# Pneumonia Prediction Project

```
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# Import packages and statements
from tensorflow.random import set seed
set seed(321)
import numpy as np
np.random.seed(123)
#import module
import pickle
!pip install lime
         Looking in indexes: <a href="https://pypi.org/simple">https://us-python.pkg.dev/colab-whee</a>
         Collecting lime
            Downloading lime-0.2.0.1.tar.gz (275 kB)
                                                                             275 kB 4.5 MB/s
        Requirement already satisfied: matplotlib in /usr/local/lib/python3.7/dist-packad
        Requirement already satisfied: numpy in /usr/local/lib/python3.7/dist-packages (:
        Requirement already satisfied: scipy in /usr/local/lib/python3.7/dist-packages (:
        Requirement already satisfied: tqdm in /usr/local/lib/python3.7/dist-packages (f:
        Requirement already satisfied: scikit-learn>=0.18 in /usr/local/lib/python3.7/dia
        Requirement already satisfied: scikit-image>=0.12 in /usr/local/lib/python3.7/dia
        Requirement already satisfied: PyWavelets>=1.1.1 in /usr/local/lib/python3.7/dis-
        Requirement already satisfied: networkx>=2.0 in /usr/local/lib/python3.7/dist-pac
        Requirement already satisfied: imageio>=2.3.0 in /usr/local/lib/python3.7/dist-pageio>=2.3.0 in /usr/local/lib/python3.
         Requirement already satisfied: tifffile>=2019.7.26 in /usr/local/lib/python3.7/d
        Requirement already satisfied: pillow!=7.1.0,!=7.1.1,>=4.3.0 in /usr/local/lib/p
        Requirement already satisfied: python-dateutil>=2.1 in /usr/local/lib/python3.7/
        Requirement already satisfied: pyparsing!=2.0.4,!=2.1.2,!=2.1.6,>=2.0.1 in /usr/
        Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.7/dist-pacl
        Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.7/dis-
         Requirement already satisfied: typing-extensions in /usr/local/lib/python3.7/dis-
        Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.7/dist-package:
         Requirement already satisfied: threadpoolctl>=2.0.0 in /usr/local/lib/python3.7/
        Requirement already satisfied: joblib>=0.11 in /usr/local/lib/python3.7/dist-pacl
         Building wheels for collected packages: lime
            Building wheel for lime (setup.py) ... done
            Created wheel for lime: filename=lime-0.2.0.1-py3-none-any.whl size=283858 shall
            Stored in directory: /root/.cache/pip/wheels/ca/cb/e5/ac701e12d365a08917bf4c61
         Successfully built lime
         Installing collected packages: lime
         Successfully installed lime-0.2.0.1
```

```
# Import packages and statements
import os
import glob
from google.colab import drive
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from tensorflow import keras
from tensorflow.keras.preprocessing.image import ImageDataGenerator, array to img, imc
from tensorflow.keras import models, layers, optimizers, regularizers, activations
from tensorflow.keras.layers import Conv2D, MaxPooling2D, Flatten, Dense, Dropout
from tensorflow.keras.callbacks import ModelCheckpoint, EarlyStopping, ReduceLROnPlate
from tensorflow.keras.applications import VGG16, VGG19
from sklearn.metrics import confusion matrix, classification report
from sklearn.utils.class_weight import compute_class_weight
import lime
from lime import lime base
from lime import lime image
from skimage.segmentation import mark boundaries
```

### Upload Data

```
from google.colab import drive
drive.mount('/content/drive')

Mounted at /content/drive

# Get current directory
print(os.getcwd())

# Get contents of the directory
print(os.listdir())

/content
['.config', 'drive', 'sample_data']

# Location of Zip File
drive_path = 'drive/MyDrive/Datasets/archive(6).zip'
local_path = '/content'
```

