2_Build_and_Train_Model

April 25, 2024

0.1 Skeleton Code

The code below provides a skeleton for the model building & training component of your project. You can add/remove/build on code however you see fit, this is meant as a starting point.

[ ]:
```
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import os
from glob import glob
%matplotlib inline
import matplotlib.pyplot as plt

##Import any other stats/DL/ML packages you may need here. E.g. Keras,␣
 ↪scikit-learn, etc.
import seaborn as sns
from itertools import chain
from skimage.io import imread,imshow
import matplotlib.image as mpimg #read png files
from scipy.ndimage import gaussian_filter
import scipy
from random import sample
import sklearn.model_selection as skl
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.layers import GlobalAveragePooling2D, Dense,␣
 ↪Dropout,Flatten,Conv2D,MaxPooling2D
from tensorflow.keras.models import Sequential, Model
from tensorflow.keras.applications.vgg16 import VGG16
from tensorflow.keras.applications.resnet import ResNet50
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.callbacks import ModelCheckpoint,␣
 ↪LearningRateScheduler,EarlyStopping, ReduceLROnPlateau
from sklearn.preprocessing import binarize
from sklearn.metrics import roc_curve, auc, precision_recall_curve,␣
 ↪confusion_matrix
```

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## Do some early processing of your metadata for easier model training:

[ ]:
```
## Load the NIH data to all_xray_df
all_xray_df = pd.read_csv('/home/shafeenkhan/Documents/My-all-programs--/
 ↪Semester-4/Aritificial Intelligence/Pneumonia_Detection_ChestX/data/
 ↪Data_Entry_2017.csv')

all_image_paths = {os.path.basename(x): x for x in
                   glob(os.path.join('/home/shafeenkhan/Documents/
 ↪My-all-programs--/Semester-4/Aritificial Intelligence/
 ↪Pneumonia_Detection_ChestX/data','images*', '*.png'))}
print('Scans found:', len(all_image_paths), ', Total Headers', all_xray_df.
 ↪shape[0])
all_xray_df['path'] = all_xray_df['Image Index'].map(all_image_paths.get)

pd.set_option('display.max_columns', None)
all_xray_df.head()
print(len(all_image_paths))
```

```
Scans found: 4999 , Total Headers 112120
4999
```

[ ]:
```
# Check the count of NaN values in the 'path' column
print(all_xray_df['path'].isnull().sum())

# Drop NaN values from the 'path' column and assign the result back to␣
 ↪all_xray_df
all_xray_df = all_xray_df.dropna(subset=['path'])

# Verify that there are no NaN values in the 'path' column after dropping
print(all_xray_df['path'].isnull().sum())
```

```
107121
0
```

[ ]:
```
## Here you may want to create some extra columns in your table with binary␣
 ↪indicators of certain diseases
## rather than working directly with the 'Finding Labels' column
```

```
all_labels=np.unique(list(chain(*all_xray_df['Finding Labels'].map(lambda x: x.
↪split('|')).tolist())))
all_labels=[x for x in all_labels if len(x)>0]
print(all_labels)

for label in all_labels:
    if len(label)>1:
        all_xray_df[label] = all_xray_df['Finding Labels'].map(lambda finding:␣
↪1.0 if label in finding else 0)


all_xray_df.head()
```

```
['Atelectasis', 'Cardiomegaly', 'Consolidation', 'Edema', 'Effusion',
'Emphysema', 'Fibrosis', 'Hernia', 'Infiltration', 'Mass', 'No Finding',
'Nodule', 'Pleural_Thickening', 'Pneumonia', 'Pneumothorax']
```

[ ]:
```
        Image Index          Finding Labels  Follow-up #  Patient ID  \
0  00000001_000.png            Cardiomegaly            0           1
1  00000001_001.png  Cardiomegaly|Emphysema            1           1
2  00000001_002.png   Cardiomegaly|Effusion            2           1
3  00000002_000.png              No Finding            0           2
4  00000003_000.png                  Hernia            0           3

  Patient Age Patient Gender View Position  OriginalImage[Width  Height]  \
0          58              M            PA                 2682     2749
1          58              M            PA                 2894     2729
2          58              M            PA                 2500     2048
3          81              M            PA                 2500     2048
4          81              F            PA                 2582     2991

  OriginalImagePixelSpacing[x     y]  Unnamed: 11  \
0                       0.143  0.143          NaN
1                       0.143  0.143          NaN
2                       0.168  0.168          NaN
3                       0.171  0.171          NaN
4                       0.143  0.143          NaN

                                                path  Atelectasis  \
0  /home/shafeenkhan/Documents/My-all-programs--/…          0.0
1  /home/shafeenkhan/Documents/My-all-programs--/…          0.0
2  /home/shafeenkhan/Documents/My-all-programs--/…          0.0
3  /home/shafeenkhan/Documents/My-all-programs--/…          0.0
4  /home/shafeenkhan/Documents/My-all-programs--/…          0.0

  Cardiomegaly  Consolidation  Edema  Effusion  Emphysema  Fibrosis  Hernia  \
0          1.0            0.0    0.0       0.0        0.0       0.0     0.0
```

```
1           1.0            0.0     0.0       0.0         1.0        0.0      0.0
2           1.0            0.0     0.0       1.0         0.0        0.0      0.0
3           0.0            0.0     0.0       0.0         0.0        0.0      0.0
4           0.0            0.0     0.0       0.0         0.0        0.0      1.0

   Infiltration  Mass  No Finding  Nodule  Pleural_Thickening  Pneumonia  \
0           0.0   0.0         0.0     0.0                 0.0        0.0
1           0.0   0.0         0.0     0.0                 0.0        0.0
2           0.0   0.0         0.0     0.0                 0.0        0.0
3           0.0   0.0         1.0     0.0                 0.0        0.0
4           0.0   0.0         0.0     0.0                 0.0        0.0

   Pneumothorax
0           0.0
1           0.0
2           0.0
3           0.0
4           0.0
```

```
[ ]: ## Here we can create a new column called 'pneumonia_class' that will allow us␣
      ↪to look at
     ## images with or without pneumonia for binary classification

     all_xray_df['pneumonia_class']=all_xray_df['Pneumonia'].replace({0.0:
      ↪'Negative',1.0:'Positive'})
     all_xray_df[all_xray_df['pneumonia_class']== 'Positive']
```

```
[ ]:           Image Index                                   Finding Labels  \
     48    00000013_010.png                    Effusion|Pneumonia|Pneumothorax
     126   00000032_012.png          Atelectasis|Consolidation|Edema|Pneumonia
     253   00000056_000.png                                   Nodule|Pneumonia
     276   00000061_012.png  Edema|Effusion|Infiltration|Pleural_Thickening…
     279   00000061_015.png                                          Pneumonia
     …                  …                                                …
     4795  00001285_001.png                       Edema|Infiltration|Pneumonia
     4796  00001285_002.png                       Edema|Infiltration|Pneumonia
     4875  00001301_039.png                           Edema|Effusion|Pneumonia
     4926  00001317_000.png                             Infiltration|Pneumonia
     4928  00001317_002.png                                          Pneumonia

           Follow-up #  Patient ID  Patient Age Patient Gender View Position  \
     48             10          13           60              M            AP
     126            12          32           55              F            AP
     253             0          56           76              M            PA
     276            12          61           77              M            AP
     279            15          61           77              M            AP
     …            …          …           …              …            …
```

```
4795              1        1285         33           M           AP
4796              2        1285         33           M           AP
4875             39        1301         57           F           AP
4926              0        1317         48           M           PA
4928              2        1317         48           M           PA

      OriginalImage[Width  Height]  OriginalImagePixelSpacing[x     y]  \
48                   3056     2544                          0.139  0.139
126                  2500     2048                          0.168  0.168
253                  2500     2048                          0.168  0.168
276                  3056     2544                          0.139  0.139
279                  3056     2544                          0.139  0.139
…                       …      …                              …     …
4795                 2500     2048                          0.168  0.168
4796                 2500     2048                          0.168  0.168
4875                 2500     2048                          0.168  0.168
4926                 2954     2991                          0.143  0.143
4928                 2992     2991                          0.143  0.143

      Unnamed: 11                                              path  \
48            NaN  /home/shafeenkhan/Documents/My-all-programs--/…
126           NaN  /home/shafeenkhan/Documents/My-all-programs--/…
253           NaN  /home/shafeenkhan/Documents/My-all-programs--/…
276           NaN  /home/shafeenkhan/Documents/My-all-programs--/…
279           NaN  /home/shafeenkhan/Documents/My-all-programs--/…
…             …                                                  …
4795          NaN  /home/shafeenkhan/Documents/My-all-programs--/…
4796          NaN  /home/shafeenkhan/Documents/My-all-programs--/…
4875          NaN  /home/shafeenkhan/Documents/My-all-programs--/…
4926          NaN  /home/shafeenkhan/Documents/My-all-programs--/…
4928          NaN  /home/shafeenkhan/Documents/My-all-programs--/…

      Atelectasis  Cardiomegaly  Consolidation  Edema  Effusion  Emphysema  \
48            0.0           0.0            0.0    0.0       1.0        0.0
126           1.0           0.0            1.0    1.0       0.0        0.0
253           0.0           0.0            0.0    0.0       0.0        0.0
276           0.0           0.0            0.0    1.0       1.0        0.0
279           0.0           0.0            0.0    0.0       0.0        0.0
…             …            …            …    …      …       …
4795          0.0           0.0            0.0    1.0       0.0        0.0
4796          0.0           0.0            0.0    1.0       0.0        0.0
4875          0.0           0.0            0.0    1.0       1.0        0.0
4926          0.0           0.0            0.0    0.0       0.0        0.0
4928          0.0           0.0            0.0    0.0       0.0        0.0

      Fibrosis  Hernia  Infiltration  Mass  No Finding  Nodule  \
48         0.0     0.0           0.0   0.0         0.0     0.0
```

```
126         0.0     0.0           0.0    0.0         0.0     0.0
253         0.0     0.0           0.0    0.0         0.0     1.0
276         0.0     0.0           1.0    0.0         0.0     0.0
279         0.0     0.0           0.0    0.0         0.0     0.0
…        …      …           …    …         …      …
4795        0.0     0.0           1.0    0.0         0.0     0.0
4796        0.0     0.0           1.0    0.0         0.0     0.0
4875        0.0     0.0           0.0    0.0         0.0     0.0
4926        0.0     0.0           1.0    0.0         0.0     0.0
4928        0.0     0.0           0.0    0.0         0.0     0.0

      Pleural_Thickening  Pneumonia  Pneumothorax pneumonia_class
48                   0.0        1.0           1.0        Positive
126                  0.0        1.0           0.0        Positive
253                  0.0        1.0           0.0        Positive
276                  1.0        1.0           0.0        Positive
279                  0.0        1.0           0.0        Positive
…                  …         …           …            …
4795                 0.0        1.0           0.0        Positive
4796                 0.0        1.0           0.0        Positive
4875                 0.0        1.0           0.0        Positive
4926                 0.0        1.0           0.0        Positive
4928                 0.0        1.0           0.0        Positive

[65 rows x 29 columns]
```

1.1 Create your training and testing data:

Based on EDA work, the Data_Entr_2017.cvs contains 1,431 Images positive for Pneumonia and 110,689 Images negative for Pneumonia.

The data set will be split into 80% Training data and 20% for testing data.

