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### Pneumonia-Detection-with-CNN / README.md



AgathaZareth Final Edits. notebook readme FINISHED

History

1 contributor

300 lines (150 sloc) | 17.8 KB

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# pneumonia-detection---convolutional-neural-network-CNN-

*This notebook is intended for educational purposes, all scerios are hypothetical, and any resulting model(s) should not be used for any medical purposes.*

## Introduction

According to the latest publication from Meticulous Research®, the global X-ray detectors market is expected to register a CAGR of 6% during the forecast period 2022–2029 to reach \$4.30 billion by 2029. The growing adoption of digital X-ray detectors, rising demand for X-ray imaging in industrial and security markets, growing geriatric population coupled with rising prevalence of chronic diseases & respiratory infections, and increasing utilization of X-ray detectors for early diagnosis & clinical applications are considered to have a positive impact on the global X-ray detectors market [TOP 10 COMPANIES IN X-RAY DETECTORS MARKET].

GE Healthcare is among the top companies operating in the global digital radiography market [[Digital Radiography Market Size to Reach USD 19.82 Billion in 2028, Says Reports and Data](#)]. GE Healthcare is also leading the way with integration of AI into their imaging equipment and software. They currently have on the market a collection of AI algorithms embedded on X-ray systems, Critical Care Suite 2.01 (CCS), for automated measurements, case prioritization, and quality control. This application automatically analyzes images on a GE X-ray system, highlights critical information on chest X-rays, including Endotracheal Tube Positioning, Pneumothorax Triage and Notifications, Quality Care Suite2 AI algorithms that operate in parallel, and help technologists reduce image quality errors and improve efficiency [[GE Healthcare](#)].

## Business Understanding

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GE Healthcare would like to increase the marketability of their CCS system by expanding their collection of AI algorithms used when automatically analyzing images. One part of this expanded collection will screen for pneumonia. This will not only help GE Healthcare stay competitive as the market grows but it will also increase the functionality of their CCS system.

GE Healthcare needs a model that can successfully identify pneumonia.

## Objectives

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Build and test a model that can detect pneumonia using chest x-ray images, to be integrated into GE Healthcare's collection of AI algorithms embedded in the Critical Care Suite 2.01 X-ray systems.

## Data Understanding

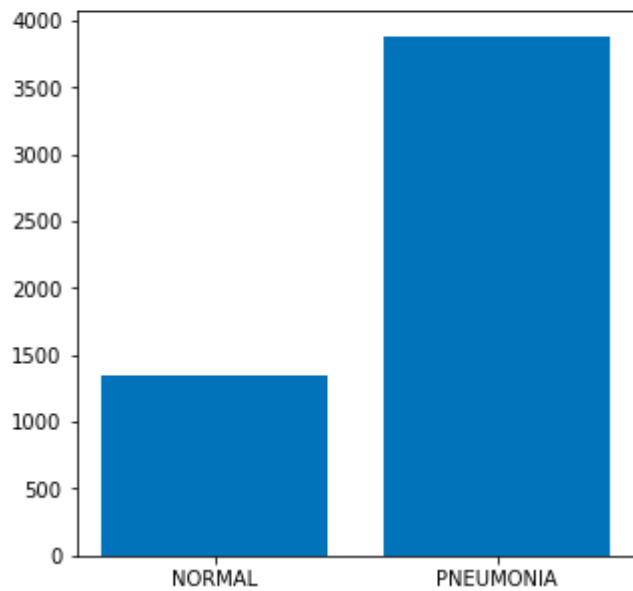
---

The dataset comes from Kermany et al. on [Mendeley Data](#). Images are from Guangzhou Women and Children's Medical Center and contain frontal chest X-rays of children and women. This is a large dataset with 5856 total radiographs; 1583 NORMAL and 4273 PNEUMONIA, both bacterial pneumonia and viral pneumonia.

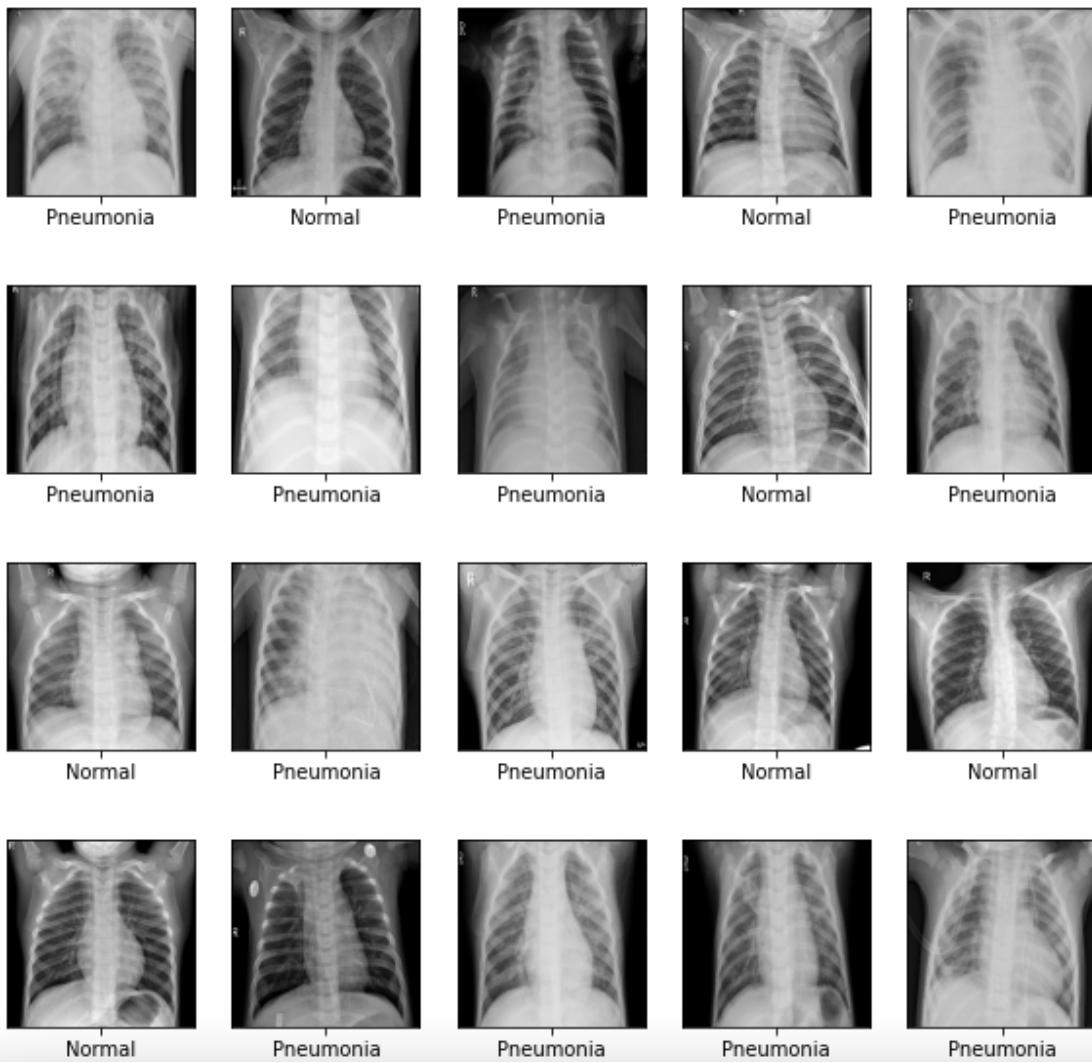
## Exploring the Data

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	label	count	percentage
0	NORMAL	1349	25.78%
1	PNEUMONIA	3883	74.22%

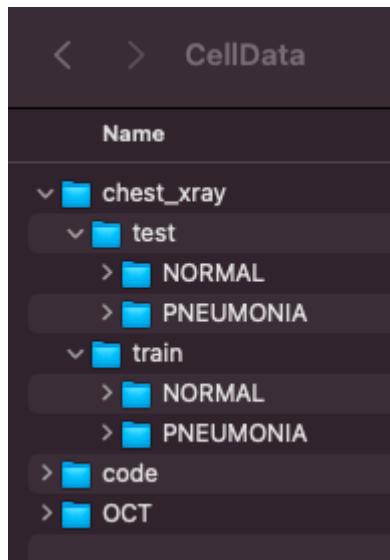


## First 20 Images from Training Data and their true label



## Data used for building models

After unzipping file from [Mendeley Data](#) there will be a `CellData` folder which contains a `chest_xray` folder. From there you will find the data is divided into a `train` and `test` folders and within these folders the images are separated into `NORMAL` and `PNEUMONIA` folders.



