FDA Submission

Your Name: Nguyen Nhat Anh Vo

Name of your Device: Pneumonia Detector

Algorithm Description

1. General Information

Intended Use Statement: Assisting radiologists in detecting pneumonia in Chest X-ray images with the view of PA/AP.

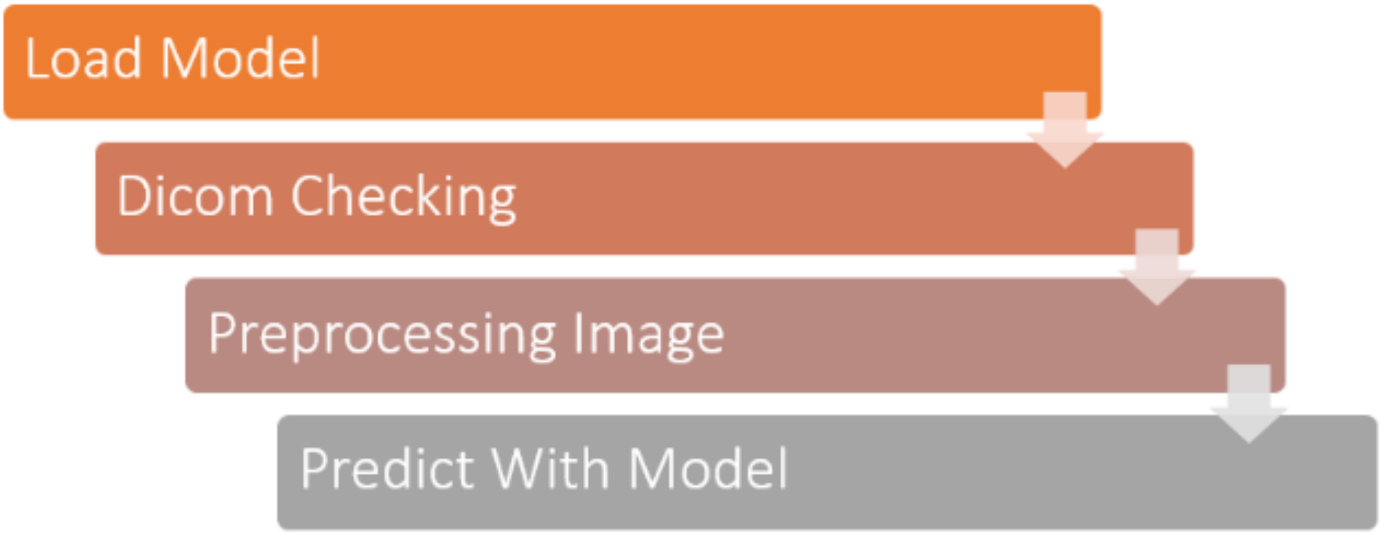
Indications for Use: It is well-used for both male and female from 1-100 years old. Patient can also exihit other diseases (Atelectasis, Cardiomegaly, Consolidation, Edema, Effusion, Emphysema, Fibrosis, Hernia, Infiltration, Mass, Nodule, Pleural_Thickening, Pneumonia, Pneumothorax) in comorbid with pneumonia.

Device Limitations: Require high-power processing GPU card to run the algorithm.

Clinical Impact of Performance:

- False Positive means the patient who is healthy is diagnosed with Pneumonia and may lead to unnecessary check of the radiologist.
- False Negative means the patient who has Pneumonia is diagnosed as healthy and may lead to missing treatment since the radiologist may depend too much on the algorithm.
- In this situation, False Negative is worst than False Positive. Because a patient with Pneumonia may not be found and does not get treated. Thus, his/her health gets worse over time.