For the training data set, the positive to negative images must be equal in number. Demographics such as age and gender must reflect the general data set. Pneumonia Positive =1144.8 counts, Pneumonia Negative = 1144.8 counts

For the validation data set, positive to negative Pneumonia cases, as well as demographics, must reflect the general data set.
Pneumonia Positive =286.2 counts, Pneumonia Negative = 22,137.8 counts

```
[ ]: def create_splits(df_name):

         ## Either build your own or use a built-in library to split your original␣
     ↪dataframe into two sets
         ## that can be used for training and testing your model
         ## It's important to consider here how balanced or imbalanced you want each␣
     ↪of those sets to be
         ## for the presence of pneumonia
```

```
    train_data, val_data=skl.train_test_split(df_name,
                                                test_size=0.2,
                                               stratify=df_name['Pneumonia'])

    #balance train_data
    p_ind=train_data[train_data['pneumonia_class']=='Positive'].index.tolist()
    n_ind=train_data[train_data['pneumonia_class']=='Negative'].index.tolist()
    n_sample = sample(n_ind,len(p_ind))
    train_data=train_data.loc[p_ind+n_sample]

    """balance val_data.  In the clinical setting where this algorithm will be␣
↪deployed,
    patients are being x-rayed based on their clinical symptoms that make␣
↪Pneumonia
    highly likely.  The prevalence of Pneumonia is about 20% of those who are␣
↪x-rayed."""
    vp_ind=val_data[val_data['pneumonia_class']=='Positive'].index.tolist()
    vn_ind=val_data[val_data['pneumonia_class']=='Negative'].index.tolist()
    vn_sample = sample(vn_ind,4*len(vp_ind))
    val_data=val_data.loc[vp_ind+vn_sample]

    return train_data, val_data
```

[ ]:
```
train_data, val_data = create_splits(all_xray_df)
```

[ ]:
```
(train_data['pneumonia_class']=='Positive').value_counts()
```

[ ]:
```
pneumonia_class
True     52
False    52
Name: count, dtype: int64
```

[ ]:
```
(val_data['pneumonia_class']=='Negative').value_counts()
```

[ ]:
```
pneumonia_class
True     52
False    13
Name: count, dtype: int64
```

train_data and val_data have the correct number of Pneuominia-positive and Pneumonia-negative cases in each set.

[ ]:
```
#check train_data distribution for changes in Age distribution of Males with␣
 ↪Pneumonia
scipy.stats.ttest_ind(all_xray_df['Patient␣
 ↪Age'][(all_xray_df['Pneumonia']==True) & (all_xray_df['Patient␣
 ↪Gender']=='M')],
                     train_data['Patient Age'][(train_data['Pneumonia']==True)␣
 ↪& (train_data['Patient Gender']=='M')]
)
```

```
[ ]: TtestResult(statistic=-0.33011002462014627, pvalue=0.7423467983668198, df=67.0)
```

```
[ ]: #check train_data distribution for changes in Age distribution of Females with␣
      ↪Pneumonia
     scipy.stats.ttest_ind(all_xray_df['Patient␣
      ↪Age'][(all_xray_df['Pneumonia']==True) & (all_xray_df['Patient␣
      ↪Gender']=='F')],
                          train_data['Patient Age'][(train_data['Pneumonia']==True)␣
      ↪& (train_data['Patient Gender']=='F')]
     )
```

```
[ ]: TtestResult(statistic=0.24749954692608628, pvalue=0.8056230495565373, df=46.0)
```

```
[ ]: train_data['Patient Gender'].value_counts()
```

```
[ ]: Patient Gender
     M    57
     F    47
     Name: count, dtype: int64
```

Train Dataset has Male 57%, Female 43%. This is similar to the overall dataset with 56.5% Male, 43.5% Female

```
[ ]: #check val_data distribution for changes in Age distribution of Males with␣
      ↪Pneumonia
     scipy.stats.ttest_ind(all_xray_df['Patient␣
      ↪Age'][(all_xray_df['Pneumonia']==True) & (all_xray_df['Patient␣
      ↪Gender']=='M')],
                          val_data['Patient Age'][(val_data['Pneumonia']== True) &␣
      ↪(val_data['Patient Gender']=='M')]
     )
```

```
[ ]: TtestResult(statistic=0.7656417861109287, pvalue=0.44780035921568495, df=46.0)
```

```
[ ]: #check val_data distribution for changes in Age distribution of Females with␣
      ↪Pneumonia
     scipy.stats.ttest_ind(all_xray_df['Patient Age'][(all_xray_df['Pneumonia']==␣
      ↪True) & (all_xray_df['Patient Gender']=='F')],
                          val_data['Patient Age'][(val_data['Pneumonia']==True) &␣
      ↪(val_data['Patient Gender']=='F')]
     )
```

```
[ ]: TtestResult(statistic=-0.7416823564620066, pvalue=0.46445589982939794, df=28.0)
```

[ ]:
```
val_data['Patient Gender'].value_counts()
```

[ ]:
```
Patient Gender
M    35
F    30
Name: count, dtype: int64
```

Validation Dataset has Male 58%, Female 42%. This is similar to the overall dataset with 56.5% Male, 43.5% Female

TTests above show that age and gender distributions in train_data and val_data reflect the general data set's demographic distributions

[ ]:
```
train_data['View Position'].value_counts()
```

[ ]:
```
View Position
PA    62
AP    42
Name: count, dtype: int64
```

Training dataset has 51.9% PA and 48.1% AP viewing position. This is similar to the overall dataset with 60% PA and 40% AP position.

[ ]:
```
val_data['View Position'].value_counts()
```

[ ]:
```
View Position
PA    37
AP    28
Name: count, dtype: int64
```

Validation dataset has 56.9% PA and 43.1% AP viewing position. This is similar to the overall dataset with 60% PA and 40% AP position.

2 Now we can begin our model-building & training

First suggestion: perform some image augmentation on your data

[ ]:
```
def my_image_augmentation_train():

    ## recommendation here to implement a package like Keras' ImageDataGenerator
    ## with some of the built-in augmentations

    ## keep an eye out for types of augmentation that are or are not␣
↪appropriate for medical imaging data
    ## Also keep in mind what sort of augmentation is or is not appropriate for␣
↪testing vs validation data

    ## STAND-OUT SUGGESTION: implement some of your own custom augmentation␣
↪that's *not*
    ## built into something like a Keras package
    my_train_idg = ImageDataGenerator(rescale = 1./255,
                                      horizontal_flip = True,
                                      height_shift_range = 0.1,
                                      width_shift_range = 0.1,
                                      rotation_range = 15,
                                      shear_range = 0.1,
                                      zoom_range = 0.1,
                                      samplewise_center = True,
                                      samplewise_std_normalization = True
                                     )
    return my_train_idg

def my_image_augmentation_val():
    my_val_idg = ImageDataGenerator(rescale = 1./255.,
                                    samplewise_center=True,
                                    samplewise_std_normalization=True
                                    )
    return my_val_idg


def make_train_gen(my_train_idg, train_df):

    ## Create the actual generators using the output of my_image_augmentation␣
 ↪for your training data
    ## Suggestion here to use the flow_from_dataframe library, e.g.:

    train_gen = my_train_idg.flow_from_dataframe(dataframe=train_df,
                                                 directory=None,
                                                 x_col = 'path',
                                                 y_col = 'pneumonia_class',
                                                 class_mode = 'binary',
                                                 target_size = (224,224),
                                                 batch_size = 16
                                                 )

    return train_gen


def make_val_gen(my_val_idg, val_df):

    val_gen = my_val_idg.flow_from_dataframe(dataframe = val_df,
                                             directory=None,
                                             x_col = "path",
                                             y_col = 'pneumonia_class',
                                             class_mode = 'binary',
                                             target_size = (224,224),
                                             batch_size = 32,
                                             shuffle=False
                                            )

    return val_gen
```

```
[ ]: val_data['path'] = val_data['path'].astype(str)
```

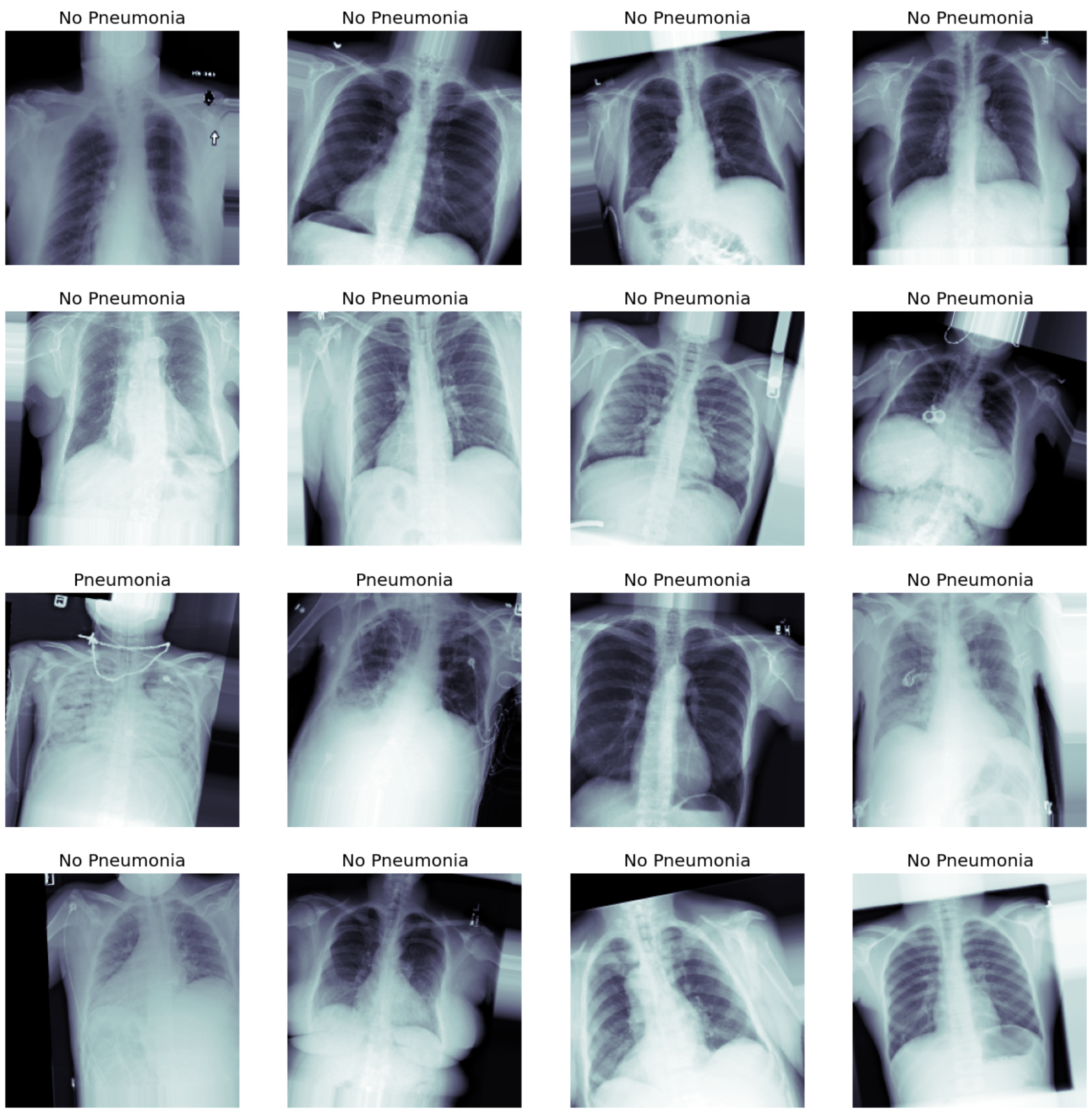
```
[ ]: ## May want to pull a single large batch of random validation data for testing␣
      ↪after each epoch:
     val_gen = make_val_gen(my_image_augmentation_val(),val_data)
     valX, valY = val_gen.next()
```

```
Found 65 validated image filenames belonging to 2 classes.
```

```
[ ]: ###### May want to look at some examples of our augmented training data.
     ## This is helpful for understanding the extent to which data is being␣
      ↪manipulated prior to training,
     ## and can be compared with how the raw data look prior to augmentation
     train_data['path'] = train_data['path'].astype(str)
     train_idg = my_image_augmentation_train()
     train_gen = make_train_gen(train_idg, train_data)

     t_x, t_y = next(train_gen)
     print("Batch Mean: " + str(t_x.mean()) + " Batch Std: " + str(t_x.std()))
     fig, m_axs = plt.subplots(4, 4, figsize = (16, 16))
     for (c_x, c_y, c_ax) in zip(t_x, t_y, m_axs.flatten()):
         c_ax.imshow(c_x[:,:,0], cmap = 'bone')
         if c_y == 1:
             c_ax.set_title('Pneumonia')
         else:
             c_ax.set_title('No Pneumonia')
         c_ax.axis('off')
```

```
Found 104 validated image filenames belonging to 2 classes.
Batch Mean: -8.920423e-09 Batch Std: 0.99999565
```