My downsampled train set will consist of 500 randomly selected images from this train folder, 250 images NORMAL and 250 PNEUMONIA . I will also create a validation set of images not used in my downsampled train set of 25 NORMAL and 25 PNEUMONIA .

# MODEL ARCHITECTURE

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## OPTIMIZERS:

SGD: "...recent studies show that Adam often leads to worse generalization performance than SGD for training deep neural networks on image classification tasks" [Adam vs. SGD: Closing the generalization gap on image classification.](#)

## ACTIVATION FUNCTION:

For hidden layers: ReLU, This is the standard activation function for hidden layers. There is no data to suggest deviating from this norm would be beneficial to this image classification task.

For output neuron: Sigmoid, because this is a binary classification we can use sigmoid function to give probability of a given image being pneumonia. These probability predictions range from 0-1 making it easy to convert to percentages if so desired.

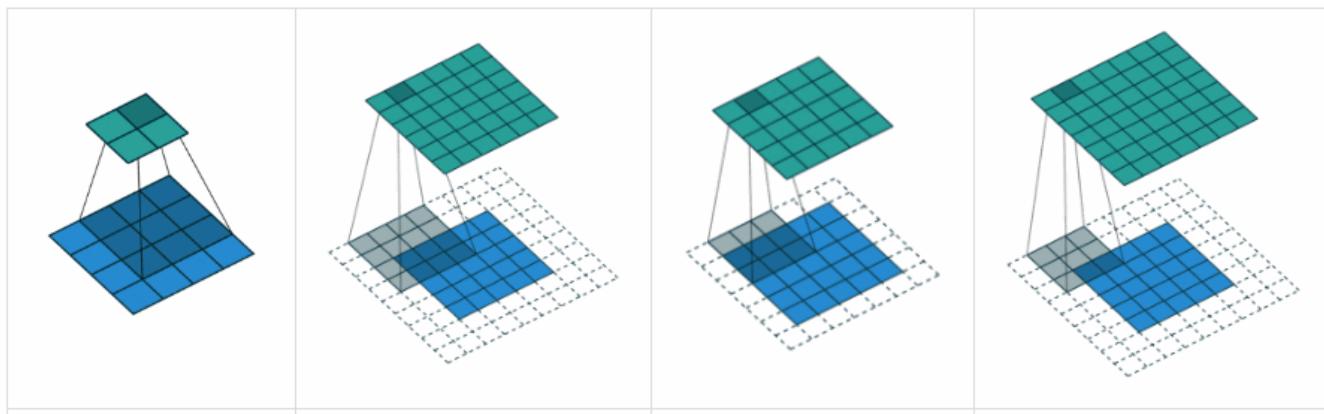
## PADDING:

For convolutional layers I will set padding equal to 'same'. This means there is one layer padding with blank pixels and the resulting pixels is the same size as the input image. It ensures that the filter is applied to all the elements of the input. Conversely, when padding is set to equal 'valid' there can be a loss of information, generally, elements on the right and the bottom of the image tend to be ignored. See below graphic from [this article](#):

padding='valid' is the first figure. The filter window stays inside the image.

padding='same' is the third figure. The output is the same size.

Visualization credits: [vdumoulin@GitHub](https://github.com/vdumoulin/conv_arithmetic)



## LOSS:

`binary_crossentropy`: This is a binary classification problem

## METRICS:

`accuracy`: I am using accuracy because I want a reliable model that does a good job at accurately labeling cases. However, false negatives are a much bigger issue than false positives so in addition to accuracy I will be focusing on pneumonia recall score from the classification report as a secondary metric for gauging model performance. And more specifically, I will be focusing on the difference between training recall scores and testing recall scores, they should be as similar as possible to show that the final model will reliably perform at the same level on new unseen data/cases as it did with the training data.

## MAXIMUM POOLING

Calculate the maximum value for each patch of the feature map. The result of using a pooling layer and creating down sampled or pooled feature maps is a summarized version of the features detected in the input [A Gentle Introduction to Pooling Layers for Convolutional Neural Networks](#).

## L2 KERNEL REGULARIZATION

L2 regularization uses a lambda coefficient of .005.

Performing L2 regularization encourages the weight values towards zero (but not exactly zero). Smaller weights reduce the impact of the hidden neurons. In that case, those hidden neurons become neglectable and the overall complexity of the neural network gets reduced, less complex models typically avoid modeling noise in the data, and therefore, there is no overfitting.

Choosing the right lambda coefficient value:

- If value is too high you run the risk of underfitting your data. Your model won't learn enough about the training data to make useful predictions.
- If value is too low you run the risk of overfitting your data. Your model will learn too much about the particularities of the training data, and won't be able to generalize to new data.

## DROPOUT

During dropout, some neurons get deactivated with a random probability P to reduce model complexity resulting in less overfitting. I am using P=.03

# Models

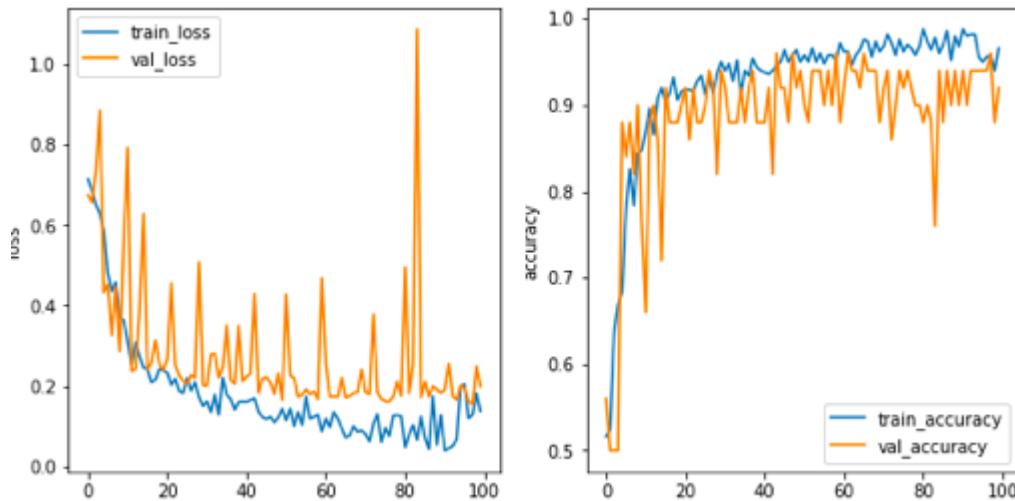
## base\_model

Baseline fully connected model without convolutional layers:

### base\_model.summary()

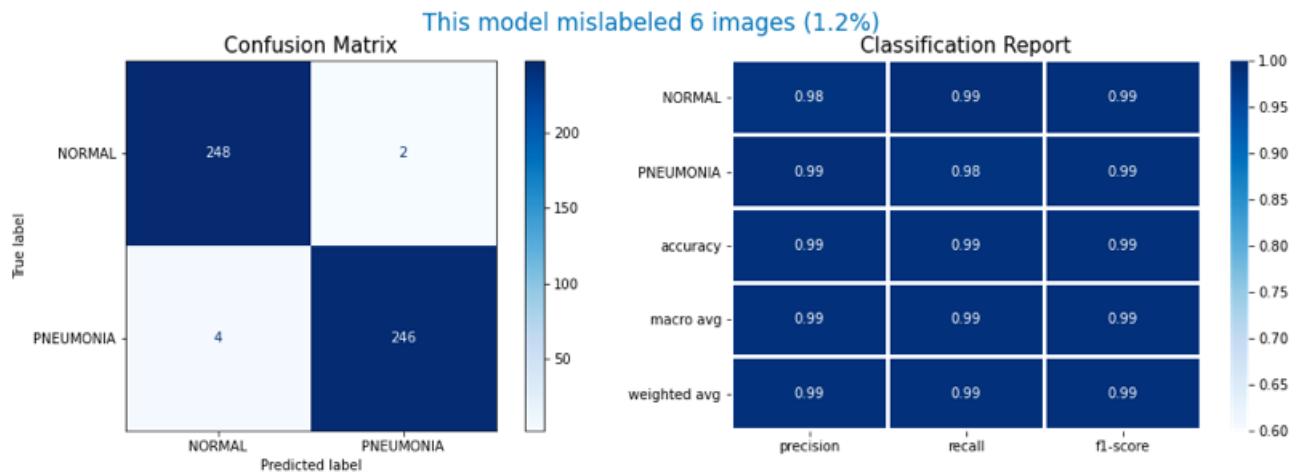
Model: "sequential"		
Layer (type)	Output Shape	Param #
dense (Dense)	(None, 100)	6553700
dense_1 (Dense)	(None, 68)	6868
dense_2 (Dense)	(None, 30)	2070
dense_3 (Dense)	(None, 1)	31
<hr/>		
Total params: 6,562,669		
Trainable params: 6,562,669		
Non-trainable params: 0		