2. Algorithm Design and Function



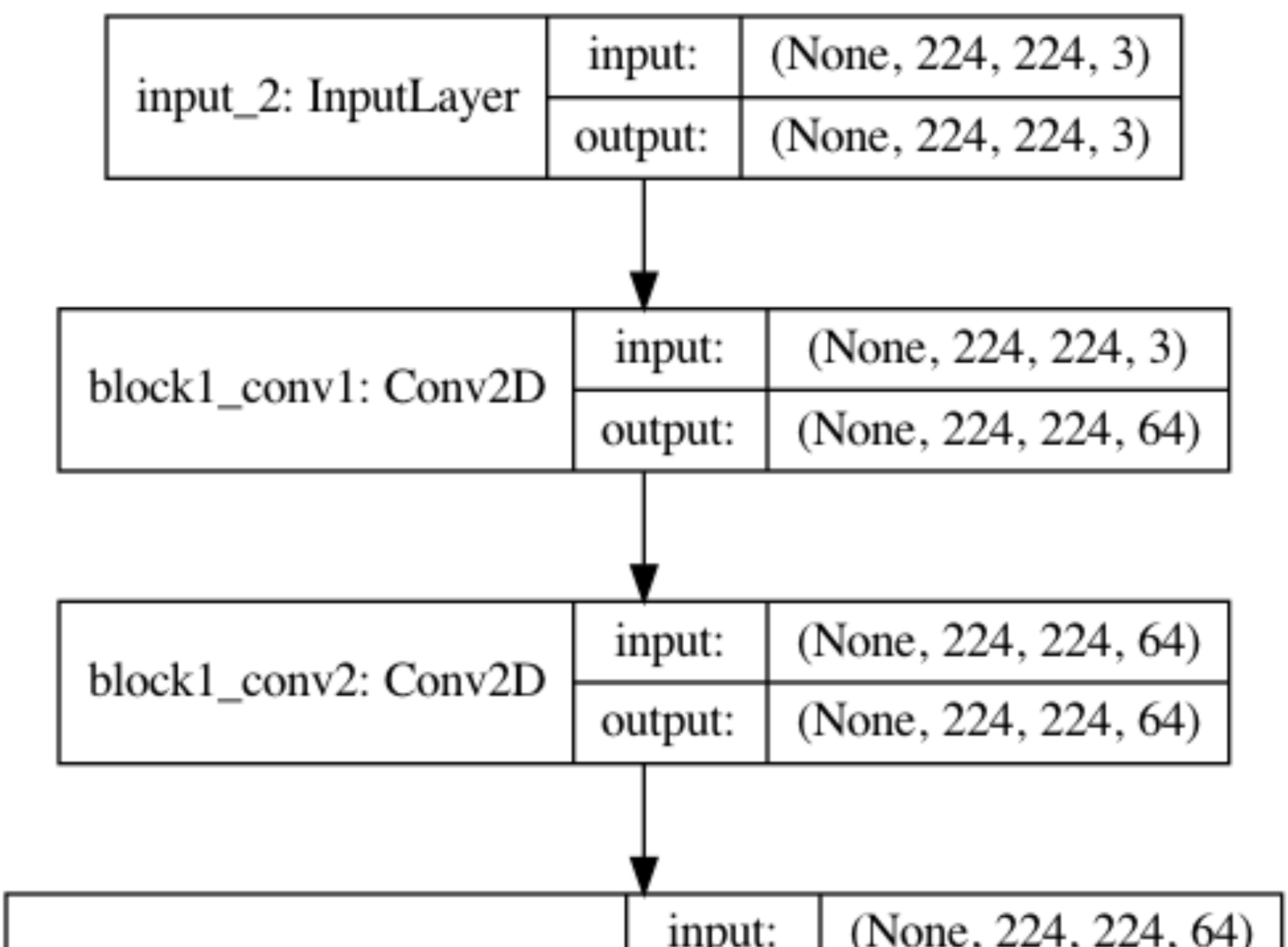
DICOM Checking Steps: Perform 3 different DICOM checks

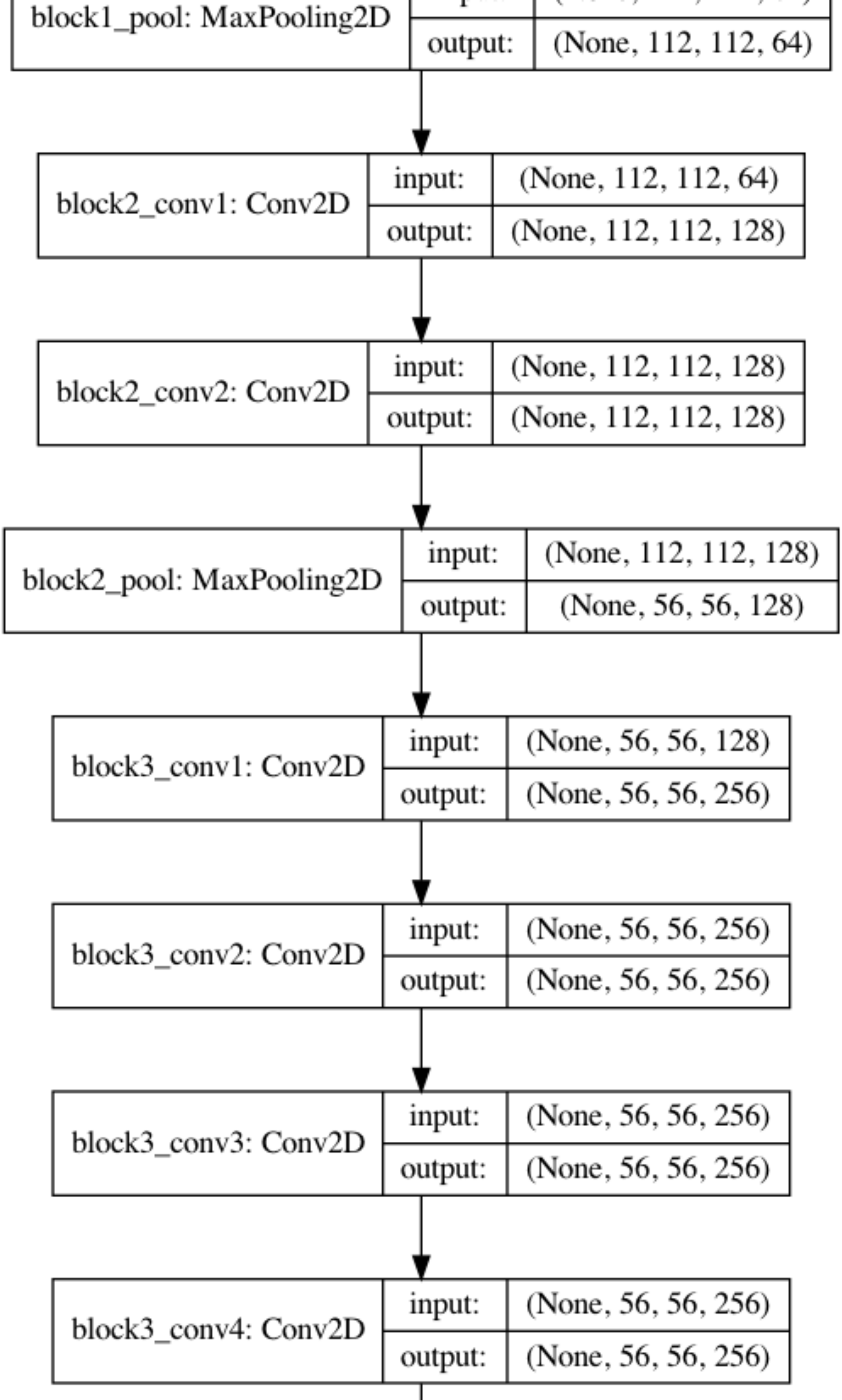
- Check patient position: Only AP or PA view will be processed
- Check image type (modality): Only DX type will be processed
- Check body part examined: Only chest taken image will be process

