Chest X-Ray Prediction

Summary

Busines and Data Understanding

This notebook will explore chest x-rays with the intent to try and predict whether a patient has pneumonia or not. The dataset is organized into 3 folders (train, test, val) and contains subfolders for each image category (Pneumonia/Normal). The folders that have been provided have close to 6,000 images from pediatric patients ages one through five. The source of the data is the Guangzhou Women and Children's Medical Center.

Data Preparation

The first step in preparing the data was performing image augmentation. This was done by expanding the size of the dataset and by creating a modified version of the existing training set images. This in turn helped to increase dataset variation and ultimately improve the ability of the model to predict new images. As well as scaling the images some of them weren't lined up properly so they had to be straightened out. Since we were predicting whether someone had pneumonia or not the images with bacterial and viral pneumonia were consolidated into one category. The libraries that were used for data preparation were:

- 1. matplotlib.pyplot for visualization
- 2. numpy for handling different arrays
- 3. pandas to handle the data
- 4. ImageDataGenerator from the tensorflow.keras.processing.image library that randomly applied defined parameters to the train set.
 - Keras and Tensorflow provide high-level APIs used for easily building and training models.

Modeling

I chose a convolutional neural network (CNN) model for this data set. The idea behind that was that a local understanding of an image is good enough. The practical benefit is that having fewer parameters greatly improves the time it takes to learn as well as reduces the amount of data required to train the model. The libraries and imports I used were:

- 1. from the tensorflow.keras.models library Sequential is imported for CNN modeling
- 2. to build the CNN architecture this notebook used tensorflow.keras.layers library which included:
 - Dense operates on the input and returns the output
 - Conv2D 2D convolution layer
 - Maxpoolin2D down samples the input along its spatial dimensions

In terms of tuning steps I chose to use EarlyStopping to help avoid overfitting the model. I also assigned weight classes because it emphasizes the weight of the minority class in order for the model to learn from all classes equally.

Evaluation

The final model upon inspection performed pretty well. The way it was evaluated was with a precision score. A prescision score in this instance was predicting pneumonia and the person actually having pneumonia or predicting normal lungs and the lungs were normal. The actual score for predicting pneumonia was an 82%. In terms of predicting healthy lungs it performed at a 90% clip. This is a good start. The validation approach I used for the model was to take a random sample from the internet and predict healthy or pneumonia lungs. It predicted, with about an 83% certainty, that the lungs were normal and they were.

Business Understanding/Stakeholders

During this project I am trying to predict, with a higher certainty, whether a person has pneumonia or not. This project is important to a few different groups of people. The first group is filled with people whom have preexisting lung conditions that make them susceptible to pneumonia. The next group is filled with people from the medical community. Specifically, x-ray technicians because they are the ones reading the results and have to be as precise as possible. Pneumonia is increasing in the population and discovering the disease earlier will provide doctors with the right knowledge on how to treat it.

Initial Data Exploration/Preparation

- The data comes from chest X-ray images (anterior-posterior) that were selected from retrospective cohorts of pediatric patients of one to five years old from Guangzhou Women and Children's Medical Center, Guangzhou.
- This data is composed of three different pieces:
 - 1. Train set
 - 2. Test set
 - 3. Validation set
- A limitation to the data set as a whole is that the images are from a very specific age range. This might create some issues with the data.
- · Importing relevant libraries to operate on the data.
- · Defining the directories for the data.
- Creating a function to help visualize our model results.

```
In [2]: # Some basic imports to start out.
# There may be more imports along the way depending on how the data is expl
# For Visualization
import matplotlib.pyplot as plt
# For handling different arrays.
import numpy as np
# For handling the data.
import pandas as pd
```

```
In [3]: #Define Directories for train, test & Validation Set
        train path = 'chest xray/train/'
        test_path = 'chest_xray/test/'
        valid_path = 'chest_xray/val/'
In [4]: # Defining results from a visualization function.
        def visualize training results(history):
            From https://machinelearningmastery.com/display-deep-learning-model-tra
            Input: keras history object (output from trained model)
            fig, (ax1, ax2) = plt.subplots(2, sharex=True)
            fig.suptitle('Model Results')
            # summarize history for accuracy
            ax1.plot(history.history['accuracy'])
            ax1.plot(history.history['val_accuracy'])
            ax1.set_ylabel('Accuracy')
            ax1.legend(['train', 'test'], loc='upper left')
            # summarize history for loss
            ax2.plot(history.history['loss'])
            ax2.plot(history.history['val_loss'])
            ax2.set_ylabel('Loss')
            ax2.legend(['train', 'test'], loc='upper left')
            plt.xlabel('Epoch')
```