## base\_model Loss and Accuracy across epochs

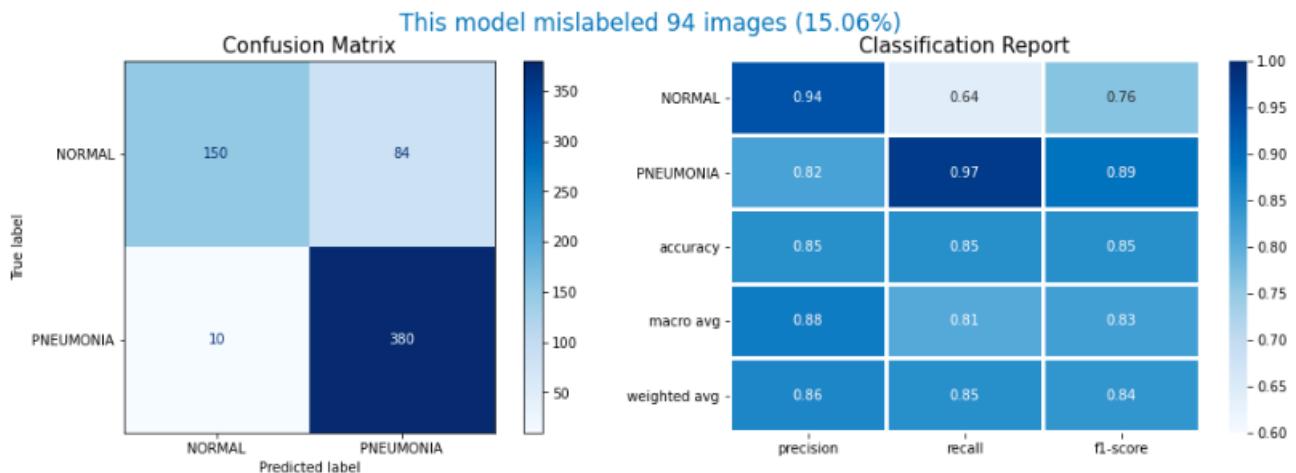


## base\_model Confusion Matrices and Classification Reports

### base\_model Train



### base\_model Test



## base\_cnn

Add convolutional layers to base\_model

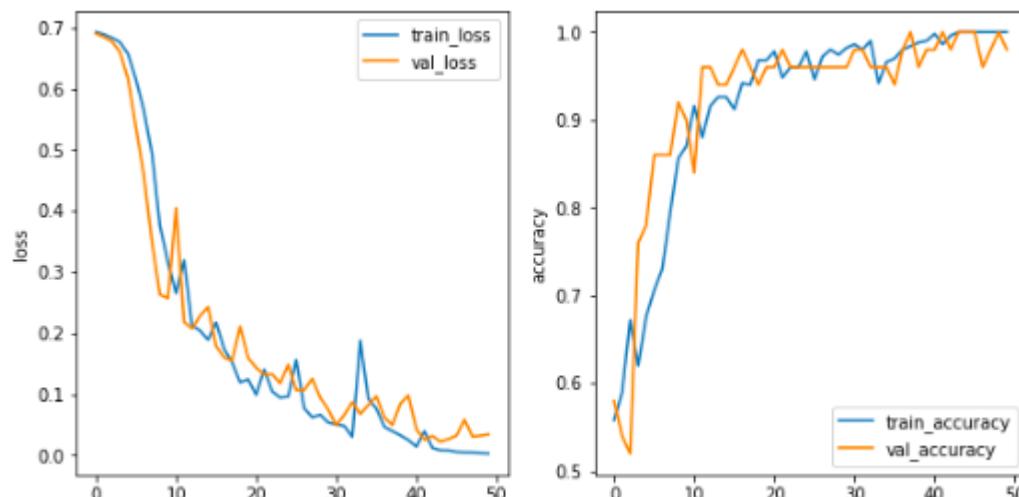
### base\_cnn.summary()

Model: "sequential\_1"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 256, 256, 100)	1000
max_pooling2d (MaxPooling2D)	(None, 128, 128, 100)	0
conv2d_1 (Conv2D)	(None, 128, 128, 80)	72080
max_pooling2d_1 (MaxPooling2D)	(None, 64, 64, 80)	0
conv2d_2 (Conv2D)	(None, 64, 64, 70)	50470
max_pooling2d_2 (MaxPooling2D)	(None, 32, 32, 70)	0
conv2d_3 (Conv2D)	(None, 32, 32, 64)	40384
max_pooling2d_3 (MaxPooling2D)	(None, 16, 16, 64)	0
flatten (Flatten)	(None, 16384)	0
dense_4 (Dense)	(None, 100)	1638500
dense_5 (Dense)	(None, 68)	6868
dense_6 (Dense)	(None, 30)	2070
dense_7 (Dense)	(None, 1)	31

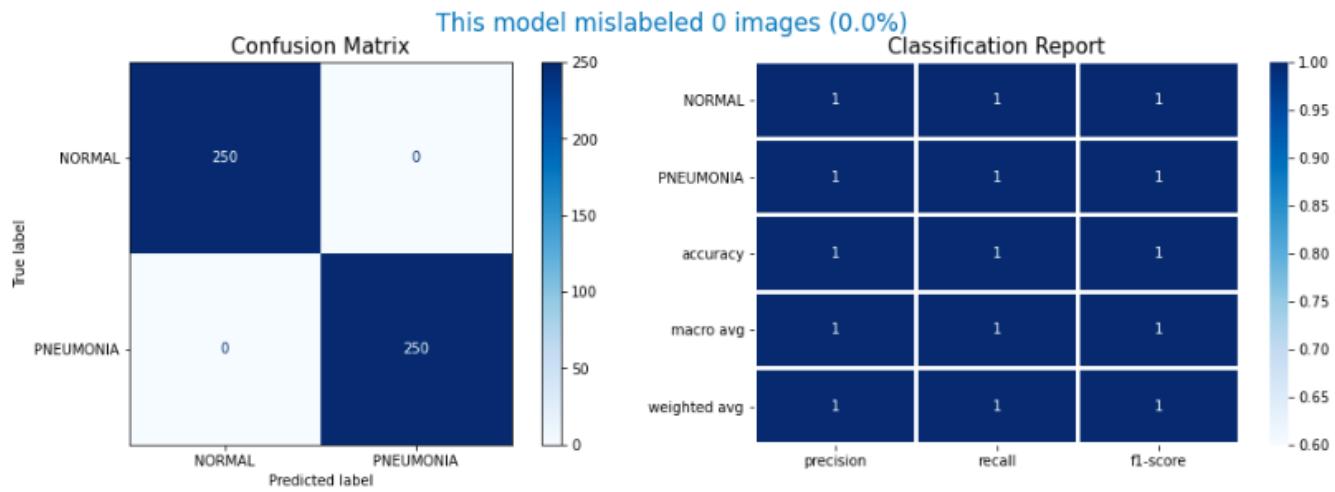
Total params: 1,811,403  
 Trainable params: 1,811,403  
 Non-trainable params: 0