## Data Preprocessing and Exploration

- Obtain and Store the Data in a train / test / val split
- Find the total number of images
- · Scale data
- · Explore the data

```
# File Paths
path train pneumonia = 'drive/MyDrive/chest xray/train/PNEUMONIA'
path train normal = 'drive/MyDrive/chest xray/train/NORMAL'
path_test_pneumonia = 'drive/MyDrive/chest_xray/test/PNEUMONIA'
path_test_normal = 'drive/MyDrive/chest_xray/test/NORMAL'
path val pneumonia = 'drive/MyDrive/chest xray/val/PNEUMONIA'
path_val_normal = 'drive/MyDrive/chest_xray/val/NORMAL'
# How many images in each set
print('Train Pneumonia', len(os.listdir(path train pneumonia)))
print('Train Normal', len(os.listdir(path train normal)))
print('Test Pneumonia', len(os.listdir(path_test_pneumonia)))
print('Test Normal', len(os.listdir(path test normal)))
print('Val Pneumonia', len(os.listdir(path val pneumonia)))
print('Val Normal', len(os.listdir(path val normal)))
    Train Pneumonia 3875
    Train Normal 1341
    Test Pneumonia 390
    Test Normal 234
    Val Pneumonia 8
    Val Normal 8
# Create data generators
# Ensure class mode is binary
# Adjust batch size for training, testing, and validation sets (number of examples use
# Use a target size of 224x224 px for each image
train generator = ImageDataGenerator(rescale=1./255).flow from directory(
                                                     'drive/MyDrive/chest xray/train',
                                                      target size=(224, 224),
                                                      batch size=5216,
                                                      class mode='binary',
                                                      seed=123)
test generator = ImageDataGenerator(rescale=1./255).flow from directory(
                                                     'drive/MyDrive/chest xray/test',
                                                      target size=(224, 224),
                                                      batch_size=624,
                                                      class mode='binary',
                                                      seed=123)
val generator = ImageDataGenerator(rescale=1./255).flow from directory(
```

```
'drive/MyDrive/chest_xray/val',
target_size=(224, 224),
batch_size=16,
class_mode='binary',
seed=123)
```

```
Found 624 images belonging to 2 classes.
    Found 16 images belonging to 2 classes.
# Create the data sets with the train/test/val splits
X_train, y_train = next(train_generator)
X_test, y_test = next(test_generator)
X val, y val = next(val generator)
# Determine which classes are which (o and 1)
print(y_test[:20])
print(y_test.shape)
train generator.class indices
    [0. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 0. 1. 0. 0. 1. 1. 1. 1. 1.]
    (624,)
    {'NORMAL': 0, 'PNEUMONIA': 1}
# Check shapes of each set
print(X train.shape)
print(X test.shape)
print(X val.shape)
    (5216, 224, 224, 3)
    (624, 224, 224, 3)
    (16, 224, 224, 3)
# Look at example of normal xray
plt.imshow(np.squeeze(X train[0]))
plt.axis('off')
plt.title('Normal X-Ray')
plt.tight layout()
plt.show()
# Check the class label ('Normal':0)
print(y train[0])
```

Found 5216 images belonging to 2 classes.

#### Normal X-Ray



```
# Look at example of pneumonia xray
plt.imshow(np.squeeze(X_train[1]))
plt.axis('off')
plt.title('Pneumonia X-Ray')
plt.tight_layout()
plt.show()
# Check class label ('Pneumonia':1)
print(y_train[1])
```

#### 0.0

#### Pneumonia X-Ray



1.0

```
# Compare the two types
fig, axes = plt.subplots(1, 2, figsize=(12, 8))
axes[0].imshow(np.squeeze(X_train[0]))
axes[1].imshow(np.squeeze(X_train[1]))
axes[0].axis('off')
axes[1].axis('off')
axes[0].set_title('Normal Chest X-Ray')
axes[1].set_title('Pneumonia Chest X-Ray')
plt.show()
```