Parameters

plt.show()

- The batch refers to the number of training examples utilized in one iteration.
- The dimension of the images we are going to define are 500x500.
- The dimension size of 500 or more with a batch size greater than 16 may result in a crash as the RAM gets completely used in such cases.
- A lower dimension size with greater batch size is one of the options to try.

```
In [5]: # Define some often used standard parameters
batch_size = 16
img_width = 500
img_height = 500
```

Creating an Image Data Generator

- We will increase the size of the image training dataset artificially by performing an Image
 Augmentation technique. Image Augmentation expands the size of the dataset by creating a
 modified version of the existing training set images that helps to increase dataset variation and
 ultimately improve the ability of the model to predict new images.
- The image generator is for:
 - 1. Train set

2. Test set

Loading up the Images

- The Image Data Generator has a class known as flow from the directory which reads the images from the folders containing the images.
- This will return the Directorylterator typetensorflow.python.keras.preprocessing.image.Directorylterator.
- Code for images can be found https://www.kaggle.com/sanwal092/intro-to-cnn-using-keras-to-predict-pneumonia)

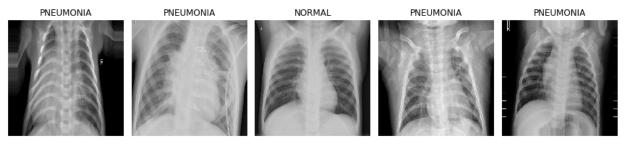
```
In [7]: train = image_gen.flow_from_directory(
              train path,
              target_size=(img_height, img_width),
              color mode='grayscale',
              class mode='binary',
              batch size=batch size
        \# Shuffle is set to as False so we can later compare it with predicted valu
        test = test data gen.flow from directory(
              test path,
              target size=(img height, img width),
              color mode='grayscale',
              shuffle=False,
              class mode='binary',
              batch size=batch size
        valid = test data gen.flow from directory(
              valid path,
              target size=(img height, img width),
              color mode='grayscale',
              class mode='binary',
              batch size=batch size
```

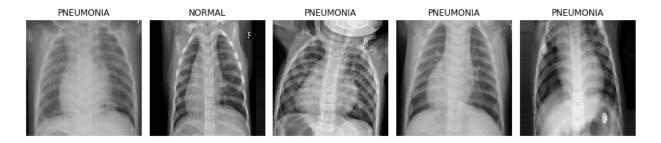
Found 5216 images belonging to 2 classes. Found 624 images belonging to 2 classes. Found 16 images belonging to 2 classes.

Images

 This is a simple preview of some of the train set images obtained from using Data Augmentation.

```
In [8]: plt.figure(figsize=(12, 12))
for i in range(0, 10):
    plt.subplot(2, 5, i+1)
    for X_batch, Y_batch in train:
        image = X_batch[0]
        dic = {0:'NORMAL', 1:'PNEUMONIA'}
        plt.title(dic.get(Y_batch[0]))
        plt.axis('off')
        plt.imshow(np.squeeze(image),cmap='gray',interpolation='nearest')
        break
plt.tight_layout()
plt.show()
```





In [9]: # Imports that will allow a CNN architecture to be created.
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense,Conv2D,Flatten,MaxPooling2D
from tensorflow.keras.callbacks import EarlyStopping,ReduceLROnPlateau

CNN

- CNN architecture is based on layers of convolution.
- The convolution layers receive input and transform the data from the image and pass it as input to the next layer.
- The transformation is known as the operation of convolution.
- It is necessary to define the number of filters for each convolution layer.
- These filters detect patterns such as edges, shapes, curves, objects, textures, or even colors.
- The more sophisticated patterns or objects it detects are more deeply layered.