### base\_cnn Loss and Accuracy across epochs

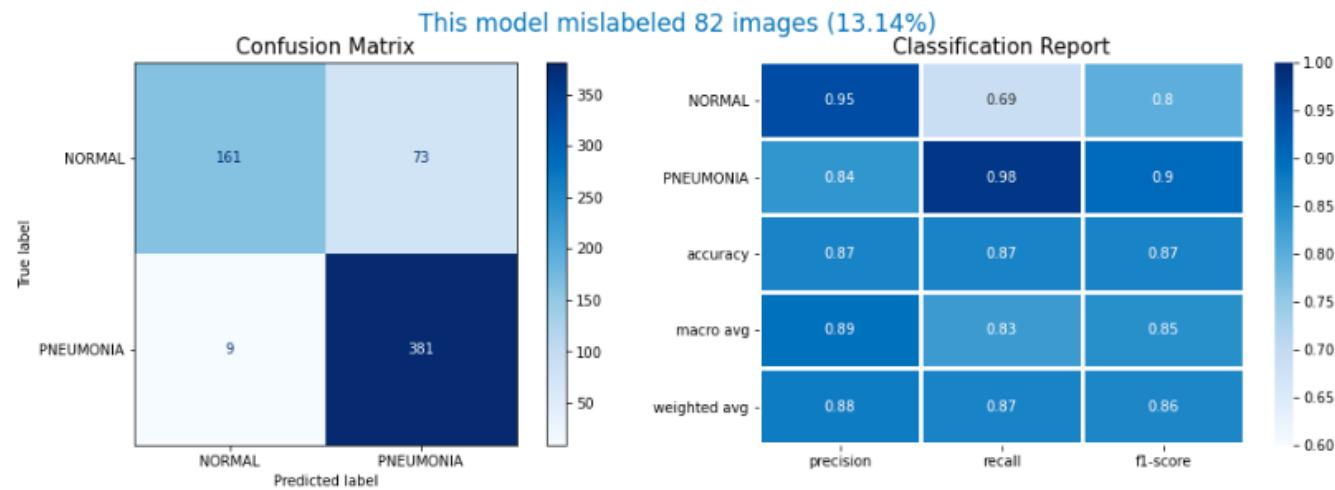


## base\_cnn Confusion Matrices and Classification Reports

### base\_cnn Train



### base\_cnn Test



## reg\_cnn

Add L2 kernel regularization to `base_cnn` model

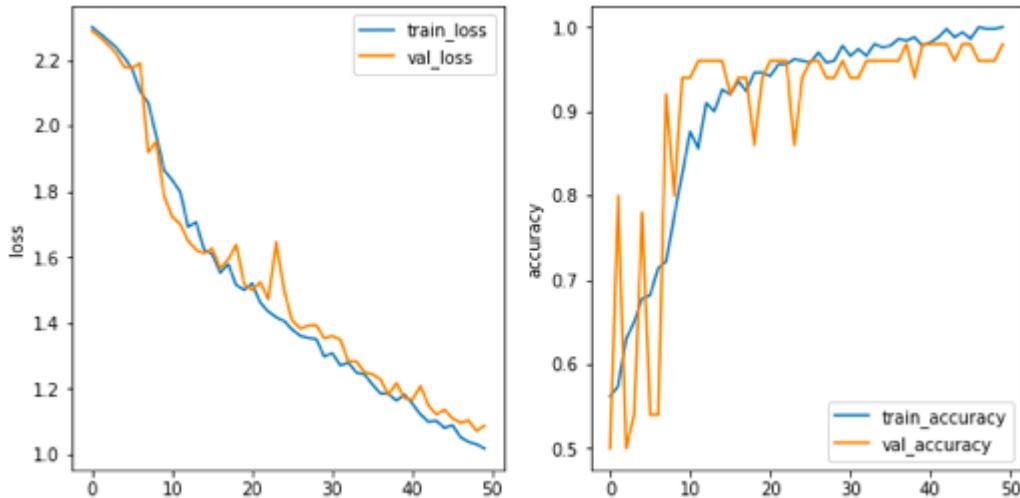
### reg\_cnn.summary()

Model: "sequential\_2"

Layer (type)	Output Shape	Param #
conv2d_4 (Conv2D)	(None, 256, 256, 100)	1000
max_pooling2d_4 (MaxPooling2D)	(None, 128, 128, 100)	0
conv2d_5 (Conv2D)	(None, 128, 128, 80)	72080
max_pooling2d_5 (MaxPooling2D)	(None, 64, 64, 80)	0
conv2d_6 (Conv2D)	(None, 64, 64, 70)	50470
max_pooling2d_6 (MaxPooling2D)	(None, 32, 32, 70)	0
conv2d_7 (Conv2D)	(None, 32, 32, 64)	40384
max_pooling2d_7 (MaxPooling2D)	(None, 16, 16, 64)	0
flatten_1 (Flatten)	(None, 16384)	0
dense_8 (Dense)	(None, 100)	1638500
dense_9 (Dense)	(None, 68)	6868
dense_10 (Dense)	(None, 30)	2070
dense_11 (Dense)	(None, 1)	31

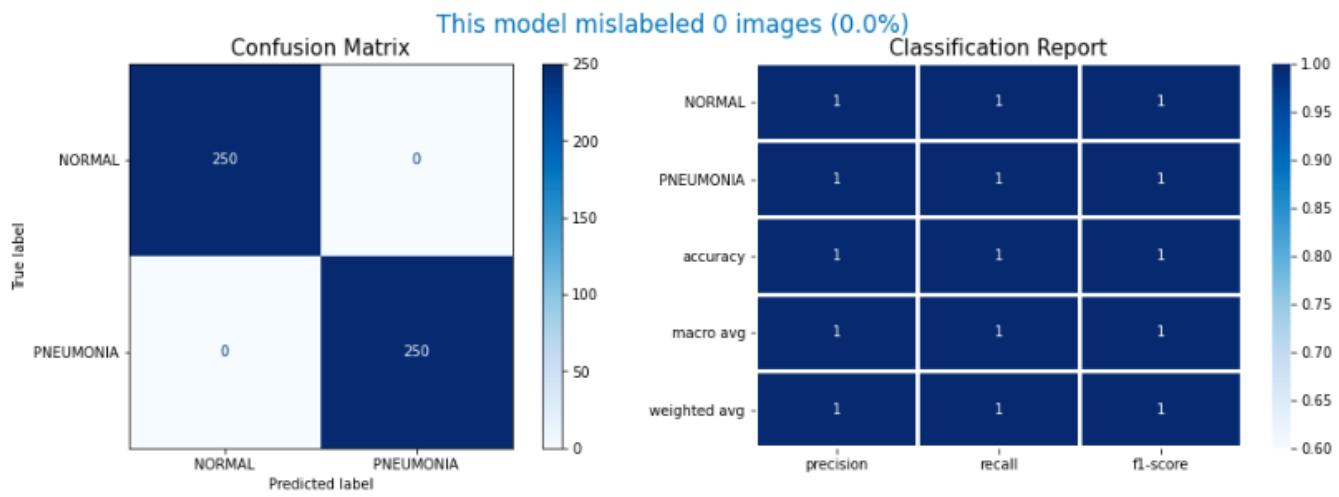
Total params: 1,811,403  
 Trainable params: 1,811,403  
 Non-trainable params: 0

## reg\_cnn Loss and Accuracy across epochs

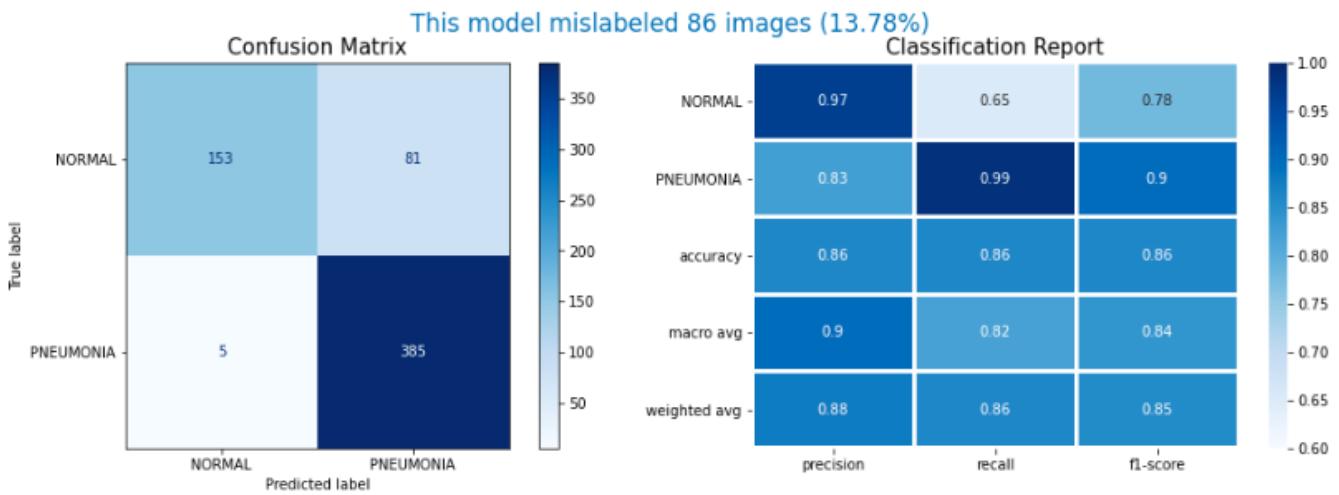


## reg\_cnn Confusion Matrices and Classification Reports

reg\_cnn Train



## reg\_cnn Test



## reduced\_nodes

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Reduce number of nodes in each layer by half