2.1 Build your model:

Recommendation here to use a pre-trained network downloaded from Keras for fine-tuning

[ ]:
```python
def load_pretrained_vgg_model(layer_of_interest):

    model = VGG16(include_top=True, weights='imagenet')
    transfer_layer = model.get_layer(layer_of_interest)
    vgg_model = Model(inputs = model.input, outputs = transfer_layer.output)

    for layer in vgg_model.layers[0:-2]:
        layer.trainable = False
    return vgg_model
```

[ ]:
```
def build_my_model(pretrained_model):

    my_model = Sequential()
    my_model.add(pretrained_model)
    my_model.add(Flatten())
    my_model.add(Dense(1024, activation = 'relu'))
    my_model.add(Dropout(0.5))
    my_model.add(Dense(512, activation = 'relu'))
    my_model.add(Dropout(0.5))
    my_model.add(Dense(256, activation = 'relu'))
    my_model.add(Dropout(0.5))
    my_model.add(Dense(1, activation = 'sigmoid'))

    optimizer = Adam(learning_rate = 1e-3)
    loss = 'binary_crossentropy'
    metrics = ['binary_accuracy']

    my_model.compile(optimizer=optimizer, loss=loss, metrics=metrics)

#    my_model_history = my_model.fit_generator(train_gen,
#                                             validation_data=(val_X, val_Y),
#                                             epochs=epochs)


    return my_model


## STAND-OUT Suggestion: choose another output layer besides just the last␣
 ↪classification layer of your modele
## to output class activation maps to aid in clinical interpretation of your␣
 ↪model's results
```

[ ]:
```
## Below is some helper code that will allow you to add checkpoints to your␣
 ↪model,
## This will save the 'best' version of your model by comparing it to previous␣
 ↪epochs of training

## Note that you need to choose which metric to monitor for your model's 'best'␣
 ↪performance if using this code.
## The 'patience' parameter is set to 10, meaning that your model will train␣
 ↪for ten epochs without seeing
## improvement before quitting

## Monitor Validation Binary accuracy, because the validation accuracy allows␣
 ↪us to see if the model can be generalized
```

```
## to images that it wasn't trained on.  Validation accuracy is chosen over␣
 ↪validation loss, because this problem
## is to detect Positive-Pneumonia or Negative-Pneumonia.

weight_path="/home/shafeenkhan/Documents/My-all-programs--/Semester-4/
 ↪Aritificial Intelligence/Pneumonia_Detection_ChestX/out{}_my_model.best.
 ↪hdf5".format('xray_class')

checkpoint = ModelCheckpoint(weight_path,
                             monitor= 'val_loss',
                             verbose=1,
                             save_best_only=True,
                             mode= 'min',
                             save_weights_only = True)

early = EarlyStopping(monitor= 'val_loss',
                      mode= 'min',
                      patience=10)

callbacks_list = [checkpoint, early]
```

2.1.1 Start training!

```
[ ]: ## train your model
vgg_model = load_pretrained_vgg_model('block5_pool')
my_model = build_my_model(vgg_model)
history = my_model.fit_generator(train_gen,
                           validation_data = val_gen,
                           epochs = 10,
                           callbacks = callbacks_list)
```

```
/tmp/ipykernel_49176/2928753405.py:4: UserWarning: `Model.fit_generator` is
deprecated and will be removed in a future version. Please use `Model.fit`,
which supports generators.
  history = my_model.fit_generator(train_gen,

Epoch 1/10
7/7 [==============================] - ETA: 0s - loss: 2.8362 - binary_accuracy:
0.3942
Epoch 00001: val_loss improved from inf to 0.51665, saving model to
/home/shafeenkhan/Documents/My-all-programs--/Semester-4/Aritificial
Intelligence/Pneumonia_Detection_ChestX/outxray_class_my_model.best.hdf5
7/7 [==============================] - 13s 2s/step - loss: 2.8362 -
binary_accuracy: 0.3942 - val_loss: 0.5166 - val_binary_accuracy: 0.8000
Epoch 2/10
7/7 [==============================] - ETA: 0s - loss: 0.9564 - binary_accuracy:
0.5000
Epoch 00002: val_loss did not improve from 0.51665
```

```
7/7 [==============================] - 12s 2s/step - loss: 0.9564 -
binary_accuracy: 0.5000 - val_loss: 0.7055 - val_binary_accuracy: 0.4462
Epoch 3/10
7/7 [==============================] - ETA: 0s - loss: 0.7032 - binary_accuracy:
0.5288
Epoch 00003: val_loss did not improve from 0.51665
7/7 [==============================] - 12s 2s/step - loss: 0.7032 -
binary_accuracy: 0.5288 - val_loss: 0.6136 - val_binary_accuracy: 0.8308
Epoch 4/10
7/7 [==============================] - ETA: 0s - loss: 0.7025 - binary_accuracy:
0.5673
Epoch 00004: val_loss did not improve from 0.51665
7/7 [==============================] - 12s 2s/step - loss: 0.7025 -
binary_accuracy: 0.5673 - val_loss: 0.6783 - val_binary_accuracy: 0.4923
Epoch 5/10
7/7 [==============================] - ETA: 0s - loss: 0.6875 - binary_accuracy:
0.5192
Epoch 00005: val_loss did not improve from 0.51665
7/7 [==============================] - 12s 2s/step - loss: 0.6875 -
binary_accuracy: 0.5192 - val_loss: 0.6213 - val_binary_accuracy: 0.6308
Epoch 6/10
7/7 [==============================] - ETA: 0s - loss: 0.6292 - binary_accuracy:
0.6923
Epoch 00006: val_loss improved from 0.51665 to 0.50458, saving model to
/home/shafeenkhan/Documents/My-all-programs--/Semester-4/Aritificial
Intelligence/Pneumonia_Detection_ChestX/outxray_class_my_model.best.hdf5
7/7 [==============================] - 12s 2s/step - loss: 0.6292 -
binary_accuracy: 0.6923 - val_loss: 0.5046 - val_binary_accuracy: 0.6923
Epoch 7/10
7/7 [==============================] - ETA: 0s - loss: 0.6977 - binary_accuracy:
0.6250
Epoch 00007: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.6977 -
binary_accuracy: 0.6250 - val_loss: 0.5563 - val_binary_accuracy: 0.6462
Epoch 8/10
7/7 [==============================] - ETA: 0s - loss: 0.5927 - binary_accuracy:
0.6731
Epoch 00008: val_loss did not improve from 0.50458
7/7 [==============================] - 11s 2s/step - loss: 0.5927 -
binary_accuracy: 0.6731 - val_loss: 0.8389 - val_binary_accuracy: 0.4462
Epoch 9/10
7/7 [==============================] - ETA: 0s - loss: 0.5755 - binary_accuracy:
0.6731
Epoch 00009: val_loss did not improve from 0.50458
7/7 [==============================] - 11s 2s/step - loss: 0.5755 -
binary_accuracy: 0.6731 - val_loss: 0.7019 - val_binary_accuracy: 0.5692
Epoch 10/10
7/7 [==============================] - ETA: 0s - loss: 0.5446 - binary_accuracy:
```

```
0.7212
Epoch 00010: val_loss did not improve from 0.50458
7/7 [==============================] - 11s 2s/step - loss: 0.5446 -
binary_accuracy: 0.7212 - val_loss: 0.5402 - val_binary_accuracy: 0.6615
```

[ ]:
```
def plot_history(history,epoch):
    plt.style.use('ggplot')
    plt.figure(figsize=(12,12))
    plt.style.use('ggplot')
    plt.plot(range(epoch),history.history['loss'],label='Loss', color='green')
    plt.plot(range(epoch),history.history['val_loss'],label='Validation_Loss',␣
 ↪color = 'red')
    plt.plot(range(epoch),history.
 ↪history['binary_accuracy'],label='Binary_Accuracy',color='blue')
    plt.plot(range(epoch),history.
 ↪history['val_binary_accuracy'],label='Validation_Bin_Accuracy',color='purple')
    plt.legend()
    plt.xlabel('Epoch')
    plt.ylabel('Loss/Accuracy')
    plt.savefig('/home/shafeenkhan/Documents/My-all-programs--/Semester-4/
 ↪Aritificial Intelligence/Pneumonia_Detection_ChestX/out/
 ↪Model_Training_Performance')
    plt.show()

    return
```