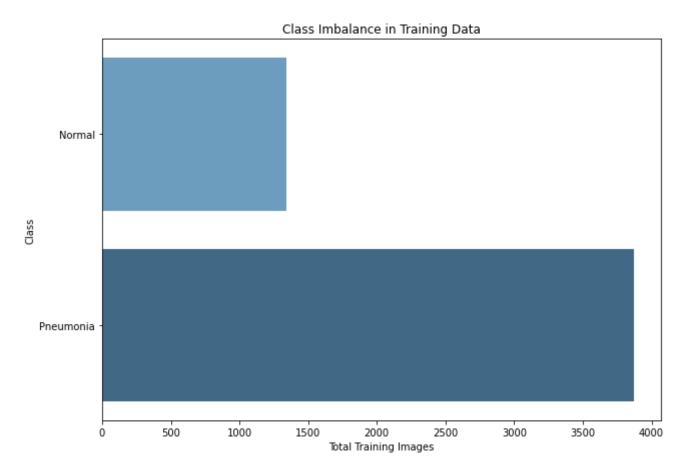






# Create bar plot to visualize class imbalance of training data

```
plt.figure(figsize=(10,7))
sns.barplot(x=[sum(y_train==0), sum(y_train==1)],
            y=['Normal', 'Pneumonia'],
            palette='Blues_d')
plt.title('Class Imbalance in Training Data')
plt.ylabel('Class')
plt.xlabel('Total Training Images')
plt.show()
```



According to the bar plot, there are far more pneumonia images than normal images.

### → Baseline CNN

This model will be our reference point. It will include the following:

- 3 convolutional layers (building blocks to produce an image)
- 3 max pooling layers (to downsample previous convolutional layers)
- 1 fully connected layer

```
baseline = models.Sequential()
baseline.add(Conv2D(32, (3, 3), activation='relu',
                    input shape=(224, 224, 3)))
baseline.add(MaxPooling2D((2, 2)))
baseline.add(Conv2D(32, (3, 3), activation='relu'))
baseline.add(MaxPooling2D(2, 2))
baseline.add(Conv2D(64, (3, 3), activation='relu'))
baseline.add(MaxPooling2D((2, 2)))
baseline.add(Flatten())
baseline.add(Dense(64, activation='relu'))
baseline.add(Dense(1, activation='sigmoid'))
baseline.compile(loss='binary crossentropy',
                optimizer='adam',
                metrics=['acc'])
# Look at summary to see all layers
baseline.summary()
```

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 222, 222, 32)	896
<pre>max_pooling2d (MaxPooling2D )</pre>	(None, 111, 111, 32)	0
conv2d_1 (Conv2D)	(None, 109, 109, 32)	9248
<pre>max_pooling2d_1 (MaxPooling 2D)</pre>	(None, 54, 54, 32)	0
conv2d_2 (Conv2D)	(None, 52, 52, 64)	18496
max_pooling2d_2 (MaxPooling	(None, 26, 26, 64)	0