Initial Baseline Model

- · Just exploring the data.
- · Seeing what an initial model spits out.
- Tried out a few initializers just to see what would happen.
- · Initializers:
 - 1. Zeros Generates 0 for all input data.
 - 2. TruncatedNormal Generates value using truncated normal distribution of input data. The truncated normal distribution is the probability distribution derived from that of a normally distributed random variable by bounding the random variable from either below or above.

```
In [1]: from keras.models import Sequential
    from keras.layers import Activation, Dense
    from keras import initializers

my_init1 = initializers.TruncatedNormal(mean = 0.0, stddev = 0.05, seed = N)

In [239]: # my_init = initializers.Zeros()
    model = Sequential()
    model.add(Conv2D(32, (3, 3), activation="relu", input_shape=(img_width, img_model.add(MaxPooling2D(pool_size = (2, 2)))
    model.add(Flatten())
    model.add(Dense(activation = 'relu', units = 128))#, kernel_initializer = m
    model.add(Dense(activation = 'relu', units = 64, kernel_initializer = my_in
    model.add(Dense(activation = 'relu', units = 32))
    model.add(Dense(activation = 'sigmoid', units = 1))
    model.compile(optimizer = 'adam', loss = 'binary_crossentropy', metrics = [
In [240]: model.summary()
```

Model: "sequential 19"

Layer (type)	Output	Shape	Param #
conv2d_35 (Conv2D)	(None,	498, 498, 32)	320
max_pooling2d_35 (MaxPooling	(None,	249, 249, 32)	0
flatten_22 (Flatten)	(None,	1984032)	0
dense_73 (Dense)	(None,	128)	253956224
dense_74 (Dense)	(None,	64)	8256
dense_75 (Dense)	(None,	32)	2080
dense_76 (Dense)	(None,	1)	33

Trainable params: 253,966,913
Non-trainable params: 0

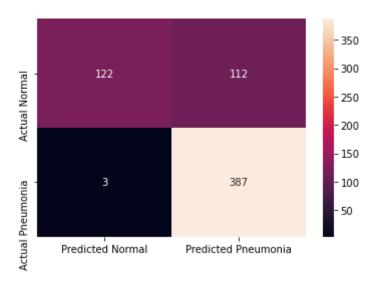
local host: 8888/notebooks/Desktop/Home/Flat Iron/Phase 4 Project/rscbjbr9sj-2/Final Notebook Chest XR ay. ipynblocal host 2 Project/rscbjbr9sj-2/Final Notebook Chest X

```
In [241]: model1 = model.fit_generator(train,
                 steps per epoch = 150,
                 epochs = 10,
                 validation_data = valid,
                 validation steps = 624)
     Epoch 1/10
     acy: 0.8042WARNING:tensorflow:Your input ran out of data; interrupting tr
     aining. Make sure that your dataset or generator can generate at least `s
     teps_per_epoch * epochs` batches (in this case, 624 batches). You may nee
     d to use the repeat() function when building your dataset.
     accuracy: 0.8042 - val_loss: 0.5976 - val_accuracy: 0.6250
     Epoch 2/10
     accuracy: 0.9104
     Epoch 3/10
     - accuracy: 0.9121
     Epoch 4/10
     accuracy: 0.9104
     Epoch 5/10
     accuracy: 0.9258
     Epoch 6/10
     accuracy: 0.9225
     Epoch 7/10
     accuracy: 0.9296
     Epoch 8/10
     accuracy: 0.9183
     Epoch 9/10
     accuracy: 0.9150
     Epoch 10/10
     accuracy: 0.9375
In [242]: test a = model.evaluate(test)
     print('The testing accuracy is :',test_a[1]*100, '%')
     ccuracy: 0.8157
     The testing accuracy is : 81.57051205635071 %
In [243]: preds1 = model.predict(test,verbose=1)
```

```
In [245]: prediction = preds1.copy()
prediction[prediction <= 0.5] = 0
prediction[prediction > 0.5] = 1
```

```
In [246]: learn.metrics import classification_report,confusion_matrix
d.DataFrame(data=confusion_matrix(test.classes, prediction, labels=[0, 1]),i
=["Predicted Normal", "Predicted Pneumonia"])
seaborn as sns
tmap(cml,annot=True, fmt="d")
```

Out[246]: <AxesSubplot:>



In [247]: print(classification_report(y_true=test.classes,y_pred=prediction,target_na

precision	recall	f1-score	support
0.98	0.52	0.68	234
0.78	0.99	0.87	390
		0.82	624
0.88	0.76	0.78	624
0.85	0.82	0.80	624
	0.98 0.78	0.98 0.52 0.78 0.99 0.88 0.76	0.98 0.52 0.68 0.78 0.99 0.87 0.82 0.88 0.76 0.78