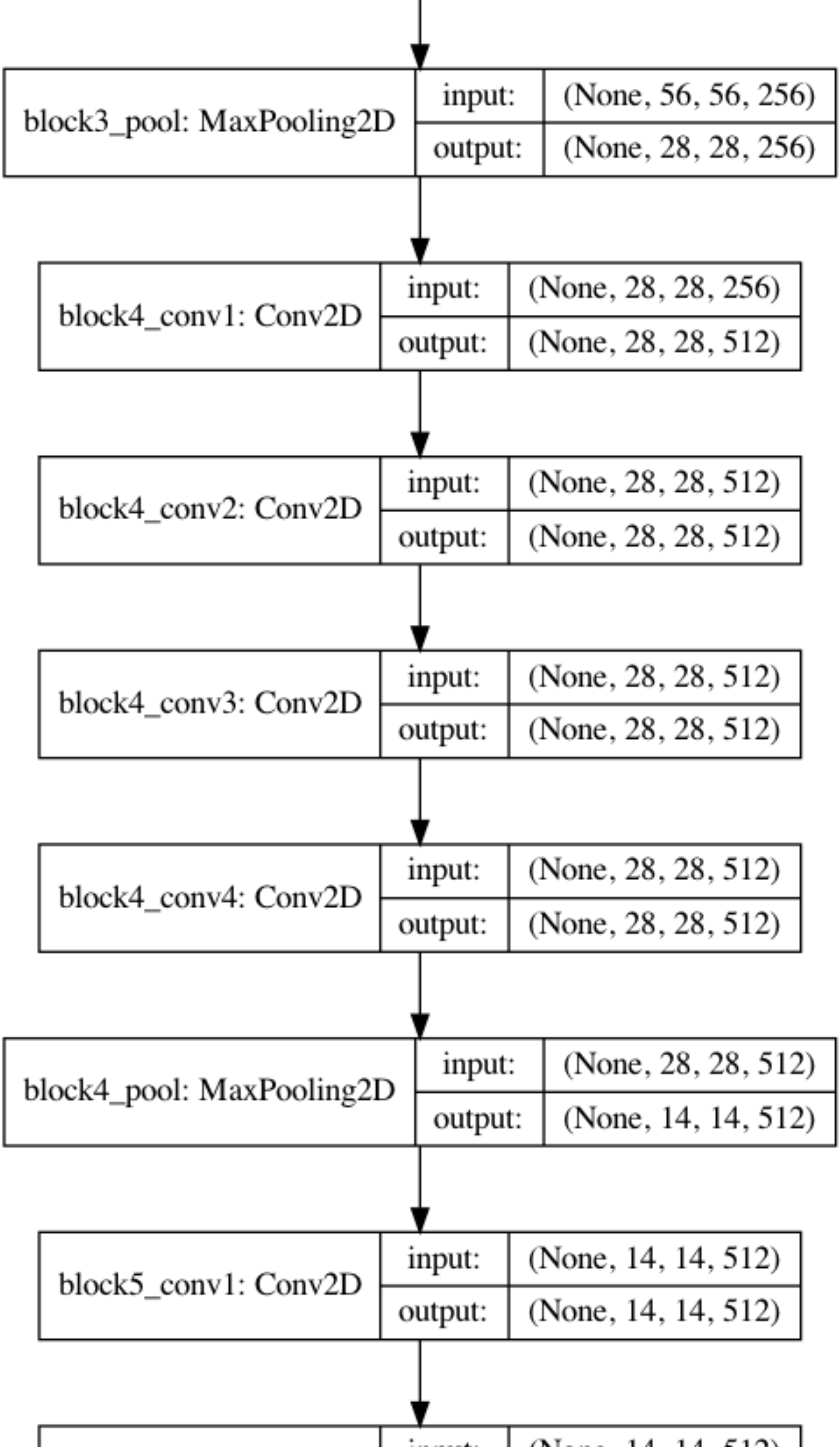
Preprocessing Steps: Rescale the image by dividing by 255.0, then normalize the image with the mean and standard deviation retrieved from the training data. Finally, resize the image to (1, 224, 224, 3) to fit in the network.