[ ]:
```
plot_history(history,10)
```

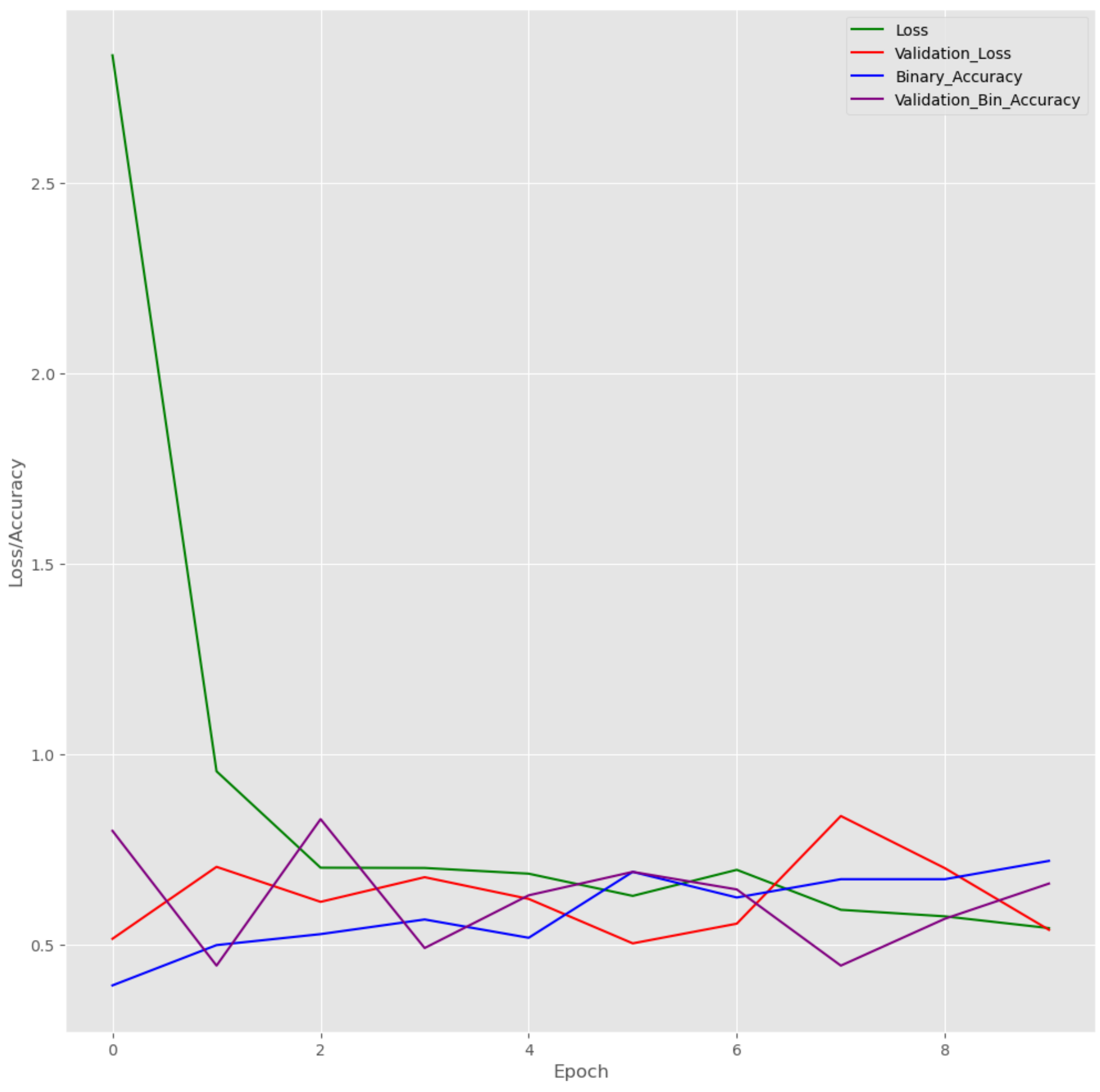


Figure 1. Model 1 Training History

```
[ ]: performance = []
```

```
[ ]: history_df=pd.DataFrame(history.history)
     performance.
       ↪append(history_df[history_df['val_loss']==min(history_df['val_loss'])])
     performance
```

```
[ ]: [       loss  binary_accuracy  val_loss  val_binary_accuracy
      5  0.629213         0.692308  0.504585             0.692308]
```

```
[ ]: def build_my_model2(pretrained_model):
         "Add one Dense layer and one Dropout Layer"
         my_model = Sequential()
         my_model.add(pretrained_model)
         my_model.add(Flatten())
         my_model.add(Dense(2048, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(1024, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(512, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(256, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(1, activation = 'sigmoid'))

         optimizer = Adam(learning_rate = 1e-3)
         loss = 'binary_crossentropy'
         metrics = ['binary_accuracy']

         my_model.compile(optimizer=optimizer, loss=loss, metrics=metrics)

         return my_model
```

```
[ ]: #Train Model #2 with Dense and Dropout Layer
     vgg_model = load_pretrained_vgg_model('block5_pool')
     my_model2 = build_my_model2(vgg_model)
     history2 = my_model2.fit_generator(train_gen,
                                        validation_data = val_gen,
                                        epochs = 10,
                                        callbacks = callbacks_list)
```

```
/tmp/ipykernel_49176/2599443291.py:4: UserWarning: `Model.fit_generator` is
deprecated and will be removed in a future version. Please use `Model.fit`,
which supports generators.
  history2 = my_model2.fit_generator(train_gen,
```

```
Epoch 1/10
7/7 [==============================] - ETA: 0s - loss: 2.6616 - binary_accuracy:
0.5385
Epoch 00001: val_loss did not improve from 0.50458
7/7 [==============================] - 13s 2s/step - loss: 2.6616 -
binary_accuracy: 0.5385 - val_loss: 1.3987 - val_binary_accuracy: 0.2000
Epoch 2/10
7/7 [==============================] - ETA: 0s - loss: 1.1645 - binary_accuracy:
0.4904
Epoch 00002: val_loss did not improve from 0.50458
7/7 [==============================] - 13s 2s/step - loss: 1.1645 -
binary_accuracy: 0.4904 - val_loss: 0.5981 - val_binary_accuracy: 0.8000
```

```
Epoch 3/10
7/7 [==============================] - ETA: 0s - loss: 0.7335 - binary_accuracy:
0.4808
Epoch 00003: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.7335 -
binary_accuracy: 0.4808 - val_loss: 0.7008 - val_binary_accuracy: 0.3231
Epoch 4/10
7/7 [==============================] - ETA: 0s - loss: 0.6806 - binary_accuracy:
0.5769
Epoch 00004: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.6806 -
binary_accuracy: 0.5769 - val_loss: 0.7176 - val_binary_accuracy: 0.3538
Epoch 5/10
7/7 [==============================] - ETA: 0s - loss: 0.7179 - binary_accuracy:
0.5192
Epoch 00005: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.7179 -
binary_accuracy: 0.5192 - val_loss: 0.6286 - val_binary_accuracy: 0.7077
Epoch 6/10
7/7 [==============================] - ETA: 0s - loss: 0.6467 - binary_accuracy:
0.6250
Epoch 00006: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.6467 -
binary_accuracy: 0.6250 - val_loss: 0.6415 - val_binary_accuracy: 0.5846
Epoch 7/10
7/7 [==============================] - ETA: 0s - loss: 0.7357 - binary_accuracy:
0.5096
Epoch 00007: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.7357 -
binary_accuracy: 0.5096 - val_loss: 0.6104 - val_binary_accuracy: 0.6923
Epoch 8/10
7/7 [==============================] - ETA: 0s - loss: 0.6939 - binary_accuracy:
0.5673
Epoch 00008: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.6939 -
binary_accuracy: 0.5673 - val_loss: 0.7228 - val_binary_accuracy: 0.5231
Epoch 9/10
7/7 [==============================] - ETA: 0s - loss: 0.6439 - binary_accuracy:
0.5769
Epoch 00009: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.6439 -
binary_accuracy: 0.5769 - val_loss: 0.7606 - val_binary_accuracy: 0.6462
Epoch 10/10
7/7 [==============================] - ETA: 0s - loss: 0.6244 - binary_accuracy:
0.6058
Epoch 00010: val_loss did not improve from 0.50458
7/7 [==============================] - 13s 2s/step - loss: 0.6244 -
binary_accuracy: 0.6058 - val_loss: 0.5859 - val_binary_accuracy: 0.6923
```

```
[ ]: plot_history(history2,10)
```