Important things to think about before starting to build a CNN model:

- 1. Always begin with a lower filter value such as 32 and begin to increase it layer wise. The patterns get nore complex so more filters are needed to capture as many combinations as possible.
- 2. Construct the model with a layer of Conv2D followed by a layer of MaxPooling.
- 3. The kernel size is a preferred odd number like 3x3.
- 4. Tanh, relu, etc. can be used for an activation function, but relu is the most preferred choice.
- 5. (input_shape) takes three arguments, the images width & height and dimension as color channel.
- 6. Flatten the input after the CNN layers and then add ANN layers.

7. Use the activation function as softmax for the last layer. If the problem is more than 2 classes, define units as the total number of classes and use sigmoid for binary classification and set unit to 1.

```
In [72]: cnn = Sequential()
         # Starting out with a lower filter of 32.
         # Max Pooling simply says to the Convolutional Neural Network that we will
         # if that is the largest information available amplitude.
         cnn.add(Conv2D(32, (3, 3), activation="relu", input_shape=(img_width, img_h
         cnn.add(MaxPooling2D(pool_size = (2, 2)))
         cnn.add(Conv2D(32, (3, 3), activation="relu"))
         cnn.add(MaxPooling2D(pool size = (2, 2)))
         cnn.add(Conv2D(32, (3, 3), activation="relu"))
         cnn.add(MaxPooling2D(pool_size = (2, 2)))
         # Increasing the filter to 64.
         cnn.add(Conv2D(64, (3, 3), activation="relu"))
         cnn.add(MaxPooling2D(pool_size = (2, 2)))
         cnn.add(Conv2D(64, (3, 3), activation="relu"))
         cnn.add(MaxPooling2D(pool size = (2, 2)))
         # Flattening is converting the data into a 1-dimensional array for inputtin
         # We flatten the output of the convolutional layers to create a single long
         cnn.add(Flatten())
         cnn.add(Dense(activation = 'relu', units = 128))
         cnn.add(Dense(activation = 'relu', units = 64))
         cnn.add(Dense(activation = 'sigmoid', units = 1))
         cnn.compile(optimizer = 'adam', loss = 'binary_crossentropy', metrics = ['a
```

CNN Summary

• Now that we have developed the model let's see what is going on!

In [73]: cnn.summary()

Model: "sequential_2"

Layer (type)	Output	Shape 	Param #
conv2d_12 (Conv2D)	(None,	498, 498, 32)	320
max_pooling2d_12 (MaxPooling	(None,	249, 249, 32)	0
conv2d_13 (Conv2D)	(None,	247, 247, 32)	9248
max_pooling2d_13 (MaxPooling	(None,	123, 123, 32)	0
conv2d_14 (Conv2D)	(None,	121, 121, 32)	9248
max_pooling2d_14 (MaxPooling	(None,	60, 60, 32)	0
conv2d_15 (Conv2D)	(None,	58, 58, 64)	18496
max_pooling2d_15 (MaxPooling	(None,	29, 29, 64)	0
conv2d_16 (Conv2D)	(None,	27, 27, 64)	36928
max_pooling2d_16 (MaxPooling	(None,	13, 13, 64)	0
flatten_5 (Flatten)	(None,	10816)	0
dense_15 (Dense)	(None,	128)	1384576
dense_16 (Dense)	(None,	64)	8256
dense_17 (Dense)	(None,	1)	65

Total params: 1,467,137
Trainable params: 1,467,137
Non-trainable params: 0

Interpretation of the Model

· Plotting CNN architecture.