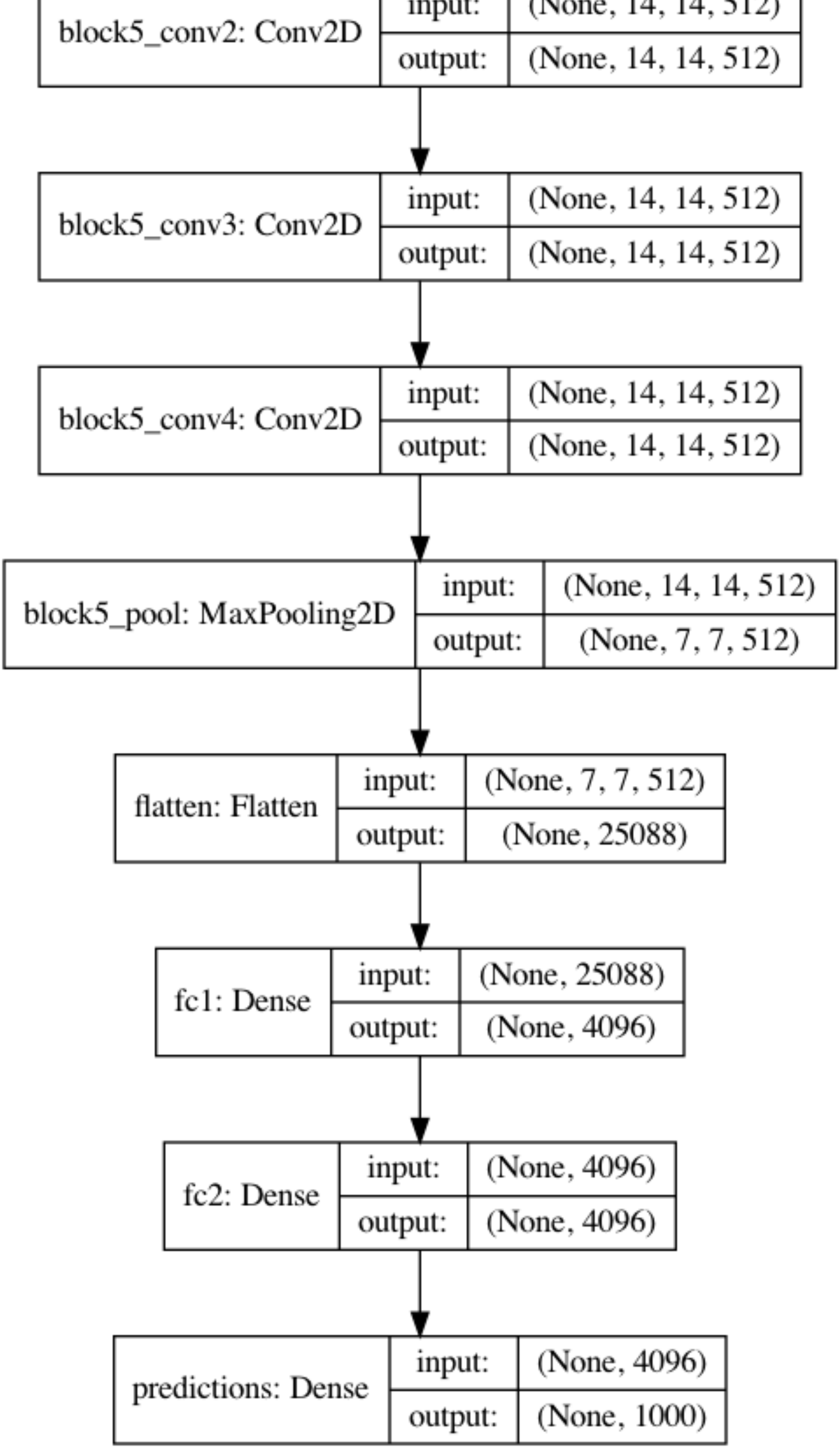
CNN Architecture:

- VGG19 model architecture is used for transfer learning.