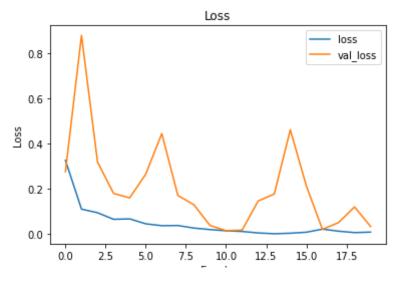
2D)

```
Epoch 2/20
Epoch 3/20
Epoch 4/20
Epoch 5/20
Epoch 6/20
Epoch 7/20
Epoch 8/20
Epoch 9/20
Epoch 10/20
Epoch 11/20
Epoch 12/20
Epoch 13/20
Epoch 14/20
Epoch 15/20
Epoch 16/20
Epoch 17/20
Epoch 18/20
```

```
Epoch 19/20
    Epoch 20/20
    # Write a function to evaliate the results of the model
def evaluate results(results, y test=y test):
 input results of model fitting.
 output loss and accuracy curves, and confusion matrix
 .....
 history = results.history
 plt.figure()
 plt.plot(history['loss'])
 plt.plot(history['val loss'])
 plt.legend(['loss', 'val loss'])
 plt.title('Loss')
 plt.xlabel('Epochs')
 plt.ylabel('Loss')
 plt.show()
 plt.figure()
 plt.plot(history['acc'])
 plt.plot(history['val_acc'])
 plt.legend(['acc', 'val acc'])
 plt.title('Accuracy')
 plt.xlabel('Epochs')
 plt.ylabel('Accuracy')
 plt.show()
 y hat test = results.model.predict(X test)
 thresh = 0.5
 y pred = (y hat test < thresh).astype(np.int)</pre>
 y_true = y_test.astype(np.int)
 cm = confusion matrix(y true, y pred)
 sns.heatmap(cm, annot=True, cmap='Blues', fmt='0.5g')
 plt.xlabel('Predictions')
 plt.ylabel('Actuals')
 plt.title('Model Confusion Matrix')
 plt.show()
 print(classification report(y true, y pred))
 print('\n')
 test loss, test acc = results.model.evaluate(X test, y test)
 print(f'Test Loss: {test loss}')
 print(f'Test Acc: {test acc}')
```

11/15/22, 12:06 PM

evaluate\_results(history)



#### **Results of Baseline:**

According to the confusion matrix, the model is mostly predicting the training class.

Due to a class imbalance-low validation and high training sets-this model is far from accurate. The model fits too well to the training set and is therefore "overfit".

For Iteration 2, I will implement an early stopping callback in attempt to balance the model. Essentially, this means that training will be stopped when the determined metric has stopped improving.

### CNN Iteration 2

- Address the class imbalance using class weights based on the results of the baseline model's confusion matrix, which shows the model is predicting mostly one class (training)
- Experiment with more epochs (the number of passes of the entire training dataset the machine learning algorithm has completed) and early stopping might prevent overfitting
- Reduce batch size to improve accuracy

```
from sklearn.utils import class_weight

# Set up our class weights
weights = compute_class_weight(class_weight = 'balanced', classes = np.unique(y_train)
weights_dict = dict(zip(np.unique(y_train), weights))
weights_dict
{0.0: 1.9448173005219984, 1.0: 0.6730322580645162}
```

support

recall f1-score

precision

```
# Set up early stopping and learning rate reduction
# Set patience to 5
early_stop = EarlyStopping(monitor='val_loss', mode='min', patience=5)
lr redox = ReduceLROnPlateau(monitor='val loss', factor=0.5, patience=5)
callbacks = [early_stop, lr_redox]
# Build model iteration 2 with improvements above and another conv layer
model2 = models.Sequential()
model2.add(Conv2D(32, (3, 3), activation='relu',
                    input_shape=(224, 224, 3)))
model2.add(MaxPooling2D((2, 2)))
model2.add(Conv2D(32, (3, 3), activation='relu'))
model2.add(MaxPooling2D(2, 2))
model2.add(Conv2D(64, (3, 3), activation='relu'))
model2.add(MaxPooling2D((2, 2)))
model2.add(Flatten())
model2.add(Dense(64, activation='relu'))
model2.add(Dense(1, activation='sigmoid'))
model2.compile(loss='binary crossentropy',
                optimizer='adam',
                metrics=['acc'])
```

#### model2.summary()

Model: "sequential\_1"

Layer (type)	Output Shape	Param #
conv2d_3 (Conv2D)	(None, 222, 222, 32)	896
<pre>max_pooling2d_3 (MaxPooling 2D)</pre>	(None, 111, 111, 32)	0
conv2d_4 (Conv2D)	(None, 109, 109, 32)	9248
<pre>max_pooling2d_4 (MaxPooling 2D)</pre>	(None, 54, 54, 32)	0
conv2d_5 (Conv2D)	(None, 52, 52, 64)	18496
<pre>max_pooling2d_5 (MaxPooling 2D)</pre>	(None, 26, 26, 64)	0
flatten_1 (Flatten)	(None, 43264)	0
dense_2 (Dense)	(None, 64)	2768960

```
dense_3 (Dense) (None, 1)
```