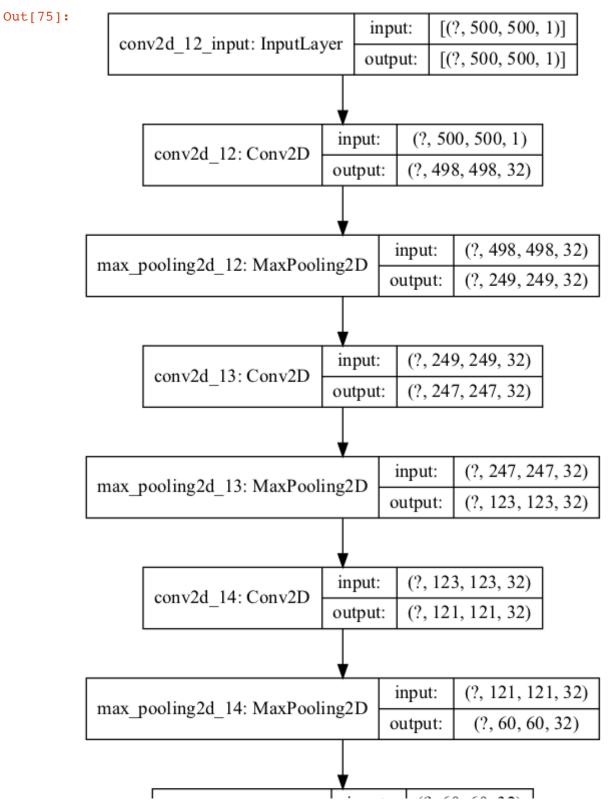
Out[74]: <tensorflow.python.keras.layers.pooling.MaxPooling2D at 0x7fb1dbd7ad30>

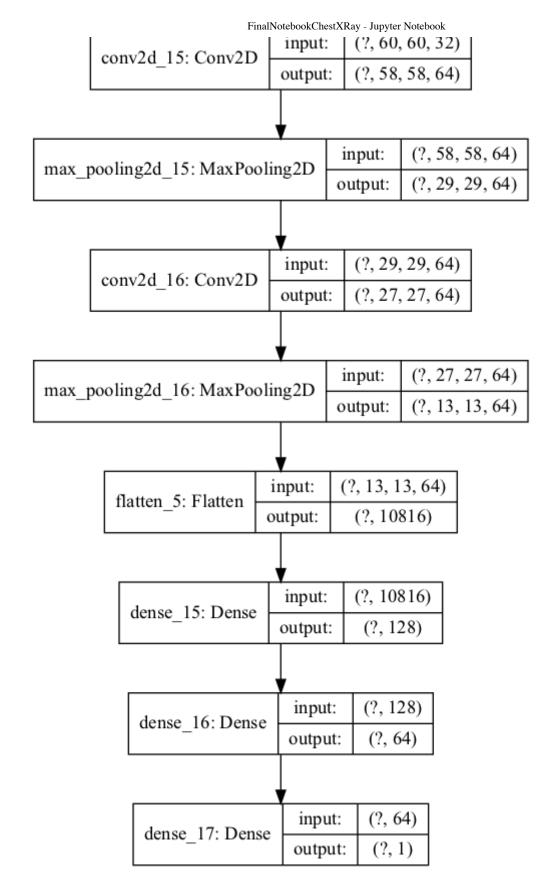
Visualizing the Model

• Link for code and model found <u>in this blog. (https://towardsdatascience.com/medical-x-ray-%EF%B8%8F-image-classification-using-convolutional-neural-network-9a6d33b1c2a)</u>

In [75]: !pip install pydot
 import graphviz
 from tensorflow.keras.utils import plot_model
 plot_model(cnn,show_shapes=True, show_layer_names=True, rankdir='TB', expan

Requirement already satisfied: pydot in /Users/patrickryan/opt/anaconda3/envs/learn-env/lib/python3.8/site-packages (1.4.2)
Requirement already satisfied: pyparsing>=2.1.4 in /Users/patrickryan/opt/anaconda3/envs/learn-env/lib/python3.8/site-packages (from pydot) (2.4.





Fitting the Model

- EarlyStopping is called to stop the epochs based on some metric (monitor) and conditions (mode, patience).
- It helps to avoid overfitting the model.
- We are telling the model to stop based on val loss metric. we need it to be a minimum.

• (patience) says that after a minimum val_loss is achieved during the next iterations if the val_loss increases in any of the 3 iterations then the training will stop at that epoch.

```
In [76]: early = EarlyStopping(monitor='val_loss', mode='min', patience=3)
    learning_rate_reduction = ReduceLROnPlateau(monitor='val_loss', patience = callbacks_list = [ early, learning_rate_reduction]
```