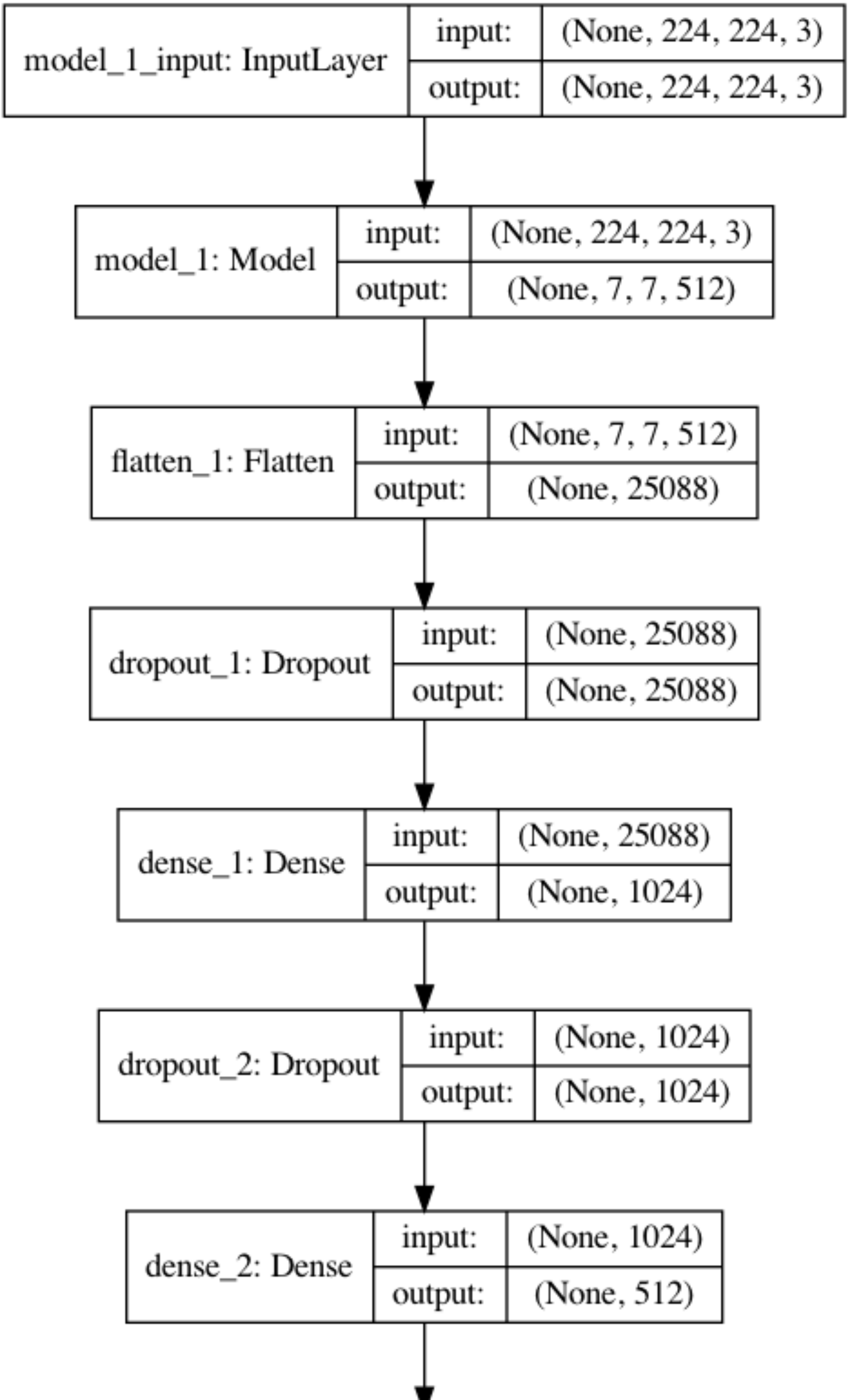


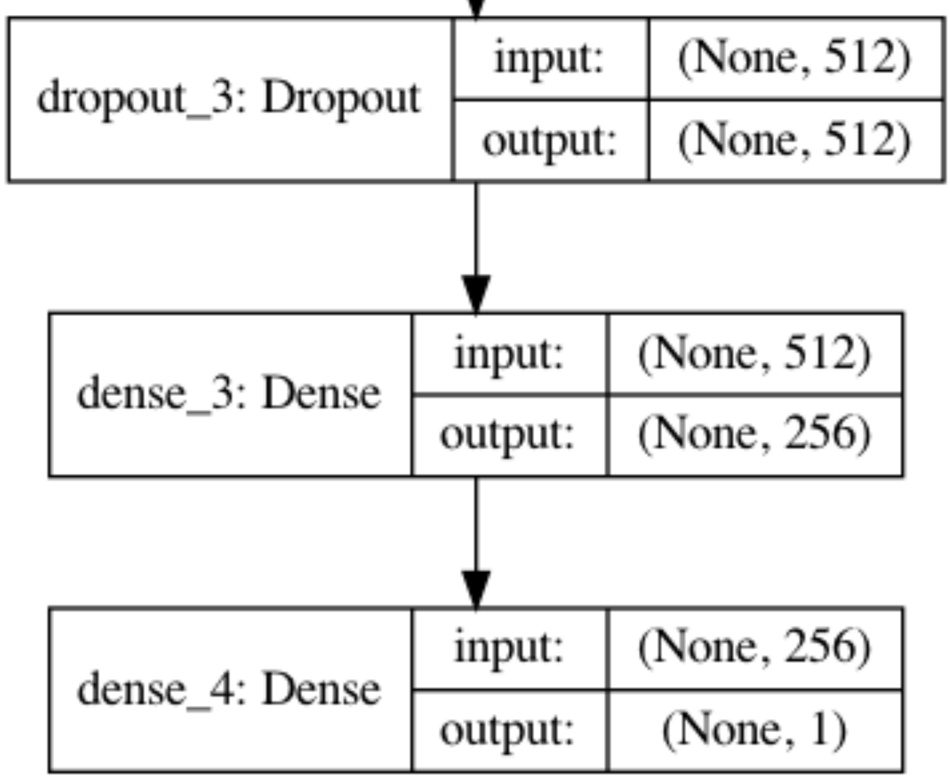

block1_pool: MaxPooling2D
output:
(None, 112, 112, 64)
block2_conv1: Conv2D
input:
(None, 112, 112, 64)
output:
(None, 112, 112, 128)
block2_conv2: Conv2D
input:
(None, 112, 112, 128)
output:
(None, 112, 112, 128)
block2_pool: MaxPooling2D
input:
(None, 112, 112, 128)
output:
(None, 56, 56, 128)
block3_conv1: Conv2D
input:
(None, 56, 56, 128)
output:
(None, 56, 56, 256)
block3_conv2: Conv2D
input:
(None, 56, 56, 256)
output:
(None, 56, 56, 256)
block3_conv3: Conv2D
input:
(None, 56, 56, 256)
output:
(None, 56, 56, 256)
block3_conv4: Conv2D
input:
(None, 56, 56, 256)
output:
(None, 56, 56, 256)


block3_pool: MaxPooling2D
input:
(None, 56, 56, 256)
output:
(None, 28, 28, 256)
block4_conv1: Conv2D
input:
(None, 28, 28, 256)
output:
(None, 28, 28, 512)
block4_conv2: Conv2D
input:
(None, 28, 28, 512)
output:
(None, 28, 28, 512)
block4_conv3: Conv2D
input:
(None, 28, 28, 512)
output:
(None, 28, 28, 512)
block4_conv4: Conv2D
input:
(None, 28, 28, 512)
output:
(None, 28, 28, 512)
block4_pool: MaxPooling2D
input:
(None, 28, 28, 512)
output:
(None, 14, 14, 512)
block5_conv1: Conv2D
input:
(None, 14, 14, 512)
output:
(None, 14, 14, 512)


block5_conv2: Conv2D
output: (None, 14, 14, 512)
block5_conv3: Conv2D
input: (None, 14, 14, 512)
output: (None, 14, 14, 512)
block5_conv4: Conv2D
input: (None, 14, 14, 512)
output: (None, 14, 14, 512)
block5_pool: MaxPooling2D
input: (None, 14, 14, 512)
output: (None, 7, 7, 512)
flatten: Flatten
input: (None, 7, 7, 512)
output: (None, 25088)
fc1: Dense
input: (None, 25088)
output: (None, 4096)
fc2: Dense
input: (None, 4096)
output: (None, 4096)
predictions: Dense
input: (None, 4096)
output: (None, 1000)

- Several custom layers are also added to the VGG19.