\_\_\_\_\_\_

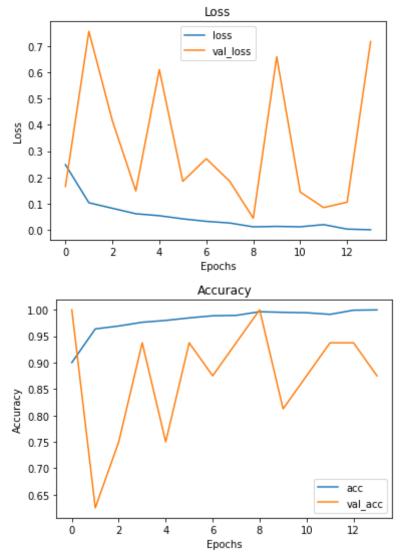
Total params: 2,797,665
Trainable params: 2,797,665
Non-trainable params: 0

results = model2.fit(X train,

\_\_\_\_\_

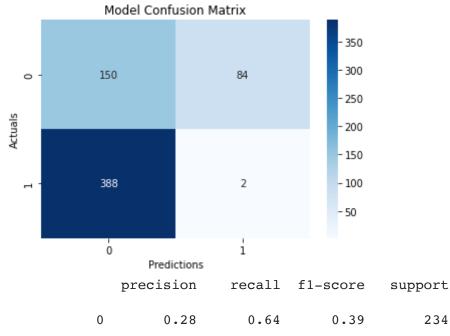
```
y_train,
  epochs=50,
  batch size=30,
  validation_data=(X_val, y_val),
  callbacks=callbacks)
Epoch 1/50
Epoch 2/50
Epoch 3/50
Epoch 4/50
Epoch 5/50
Epoch 6/50
Epoch 7/50
Epoch 8/50
Epoch 9/50
Epoch 10/50
Epoch 11/50
Epoch 12/50
Epoch 13/50
Epoch 14/50
```

evaluate results(results)



======= ] - 0s 7ms/step 20/20 [====== /usr/local/lib/python3.7/dist-packages/ipykernel\_launcher.py:29: DeprecationWarn: Deprecated in NumPy 1.20; for more details and guidance: <a href="https://numpy.org/devdo">https://numpy.org/devdo</a> /usr/local/lib/python3.7/dist-packages/ipykernel\_launcher.py:30: DeprecationWarn Deprecated in NumPy 1.20; for more details and guidance: <a href="https://numpy.org/devdo">https://numpy.org/devdo</a>

234



1	0.02	0.01	0.01	390
accuracy			0.24	624
macro avg	0.15	0.32	0.20	624
weighted avg	0.12	0.24	0.15	624

#### **Results of Iteration 2:**

Our accuracy remained largely the same, though the loss improved.

The training/validation ratio is heavily skewed. In the next iteratrion I will adjust the validation training split for greater balance.

