rate and Augmentation
 - 10.4 Model Fit

```
10.5 Scoring10.6 Accuracy and Loss Plots11. All 5 Model 4 Runs/font>
```

1. Load Libraries

```
In [2]: import numpy as np
np.random.seed(1236)

# https://www.tensorflow.org/api_docs/python/tf/random/set_seed
import tensorflow as tf
tf.random.set_seed(1236)
```

```
In [3]: # Use %matplotlib inline to enable effective coordination between Jupyter and matplotlib and display within t
        he notebook
        %matplotlib inline
        import os
        import sys
        import pandas as pd
        import matplotlib.pyplot as plt
        import keras
        from keras import backend as K
        from keras.models import Sequential
        from keras.layers import Dense, Activation, Flatten, Dropout, Conv2D, MaxPooling2D #, GlobalAveragePooling2D
        from keras import optimizers
        from keras.optimizers import Adam #, SGD
        from keras.layers.normalization import BatchNormalization
        from keras.metrics import categorical crossentropy
        from keras.utils.np utils import to categorical
        from keras.preprocessing.image import ImageDataGenerator
        from keras.models import Model
        from keras.callbacks import ReduceLROnPlateau #, EarlyStopping, ModelCheckpoint
        from keras.utils import plot model
        from keras.regularizers import 12 #, L1
        from keras import initializers #he normal
```

Using TensorFlow backend.

```
In [4]: import seaborn as sns
        from PIL import Image
        import sklearn as sk
        from sklearn.preprocessing import label binarize
        from sklearn.metrics import confusion matrix
        from sklearn.model selection import train test split
        from sklearn.preprocessing import LabelEncoder, StandardScaler
        from sklearn.metrics import classification report
        from sklearn import metrics
        import shutil
        import itertools
        from glob import glob
        from numpy.random import seed
        import pydot
        import time
        import cv2
```

In [5]: import autoreload %load_ext watermark %load_ext autoreload %autoreload 2 %watermark -a 'WForsythe' -d -t -v -p numpy,pandas,keras,sklearn,tensorflow,seaborn,cv2

WForsythe 2020-02-22 14:36:10

CPython 3.7.6
IPython 7.11.1

numpy 1.18.1
pandas 0.25.3
keras 2.3.1
sklearn 0.22.1
tensorflow 2.0.0
seaborn 0.9.0

cv2 4.2.0

2 Read & Process Data

2.1 Look inside HAM1000 directory

The only files and folders from the HAM10000 directory needed to complete this project were the two image folders and the metadata file.

```
In [5]: ham_folder = 'C:\HAM10000'
    print(os.listdir(ham_folder))

['HAM10000_images_part_1', 'HAM10000_images_part_2', 'HAM10000_metadata.csv', 'hmnist_28_28_L.csv', 'hmnist_8_8_RGB.csv']
```

2.2 Read metadata and encode lables

This operation includes creating a new column with dx labels converted to class numbers

```
In [6]: # Source: https://github.com/00chengh/Skin-Cancer-HAM10000/blob/master/Final%20Capstone%20-%20Skin%20Cancer.i
pynb
# Source: https://www.kaggle.com/sid321axn/step-wise-approach-cnn-model-77-0344-accuracy
# Source: https://www.kaggle.com/hashbanger/skin-lesion-identification

metadata = pd.read_csv('C:\HAM10000\HAM10000_metadata.csv')
print(metadata.shape)

lab_enc = LabelEncoder()
lab_enc.fit(metadata['dx'])
LabelEncoder()
print(list(lab_enc.classes_))

metadata['label'] = lab_enc.transform(metadata["dx"]) # Converts Labels to class numbers
metadata.head(15)
```

(10015, 7)
['akiec', 'bcc', 'bkl', 'df', 'mel', 'nv', 'vasc']

Out[6]:

	lesion_id	image_id	dx	dx_type	age	sex	localization	label
0	HAM_0000118	ISIC_0027419	bkl	histo	80.0	male	scalp	2
1	HAM_0000118	ISIC_0025030	bkl	histo	80.0	male	scalp	2
2	HAM_0002730	ISIC_0026769	bkl	histo	80.0	male	scalp	2
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp	2
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear	2
5	HAM_0001466	ISIC_0027850	bkl	histo	75.0	male	ear	2
6	HAM_0002761	ISIC_0029176	bkl	histo	60.0	male	face	2
7	HAM_0002761	ISIC_0029068	bkl	histo	60.0	male	face	2
8	HAM_0005132	ISIC_0025837	bkl	histo	70.0	female	back	2
9	HAM_0005132	ISIC_0025209	bkl	histo	70.0	female	back	2
10	HAM_0001396	ISIC_0025276	bkl	histo	55.0	female	trunk	2
11	HAM_0004234	ISIC_0029396	bkl	histo	85.0	female	chest	2
12	HAM_0004234	ISIC_0025984	bkl	histo	85.0	female	chest	2
13	HAM_0001949	ISIC_0025767	bkl	histo	70.0	male	trunk	2
14	HAM_0001949	ISIC_0032417	bkl	histo	70.0	male	trunk	2

3 Merge image folders and create lesion type dictionary

```
In [8]: # Source: https://github.com/00chengh/Skin-Cancer-HAM10000/blob/master/Final%20Capstone%20-%20Skin%20Cancer.i
        pynb
        # Source: https://www.kaggle.com/sid321axn/step-wise-approach-cnn-model-77-0344-accuracy
        # Source: https://www.kagale.com/hashbanger/skin-lesion-identification
        base folder = os.path.join('...', ham folder)
        # Merge image folders HAM10000 images part1 and HAM10000 images part2
        imageid_path_dict = {os.path.splitext(os.path.basename(x))[0]: x
                             for x in glob(os.path.join(base_folder, '*', '*.jpg'))}
        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'
```

4 Add New Columns

```
In [10]: # Source: https://github.com/00chengh/Skin-Cancer-HAM10000/blob/master/Final%20Capstone%20-%20Skin%20Cancer.i
pynb
# Source: https://www.kaggle.com/sid321axn/step-wise-approach-cnn-model-77-0344-accuracy
# Source: https://www.kaggle.com/hashbanger/skin-lesion-identification

ham_df = pd.read_csv(os.path.join(base_folder, 'HAM10000_metadata.csv'))

# Create new columns
ham_df['path'] = ham_df['image_id'].map(imageid_path_dict.get) # Map image paths to image_ids
ham_df['cell_type'] = ham_df['dx'].map(lesion_type_dict.get) # create cell type column from dx with full class
s names
ham_df['cell_type_idx'] = pd.Categorical(ham_df['cell_type']).codes # Convert cell type to categorical
```