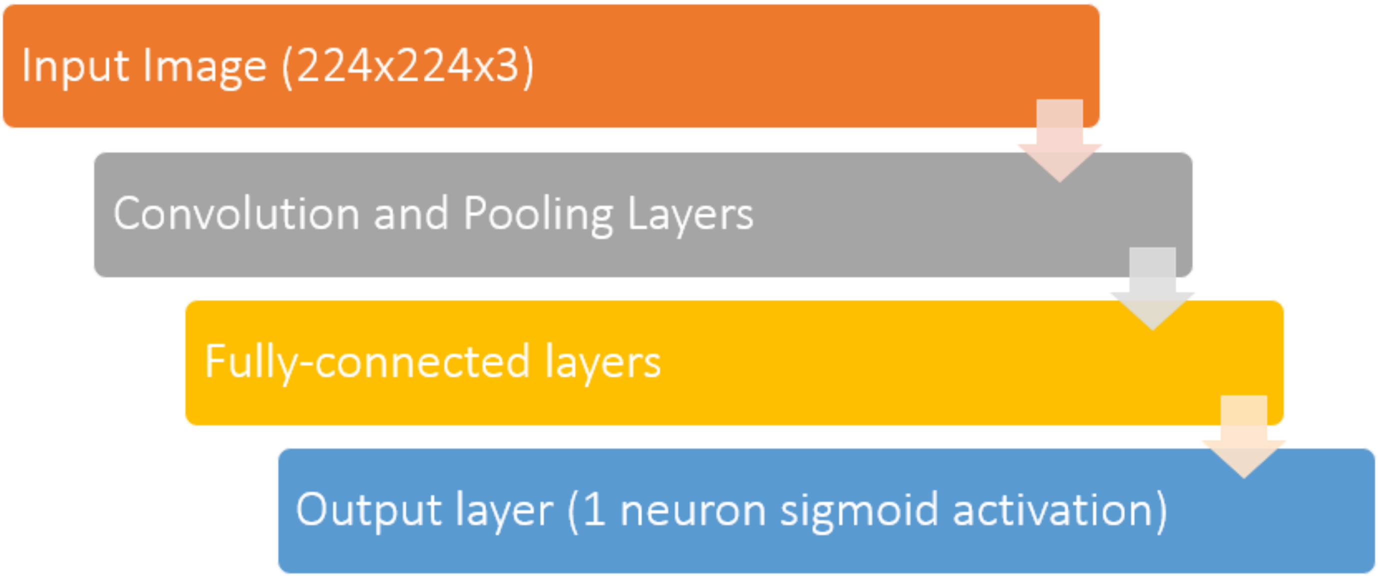




- Model Summary

```
Model: "sequential_1"
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
model_1 (Model)              (None, 7, 7, 512)         20024384
_________________________________________________________________
flatten_1 (Flatten)          (None, 25088)             0
_________________________________________________________________
dropout_1 (Dropout)          (None, 25088)             0
_________________________________________________________________
dense_1 (Dense)              (None, 1024)              25691136
_________________________________________________________________
dropout_2 (Dropout)          (None, 1024)              0
_________________________________________________________________
dense_2 (Dense)              (None, 512)               524800
_________________________________________________________________
dropout_3 (Dropout)          (None, 512)               0
_________________________________________________________________
dense_3 (Dense)              (None, 256)               131328
_________________________________________________________________
dense_4 (Dense)              (None, 1)                 257
=================================================================
Total params: 46,371,905
Trainable params: 28,707,329
Non-trainable params: 17,664,576
```