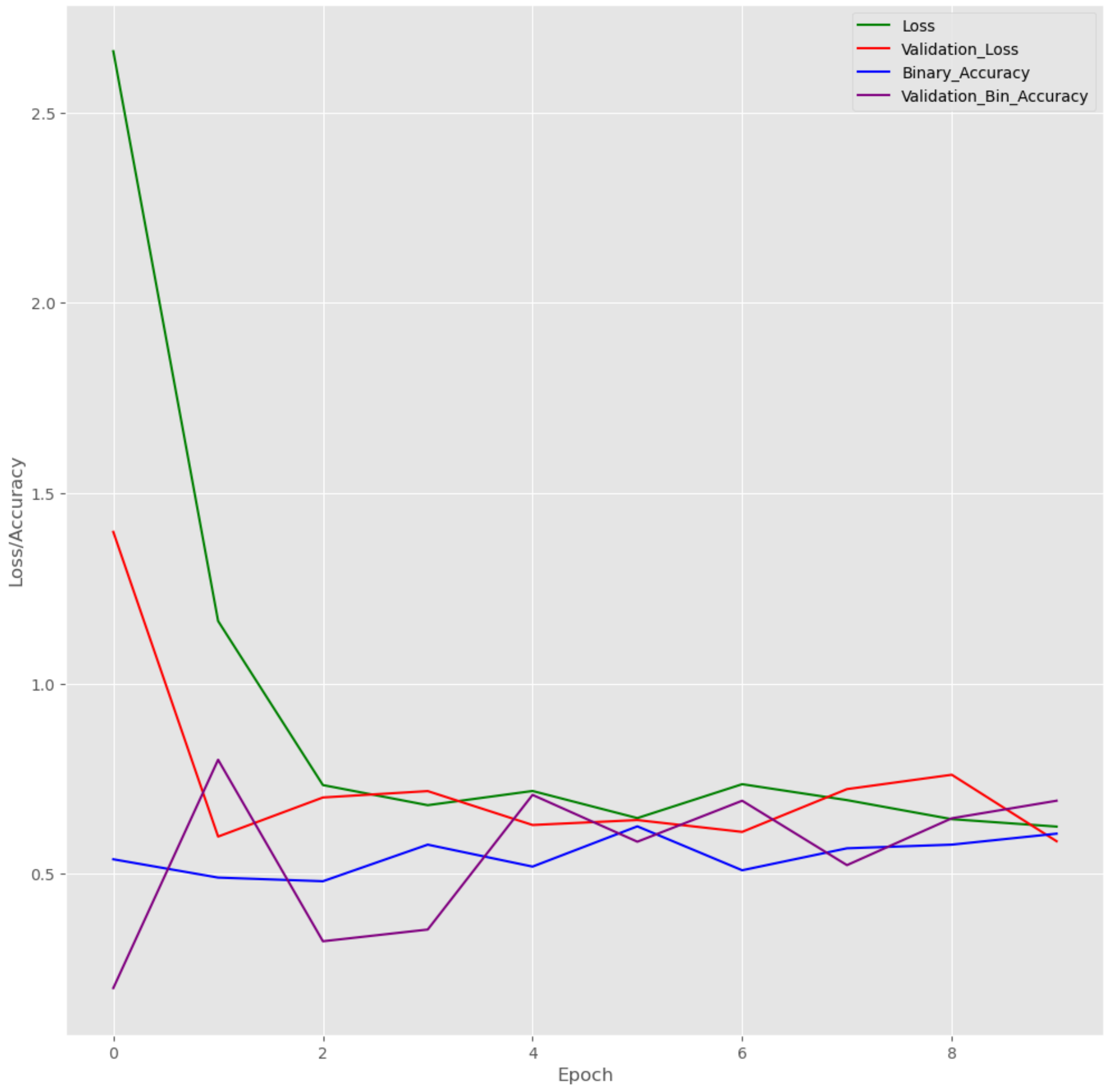


Figure 2. Model 2 Training History

```
[ ]: history2_df=pd.DataFrame(history2.history)
     performance.
      ↪append(history2_df[history2_df['val_loss']==min(history2_df['val_loss'])])
     performance
```

```
[ ]: [       loss  binary_accuracy  val_loss  val_binary_accuracy
      5  0.629213         0.692308  0.504585             0.692308,
             loss  binary_accuracy  val_loss  val_binary_accuracy
      9  0.624362         0.605769  0.585881             0.692308]
```

```
[ ]: def build_my_model3(pretrained_model):
         "Change Learning rate from 1e-3 to 1e-4"
         my_model = Sequential()
         my_model.add(pretrained_model)
         my_model.add(Flatten())
         my_model.add(Dense(2048, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(1024, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(512, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(256, activation = 'relu'))
         my_model.add(Dropout(0.5))
         my_model.add(Dense(1, activation = 'sigmoid'))

         optimizer = Adam(learning_rate = 1e-4)
         loss = 'binary_crossentropy'
         metrics = ['binary_accuracy']

         my_model.compile(optimizer=optimizer, loss=loss, metrics=metrics)

         return my_model
```

```
[ ]: #Train Model3
     vgg_model = load_pretrained_vgg_model('block5_pool')
     my_model3 = build_my_model3(vgg_model)
     history3 = my_model3.fit_generator(train_gen,
                                        validation_data = val_gen,
                                        epochs = 10,
                                        callbacks = callbacks_list)
```

```
/tmp/ipykernel_49176/3601672078.py:4: UserWarning: `Model.fit_generator` is
deprecated and will be removed in a future version. Please use `Model.fit`,
which supports generators.
  history3 = my_model3.fit_generator(train_gen,
```

```
Epoch 1/10
7/7 [==============================] - ETA: 0s - loss: 0.9464 - binary_accuracy:
0.5577
Epoch 00001: val_loss did not improve from 0.50458
7/7 [==============================] - 13s 2s/step - loss: 0.9464 -
binary_accuracy: 0.5577 - val_loss: 0.6719 - val_binary_accuracy: 0.6462
Epoch 2/10
7/7 [==============================] - ETA: 0s - loss: 1.0774 - binary_accuracy:
0.4712
Epoch 00002: val_loss did not improve from 0.50458
7/7 [==============================] - 13s 2s/step - loss: 1.0774 -
binary_accuracy: 0.4712 - val_loss: 0.6003 - val_binary_accuracy: 0.8000
```

```
Epoch 3/10
7/7 [==============================] - ETA: 0s - loss: 1.1647 - binary_accuracy:
0.4808
Epoch 00003: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 1.1647 -
binary_accuracy: 0.4808 - val_loss: 0.7694 - val_binary_accuracy: 0.2154
Epoch 4/10
7/7 [==============================] - ETA: 0s - loss: 1.0219 - binary_accuracy:
0.5192
Epoch 00004: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 1.0219 -
binary_accuracy: 0.5192 - val_loss: 0.7347 - val_binary_accuracy: 0.3385
Epoch 5/10
7/7 [==============================] - ETA: 0s - loss: 0.9479 - binary_accuracy:
0.5000
Epoch 00005: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.9479 -
binary_accuracy: 0.5000 - val_loss: 0.6512 - val_binary_accuracy: 0.7077
Epoch 6/10
7/7 [==============================] - ETA: 0s - loss: 1.0226 - binary_accuracy:
0.4808
Epoch 00006: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 1.0226 -
binary_accuracy: 0.4808 - val_loss: 0.6370 - val_binary_accuracy: 0.8154
Epoch 7/10
7/7 [==============================] - ETA: 0s - loss: 0.9600 - binary_accuracy:
0.5000
Epoch 00007: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.9600 -
binary_accuracy: 0.5000 - val_loss: 0.7404 - val_binary_accuracy: 0.2462
Epoch 8/10
7/7 [==============================] - ETA: 0s - loss: 0.8555 - binary_accuracy:
0.5385
Epoch 00008: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.8555 -
binary_accuracy: 0.5385 - val_loss: 0.6840 - val_binary_accuracy: 0.5692
Epoch 9/10
7/7 [==============================] - ETA: 0s - loss: 0.7548 - binary_accuracy:
0.5481
Epoch 00009: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.7548 -
binary_accuracy: 0.5481 - val_loss: 0.6526 - val_binary_accuracy: 0.6769
Epoch 10/10
7/7 [==============================] - ETA: 0s - loss: 0.7076 - binary_accuracy:
0.5865
Epoch 00010: val_loss did not improve from 0.50458
7/7 [==============================] - 12s 2s/step - loss: 0.7076 -
binary_accuracy: 0.5865 - val_loss: 0.6288 - val_binary_accuracy: 0.7692
```

```
[ ]: model3_plot = plot_history(history3,10)
```

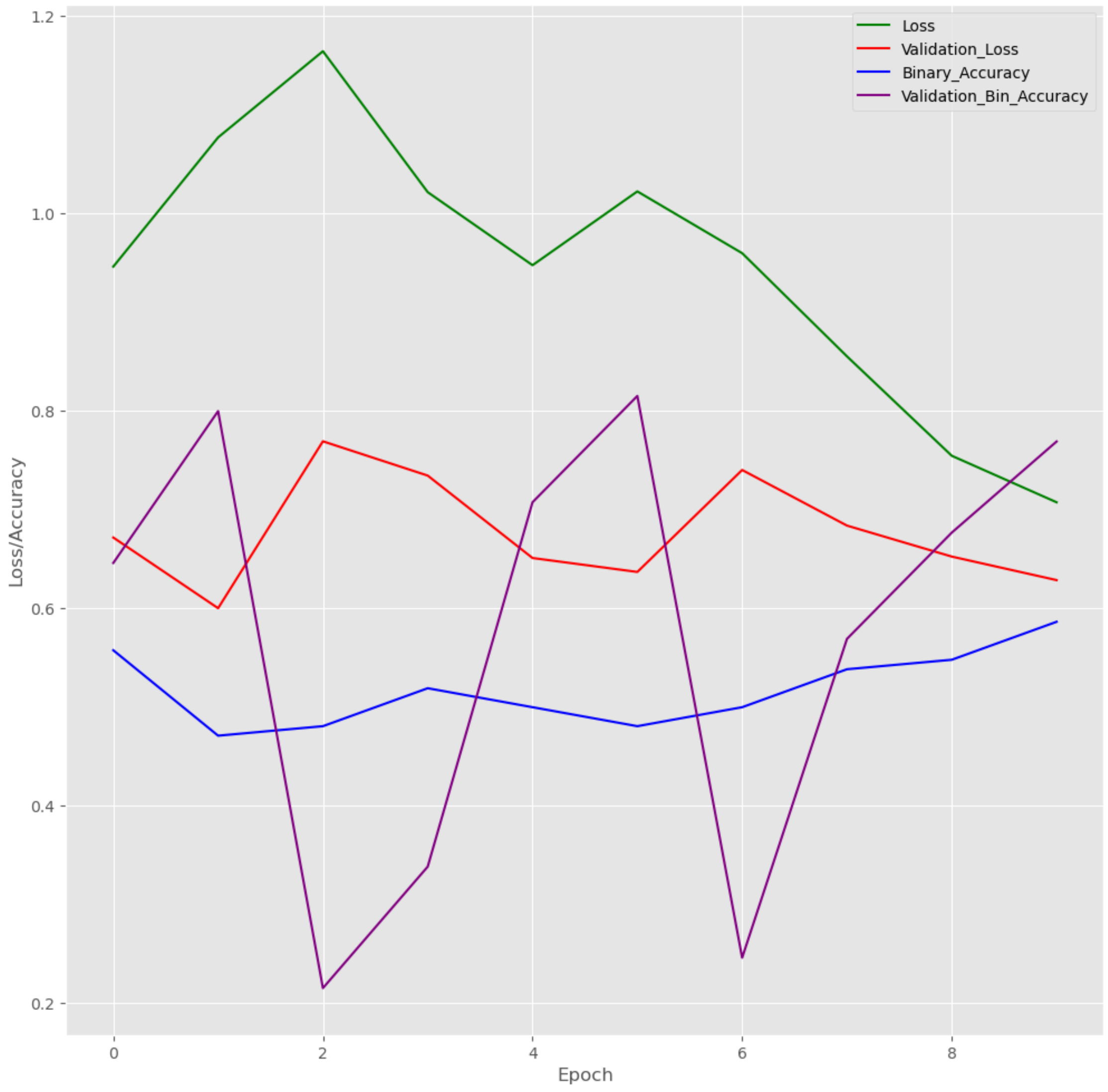


Figure 3. Model 3 Training History

```
[ ]: history3_df=pd.DataFrame(history3.history)
     performance.
       ↪append(history3_df[history3_df['val_loss']==min(history3_df['val_loss'])])
```

```
[ ]: performance
```

```
[ ]: [       loss  binary_accuracy  val_loss  val_binary_accuracy
      5  0.629213         0.692308  0.504585             0.692308,
             loss  binary_accuracy  val_loss  val_binary_accuracy
      9  0.624362         0.605769  0.585881             0.692308,
       loss  binary_accuracy  val_loss  val_binary_accuracy
 1  1.077354         0.471154  0.600309                 0.8]
```

Model 1 has the lowest val_loss. Proceed with Model 1

After training for some time, look at the performance of your model by plotting some performance statistics: Note, these figures will come in handy for your FDA documentation later in the project

```
[ ]: vgg_model = load_pretrained_vgg_model('block5_pool')
     my_model1 = build_my_model(vgg_model)
     my_model1.summary()
```

```
Model: "sequential_12"

_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 model_12 (Functional)       (None, 7, 7, 512)         14714688

 flatten_12 (Flatten)        (None, 25088)             0

 dense_54 (Dense)            (None, 1024)              25691136

 dropout_42 (Dropout)        (None, 1024)              0

 dense_55 (Dense)            (None, 512)               524800

 dropout_43 (Dropout)        (None, 512)               0

 dense_56 (Dense)            (None, 256)               131328

 dropout_44 (Dropout)        (None, 256)               0

 dense_57 (Dense)            (None, 1)                 257

=================================================================
Total params: 41,062,209
Trainable params: 28,707,329
Non-trainable params: 12,354,880
_________________________________________________________________
```

```
[ ]: ## After training, make some predictions to assess your model's overall␣
      ↪performance
     ## Note that detecting pneumonia is hard even for trained expert radiologists,
     ## so there is no need to make the model perfect.

     vgg_model = load_pretrained_vgg_model('block5_pool')
     my_model1 = build_my_model(vgg_model)
```

```
my_model1.load_weights(weight_path)
val_gen.reset()
pred_Y = my_model1.predict(val_gen, verbose = True)
```

```
3/3 [==============================] - 4s 994ms/step
```

```
[ ]: pred_Y.shape
```

```
[ ]: (65, 1)
```

```
[ ]: val_gen.labels
```

```
[ ]: [1,
      1,
      1,
      1,
      1,
      1,
      1,
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      1,
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```

[ ]:
```
pred_Y = pred_Y.flatten().tolist()
```

[ ]:
```
predictions_df=pd.DataFrame({'Label':val_gen.labels,'Predict':pd.
  ↪Series(pred_Y)})
predictions_df.sort_values('Label',ascending=False).head(10)
```

[ ]:
```
    Label   Predict
0       1  0.662846
7       1  0.647125
1       1  0.214297
11      1  0.724178
10      1  0.624843
9       1  0.160731
8       1  0.195216
12      1  0.401560
6       1  0.573180
5       1  0.747797
```

```
[ ]: predictions_df[predictions_df['Label']==1.0]
```

```
[ ]:     Label   Predict
    0       1  0.662846
    1       1  0.214297
    2       1  0.715125
    3       1  0.574234
    4       1  0.896850
    5       1  0.747797
    6       1  0.573180
    7       1  0.647125
    8       1  0.195216
    9       1  0.160731
    10      1  0.624843
    11      1  0.724178
    12      1  0.401560
```

```
[ ]: predictions_df.to_csv('/home/shafeenkhan/Documents/My-all-programs--/Semester-4/
      ↪Aritificial Intelligence/Pneumonia_Detection_ChestX/out/
      ↪Predictions_best_model.csv')
```

```
[ ]: predictions_df= pd.read_csv('/home/shafeenkhan/Documents/My-all-programs--/
      ↪Semester-4/Aritificial Intelligence/Pneumonia_Detection_ChestX/out/
      ↪Predictions_best_model.csv')
     predictions_df
```