In [11]: ham_df

Out[11]:

	lesion_id	image_id	dx	dx_type	age	sex	localization	path	cell_
0	HAM_0000118	ISIC_0027419	bkl	histo	80.0	male	scalp	C:\HAM10000\HAM10000_images_part_1\ISIC_002741	B kera le
1	HAM_0000118	ISIC_0025030	bkl	histo	80.0	male	scalp	C:\HAM10000\HAM10000_images_part_1\ISIC_002503	B kera le
2	HAM_0002730	ISIC_0026769	bkl	histo	80.0	male	scalp	C:\HAM10000\HAM10000_images_part_1\ISIC_002676	B kera le
3	HAM_0002730	ISIC_0025661	bkl	histo	80.0	male	scalp	C:\HAM10000\HAM10000_images_part_1\ISIC_002566	B kera le
4	HAM_0001466	ISIC_0031633	bkl	histo	75.0	male	ear	C:\HAM10000\HAM10000_images_part_2\ISIC_003163	B kera le
10010	HAM_0002867	ISIC_0033084	akiec	histo	40.0	male	abdomen	C:\HAM10000\HAM10000_images_part_2\ISIC_003308	A kera
10011	HAM_0002867	ISIC_0033550	akiec	histo	40.0	male	abdomen	C:\HAM10000\HAM10000_images_part_2\ISIC_003355	A kera
10012	HAM_0002867	ISIC_0033536	akiec	histo	40.0	male	abdomen	C:\HAM10000\HAM10000_images_part_2\ISIC_003353	Д kera
10013	HAM_0000239	ISIC_0032854	akiec	histo	80.0	male	face	C:\HAM10000\HAM10000_images_part_2\ISIC_003285	A kera
10014	HAM_0003521	ISIC_0032258	mel	histo	70.0	female	back	C:\HAM10000\HAM10000_images_part_2\ISIC_003225	Mela

10015 rows × 10 columns

```
In [12]: ham_df.dx.unique()
Out[12]: array(['bkl', 'nv', 'df', 'mel', 'vasc', 'bcc', 'akiec'], dtype=object)
```

5 Clean Data

5.1

```
In [13]: ham_df.info()
         <class 'pandas.core.frame.DataFrame'>
         RangeIndex: 10015 entries, 0 to 10014
         Data columns (total 10 columns):
         lesion id
                          10015 non-null object
         image_id
                          10015 non-null object
                          10015 non-null object
         dx
         dx_type
                          10015 non-null object
                           9958 non-null float64
         age
                          10015 non-null object
         sex
                          10015 non-null object
         localization
                           10015 non-null object
         path
         cell type
                          10015 non-null object
         cell type idx
                           10015 non-null int8
         dtypes: float64(1), int8(1), object(8)
         memory usage: 714.1+ KB
```

5.2 Check for missing values indicated in ham_df.info()

```
In [14]: ham_df.isnull().sum()
Out[14]: lesion_id
                            0
         image_id
                            0
          dx
         dx_type
                           57
          age
                            0
          sex
         localization
         path
         cell_type
         cell_type_idx
         dtype: int64
```

5.3 Use mean of age to fill age missing values

```
In [15]: ham_df['age'].fillna((ham_df['age'].mean()), inplace=True)
         ham_df.isnull().sum()
Out[15]: lesion_id
                           0
         image_id
                           0
          dx
         dx_type
          age
          sex
         localization
         path
         cell_type
                           0
         cell_type_idx
         dtype: int64
```

5.3.1 Re-check to make sure that all the data is present

```
In [16]: ham_df.info()
         <class 'pandas.core.frame.DataFrame'>
         RangeIndex: 10015 entries, 0 to 10014
         Data columns (total 10 columns):
         lesion id
                          10015 non-null object
         image id
                          10015 non-null object
         dx
                          10015 non-null object
         dx_type
                          10015 non-null object
                           10015 non-null float64
         age
         sex
                          10015 non-null object
         localization
                          10015 non-null object
                           10015 non-null object
         path
                          10015 non-null object
         cell type
         cell type idx
                           10015 non-null int8
         dtypes: float64(1), int8(1), object(8)
         memory usage: 714.1+ KB
```

6 Exploratory Data Analysis (EDA)

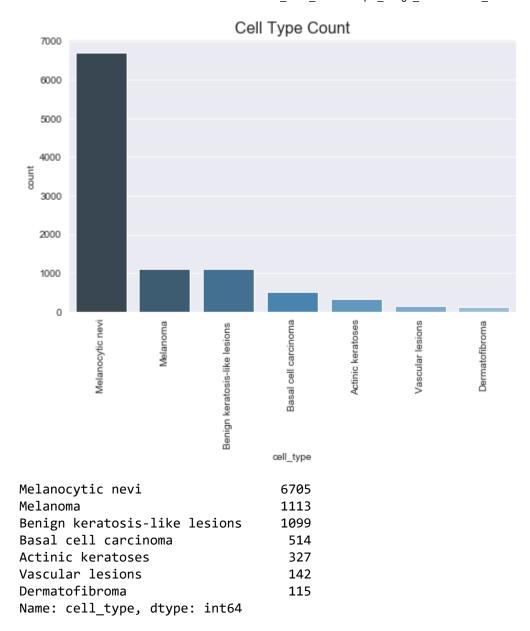
Although exploratory data analysis (EDA) performed was wide ranging, the primary consideration was the relative differences between cell type counts.

Figures script adapted from:

```
https://jakevdp.github.io/PythonDataScienceHandbook/04.14-visualization-with-seaborn.html https://flynn.gg/blog/better-matplotlib-charts/https://seaborn.pydata.org/tutorial/categorical.html https://seaborn.pydata.org/examples/grouped_boxplot.html
```

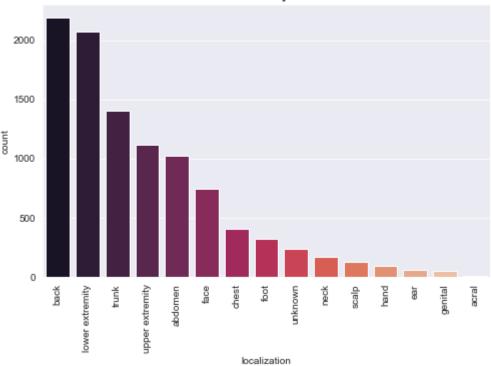
6.1 Cell Type Count

This image dataset is highly imbalanced with one class of seven, Melanocytic nevi, filling 67% of the space. Between the imbalance bias, resizing the image size from 650x450 to 160x120 (a 93% pixel count reduction), and image color similarity this classification problem is an especially difficult exercise regarding model accuracy.



6.2 General Anatomy Site Count

General Anatomy Site Count

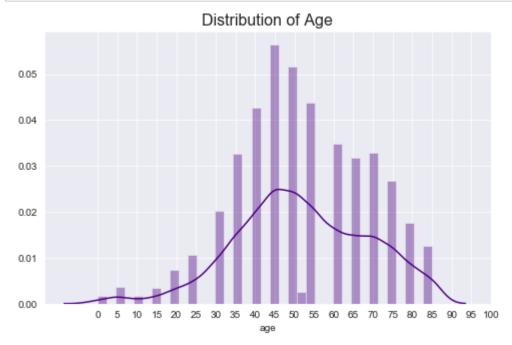


back	2192
lower extremity	2077
trunk	1404
upper extremity	1118
abdomen	1022
face	745
chest	407
foot	319
unknown	234
neck	168
scalp	128
hand	90
ear	56
genital	48
acral	7