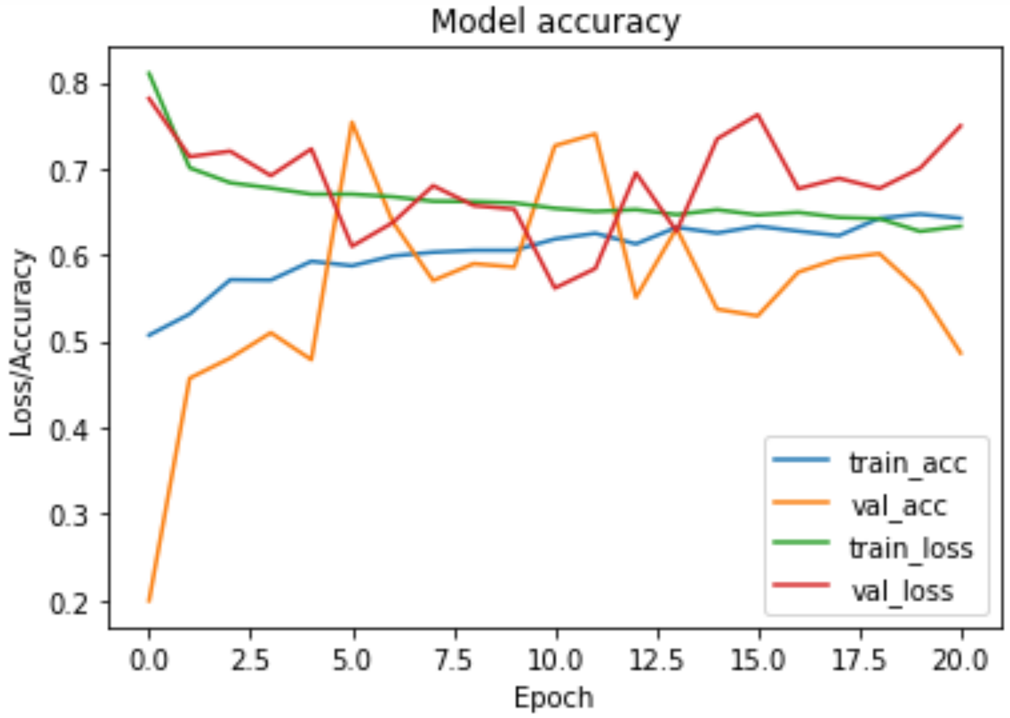
- Model Flowchart

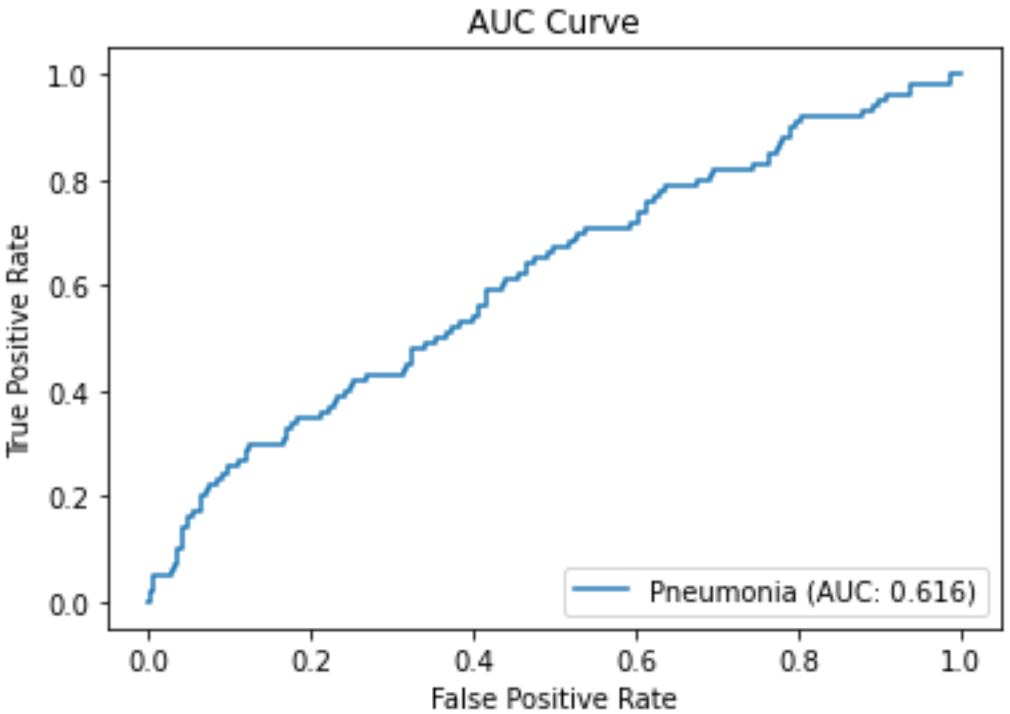


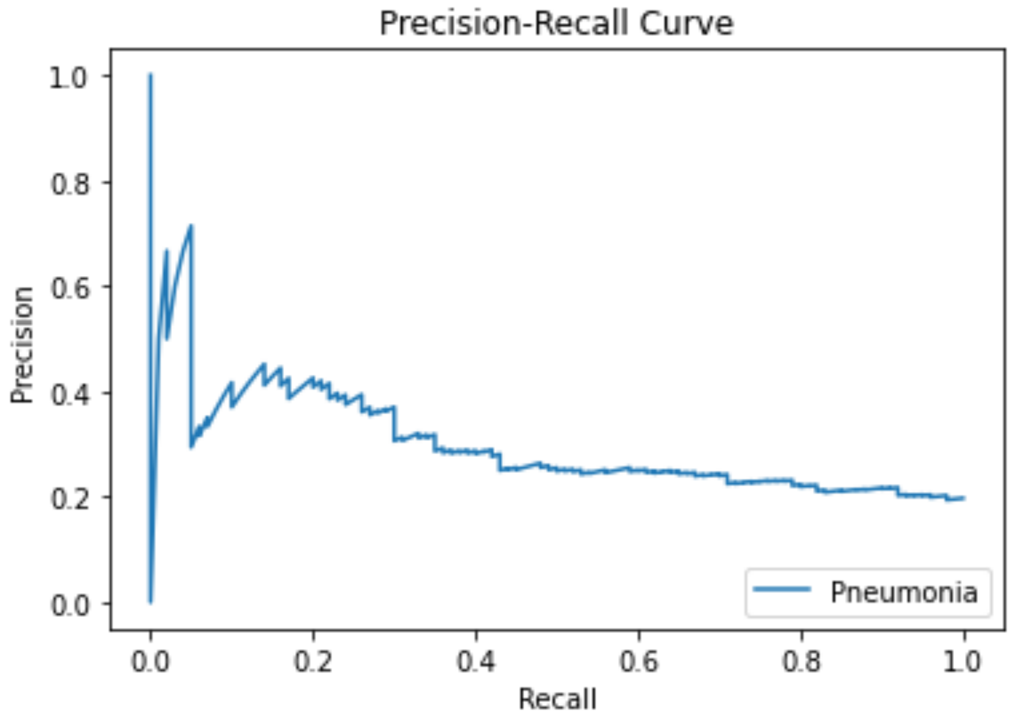
3. Algorithm Training

Parameters:

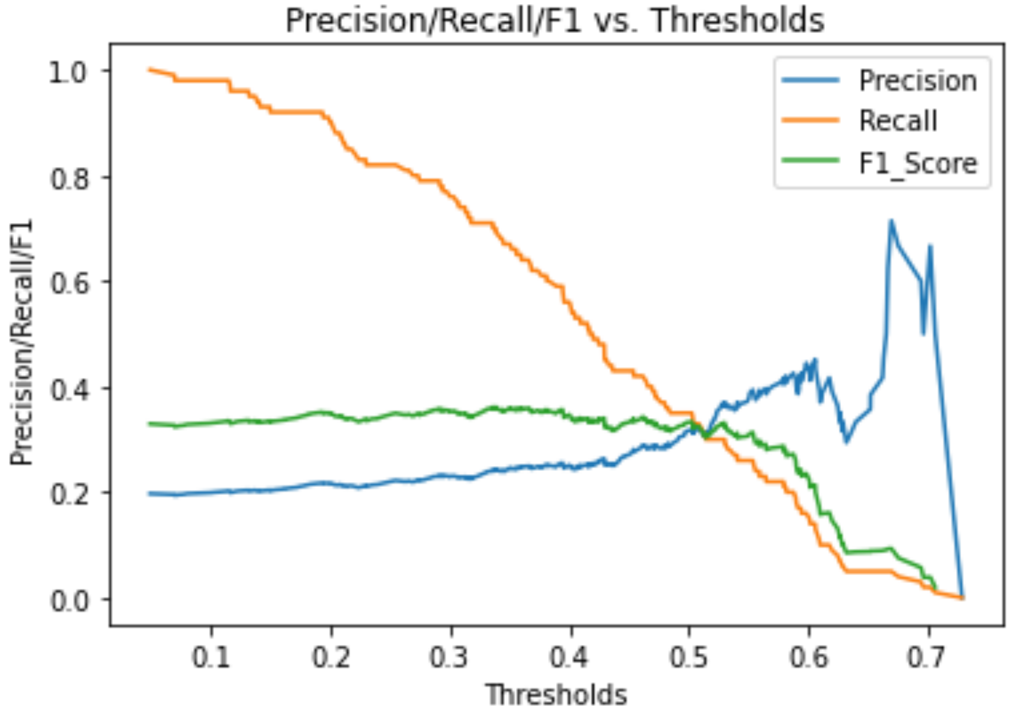
- Augmentation used:
  - Horizonal Flip
  - Height Shift Range = 0.1
  - Width Shift Range = 0.1
  - Rotation Range = 20
  - Shear Range = 0.1
  - Zoom Range = 0.1
- Batch size = 32
- Optimizer learning rate = 3e-4
- Layers of pre-existing architecture that were frozen: First 20 layers
- Layers of pre-existing architecture that were fine-tuned: None
- Layers added to pre-existing architecture:
  - Flatten
  - Dropout 0.5
  - Dense 1024, Activation = ReLU
  - Dropout 0.5
  - Dense 512, Activation = ReLU
  - Dropout 0.5
  - Dense 256, Activation = ReLU
  - Dense 1, Activation = Sigmoid


Model accuracy
Loss/Accuracy
Epoch
train_acc
val_acc
train_loss
val_loss


AUC Curve
True Positive Rate
False Positive Rate
Pneumonia (AUC: 0.616)



Final Threshold and Explanation:



- Based on the F1-Score vs Threshold Chart, to balance between the Precision and Recall, the threshold of 0.728 will give the max value of F1-Score.

4. Databases

- The databases contains 112,120 X-Ray images. The number of Pneumonia Positive images is only 1430 (1.27%).
- Therefore, to split the databases for training, I will have to:
  - Obtain all the postive cases of Pneumonia.
  - Divide the positive cases into 80%-20% for the Training and Validation

Dataset.

Description of Training Dataset:

- Balance the number of negative and positive cases in the training data.

Description of Validation Dataset:

- Make the number of negative cases 4 times bigger the positive cases to somehow reflect the real-world clinical setting

5. Ground Truth

- The ground truth is NLP-derived labels. NLP at this stage is not complex enough to capture all the existing information of the reports. Hence, the accuracy is roughly 90%.

6. FDA Validation Plan

Patient Population Description for FDA Validation Dataset:

- Male and female patients in the age of 1 to 100. The gender distribution is slightly toward Male patient, the male to female ratio is approximately 1.2
- The patient may exihibit the following comorbid with Pneumonia: Atelectasis, Cardiomegaly, Consolidation, Edema, Effusion, Emphysema, Fibrosis, Hernia, Infiltration, Mass, Nodule, Pleural_Thickening, Pneumonia, Pneumothorax -
- The X-Ray Dicom file should has the following properties:
  - Patient Postition: AP or PA
  - Image Type: DX
  - Body Part Examined: CHEST

Ground Truth Acquisition Methodology:

- Establish a silver standard of radiologist reading

Algorithm Performance Standard:

	F1 Score (95% CI)
Radiologist 1	0.383 (0.309, 0.453)
Radiologist 2	0.356 (0.282, 0.428)
Radiologist 3	0.365 (0.291, 0.435)
Radiologist 4	0.442 (0.390, 0.492)
Radiologist Avg.	0.387 (0.330, 0.442)
CheXNet	0.435 (0.387, 0.481)

- The F1-Score should be approximately 0.435 to out-perform the current state-of-the-art method (CheXNet) [https://arxiv.org/pdf/1711.05225.pdf (https://arxiv.org/pdf/1711.05225.pdf)]