Assigning Class Weights

- · It is good practice to assign class weights.
- It emphasizes the weight of the minority class in order for the model to learn from all classes equally.

```
Epoch 1/10
acy: 0.9181WARNING:tensorflow:Your input ran out of data; interrupting tr
aining. Make sure that your dataset or generator can generate at least `s
teps per epoch * epochs` batches (in this case, 624 batches). You may nee
d to use the repeat() function when building your dataset.
accuracy: 0.9181 - val_loss: 0.5699 - val_accuracy: 0.8125
Epoch 2/10
accuracy: 0.9087
Epoch 3/10
accuracy: 0.9119
Epoch 4/10
accuracy: 0.9131
Epoch 5/10
accuracy: 0.9325
Epoch 6/10
accuracy: 0.9250
Epoch 7/10
accuracy: 0.9175
Epoch 8/10
accuracy: 0.9275
Epoch 9/10
accuracy: 0.9287
Epoch 10/10
accuracy: 0.9287
```

Defining the Results of the Visualization Function

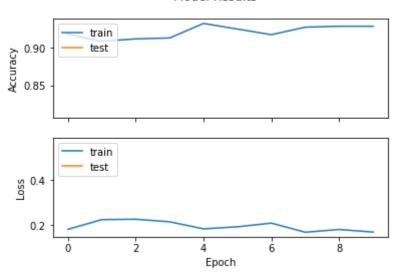
```
In [207]: test_accu = cnn.evaluate_generator(test, 100)
#test_accu = cnn.evaluate(test_set, len(validation_generator), verbose=0)
print("Test loss:", test_accu[0])
print("Test accuracy:", test_accu[1])

visualize_training_results(cnn_model)
```

WARNING:tensorflow:Your input ran out of data; interrupting training. Mak e sure that your dataset or generator can generate at least `steps_per_ep och * epochs` batches (in this case, 100 batches). You may need to use the repeat() function when building your dataset.

Test loss: 0.5063505172729492 Test accuracy: 0.8413461446762085

Model Results



Evaluate

- · Find the models accuracy.
- · Predicting the test dataset.
- Taking a peak at some of the performance measurement metrics in detail to evaluate our model.

- · The activation function of the last layer is sigmoid.
- This allows the model to give a prediction in the 0 to 1 range and not an exact classification as 0 or 1.
- So we categorize all the values in the 0.5 to 1 range as 0 and less than 0.5 as 1.
- Note: 0 denotes a normal case and 1 denotes a case of pneumonia.

```
In [210]: predictions = preds.copy()
    predictions[predictions <= 0.5] = 0
    predictions[predictions > 0.5] = 1
```

Confusion Matrix

- The upper left (true positive) denotes the number of images correctly predicted as normal cases.
- The bottom right (true negative) denotes the correctly predicted number of images as cases of pneumonia.
- The upper right denotes the number of incorrectly predicted images but were actually normal cases.
- The lower left denotes the number of incorrectly predicted images that were actually pneumonia cases.

```
In [211]: from sklearn.metrics import classification_report,confusion_matrix
    cm = pd.DataFrame(data=confusion_matrix(test.classes, predictions, labels=[
        columns=["Predicted Normal", "Predicted Pneumonia"])
    import seaborn as sns
    sns.heatmap(cm,annot=True, fmt="d")
```

Out[211]: <AxesSubplot:>



Classification Report

- Precision = TruePositives / (TruePositives + FalsePositives)
 - The precision score explains how precise/accurate your model is out of those predicted positive. Meaning, how many of them are actually positive.
- Recall = TruePositives / (TruePositives + FalseNegatives)
 - Recall calculates how many of the actual positives our model captured through labeling them as positive (true positive).
- F1 = (2 * Precision * Recall) / (Precision + Recall)
 - F1 Score can be a better measure to use if we need to seek a balance between precision and recall. Especially if there is an uneven class distribution (large number of actual negatives).

In [212]: print(classification_report(y_true=test.classes,y_pred=predictions,target_n