```
[ ]:     Unnamed: 0  Label   Predict
    0            0      1  0.662846
    1            1      1  0.214297
    2            2      1  0.715125
    3            3      1  0.574234
    4            4      1  0.896850
    ..         …     …         …
    60          60      0  0.112950
    61          61      0  0.479327
    62          62      0  0.072709
    63          63      0  0.266347
    64          64      0  0.074272

    [65 rows x 3 columns]
```

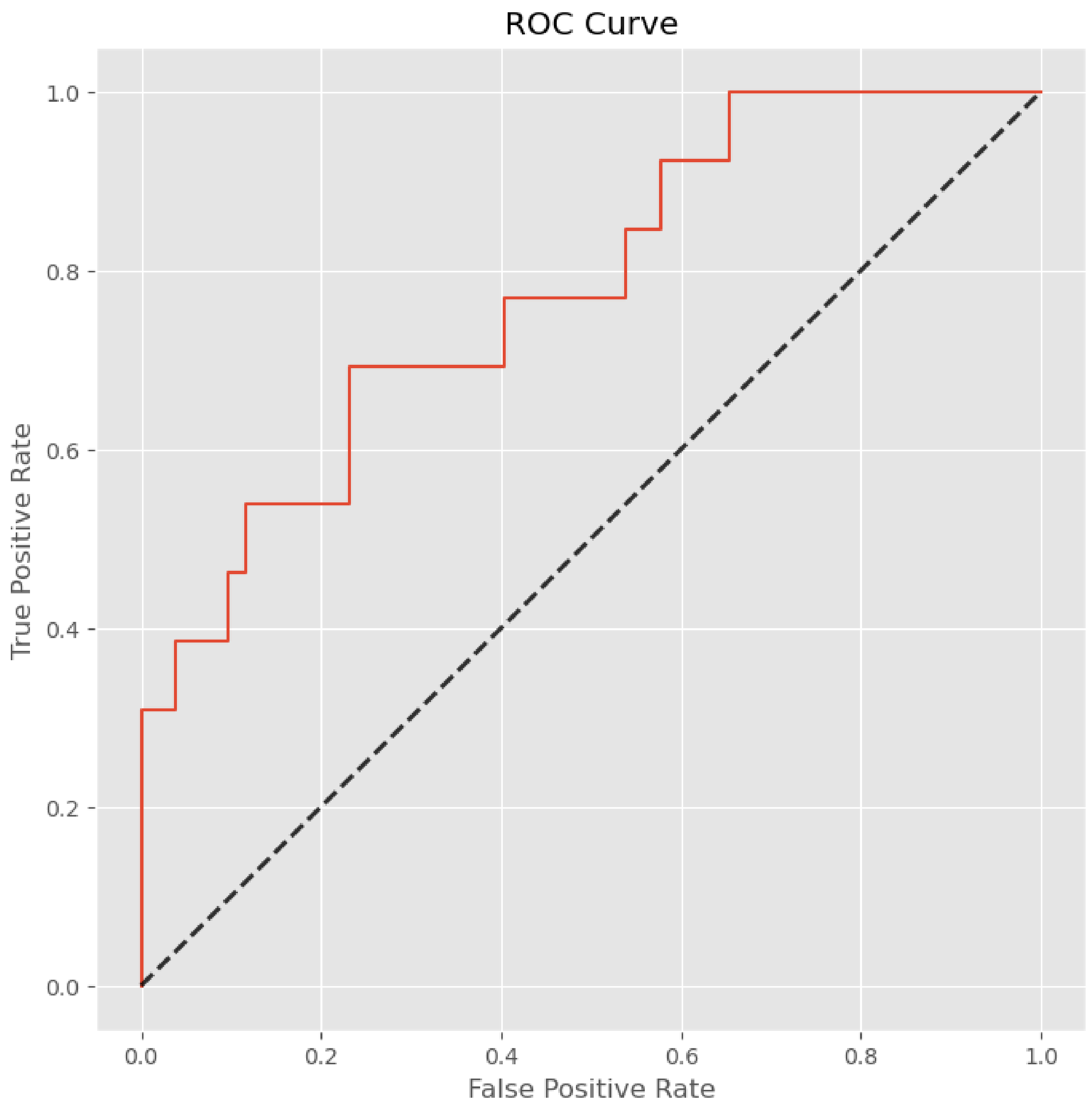
3 ROC, Precision-Recall Curve, F1 Plot

```
[ ]: def plot_roc(t_y, p_y):

         fpr, tpr, thresholds = roc_curve(t_y, p_y, pos_label = 1)
     #    np.append(thresholds, 1)
```

```
    plt.plot(fpr,tpr)
    plt.style.use('ggplot')
    plt.title('ROC Curve')
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.plot([0, 1], [0, 1], linestyle='--', lw=2,␣
↪color='black',label='Chance', alpha=.8)
    plt.savefig('/home/shafeenkhan/Documents/My-all-programs--/Semester-4/
↪Aritificial Intelligence/Pneumonia_Detection_ChestX/out/ROC_Curve')
    plt.show()

    return fpr, tpr, thresholds

## what other performance statistics do you want to include here besides AUC?


def plot_precision_recall_curve(t_y, p_y):
    precision, recall, threshold = precision_recall_curve(t_y,p_y,pos_label = 1)
    threshold = np.append(threshold, 1)
    plt.style.use('ggplot')
    plt.plot(precision, recall)
    plt.title('Precision-Recall Curve')
    plt.xlabel('Precision')
    plt.ylabel('Recall')
    plt.savefig('/home/shafeenkhan/Documents/My-all-programs--/Semester-4/
↪Aritificial Intelligence/Pneumonia_Detection_ChestX/out/
↪Precision_Recall_Curve')
    plt.show()

    return precision, recall, threshold

def calc_f1(prec,recall):
    return 2*(prec*recall)/(prec+recall)

def plot_f1(t_y,p_y):
    precision, recall, threshold = plot_precision_recall_curve(t_y,p_y)
    f1 = calc_f1(precision, recall)
    plt.style.use('ggplot')
    plt.plot(threshold, f1)
    plt.title('F1 vs Threshold')
    plt.xlabel('Threshold')
    plt.ylabel('F1')
    plt.savefig('/home/shafeenkhan/Documents/My-all-programs--/Semester-4/
↪Aritificial Intelligence/Pneumonia_Detection_ChestX/out/F1_Threshold')
    plt.show()

    return precision, recall, f1, threshold
```

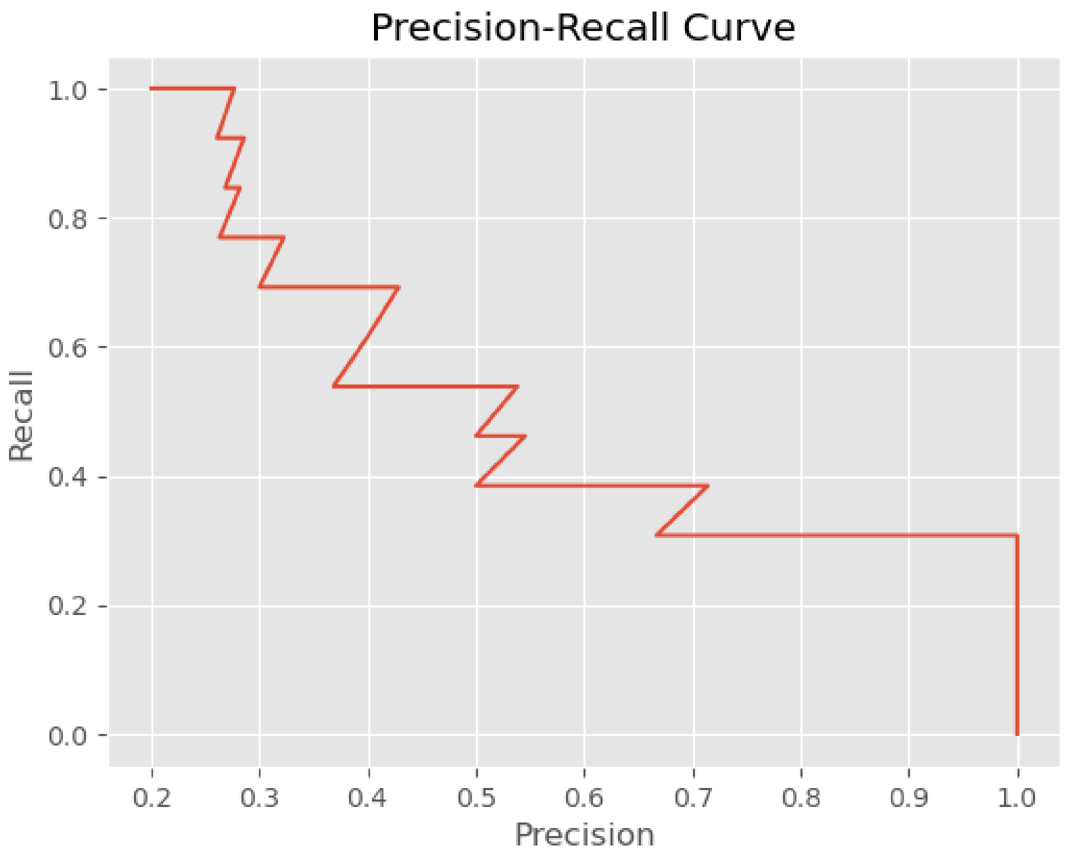
```
def plot_auc(t_y, p_y):
    fig, ax = plt.subplots(figsize=(8,8))
    plt.style.use('ggplot')
    fpr, tpr, thresholds = plot_roc(t_y, p_y)
    res = auc(fpr, tpr)
    print("AUC-ROC is: " + str(res))
    return fpr, tpr, thresholds, res
```

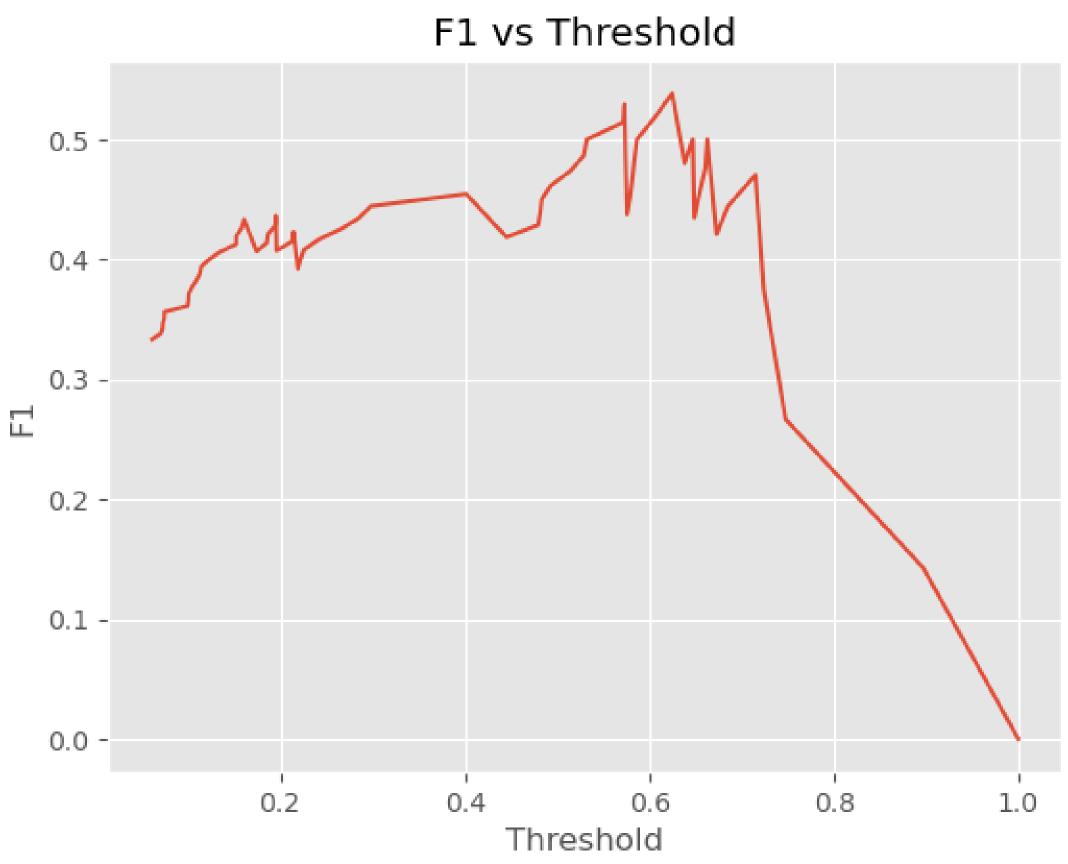
```
[ ]: fpr, tpr, thresholds_ROC, AUC =␣
      ↪plot_auc(predictions_df['Label'],predictions_df['Predict'])
```