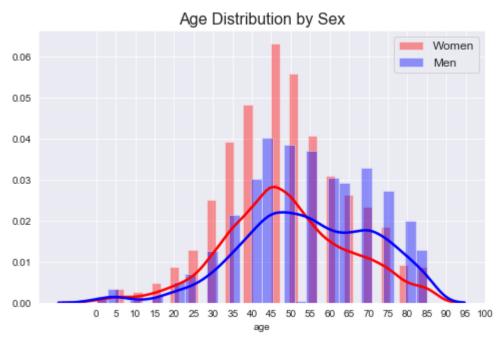
Name: localization, dtype: int64

6.3 Distribution of Age

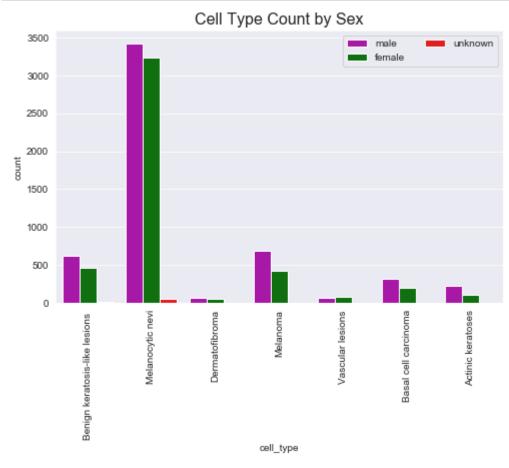
```
In [84]: sns.set_style("darkgrid")
    plt.figure(figsize=(8,5))
    plt.title('Distribution of Age',fontsize=16)
    sns.distplot(ham_df['age'], color= 'indigo')
    #plt.title('Overall Distribution')
    plt.xticks(list(range(0,105,5)))
plt.show()
```



6.4 Age Distribution by Sex



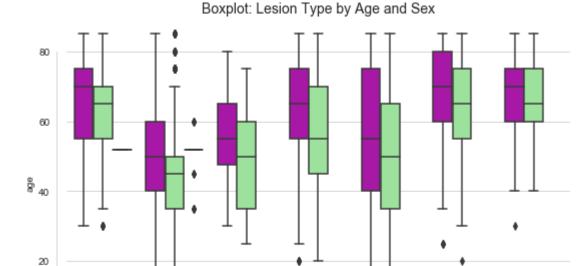
6.5 Cell Type Count by Sex



sex male female unknown

akiec

6.6 Lesion Type by Age and Sex



mel

vasc

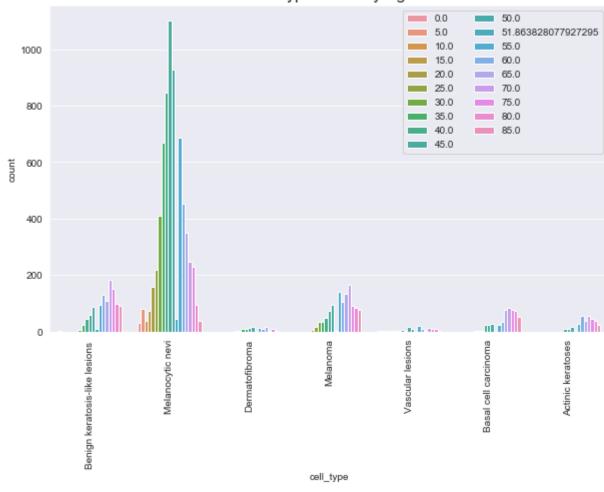
bcc

df

6.7 Count Plot: Cell Type Count by Age

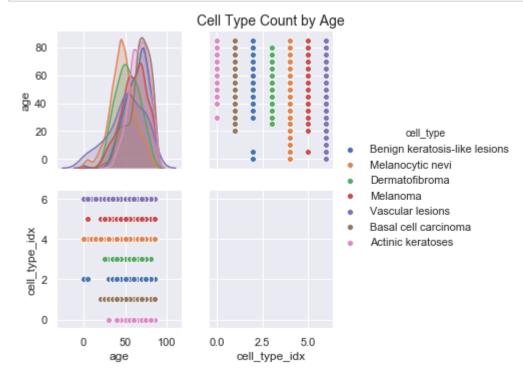
bkl

Cell Type Count by Age



6.8 Pairs Plot Cell Type by Age

```
In [90]: sns.set(style="darkgrid")
    sns.pairplot(ham_df, hue="cell_type")
    plt.title('Cell Type Count by Age',fontsize=14)
    plt.show()
```



Seaborn Pairs Plot

The following two cells saved here are for future reference.

* Author: Mader, K

* Title: Dermatology MNIST: Loading and Processing

* Date: 2019

* Code version: n.a.

* Availability: https://www.kaggle.com/kmader/dermatology-mnist-loading-and-processing

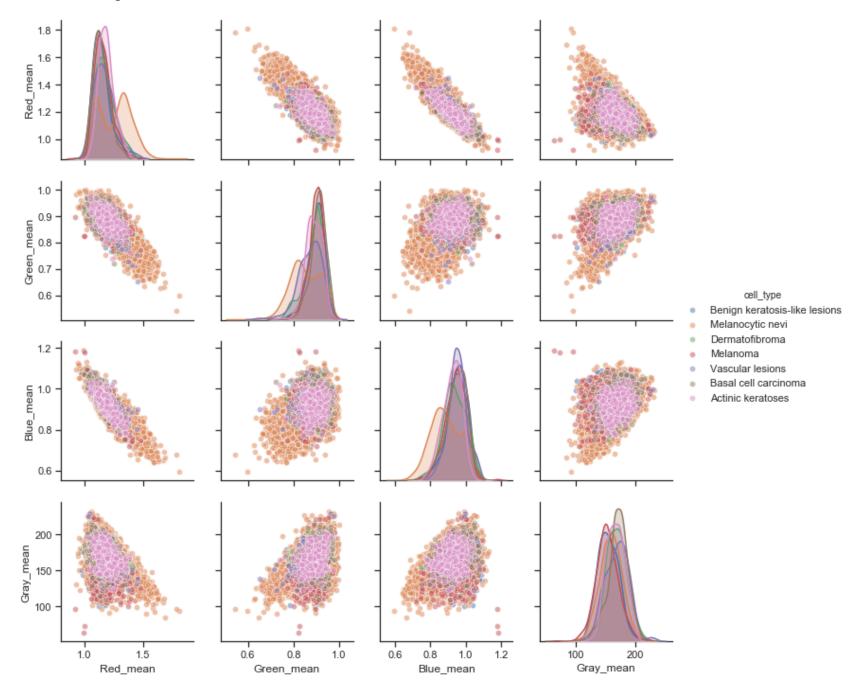
Get and normalize color channel information

Out[95]:

	Red_mean	Green_mean	Blue_mean	Gray_mean
2338	1.095006	0.865439	1.039555	173.623385
9036	1.150141	0.875402	0.974456	129.212778
5726	1.264748	0.849982	0.885269	173.883142
1591	1.192256	0.862743	0.945002	157.451441
5860	1.547749	0.708018	0.744233	121.210295
6260	1.314572	0.804819	0.880610	162.674201
856	1.214301	0.881434	0.904264	139.299271
1630	1.201904	0.913005	0.885091	166.863333
4567	1.252020	0.850425	0.897556	195.313646
8221	1.237955	0.836908	0.925137	168.624618

Pairs Plot: Cell Type

Out[96]: <seaborn.axisgrid.PairGrid at 0x21c41411b48>



7 Resize Images

7.1 Compare image size characteristics

```
Compare resized image resolution: 600x450 vs. 160x120
```

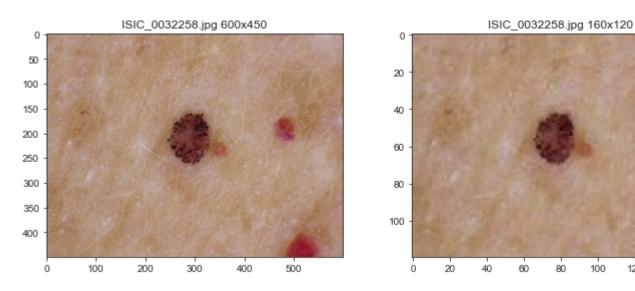
The side-by-side image comparisons (7.1.1 and 7.1.2) shows some reduction in resolution. How much of an affect using a 160x120 resized image compared to the original size had regarding test accuracy is undetermined.

```
In [38]: img_ISIC_0032258 = Image.open('C:\ham10000\HAM10000_images_part_2\ISIC_0032258.jpg')
img_ISIC_0032259 = Image.open('C:\ham10000\HAM10000_images_part_2\ISIC_0032259.jpg')
img_ISIC_0032258_160x120 = img_ISIC_0032258.resize((160,120), Image.ANTIALIAS)
img_ISIC_0032258_160x120.save('D:\MSDS692\img_ISIC_0032258_160x120.jpg')
img_ISIC_0032259_160x120 = img_ISIC_0032259.resize((160,120), Image.ANTIALIAS)
img_ISIC_0032259_160x120.save('D:\MSDS692\img_ISIC_0032259_160x120.jpg')
```