## reduced\_nodes.summary()

Model: "sequential\_3"

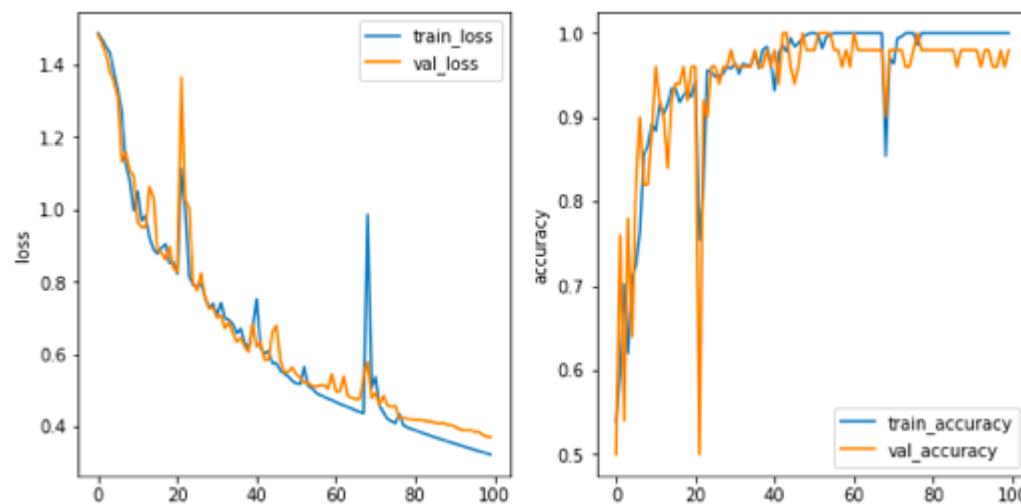
Layer (type)	Output Shape	Param #
conv2d_8 (Conv2D)	(None, 256, 256, 50)	500
max_pooling2d_8 (MaxPooling2D)	(None, 128, 128, 50)	0
conv2d_9 (Conv2D)	(None, 128, 128, 40)	18040
max_pooling2d_9 (MaxPooling2D)	(None, 64, 64, 40)	0
conv2d_10 (Conv2D)	(None, 64, 64, 35)	12635
max_pooling2d_10 (MaxPooling2D)	(None, 32, 32, 35)	0
conv2d_11 (Conv2D)	(None, 32, 32, 32)	10112
max_pooling2d_11 (MaxPooling2D)	(None, 16, 16, 32)	0
flatten_2 (Flatten)	(None, 8192)	0
dense_12 (Dense)	(None, 50)	409650
dense_13 (Dense)	(None, 34)	1734
dense_14 (Dense)	(None, 15)	525
dense_15 (Dense)	(None, 1)	16

Total params: 453,212

Trainable params: 453,212

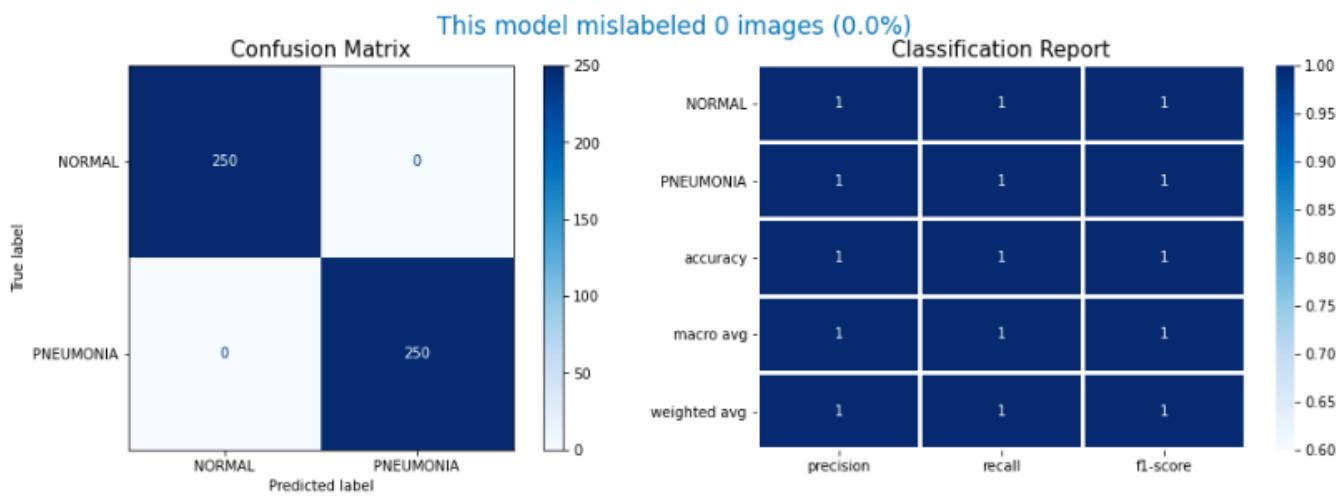
Non-trainable params: 0

## reduced\_nodes Loss and Accuracy across epochs

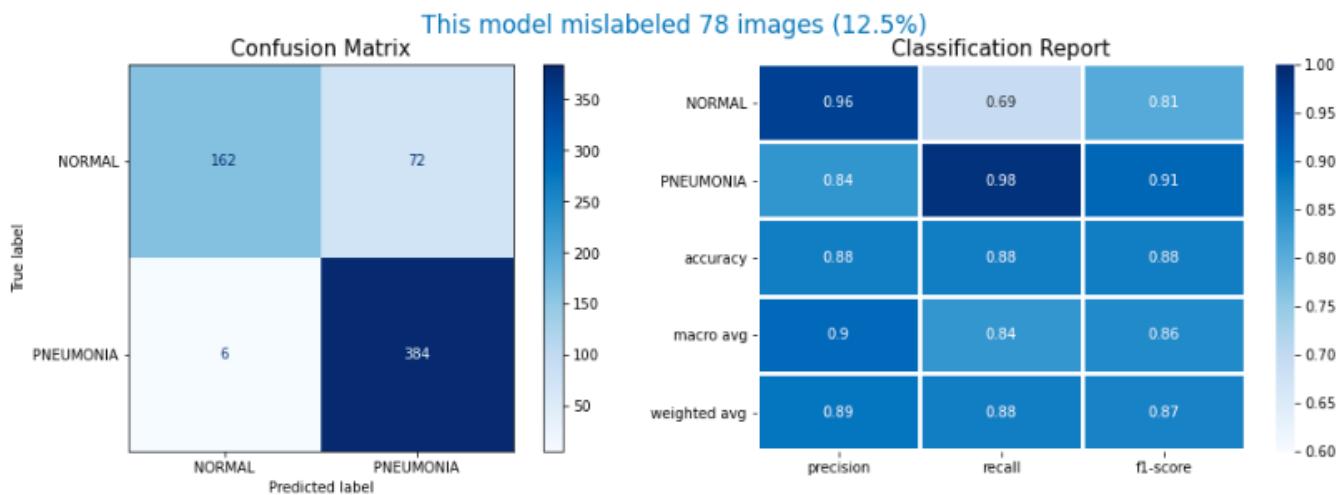


## reduced\_nodes Confusion Matrices and Classification Reports

### reduced\_nodes Train



## reduced\_nodes Test



## dropout

Add dropout to `reduced_nodes` model

### `dropout.summary()`

Model: "sequential\_4"