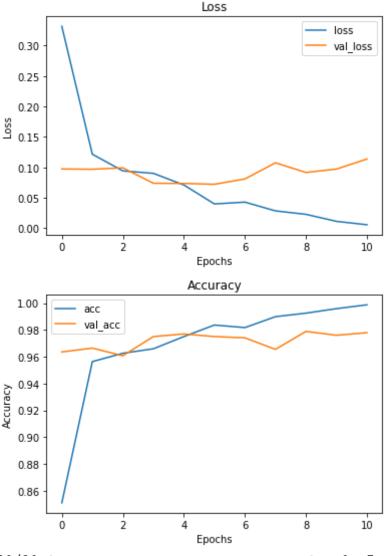
### → CNN Iteration 3

I will rework the validation size see if if this improves the loss and accuracy curves.

```
mod3 = models.Sequential()
mod3.add(Conv2D(32, (3, 3), activation='relu',
                input_shape=(224, 224, 3)))
mod3.add(MaxPooling2D((2, 2)))
mod3.add(Conv2D(32, (3, 3), activation='relu'))
mod3.add(MaxPooling2D(2, 2))
mod3.add(Conv2D(64, (3, 3), activation='relu'))
mod3.add(MaxPooling2D((2, 2)))
mod3.add(Flatten())
mod3.add(Dense(64, activation='relu'))
mod3.add(Dense(1, activation='sigmoid'))
mod3.compile(loss='binary crossentropy',
             optimizer='adam',
             metrics=['acc'])
results = mod3.fit(X train,
               y train,
               epochs=50,
               batch size=30,
               validation split=.2,
               class weight=weights dict,
               callbacks=callbacks)
   Epoch 1/50
   Epoch 2/50
   Epoch 3/50
```

```
Epoch 4/50
Epoch 5/50
Epoch 6/50
Epoch 7/50
Epoch 8/50
Epoch 9/50
Epoch 10/50
Epoch 11/50
```

evaluate\_results(results)



#### **Results of Iteration 3:**

The curves significantly improved. Model 3a improved a bit here. In the next iteration, I will keep this validation split instead of using the tiny validation set.

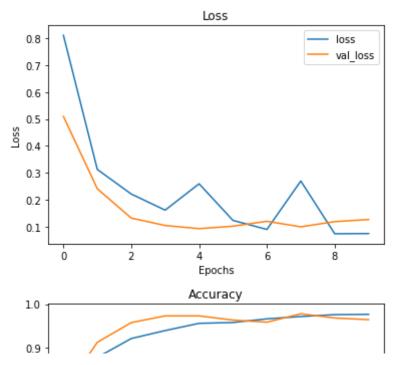
### CNN Iteration 4

In this iteration, I will add 2 convolutional layers per max pooling layer.

- I will also add convolutional layers will help detect more of the edges/nuances in the images with pneumonia
- I will also add another 2 blocks of layers (make the model deeper)
- Continue using 'RMSprop' as the optimizer

```
mod4 = models.Sequential()
```

```
mod4.add(Conv2D(32, (3, 3), activation='relu',
            input shape=(224, 224, 3)))
mod4.add(Conv2D(32, (3, 3), activation='relu'))
mod4.add(MaxPooling2D((2, 2)))
mod4.add(Conv2D(32, (3, 3), activation='relu'))
mod4.add(Conv2D(32, (3, 3), activation='relu'))
mod4.add(MaxPooling2D(2, 2))
mod4.add(Conv2D(64, (3, 3), activation='relu'))
mod4.add(Conv2D(64, (3, 3), activation='relu'))
mod4.add(MaxPooling2D((2, 2)))
mod4.add(Conv2D(64, (3, 3), activation='relu'))
mod4.add(Conv2D(64, (3, 3), activation='relu'))
mod4.add(MaxPooling2D((2, 2)))
mod4.add(Flatten())
mod4.add(Dense(128, activation='relu'))
mod4.add(Dense(64, activation='relu'))
mod4.add(Dense(1, activation='sigmoid'))
mod4.compile(loss='binary_crossentropy',
          optimizer='RMSprop',
          metrics=['acc'])
results = mod4.fit(X train,
           y train,
            epochs=50,
            batch size=32,
            validation split=.2,
            class weight=weights dict,
            callbacks=[early stop])
  Epoch 1/50
   Epoch 2/50
   131/131 [======
              Epoch 3/50
   Epoch 4/50
   Epoch 5/50
   Epoch 6/50
   131/131 [======
              Epoch 7/50
   Epoch 8/50
```



#### **Results of Iteration 4:**

There is significant model improvement in this iteration! According to the classification report and confusion matrix, the model is prediction normal x-rays very well.