7.1.1 Image ISIC_0032258.jpg

```
In [39]:
         sns.set style("ticks")
         from PIL import Image
         plt.figure(figsize=(12, 9))
         plt.subplot(2,2,1)
         imSize1 = Image.open('C:\ham10000\HAM10000_images_part_2\ISIC_0032258.jpg')
         plt.title('ISIC_0032258.jpg 600x450')
         plt.imshow(imSize1)
         plt.subplot(2,2,2)
         ISIC_0032258_160x120 = Image.open('D:\MSDS692\img_ISIC_0032258_160.jpg')
         plt.title('ISIC_0032258.jpg 160x120')
         plt.imshow(ISIC_0032258_160x120)
         print(imSize1.mode, imSize1.format)
         plt.show()
```

RGB JPEG



7.1.2 Image ISIC_0032259.jpg

120

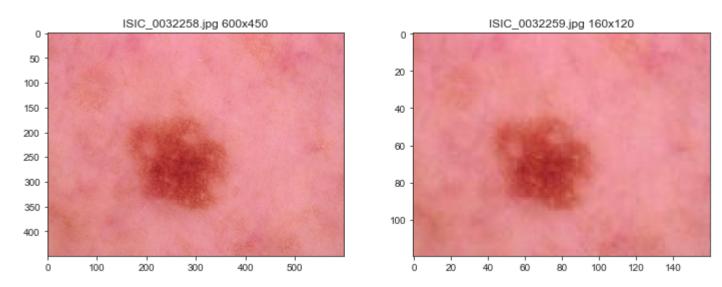
```
In [46]: plt.figure(figsize=(12, 9))

plt.subplot(2,2,1)
    imSize1 = Image.open('C:\ham10000\HAM10000_images_part_2\ISIC_0032258.jpg')
    plt.imshow(imSize1)
    plt.title('ISIC_0032258.jpg 600x450')
    plt.imshow(imSize2)

plt.subplot(2,2,2)
    ISIC_0032259_160x120 = Image.open('D:\MSDS692\img_ISIC_0032259_160x120.jpg')
    plt.title('ISIC_0032259.jpg 160x120')
    plt.imshow(ISIC_0032259_160x120)

print(imSize2.mode, imSize2.format)
    plt.show()
```

RGB JPEG



7.2 Resize Images for Model Input

Image .resize(width, height) to produce input shape (height, width, channels) Settled on image size **160x120**.

Tested other sizes listed below with *mixed* results. The (120, 160, 3) input shape was a compromise between speed, resolution, and memory limit.

```
In [17]: ham df['image'] = ham df['path'].map(lambda x: np.asarray(Image.open(x).resize((160,120)))) #
In [ ]:
         ##.resize(height, width)
         #ham df['image'] = ham df['path'].map(lambda x: np.asarray(Image.open(x).resize((100, 75))))
         #ham df['image'] = ham df['path'].map(lambda x: np.asarray(Image.open(x).resize((128, 96))))
         #ham df['image'] = ham df['path'].map(lambda x: np.asarray(Image.open(x).resize((180, 135))))
         #ham df['image'] = ham df['path'].map(lambda x: np.asarray(Image.open(x).resize((240, 180))))
         #ham df['image'] = ham df['path'].map(lambda x: np.asarray(Image.open(x).resize((224,224))))
In [18]: print(ham df['image'].map(lambda x: x.shape))
                  (120, 160, 3)
         0
         1
                  (120, 160, 3)
         2
                  (120, 160, 3)
         3
                  (120, 160, 3)
         4
                  (120, 160, 3)
         10010
                  (120, 160, 3)
                  (120, 160, 3)
         10011
                  (120, 160, 3)
         10012
                  (120, 160, 3)
         10013
         10014
                  (120, 160, 3)
         Name: image, Length: 10015, dtype: object
```

7.3 A sample of skin lesion images

```
In [57]: sns.set_style("ticks")
    plt.figure(figsize=(15,15))
    for i in range(49):
        plt.subplot(7,7,i+1)
        plt.xticks([])
        plt.yticks([])
        plt.grid(False)
        plt.imshow(ham_df['image'][i])
plt.show()
```

















Preprocess

The following processes were sourced or adapted from these sites and notebooks:

```
https://www.datacamp.com/community/tutorials/convolutional-neural-networks-python
https://github.com/00chengh/Skin-Cancer-HAM10000/blob/master/Final%20Capstone%20-%20Skin%20Cancer.ipynb
https://www.kaggle.com/sid321axn/step-wise-approach-cnn-model-77-0344-accuracy
https://www.kaggle.com/hashbanger/skin-lesion-identification
```

```
In [19]: features=ham_df.drop(columns=['cell_type_idx'],axis=1)
    target=ham_df['cell_type_idx']
```

8.1 Train Test Validate

8.1.1 Split: train / test = 80 / 20

```
In [21]: trainX, testX, trainY, testY = train_test_split(features, target, test_size=0.20,random_state=1234)
```

8.1.2 Change to a Numpy array

```
In [22]: x_train = np.asarray(trainX['image'].tolist())
x_test = np.asarray(testX['image'].tolist())
```

8.1.3 Standardize

```
In [23]: 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)

    x_train = (x_train - x_train_mean)/x_train_std
    x_test = (x_test - x_test_mean)/x_test_std
```

8.1.4 One-hot encoding: Convert output to categorical crossentropy

```
In [24]: y_train = to_categorical(trainY, 7)
y_test = to_categorical(testY, 7)
```

8.1.5 Split: train / validation = 0.87 / 0.13

Chose validation size at 13% of train. Obtained slightly better results than using a 90/10 and other splits.

```
In [25]: x_train, x_validate, y_train, y_validate = train_test_split(x_train, y_train, test_size = 0.13, random_state = 2)
```

8.1.6 Reshape images to 3 dimensions

```
In [26]: x_train = x_train.reshape(x_train.shape[0], *(120, 160, 3))
x_test = x_test.reshape(x_test.shape[0], *(120, 160, 3))
x_validate = x_validate.reshape(x_validate.shape[0], *(120, 160, 3))
```

8.1.6.1 Confirm shape

```
In [27]: print(x_train.shape)
    print(y_train.shape)
    print(x_test.shape)
    print(x_validate.shape)

(6970, 120, 160, 3)
    (6970, 7)
    (2003, 120, 160, 3)
    (1042, 120, 160, 3)
```

Test Model

This section includes a test CNN model. The test model was provided primarily as an example starting point.