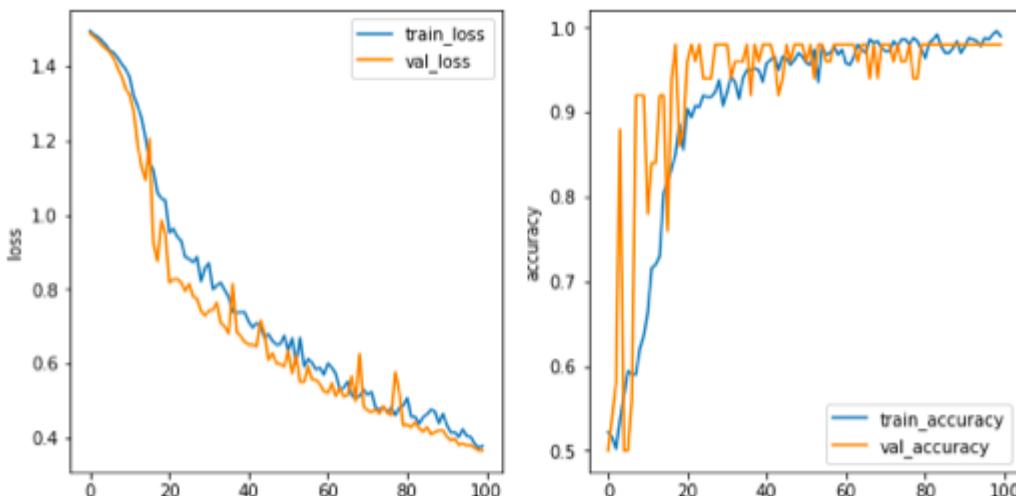
Layer (type)	Output Shape	Param #
conv2d_12 (Conv2D)	(None, 256, 256, 50)	500
max_pooling2d_12 (MaxPooling)	(None, 128, 128, 50)	0
conv2d_13 (Conv2D)	(None, 128, 128, 40)	18040
max_pooling2d_13 (MaxPooling)	(None, 64, 64, 40)	0
conv2d_14 (Conv2D)	(None, 64, 64, 35)	12635
max_pooling2d_14 (MaxPooling)	(None, 32, 32, 35)	0
conv2d_15 (Conv2D)	(None, 32, 32, 32)	10112
max_pooling2d_15 (MaxPooling)	(None, 16, 16, 32)	0
flatten_3 (Flatten)	(None, 8192)	0
dropout (Dropout)	(None, 8192)	0
dense_16 (Dense)	(None, 50)	409650
dropout_1 (Dropout)	(None, 50)	0
dense_17 (Dense)	(None, 34)	1734
dropout_2 (Dropout)	(None, 34)	0
dense_18 (Dense)	(None, 15)	525
dropout_3 (Dropout)	(None, 15)	0
dense_19 (Dense)	(None, 1)	16

Total params: 453,212

Trainable params: 453,212

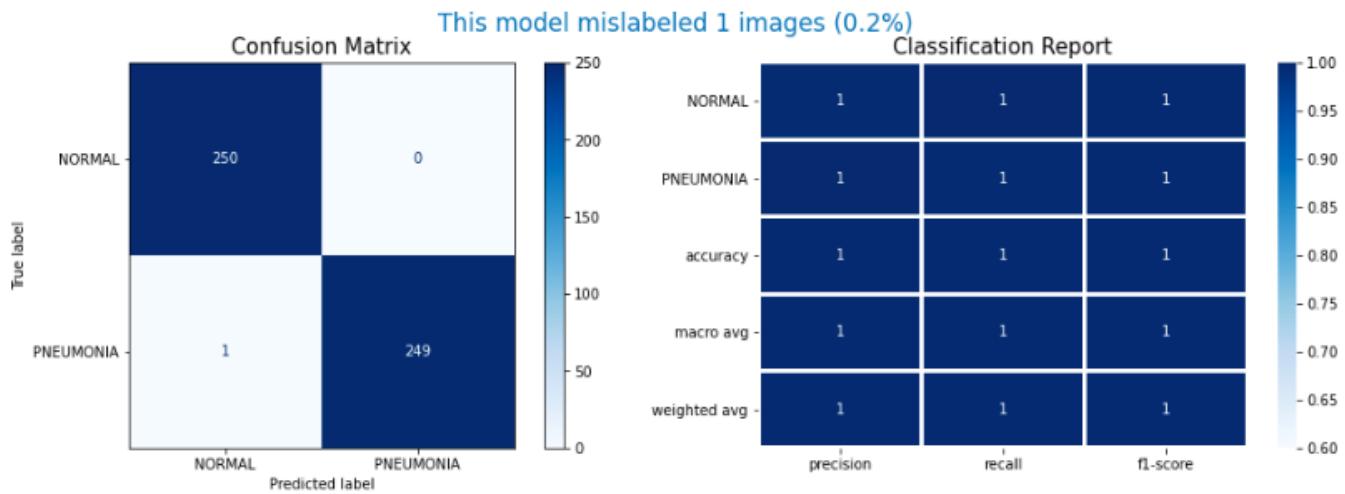
Non-trainable params: 0

## dropout Loss and Accuracy across epochs

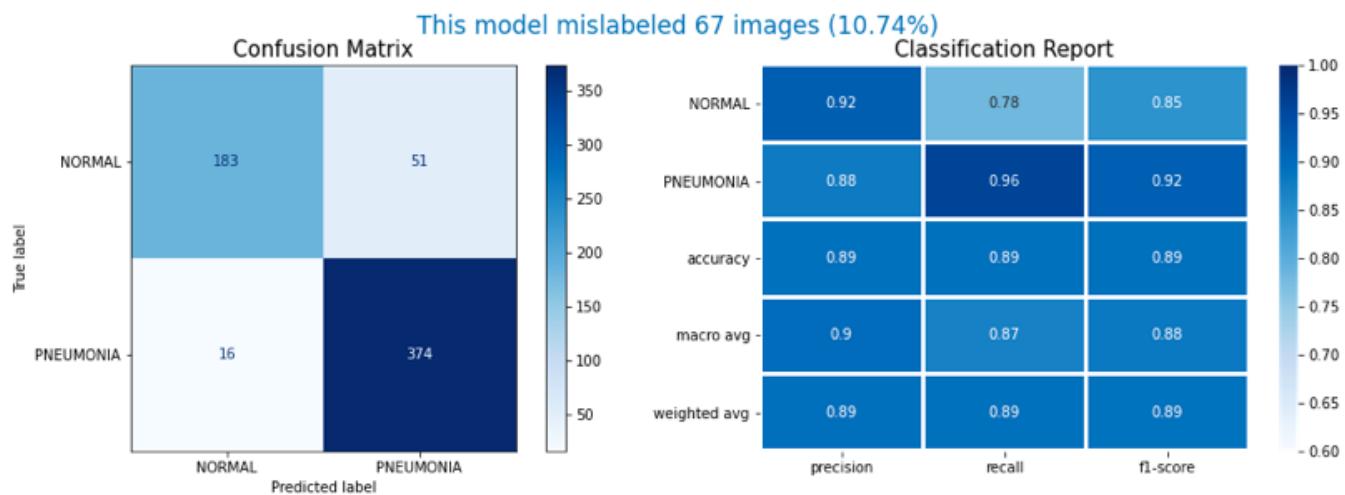


## dropout Confusion Matrices and Classification Reports

## dropout Train



## dropout Test



# Compare the models

compare df:

	<b>pneumonia_recall</b>	<b>misclassified</b>	<b>accuracy</b>
<b>base_train</b>	0.98	0.010	0.99
<b>base_test</b>	0.97	0.150	0.85
<b>cnn_train</b>	1.00	0.000	1.00
<b>cnn_test</b>	0.98	0.131	0.87
<b>reg_train</b>	1.00	0.000	1.00
<b>reg_test</b>	0.99	0.139	0.86
<b>reduced_train</b>	1.00	0.000	1.00
<b>reduced_test</b>	0.98	0.125	0.88
<b>drop_train</b>	1.00	0.002	1.00
<b>drop_test</b>	0.96	0.107	0.89

metrics\_df :

	<b>train_loss</b>	<b>train_acc</b>	<b>test_loss</b>	<b>test_acc</b>	<b>loss_diff</b>	<b>acc_diff</b>
<b>base_model</b>	0.040549	0.988	0.598990	0.849359	0.558442	0.138641
<b>base_cnn</b>	0.001954	1.000	0.899908	0.868590	0.897954	0.131410
<b>reg_cnn</b>	1.012247	1.000	1.839380	0.862179	0.827133	0.137821
<b>reduced_nodes</b>	0.321644	1.000	1.059986	0.875000	0.738342	0.125000
<b>dropout</b>	0.348353	0.998	0.967050	0.892628	0.618697	0.105372

My goal for adding dropout was to close the gap between the training and test loss difference and train and test accuracy difference. The metrics\_df shows that this dropout model did infact reduce that gap from the previous model iteration. However, the compare df shows that while the accuracy improved with this dropout model, the pneumonia recall score for test data dropped. You can also explore this in greater detail by comparing the confusion matrices and classification reports of the train data from the last two models.