Only a few "normal" images were classified as having pneumonia (False Positives). However, there are still many images with pneumonia misclassified as normal (False Negatives).

I will do another iteration on this model to improve accuracy.

Deprecated in Numbry 1 20. for more details and quidance. https://numbry.org/devider

### CNN Iteration 5

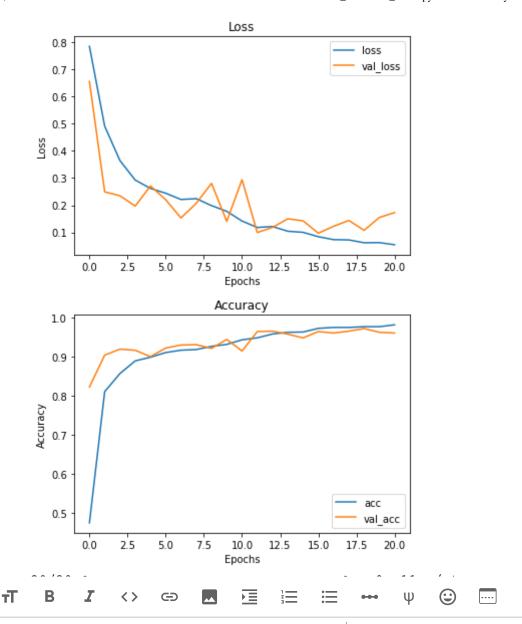
In this iteration, I attempt to pull more features out of images by deepening the neural network.

```
mod5.add(MaxPooling2D((2, 2)))
mod5.add(Conv2D(64, (3, 3), activation='relu'))
mod5.add(Conv2D(64, (3, 3), activation='relu'))
mod5.add(MaxPooling2D((2, 2)))
mod5.add(Conv2D(128, (3, 3), activation='relu'))
mod5.add(Conv2D(128, (3, 3), activation='relu'))
mod5.add(MaxPooling2D((2, 2)))
mod5.add(Flatten())
mod5.add(Dense(128, activation='relu'))
mod5.add(Dense(64, activation='relu'))
mod5.add(Dense(1, activation='sigmoid'))
mod5.compile(loss='binary crossentropy',
      optimizer='RMSprop',
      metrics=['acc'])
results = mod5.fit(X train,
        y train,
        epochs=50,
        batch_size=32,
        validation split=.2,
        class weight=weights dict,
        callbacks=[early stop])
 Epoch 1/50
  Epoch 2/50
  Epoch 3/50
  Epoch 4/50
  Epoch 5/50
  Epoch 6/50
  Epoch 7/50
  Epoch 8/50
  Epoch 9/50
  Epoch 10/50
  Epoch 11/50
  Epoch 12/50
  Epoch 13/50
```

```
Epoch 14/50
Epoch 15/50
Epoch 16/50
Epoch 17/50
Epoch 18/50
Epoch 19/50
Epoch 20/50
Epoch 21/50
```

evaluate\_results(results)

C→



\*\*Results of Iteration 5\*\*

When we look at all the models, model 4 ha False Negatives than most of the other models.

\*\*Which model is the best fit?\*\*

In · diagnosing · pneumonia, · the · best · practice
Negatives.

\*\*Iteration 4\*\* has less false negatives a reduce the number of False Negatives. of the other models. Iteration 4 also has be considered our final, best model. Iteration 4 has less false negatives and

#### **Results of Iteration 5**

When we look at all the models, model 4 has the best accuracy (82%), and less False Negatives than most of the other models.

#### Which model is the best fit?

In diagnosing pneumonia, the best practice is to reduce the number of False Negatives.