Test Model Architecture

```
In [74]: | # CNN Model Architecture
         input_shape = (120, 160, 3)
         num classes = 7
         modelT = Sequential()
         modelT.add(Conv2D(16, (3, 3), padding='same',input shape=input shape, activation='relu'))
         modelT.add(BatchNormalization())
         modelT.add(MaxPooling2D(2, 2))
         modelT.add(Dropout(0.25))
         modelT.add(Conv2D(32, (3, 3), padding='same', activation='relu'))
         modelT.add(BatchNormalization())
         modelT.add(MaxPooling2D(2, 2))
         modelT.add(Dropout(0.25))
         modelT.add(Conv2D(64, (3, 3), padding='same', activation='relu'))
         modelT.add(BatchNormalization())
         modelT.add(MaxPooling2D(2, 2))
         modelT.add(Dropout(0.25))
         modelT.add(Flatten())
         modelT.add(Dense(128, activation='relu'))
         modelT.add(BatchNormalization())
         modelT.add(Dropout(0.5))
         modelT.add(Dense(num classes, activation='softmax'))
         modelT.compile(optimizer = 'adam', loss = "categorical crossentropy", metrics=["accuracy"])
         modelT.summary()
```

Model: "sequential_5"

Layer (type)	Output	Shape	Param #
conv2d_33 (Conv2D)	(None,	120, 160, 16)	448
batch_normalization_26 (Batc	(None,	120, 160, 16)	64
max_pooling2d_15 (MaxPooling	(None,	60, 80, 16)	0
dropout_17 (Dropout)	(None,	60, 80, 16)	0
conv2d_34 (Conv2D)	(None,	60, 80, 32)	4640
batch_normalization_27 (Batc	(None,	60, 80, 32)	128
max_pooling2d_16 (MaxPooling	(None,	30, 40, 32)	0
dropout_18 (Dropout)	(None,	30, 40, 32)	0
conv2d_35 (Conv2D)	(None,	30, 40, 64)	18496
batch_normalization_28 (Batc	(None,	30, 40, 64)	256
max_pooling2d_17 (MaxPooling	(None,	15, 20, 64)	0
dropout_19 (Dropout)	(None,	15, 20, 64)	0
flatten_3 (Flatten)	(None,	19200)	0
dense_7 (Dense)	(None,	128)	2457728
batch_normalization_29 (Batc	(None,	128)	512
dropout_20 (Dropout)	(None,	128)	0
dense_8 (Dense)	(None,	7)	903
=======================================	======		========

Total params: 2,483,175
Trainable params: 2,482,695
Non-trainable params: 480

file:///C:/Users/wmadi/Downloads/A_CNN_Dermoscopic_Image_Classification_Practicum1_HAM10000.html

Test Model Train Fit

```
Running Model T without data augmentation.
Train on 6970 samples, validate on 2003 samples
Epoch 1/20
4 - val accuracy: 0.6161
Epoch 2/20
0 - val accuracy: 0.4638
Epoch 3/20
9 - val accuracy: 0.5307
Epoch 4/20
5 - val accuracy: 0.5607
Epoch 5/20
9 - val accuracy: 0.5791
Epoch 6/20
7 - val accuracy: 0.6550
Epoch 7/20
1 - val accuracy: 0.6685
Epoch 8/20
4 - val accuracy: 0.7179
Epoch 9/20
7 - val accuracy: 0.7384
Epoch 10/20
8 - val accuracy: 0.7154
Epoch 11/20
0 - val_accuracy: 0.7124
Epoch 12/20
6 - val accuracy: 0.7234
Epoch 13/20
8 - val accuracy: 0.7249
```

```
Epoch 14/20
8 - val accuracy: 0.7284
Epoch 15/20
3 - val accuracy: 0.6995
Epoch 16/20
1 - val_accuracy: 0.7309
Epoch 17/20
1 - val accuracy: 0.7149
Epoch 18/20
5 - val accuracy: 0.7274
Epoch 19/20
8 - val accuracy: 0.7229
Epoch 20/20
3 - val accuracy: 0.7499
272.37962341308594 seconds
```

Test Model Evaluation

```
In [77]: # Model T evaluation
    print('------')
    print('Model T evaluation without data augumentation.')
    print('------')
    scores = modelT.evaluate(x_test, y_test, verbose=2)

    print("CNN Error: %.2f%" % (100-scores[1]*100))
    print("CNN Acc: %.2f%" % (scores[1]*100))

    final_loss, final_acc = modelT.evaluate(x_test, y_test, verbose=0)
    print("Final loss: {0:.4f}".format(final_loss, final_acc))
```

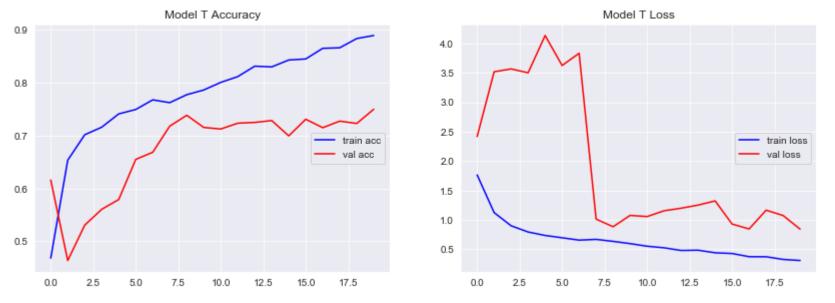
Model T evaluation without data augumentation.

CNN Error: 25.01% CNN Acc: 74.99% Final loss: 0.8403

Test Model Accuracy and Loss Plots

```
In [78]: sns.set_style("darkgrid")
   plt.figure(figsize=(14,10))
   plt.subplot(2,2,1)
   plt.plot(ModelT.history['accuracy'], 'b', label="Training accuracy")
   plt.plot(ModelT.history['val_accuracy'], 'r', label="Validation accuracy")
   plt.legend(['train acc', 'val acc'], loc='center right')
   plt.title('Model T Accuracy')

plt.subplot(2,2,2)
   plt.plot(ModelT.history['loss'], 'b', label= "Training loss")
   plt.plot(ModelT.history['val_loss'], 'r', label="validation loss")
   plt.legend(['train loss', 'val loss'], loc='center right')
   plt.title('Model T Loss')
   plt.show()
```



Set the learning rate reduction and add data augumentation to the Test Model

```
In [79]: # Source: https://github.com/00chengh/Skin-Cancer-HAM10000/blob/master/Final%20Capstone%20-%20Skin%20Cancer.i
         pynb
         # Source: https://www.kaggle.com/sid321axn/step-wise-approach-cnn-model-77-0344-accuracy
         lr reduction = ReduceLROnPlateau(
             monitor='val accuracy',
             patience=4, # 3
             verbose=1,
             factor=0.5,
             # factor=0.3,
             min lr=0.0000001)
         # data augmentation added to help reduce overfitting
         train datagen = ImageDataGenerator(
             rotation range = 20, # 45, 90
             width shift range = 0.2, # 0.1
             height shift range = 0.2, # 0.1
             shear range = 0.1, # 0.2
             zoom_range = 0.1, # 0.2, 0.3
             horizontal flip = True,
             #vertical flip=True,
```