```
AUC-ROC is: 0.7781065088757396
```

[ ]:
```
precision, recall, f1, thresholds_f1 =␣
  ↪plot_f1(predictions_df['Label'],predictions_df['Predict'])
```





```
[ ]: recall_df = pd.DataFrame({"Precision":precision, "Threshold":thresholds_f1,␣
      ↪"Recall":recall, "F1":f1})
```

Once you feel you are done training, you'll need to decide the proper classification threshold that optimizes your model's performance for a given metric (e.g. accuracy, F1, precision, etc. You decide)

```
[ ]: ## Find the threshold that optimize your model's performance,
     ## and use that threshold to make binary classification. Make sure you take all␣
      ↪your metrics into consideration.

     ## If, this model can be used for screening studyies where High Recall is␣
      ↪required,
     ## reducing false negatives at the expense of more false positives.  This would
     ## be found on the ROC curve where the distance away from Chance prediction is␣
      ↪greatest.

     def find_ROC_thresh(fpr,tpr,thresh):
         dist1=0
         dist2=0
```

```
    tprmax = 0
    for i in range(len(fpr)):
        dist2 = tpr[i] - fpr[i]
        if dist2 > dist1:
            dist1 = dist2
            tprmax=tpr[i]
        else:
            continue
    df = pd.DataFrame({'fpr':fpr,'tpr':tpr,'threshold':thresh})
    threshmax = df['threshold'][df['tpr']==tprmax].iloc[-1]
    return threshmax

## If this model is used for confirming a diagnosis, high precision is desired.
## An F1 Score is maximized where there is a balance between precision and␣
 ↪recall.
## The corresponding threshold for that F1 Score should be chosen.

def find_F1_thresh(f1,thresh):
    df = pd.DataFrame({'f1':f1,'threshold':thresh})
    threshmax = df['threshold'][df['f1']==df['f1'].max()] .iloc[-1]
    return threshmax
```

```
[ ]: thresh_ROC = find_ROC_thresh(fpr,tpr, thresholds_ROC)
     print("thresh_ROC is " + str(thresh_ROC))
```

```
thresh_ROC is 0.4451873004436493
```

```
[ ]: thresh_F1 = find_F1_thresh(f1, thresholds_f1)
     print("Maximium F1-score is {} \nThreshhold for this F1-score is {}".
      ↪format(str(np.max(f1)), str(thresh_F1)))
```

```
Maximium F1-score is 0.5384615384615384
Threshhold for this F1-score is 0.624842643737793
```

```
[ ]: val_gen_labels= pd.DataFrame(val_gen.labels)
     val_Pos_labels= val_gen_labels[val_gen_labels[0] > 0]
     val_Pos_labels
     val_Pos_ind=val_Pos_labels.index
     val_Pos_ind
```

```
[ ]: Index([0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12], dtype='int64')
```

```
[ ]: val_filenames = np.array(val_gen.filenames)
     val_labels=np.array(val_gen.labels)
```

```
[ ]: ## Let's look at some examples of true vs. predicted with our best model based␣
      ↪on thresh_ROC:
     Thresh=thresh_ROC
```

```python
fig, m_axs = plt.subplots(10, 10, figsize = (16, 16))
i = 0
for (c_x, c_y, c_ax) in zip(val_filenames[val_Pos_ind],␣
 ↪val_labels[val_Pos_ind], m_axs.flatten()):
    c_ax.imshow(imread(c_x), cmap = 'bone')
    if c_y == 1:
        if pred_Y[i] > Thresh:
            c_ax.set_title('1, 1')
        else:
            c_ax.set_title('1, 0')
    else:
        if pred_Y[i] > Thresh:
            c_ax.set_title('0, 1')
        else:
            c_ax.set_title('0, 0')
    c_ax.axis('off')
    i=i+1
```

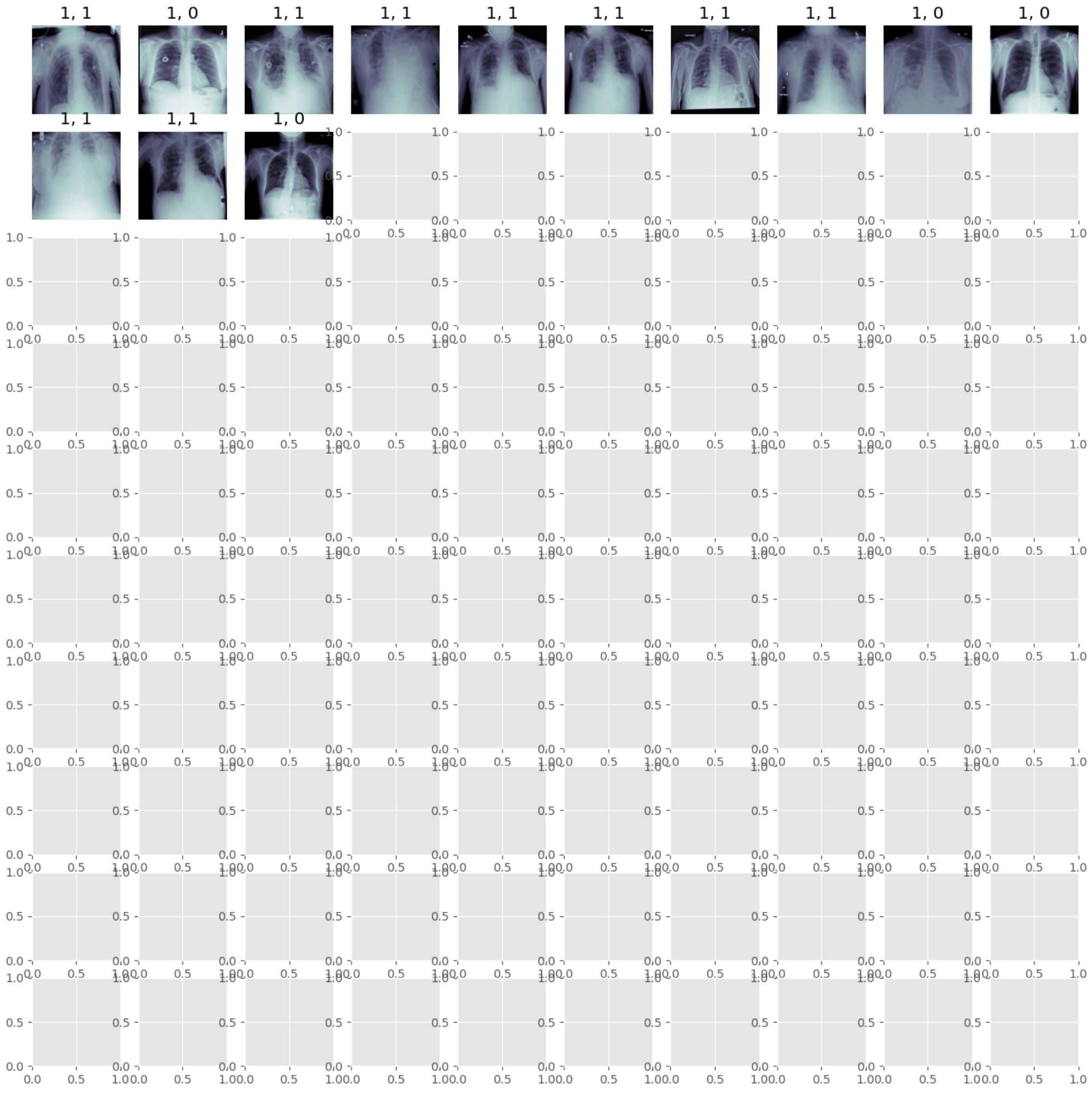


Figure 4. 100 Images with titles showing "Label Value, Prediction Value" for pneumonia, using ROC Threshold

[ ]:
```
#ROC Threshold Confusion Matrix:
pred_YROC = []

for x in range(len(pred_Y)):
    if pred_Y[x] > thresh_ROC:
        pred_YROC.append(1)
    else:
        pred_YROC.append(0)

tn,fp,fn,tp =confusion_matrix(val_gen.labels,pred_YROC).ravel()
```

```
print (tp, fp,"\n",fn,tn)
```

```
9 20
 4 32
```

```
[ ]: ## Let's look at some examples of true vs. predicted with our best model based␣
     ↪on thresh_F1:
     Thresh=thresh_F1