At this point I need to move forward with selecting a final model. I can chose the higher accuracy dropout model, or the higher recall score of reduced\_nodes model.

Because the intent of this model is to flag cases of concern, I will go with the higher recall score model, `reduced_nodes`, so that fewer cases are given a false negative label of `NORMAL`. This may result in increased number of cases prioritized for immediate review from radiologists however, I will capture as many true pneumonia cases as possible which in the end will result in expedited treatment for these patients.

## Final Model

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For the above mentioned reasons I have chosen my final model to be the `reduced_nodes` model. For the `final_model` I downsampled the pneumonia class to match that of the normal class. This will bring the total number of training images to 2698 with an even split of both classes. I then selected 25 from each class for validation data.

### final\_model Architecture

---

```
final_model = models.Sequential()
final_model.add(layers.Conv2D(50, (3, 3), padding='same', activation='relu', input_shape=(256, 256, 1)))
final_model.add(layers.MaxPooling2D((2, 2)))

final_model.add(layers.Conv2D(40, (3, 3), padding='same', activation='relu'))
final_model.add(layers.MaxPooling2D((2, 2)))

final_model.add(layers.Conv2D(35, (3, 3), padding='same', activation='relu'))
final_model.add(layers.MaxPooling2D((2, 2)))

final_model.add(layers.Conv2D(32, (3, 3), padding='same', activation='relu'))
final_model.add(layers.MaxPooling2D((2, 2)))

final_model.add(layers.Flatten())

final_model.add(layers.Dense(32, kernel_regularizer=regularizers.l2(.005), activation='relu'))
final_model.add(layers.Dense(16, kernel_regularizer=regularizers.l2(.005), activation='relu'))
final_model.add(layers.Dense(5, kernel_regularizer=regularizers.l2(.005), activation='relu'))
final_model.add(layers.Dense(1, activation='sigmoid'))

final_model.compile(optimizer='SGD',
                    loss='binary_crossentropy',
                    metrics=['accuracy'])

final_model.summary()
```

### final\_model Summary

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**Model: "sequential\_7"**

Layer (type)	Output Shape	Param #
conv2d_24 (Conv2D)	(None, 256, 256, 50)	500
max_pooling2d_24 (MaxPooling)	(None, 128, 128, 50)	0
conv2d_25 (Conv2D)	(None, 128, 128, 40)	18040
max_pooling2d_25 (MaxPooling)	(None, 64, 64, 40)	0
conv2d_26 (Conv2D)	(None, 64, 64, 35)	12635
max_pooling2d_26 (MaxPooling)	(None, 32, 32, 35)	0
conv2d_27 (Conv2D)	(None, 32, 32, 32)	10112
max_pooling2d_27 (MaxPooling)	(None, 16, 16, 32)	0
flatten_6 (Flatten)	(None, 8192)	0
dense_28 (Dense)	(None, 32)	262176
dense_29 (Dense)	(None, 16)	528
dense_30 (Dense)	(None, 5)	85
dense_31 (Dense)	(None, 1)	6

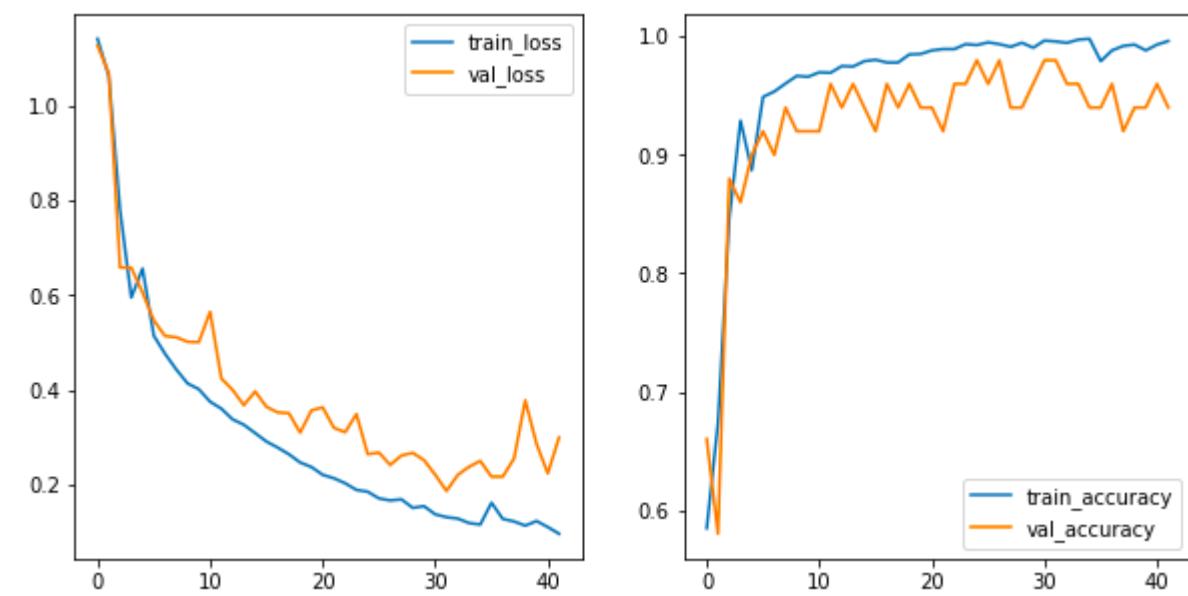
Total params: 304,082

Trainable params: 304,082

Non-trainable params: 0

## final\_model Loss and Accuracy across epochs

### Plot



**NOTES:** The early stopping was triggered after 42 epochs. It took approximately 180 seconds per epoch on this machine. It is clear from the above plots that this model is still slightly over trained (take note of the scale of y axis). Next Steps will discuss options to address this.

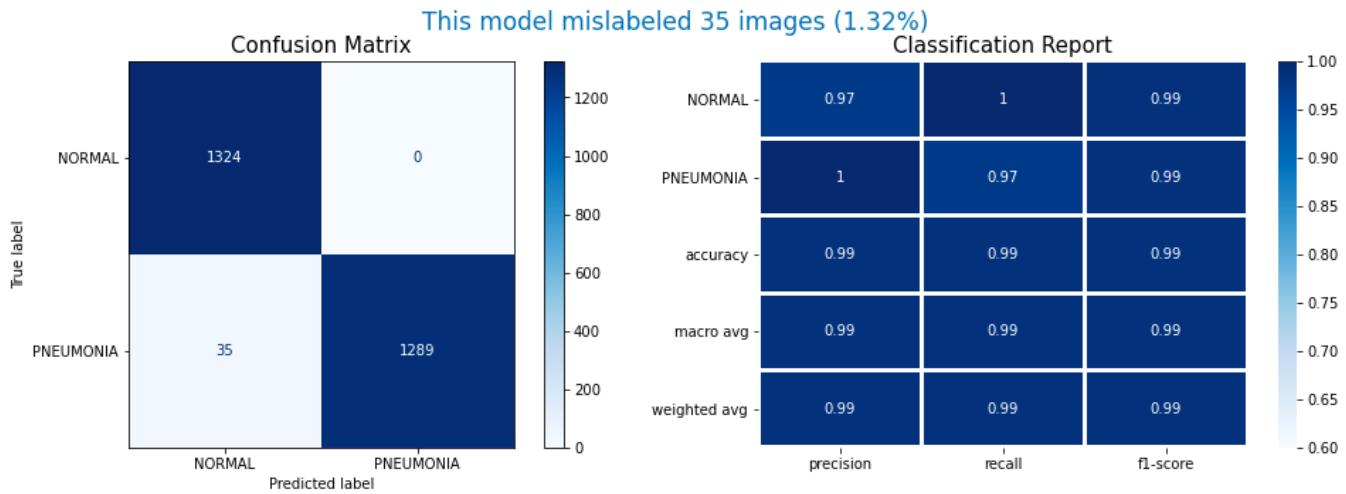
## Compare with compare df

	pneumonia_recall	misclassified	accuracy
<b>base_train</b>	0.98	0.010	0.99
<b>base_test</b>	0.97	0.150	0.85
<b>cnn_train</b>	1.00	0.000	1.00
<b>cnn_test</b>	0.98	0.131	0.87
<b>reg_train</b>	1.00	0.000	1.00
<b>reg_test</b>	0.99	0.139	0.86
<b>reduced_train</b>	1.00	0.000	1.00
<b>reduced_test</b>	0.98	0.125	0.88
<b>drop_train</b>	1.00	0.002	1.00
<b>drop_test</b>	0.96	0.107	0.89
<b>final_train</b>	0.97	0.013	0.99
<b>final_test</b>	0.97	0.088	0.91