Train modelT with Augmentation

```
In [80]: # Source: https://github.com/00chengh/Skin-Cancer-HAM10000/blob/master/Final%20Capstone%20-%20Skin%20Cancer.i
        pynb
        # Source: https://www.kaggle.com/sid321axn/step-wise-approach-cnn-model-77-0344-accuracy
        # Source: https://www.kaggle.com/hashbanger/skin-lesion-identification
        Epochs=20
        batchSize=64
        t0=time.time()
        print('----')
        print('Running Model T [BatchNorm / Droput] with Augumentation.')
        print('----')
        ModelT = modelT.fit(train datagen.flow(x train,y train, batch size=batchSize),
                                  epochs = Epochs, validation data = (x validate, y validate),
                                  verbose = 1, steps per epoch=x train.shape[0] / batchSize,
                                  callbacks=[lr reduction])
        t1=time.time()
        print(t1-t0," seconds")
```

```
Running Model T [BatchNorm / Droput] with Augumentation.
Epoch 1/20
0 - val accuracy: 0.7418
Epoch 2/20
4 - val accuracy: 0.7572
Epoch 3/20
1 - val accuracy: 0.7486
Epoch 4/20
2 - val accuracy: 0.7601
Epoch 5/20
109/108 [=============== ] - 21s 197ms/step - loss: 0.7105 - accuracy: 0.7389 - val loss: 0.723
1 - val accuracy: 0.7687
Epoch 6/20
8 - val accuracy: 0.7438
Epoch 7/20
9 - val_accuracy: 0.7678
Epoch 8/20
6 - val accuracy: 0.7524
Epoch 9/20
6 - val accuracy: 0.7524
Epoch 00009: ReduceLROnPlateau reducing learning rate to 0.00050000000237487257.
Epoch 10/20
0 - val accuracy: 0.7553
Epoch 11/20
7 - val accuracy: 0.7553
Epoch 12/20
4 - val accuracy: 0.7630
Epoch 13/20
```

```
9 - val accuracy: 0.7476
Epoch 00013: ReduceLROnPlateau reducing learning rate to 0.0002500000118743628.
Epoch 14/20
0 - val accuracy: 0.7601
Epoch 15/20
2 - val accuracy: 0.7649
Epoch 16/20
9 - val accuracy: 0.7572
Epoch 17/20
5 - val accuracy: 0.7802
Epoch 18/20
4 - val accuracy: 0.7706
Epoch 19/20
1 - val accuracy: 0.7630
Epoch 20/20
2 - val accuracy: 0.7562
435.7690336704254 seconds
```

Evaluate Test Model Test Accuracy and Loss

Test Model Accuracy and Loss Plots after Augumentation

```
In [82]: sns.set_style("darkgrid")
    plt.figure(figsize=(14,10))
    plt.subplot(2,2,1)
    plt.plot(ModelT.history['accuracy'], 'b', label="Training accuracy")
    plt.plot(ModelT.history['val_accuracy'], 'r', label="Validation accuracy")
    plt.legend(['train acc', 'val acc'], loc='center right')
    plt.title('Model T Accuracy')

plt.subplot(2,2,2)
    plt.plot(ModelT.history['loss'], 'b', label= "Training loss")
    plt.plot(ModelT.history['val_loss'], 'r', label="validation loss")
    plt.legend(['train loss', 'val loss'], loc='center right')
    plt.title('Model T Loss')
    plt.show()
```





10 Final Model

Average Test Score 80.14%

Chausina Madal 4 Den 40

Tested multiple configurations including hyperparameters before settling on this final architecture and tuning. This model, Model 4, was one of six seperate architectures attempted. Metrics included CNN (test) accuracy and loss, which was the primary metric, plus f1-scores in a classification report, AUC (area under curve) score, jaccard similarity score, and confusion matrix. The optimizer was Adam set at the default value and loss was categorical cross entropy.

Model 4 input included 160x120 3 channel images resized from 600x450. This final model included 9 convolutions in 4 groups, a 2 dense group, flatten, and the output layer. Conv Group 1 had three convolutions: A slightly different approach than usual. Conv Groups 2, 3, and 4 each contained two convolutions. In addition, the input convolution (Conv layer 1) had 16 kernel filters while the following two convolutions in group 1 each included 32 kernel filters. For the dense layers 1024 kernels worked better than larger or smaller sized kernels. Each convolution layer included 3x3 filters, which is best to discern small and local features (Ramesh, 2018).

Also included were BatchNormalization, MaxPooling2D, and Dropout layers. An added kernel regulizer I2 set at 0.01 to help manage overfitting was added to each Conv2D, and to each Dense layer.

Shown in Table 1 are scores for separate runs and the average for each score type. Score types included CNN (test) score, AUC Score, and f1 scores for model accuracy, melanoma, and basil cell carcinoma. CNN score is also referenced as the test score and as the classification score.

CNN (test) Scores were very close to one another. The best test score was 80.38% (run #4) and the best AUC Score was 0.7872 (run #5). An AUC Score may be a better indicator of how well of a fit the model is than the CNN score. The average difference between test and AUC was 2.6 %.

10.1 Table 1

```
In [6]: import pandas as pd
    scoresTable = pd.read_csv('D:\MSDS692\Scores.csv')
    scoresTable
```

Out[6]:

	Model Run	CNN Score	AUC Score	f1 Accuracy	f1 Melanoma	f1 Basil Cell
0	1	0.8033	0.7705	0.80.	0.54	0.61.
1	2	0.7988	0.7805	0.80.	0.51	0.61.
2	3	0.8038	0.7774	0.80.	0.59	0.60.
3	4	0.7998	0.7872	0.80.	0.54	0.58.
4	5	0.8013	0.7867	0.80.	0.55	0.62.
5	Average	0.8014	0.7805	0.80.	0.55	0.60.

10.2 CNN Model Architecture

```
In [28]: from keras.regularizers import 12 #, L1
         np.random.seed(168)
         inputShape = (120, 160, 3)
         num classes = 7
         kreg = 12(0.01) # adding a regularizer to a layer adds a new loss # 0.001 or 0.0001
         \#area = L1(0.01)
         def model4():
             ### Model 4
             ## A model with 9 convolutions in 4 groups,
             ## A 2 dense group, a flatten, and an output layer
             ## Conv2D
                 # Activation: relu
                 # Padding: same except first Conv2D = valid
                 # kernel regularizer: L2 added to dense layers and some convolution layers
                 # Batch Normalization added to each conv layers group
                 # Max Pooling added to each conv layers group
                 # Dropout added to each group
             ## Output
                 # Batch Normalization
                 # activation: Softmax
             ## Compile
                 # Metric: Accuracy
                 # Optimizer: Adam
                 # Loss: categorical cross entropy
             model = Sequential()
             # conv group 1
             model.add(Conv2D(16, (3, 3), padding='valid', input_shape=inputShape, activation='relu'))
             model.add(BatchNormalization())
             model.add(Conv2D(32, (3, 3), padding='same', kernel regularizer=kreg, activation='relu'))
             model.add(Conv2D(32, (3, 3), padding='same', kernel regularizer=kreg, activation='relu'))
             model.add(BatchNormalization())
             model.add(MaxPooling2D())
             model.add(Dropout(0.25))
             # conv group 2
             model.add(Conv2D(64, (3, 3), padding='same', kernel regularizer=kreg, activation='relu'))
             model.add(Conv2D(64, (3, 3), padding='same', kernel regularizer=kreg, activation='relu'))
             model.add(BatchNormalization())
```

```
model.add(MaxPooling2D())
   model.add(Dropout(0.25))
   # conv group 3
   model.add(Conv2D(128, (3, 3), padding='same', kernel regularizer=kreg, activation='relu'))
   model.add(Conv2D(128, (3, 3), padding='same', kernel regularizer=kreg, activation='relu'))
   model.add(BatchNormalization())
   model.add(MaxPooling2D())
   model.add(Dropout(0.25))
   # conv group 4
   model.add(Conv2D(256, (3, 3), padding='same', kernel_regularizer=kreg, activation='relu'))
   model.add(Conv2D(256, (3, 3), padding='same', kernel regularizer=kreg, activation='relu'))
   model.add(BatchNormalization())
   model.add(MaxPooling2D())
   model.add(Dropout(0.25))
   # flatten
   model.add(Flatten())
   # dense group
   model.add(Dense(1024, kernel regularizer=kreg, activation='relu'))
   model.add(Dense(1024, kernel regularizer=kreg, activation='relu'))
   model.add(BatchNormalization())
   model.add(Dropout(0.25))
   # output
   model.add(Dense(num classes))
   model.add(BatchNormalization())
   model.add(Activation('softmax'))
   # model compile
   model.compile(loss = 'categorical crossentropy', optimizer= 'adam', metrics=['accuracy'])
   return model
model4 = model4()
model4.summary()
```