     fig, m_axs = plt.subplots(10, 10, figsize = (16, 16))
     i = 0
     for (c_x, c_y, c_ax) in zip(val_filenames[val_Pos_ind],␣
      ↪val_labels[val_Pos_ind], m_axs.flatten()):
         c_ax.imshow(imread(c_x), cmap = 'bone')
         if c_y == 1:
             if pred_Y[i] > Thresh:
                 c_ax.set_title('1, 1')
             else:
                 c_ax.set_title('1, 0')
         else:
             if pred_Y[i] > Thresh:
                 c_ax.set_title('0, 1')
             else:
                 c_ax.set_title('0, 0')
         c_ax.axis('off')
         i=i+1
```

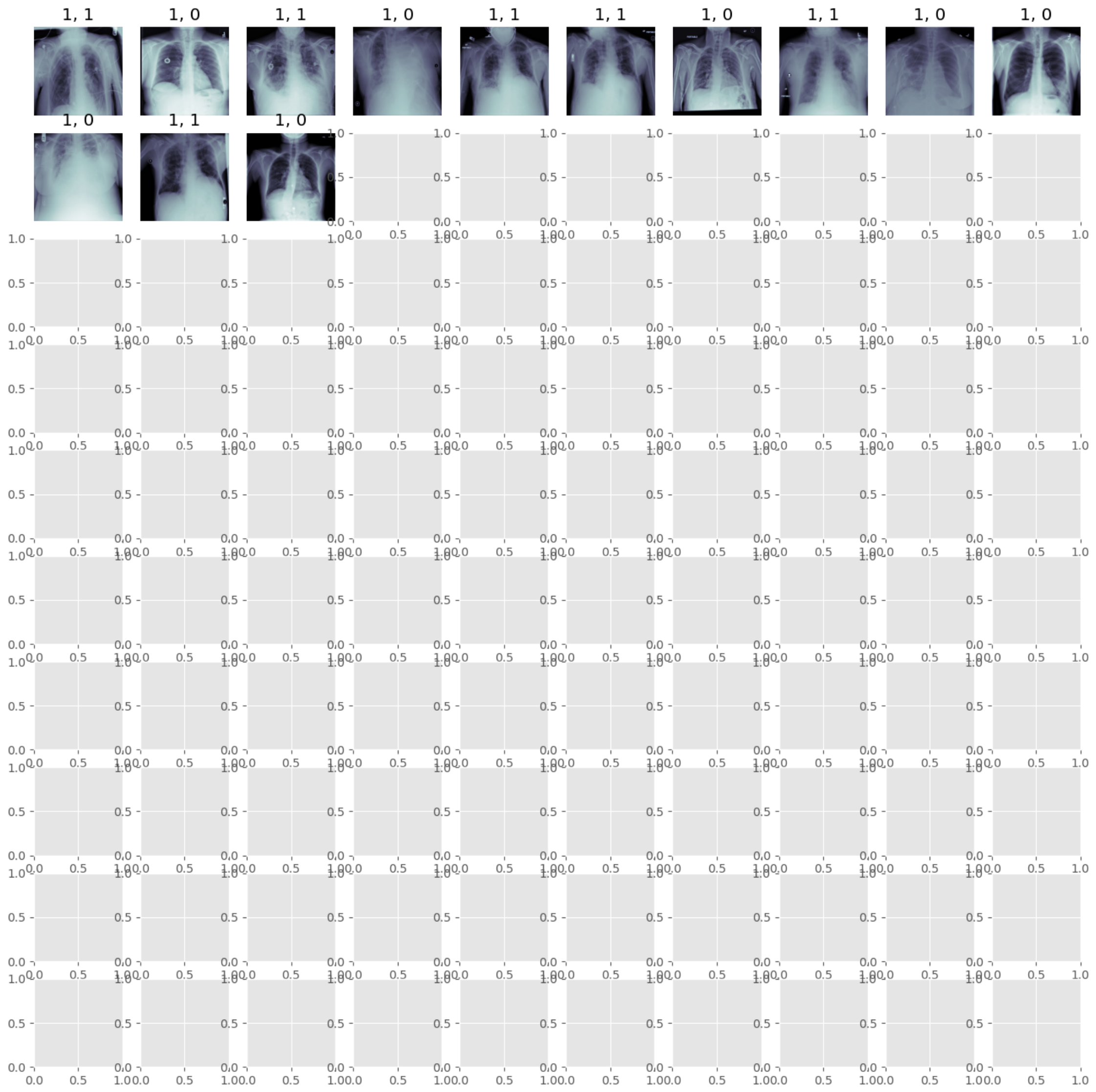


Figure 5. 100 Images with titles showing "Label Value, Prediction Value" for pneumonia, using F1-score Threshold

[ ]:
```
#F1 Threshold Confusion Matrix:
pred_YF1 = []

for x in range(len(pred_Y)):
    if pred_Y[x] > thresh_F1:
        pred_YF1.append(1)
    else:
        pred_YF1.append(0)

tn,fp,fn,tp = confusion_matrix(val_gen.labels,pred_YF1).ravel()
```

```
print (tp, fp,"\n",fn,tn)
```

```
6 6
 7 46
```

```
[ ]: #Maximize Recall.  Choose Threshold at recall at 0.8.
     recall_df[recall_df['Recall']>0.8]
```

```
[ ]:     Precision  Threshold    Recall        F1
    0    0.200000   0.061094  1.000000  0.333333
    1    0.203125   0.069927  1.000000  0.337662
    2    0.206349   0.072170  1.000000  0.342105
    3    0.209677   0.072709  1.000000  0.346667
    4    0.213115   0.074245  1.000000  0.351351
    5    0.216667   0.074272  1.000000  0.356164
    6    0.220339   0.099344  1.000000  0.361111
    7    0.224138   0.100466  1.000000  0.366197
    8    0.228070   0.100620  1.000000  0.371429
    9    0.232143   0.104352  1.000000  0.376812
    10   0.236364   0.108806  1.000000  0.382353
    11   0.240741   0.112950  1.000000  0.388060
    12   0.245283   0.114259  1.000000  0.393939
    13   0.250000   0.122875  1.000000  0.400000
    14   0.254902   0.134626  1.000000  0.406250
    15   0.260000   0.152164  1.000000  0.412698
    16   0.265306   0.152212  1.000000  0.419355
    17   0.270833   0.158203  1.000000  0.426230
    18   0.276596   0.160731  1.000000  0.433333
    19   0.260870   0.174366  0.923077  0.406780
    20   0.266667   0.185404  0.923077  0.413793
    21   0.272727   0.186641  0.923077  0.421053
    22   0.279070   0.194798  0.923077  0.428571
    23   0.285714   0.195216  0.923077  0.436364
    24   0.268293   0.196007  0.846154  0.407407
    25   0.275000   0.212979  0.846154  0.415094
    26   0.282051   0.214297  0.846154  0.423077
```

```
[ ]: ## Let's look at some examples of true vs. predicted with our best model␣
      ↪maximizing Recall.  Recall=0.80:
     Thresh =  0.355

     fig, m_axs = plt.subplots(10, 10, figsize = (16, 16))
     i = 0
     for (c_x, c_y, c_ax) in zip(val_filenames[val_Pos_ind],␣
      ↪val_labels[val_Pos_ind], m_axs.flatten()):
         c_ax.imshow(imread(c_x), cmap = 'bone')
         if c_y == 1:
```

```
        if pred_Y[i] > Thresh:
            c_ax.set_title('1, 1')
        else:
            c_ax.set_title('1, 0')
    else:
        if pred_Y[i] > Thresh:
            c_ax.set_title('0, 1')
        else:
            c_ax.set_title('0, 0')
    c_ax.axis('off')
    i=i+1
```

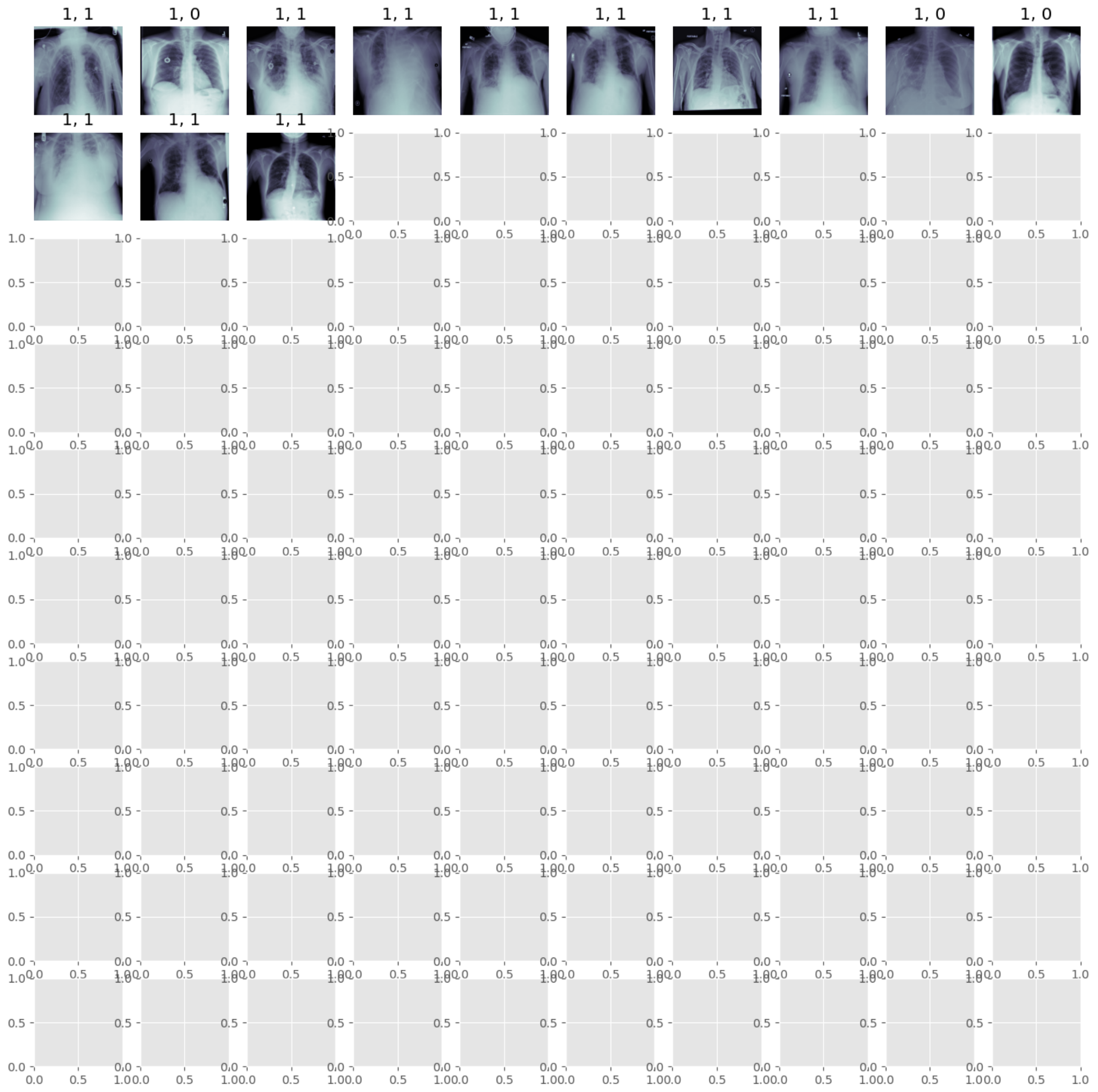


Figure 6. 100 Images with titles showing "Label Value, Prediction Value" for pneumonia, using

Recall Threshold

[ ]:
```
thresh_recall = 0.355

pred_Yrecall = []

for x in range(len(pred_Y)):
    if pred_Y[x] > thresh_recall:
        pred_Yrecall.append(1)
    else:
        pred_Yrecall.append(0)

tn,fp,fn,tp = confusion_matrix(val_gen.labels,pred_Yrecall).ravel()
print (tp, fp,"\n",fn,tn)
```

```
10 21
 3 31
```

#### The performance of three thresholds was explored by optimizing by ROC, by F1, and by maximizing Recall.

1. Optimize Threshold value by ROC is seen above. Based on images from the validation set with Positive Pneumonia labels, we see that the threshold value from ROC (0.24046) identifies some Positive Pneumonia labels correctly. Based on it's corresponding confusion matrix, it yields 219 TP, 67 FN, 701 FP.

2. Optimize Threshold value by F1. Based on images from the validation set with Positive Pneumonia labels, we see that the threshold value from F1 (0.24509) identifies some Positive Pneumonia labels correctly. Based on it's corresponding confusion matrix, it yields 218 TP and 68 FN, 692 FP. The performance is similar to optimizing by ROC. With this threshold, the F1 score is 0.366.

3. Maximize recall. A threshold value of 0.355 was chosen where Recall is above 0.80. It's corresponding confusion matrix, it yields 124 TP, 162 FN, with 351 FP. Though this method should have favored increasing TP at the cost of FN, this did not yield a result that is more aggressive that optimizing by ROC or F1.

For this project, model1 is the best architecture and its optimal threshold value is 0.24509 as determined from F1. This combination yields a F1 score of 0.366.

[ ]:
```
## Just save model architecture to a .json:
model_json = my_model1.to_json()

with open("/home/shafeenkhan/Documents/My-all-programs--/Semester-4/Aritificial␣
↪Intelligence/Pneumonia_Detection_ChestX/out/my_model1.json", "w") as␣
↪json_file:
    json_file.write(model_json)
```