**Iteration 4** has less false negatives and less false positives than most of the other models. Iteration 4 also has an accuracy score of 82%. It will be considered our final, best model.

```
final_cnn_path = 'drive/MyDrive/Datasets/final_pre_trained_cnn.hd5'

mod5.save(final_cnn_path)

WARNING:absl:Found untraced functions such as _jit_compiled_convolution_op, _jit_

# Reload model
final_model = models.load_model(final_cnn_path)
```

## Image Feature Exploration

Use the Lime package to explore the features that lead to each classification.

I implemented Lime with information from this article.

```
# Get random image and label
label = y_train[2]
img = X_train[2]
img = img.astype('double')
# Get model pred
pred = mod5.predict(np.array([img]))
pred class = int(pred.round())
# Print true class, predicted class and image
print('True Class:', label)
print('Predicted Class:', pred class)
array to img(img)
    NameError
                                                 Traceback (most recent call last)
     <ipython-input-1-caadc7112d5d> in <module>
           1 # Get random image and label
     ---> 2 label = y_train[2]
           3 \text{ img} = X \text{ train}[2]
           5 img = img.astype('double')
    NameError: name 'y train' is not defined
      SEARCH STACK OVERFLOW
# Make an explainer
explainer = lime image.LimeImageExplainer()
```

 100%

2000/2000 [00:17<00:00, 109.85it/s]

```
1/1 [======= ] - 0s 128ms/step
1/1 [======= ] - 0s 21ms/step
1/1 [======] - 0s 22ms/step
1/1 [======= ] - 0s 21ms/step
1/1 [======] - 0s 21ms/step
1/1 [======= ] - 0s 23ms/step
1/1 [======= ] - 0s 21ms/step
1/1 [======= ] - 0s 22ms/step
1/1 [======= ] - 0s 22ms/step
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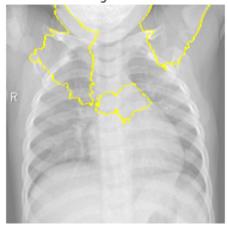
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 # Get random image and label
label = y train[0]
img = X train[0]
# Get model prediction
pred = mod5.predict(np.array([img]))
pred class = int(pred.round())
# Print true class, predicted class and image
print('True Class:', label)
```

```
print('Predicted Class:', pred_class)
array_to_img(img)
```

1/1 [=======] - 0s 19ms/step
True Class: 0.0
Predicted Class: 0



#### Features Contributing to Normal Classification



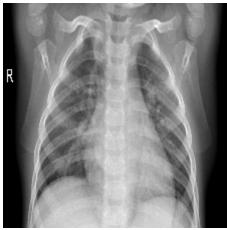
```
# Get a random image at index 2
label2 = y_train[1]
img2 = X_train[1]
img2 = img2.astype('double')

# Get model prediction
pred2 = mod5.predict(np.array([img2]))
pred_class2 = int(pred.round())
```

```
# Print true class, predicted class and image
print('True Class:', label2)
print('Predicted Class:', pred_class2)
array_to_img(img2)
```

1/1 [======] - Os 21ms/step

True Class: 1.0
Predicted Class: 0



100%

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fig, axes = plt.subplots(1, 2, figsize=(12, 8))
axes[0].imshow(mark boundaries(temp / 2 + 0.5, mask))
axes[1].imshow(mark_boundaries(temp2 / 2 + 0.5, mask2))
axes[0].axis('off')
axes[1].axis('off')
axes[0].set title('Correct Normal Classification')
axes[1].set title('Incorrect Pneumonia Classification')
plt.show()
```

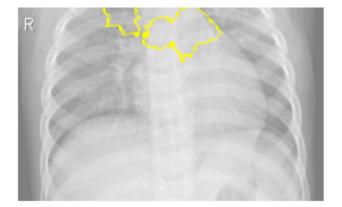
1/1 [======= ] - 0s 20ms/step

Correct Normal Classification



Incorrect Pneumonia Classification







Colab paid products - Cancel contracts here

0s

completed at 10:02 AM

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