Model: "sequential_1"

Layer (type)	Output Shape	Param #
conv2d_1 (Conv2D)	(None, 120, 160, 16)	448
batch_normalization_1 (Batch	(None, 120, 160, 16)	64
conv2d_2 (Conv2D)	(None, 120, 160, 32)	4640
conv2d_3 (Conv2D)	(None, 120, 160, 32)	9248
batch_normalization_2 (Batch	(None, 120, 160, 32)	128
max_pooling2d_1 (MaxPooling2	(None, 60, 80, 32)	0
dropout_1 (Dropout)	(None, 60, 80, 32)	0
conv2d_4 (Conv2D)	(None, 60, 80, 64)	18496
conv2d_5 (Conv2D)	(None, 60, 80, 64)	36928
batch_normalization_3 (Batch	(None, 60, 80, 64)	256
max_pooling2d_2 (MaxPooling2	(None, 30, 40, 64)	0
dropout_2 (Dropout)	(None, 30, 40, 64)	0
conv2d_6 (Conv2D)	(None, 30, 40, 128)	73856
conv2d_7 (Conv2D)	(None, 30, 40, 128)	147584
batch_normalization_4 (Batch	(None, 30, 40, 128)	512
max_pooling2d_3 (MaxPooling2	(None, 15, 20, 128)	0
dropout_3 (Dropout)	(None, 15, 20, 128)	0
conv2d_8 (Conv2D)	(None, 15, 20, 256)	295168
conv2d_9 (Conv2D)	(None, 15, 20, 256)	590080
batch_normalization_5 (Batch	(None, 15, 20, 256)	1024

max_pooling2d_4 (MaxPooling2	(None,	7, 10, 256)	0
dropout_4 (Dropout)	(None,	7, 10, 256)	0
flatten_1 (Flatten)	(None,	17920)	0
dense_1 (Dense)	(None,	1024)	18351104
dense_2 (Dense)	(None,	1024)	1049600
batch_normalization_6 (Batch	(None,	1024)	4096
dropout_5 (Dropout)	(None,	1024)	0
dense_3 (Dense)	(None,	7)	7175
batch_normalization_7 (Batch	(None,	7)	28
activation_1 (Activation)	(None,	7)	0
Total params: 20,590,435 Trainable params: 20,587,381 Non-trainable params: 3,054	=====		=======

10.3 Set Learning Rate and Augmentation

```
In [29]: | lrReduction = ReduceLROnPlateau(
             monitor='val accuracy',
             patience=3, # patience=3 gave slightly better results than 4, 2, 5
             verbose=1,
             factor=0.5,
             #factor=0.3,
             min_lr=0.0000001
         trainDatagen = ImageDataGenerator(
             rotation_range = 20, # Tried a variety of rotations but made little difference
             width shift range = 0.1, # 0.2
             height shift range = 0.1, # 0.2
             #shear range = 0.1, # 0.2
             zoom range = 0.1, # 0.2, 0.3
             horizontal flip = True,
             #vertical flip = True # tended to add a bit more overfitting
         trainDatagen.fit(x train) # fit the training data in order to augment.
```

10.4 Model Fit

Source: https://github.com/00chengh/Skin-Cancer-HAM10000/blob/master/Final%20Capstone%20-%20Skin%20Cancer.ipynb

Source: https://www.kaggle.com/sid321axn/step-wise-approach-cnn-model-77-0344-accuracy

Source: https://www.kaggle.com/hashbanger/skin-lesion-identification

```
Running Model 4 - Data Augumentation Included.
Epoch 1/50
- val accuracy: 0.6747
Epoch 2/50
54/54 [=========================== ] - 28s 525ms/step - loss: 3.7633 - accuracy: 0.6511 - val loss: 3.0765
- val accuracy: 0.6747
Epoch 3/50
- val accuracy: 0.6747
Epoch 4/50
- val accuracy: 0.6747
Epoch 00004: ReduceLROnPlateau reducing learning rate to 0.0005000000237487257.
Epoch 5/50
- val accuracy: 0.6737
Epoch 6/50
- val accuracy: 0.6737
Epoch 7/50
54/54 [========================== ] - 29s 528ms/step - loss: 1.7169 - accuracy: 0.7296 - val loss: 1.7642
- val accuracy: 0.6766
Epoch 8/50
- val accuracy: 0.6900
Epoch 9/50
54/54 [=========================== ] - 29s 530ms/step - loss: 1.5374 - accuracy: 0.7428 - val loss: 1.5404
- val accuracy: 0.7131
Epoch 10/50
54/54 [========================== ] - 29s 534ms/step - loss: 1.4674 - accuracy: 0.7463 - val loss: 1.4655
- val accuracy: 0.7274
Epoch 11/50
54/54 [========================= ] - 28s 519ms/step - loss: 1.4425 - accuracy: 0.7419 - val loss: 1.3844
- val accuracy: 0.7457
Epoch 12/50
- val accuracy: 0.7457
Epoch 13/50
54/54 [=========================== ] - 29s 528ms/step - loss: 1.3297 - accuracy: 0.7559 - val_loss: 1.2546
```

```
- val accuracy: 0.7418
Epoch 14/50
- val accuracy: 0.7745
Epoch 15/50
- val accuracy: 0.7591
Epoch 16/50
- val accuracy: 0.7591
Epoch 17/50
- val accuracy: 0.7562
Epoch 00017: ReduceLROnPlateau reducing learning rate to 0.0002500000118743628.
Epoch 18/50
- val accuracy: 0.7649
Epoch 19/50
- val accuracy: 0.7764
Epoch 20/50
- val accuracy: 0.7783
Epoch 21/50
- val accuracy: 0.7591
Epoch 22/50
- val accuracy: 0.7821
Epoch 23/50
- val accuracy: 0.7534
Epoch 24/50
- val accuracy: 0.7802
Epoch 25/50
- val accuracy: 0.7783
Epoch 00025: ReduceLROnPlateau reducing learning rate to 0.0001250000059371814.
Epoch 26/50
```

```
- val accuracy: 0.7927
Epoch 27/50

    val accuracy: 0.7802

Epoch 28/50
- val accuracy: 0.7860
Epoch 29/50
- val accuracy: 0.7774
Epoch 00029: ReduceLROnPlateau reducing learning rate to 6.25000029685907e-05.
Epoch 30/50
- val accuracy: 0.7889
Epoch 31/50
- val accuracy: 0.7898
Epoch 32/50
- val accuracy: 0.7956
Epoch 33/50
- val accuracy: 0.7937
Epoch 34/50
- val accuracy: 0.8023
Epoch 35/50
- val accuracy: 0.8061
Epoch 36/50

    val accuracy: 0.8052

Epoch 37/50
- val accuracy: 0.8061
Epoch 38/50
- val accuracy: 0.8023
Epoch 00038: ReduceLROnPlateau reducing learning rate to 3.125000148429535e-05.
Epoch 39/50
```

```
    val accuracy: 0.8052

Epoch 40/50
- val accuracy: 0.7937
Epoch 41/50
- val accuracy: 0.7937
Epoch 00041: ReduceLROnPlateau reducing learning rate to 1.5625000742147677e-05.
Epoch 42/50
- val accuracy: 0.8004
Epoch 43/50
- val accuracy: 0.7975
Epoch 44/50
- val accuracy: 0.7956
Epoch 00044: ReduceLROnPlateau reducing learning rate to 7.812500371073838e-06.
Epoch 45/50
- val accuracy: 0.7956
Epoch 46/50
- val_accuracy: 0.8042
Epoch 47/50
- val accuracy: 0.8013
Epoch 00047: ReduceLROnPlateau reducing learning rate to 3.906250185536919e-06.
Epoch 48/50
- val accuracy: 0.7965
Epoch 49/50
- val accuracy: 0.7927
Epoch 50/50
- val accuracy: 0.7937
Epoch 00050: ReduceLROnPlateau reducing learning rate to 1.9531250927684596e-06.
1436.3482639789581 seconds
```