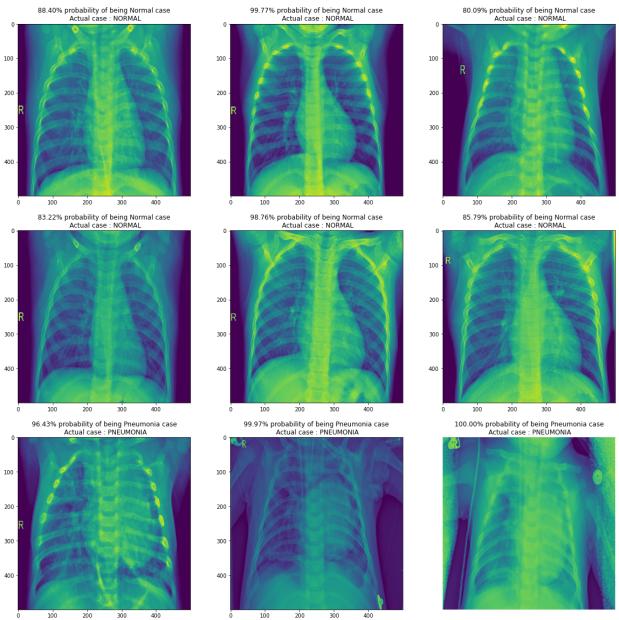
	precision	recall	f1-score	support
NORMAL	0.90	0.65	0.75	234
PNEUMONIA	0.82	0.96	0.88	390
accuracy			0.84	624
macro avg	0.86	0.80	0.82	624
weighted avg	0.85	0.84	0.83	624

Visualizing Some of the Predicted Values

• Code for imaging can be found https://towardsdatascience.com/medical-x-ray- %EF%B8%8F-image-classification-using-convolutional-neural-network-9a6d33b1c2a)

```
In [213]: # This code extracts the images from the test data iterator without shuffli
# x contains image array and y has labels
test.reset()
x=np.concatenate([test.next()[0] for i in range(test.__len__())])
y=np.concatenate([test.next()[1] for i in range(test.__len__())])
print(x.shape)
print(y.shape)
(624, 500, 500, 1)
(624,)
```

```
In [214]: dic = {0:'NORMAL', 1:'PNEUMONIA'}
plt.figure(figsize=(20,20))
for i in range(0+228, 9+228):
    plt.subplot(3, 3, (i-228)+1)
    if preds[i, 0] >= 0.5:
        out = ('{:.2%} probability of being Pneumonia case'.format(preds[i] else:
        out = ('{:.2%} probability of being Normal case'.format(1-preds[i][ plt.title(out+"\n Actual case : "+ dic.get(y[i]))
    plt.imshow(np.squeeze(x[i]))
plt.axis('off')
plt.show()
```



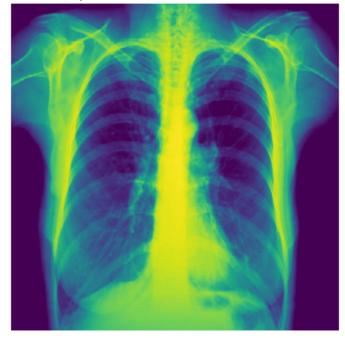
Testing on a Random Sample (for fun)

- Picking a random image out (just googled chest x-ray).
- Processing the image.
- · Predicting from the random image obtained.

· Visualizing the random sample.

```
In [215]: # Testing a random Chest X-Ray from the internet.
          random_path = 'chest_xray/X-Ray-Chest-random-32202353-500-400.jpg'
          from tensorflow.keras.preprocessing import image
          random img = image.load img(random path, target size=(500, 500), color mode
          # Preprocessing the image.
          pp random img = image.img to array(random_img)
          pp random img = pp random img/255
          pp random img = np.expand dims(pp random img, axis=0)
          # Predicting the accuracy of the random chest x-ray.
          random preds= cnn.predict(pp random img)
          # Visualize the random sample.
          plt.figure(figsize=(6,6))
          plt.axis('off')
          if random preds>= 0.5:
              out = ('I am {:.2%} percent confirmed that this is a Pneumonia case'.fo
          else:
              out = ('I am {:.2%} percent confirmed that this is a Normal case'.forma
          plt.title("A Random Chest X-Ray\n"+out)
          plt.imshow(np.squeeze(pp random img))
          plt.show()
```

A Random Chest X-Ray I am 83.22% percent confirmed that this is a Normal case



Conclusion

Based on the model and all of the tuning I obtained precision scores of 82% for predicting pneumonia and 90% for predicting healthy lungs. This was corroborated by examining a random sample from the internet. This sample was tested and had an 83.22% chance of being noraml and

they were. A reduction in false negatives was also achieved by tuning the parameters. This is good because we don't want to tell someone they are healthy when they are not.

Going Forward

In terms of what could be done to make this even better I would start by tuning the parameters a little more. I would also try adding more relevant data to the source. This will allow for even more accurate predictions going forward.