file:///C:/Users/wmadi/Downloads/A CNN Dermoscopic Image Classification Practicum1 HAM10000.html

Scoring

10.5.1 Assess Accuracy and Loss Scores

I decided to present the lowest scored model run of five runs rather than the highest scored run.

10.5.2 Predict and Transform to One-hot

```
In [ ]: y_pred = np.argmax(model4.predict(x_test), axis=1)
    y_true = np.argmax(y_test, axis=1)
```

10.5.3 Assign Target Names

10.5.4 Process Classification Report

```
In [33]: # Precision = True Positives / (True Positives + False Positives)
    # Recall = True Positives / (True Positives + False Negatives)
    # A balance between precison and recall: f1-score = 2*(1/((1/precision) + (1/recall)))

from sklearn.metrics import classification_report
    print('Model 4 Classification Report')
    print('-----')

model4_report= classification_report(y_true, y_pred, target_names=targetNames)
    print(model4_report)
```

Model 4 Classification Report

	precision	recall	f1-score	support
Actinic keratoses	0.55	0.48	0.51	60
Basal cell carcinoma	0.61	0.55	0.58	97
Benign keratosis-like lesions	0.57	0.65	0.61	224
Dermatofibroma	0.41	0.48	0.44	27
Melanocytic nevi	0.88	0.94	0.91	1320
Melanoma	0.69	0.41	0.51	246
Vascular lesions	0.96	0.79	0.87	29
accuracy			0.80	2003
macro avg	0.67	0.61	0.63	2003
weighted avg	0.79	0.80	0.79	2003

10.5.5 Compute Area Under Curve (AUC)

```
In [34]:
         Author: Plog, E
         Title: AUC ROC Curve Scoring Function for Multi-class Classification
         Date: 2018
         Code version: n.a.
         Availability: https://medium.com/@ploq397/auc-roc-curve-scoring-function-for-multi-class-classification-98228
         71a6659
         111
         from sklearn.metrics import roc auc score
         from sklearn import preprocessing
         def multiclass_roc_auc_score(y_test, y_pred, average="macro"):
            lb = preprocessing.LabelBinarizer()
            lb.fit(y test)
            y test1 = lb.transform(y test)
            y pred1 = lb.transform(y pred)
            return roc auc score(y test1, y pred1, average=average)
         aucScore =multiclass_roc_auc_score(y_test, y_pred)
         print('----')
         print('Model 4 Area Under Curve')
         print('-----')
         print("AUC: %.2f%%" % (aucScore*100)) # Add to show as a %
        Model 4 Area Under Curve
         AUC: 78.05%
```

10.5.6 Show Confusion Matrix



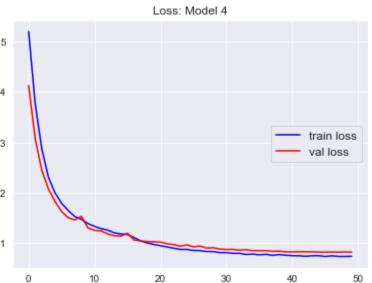
10.6 Accuracy and Loss Plots

```
In [38]:
    sns.set_style("darkgrid")
    plt.figure(figsize=(14,10))
    plt.subplot(2,2,1)
    plt.plot(Model4.history['accuracy'], 'b', label="Training accuracy")
    plt.plot(Model4.history['val_accuracy'], 'r', label="Validation accuracy")
    plt.legend(['train acc', 'val acc'], loc='center right', fontsize='12')
    plt.title('Accuracy: Model 4')

    plt.subplot(2,2,2)
    plt.plot(Model4.history['loss'], 'b', label= "Training loss")
    plt.plot(Model4.history['val_loss'], 'r', label="validation loss")
    plt.legend(['train loss', 'val loss'], loc='center right', fontsize='12')
    plt.title('Loss: Model 4')
```

Out[38]: Text(0.5, 1.0, 'Loss: Model 4')





11 All Model 4 Runs

Table 1

In [8]: scoresTable = pd.read_csv('D:\MSDS692\Scores.csv')
scoresTable

Out[8]:

	Model Run	CNN Score	AUC Score	f1 Accuracy	f1 Melanoma	f1 Basil Cell
0	1	0.8033	0.7705	0.80.	0.54	0.61.
1	2	0.7988	0.7805	0.80.	0.51	0.61.
2	3	0.8038	0.7774	0.80.	0.59	0.60.
3	4	0.7998	0.7872	0.80.	0.54	0.58.
4	5	0.8013	0.7867	0.80.	0.55	0.62.
5	Average	0.8014	0.7805	0.80.	0.55	0.60.

Run 1

```
print('-----')
In [30]:
       print('Model 4 Accuracy and Loss Scores')
       print('----')
       scores = model4.evaluate(x_test, y_test, verbose=2)
       print("CNN Error: %.2f%%" % (100-scores[1]*100))
       print("CNN Acc: %.2f%%" % (scores[1]*100))
       final loss, final acc = model4.evaluate(x test, y test, verbose=1)
       print("Final loss: {0:.4f}".format(final loss, final acc))
       print('----')
       Model 4 Accuracy and Loss Scores
       ______
       CNN Error: 19.67%
       CNN Acc: 80.33%
       2003/2003 [========== ] - 3s 1ms/step
       Final loss: 0.8574
```

Final loss: 0.9667

CNN Acc: 80.38%

Final loss: 0.9349

2003/2003 [============] - 3s 1ms/step

Final loss: 0.9164

2003/2003 [==========] - 3s 1ms/step

```
In [31]: | print('----')
       print('Model 4 Accuracy and Loss Scores')
       print('----')
       scores = model4.evaluate(x_test, y_test, verbose=2)
       print("CNN Error: %.2f%%" % (100-scores[1]*100))
       print("CNN Acc: %.2f%%" % (scores[1]*100))
       final loss, final acc = model4.evaluate(x test, y test, verbose=1)
       print("Final loss: {0:.4f}".format(final loss, final acc))
       print('----')
       Model 4 Accuracy and Loss Scores
       _____
       CNN Error: 19.87%
       CNN Acc: 80.13%
       2003/2003 [=========== ] - 3s 2ms/step
       Final loss: 0.8980
In [ ]:
```