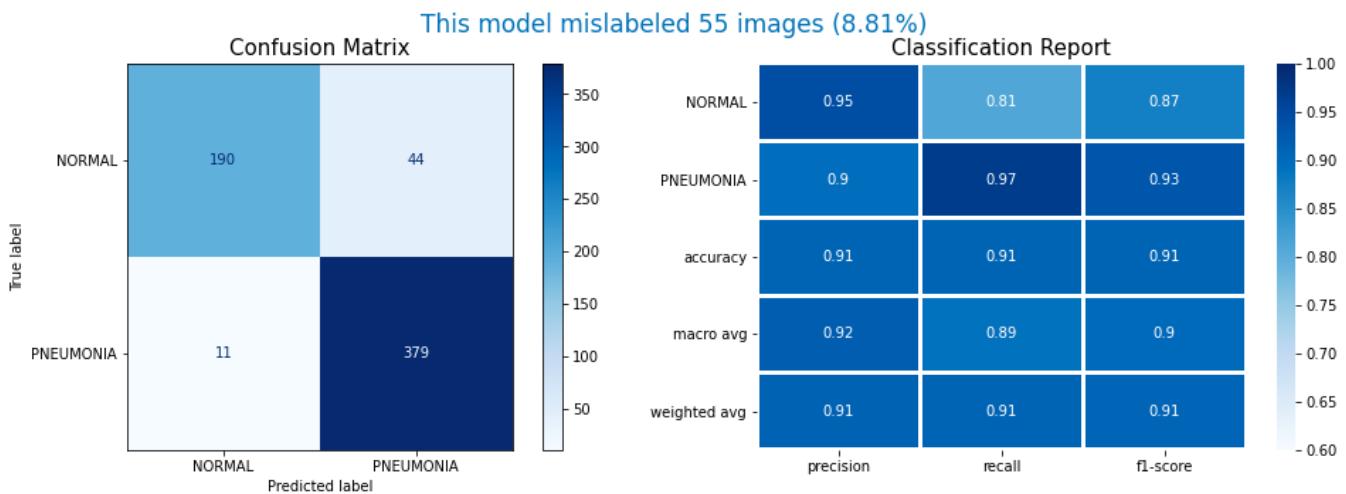
**NOTES:** There is still a very high accuracy with both train and test data, ~98.7% and ~91.2% respectively. Additionally, the differences between training and test, loss and accuracy are the lowest in this final model. Remember, this is the `reduce_nodes` model and the only difference is the amount of data that has been used to train the model.

# final\_model Confusion Matrices and Classification Reports

## final\_model Train

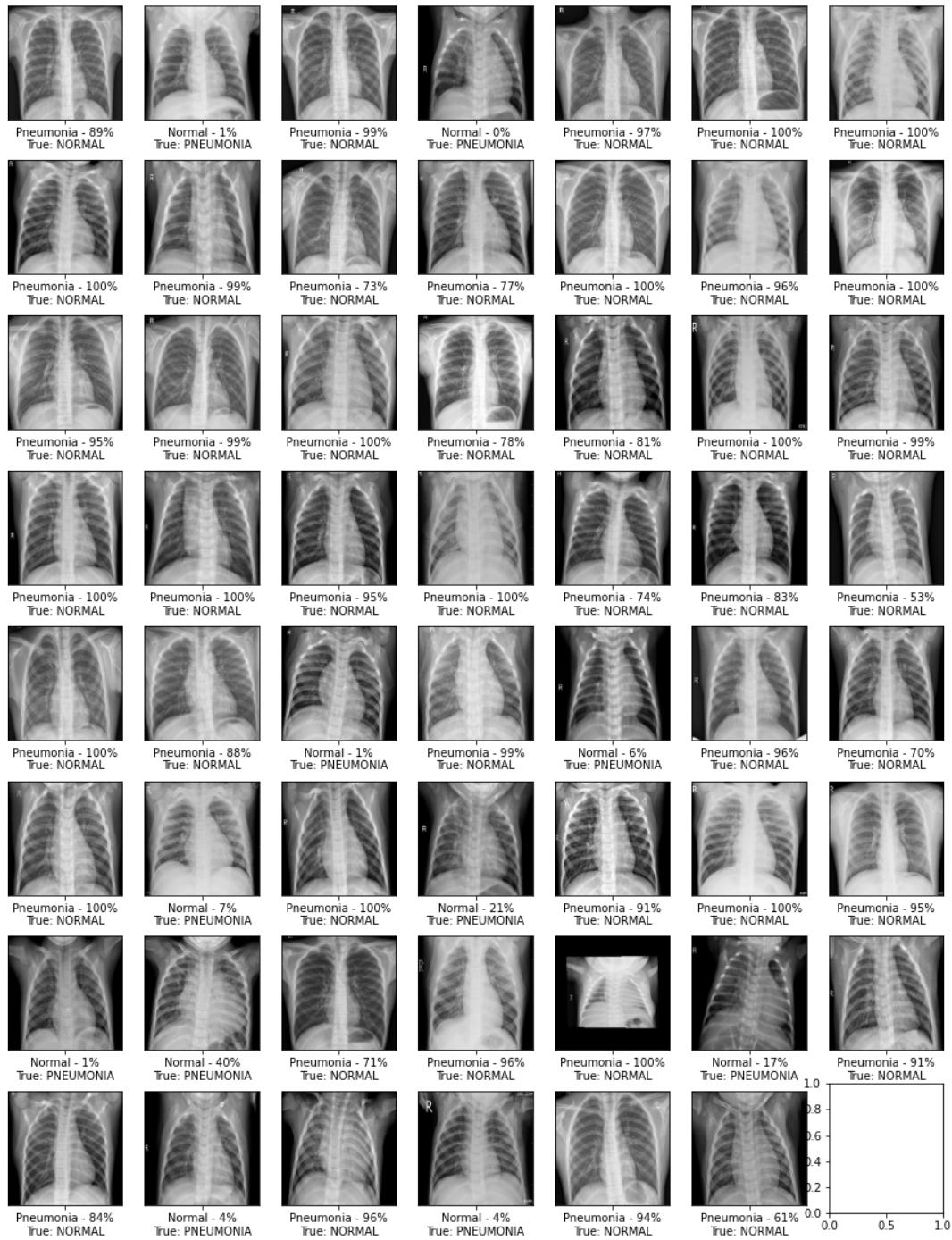


## final\_model Test



[View misclassified images from testing data](#)

Images the final\_model misclassified: predicted\_class - predicted\_probability\_of\_pneumonia.



## Final evaluation

## metrics\_df

	<b>train_loss</b>	<b>train_acc</b>	<b>test_loss</b>	<b>test_acc</b>	<b>loss_diff</b>	<b>acc_diff</b>
<b>base_model</b>	0.040549	0.988000	0.598990	0.849359	0.558442	0.138641
<b>base_cnn</b>	0.001954	1.000000	0.899908	0.868590	0.897954	0.131410
<b>reg_cnn</b>	1.012247	1.000000	1.839380	0.862179	0.827133	0.137821
<b>reduced_nodes</b>	0.321644	1.000000	1.059986	0.875000	0.738342	0.125000
<b>dropout</b>	0.348353	0.998000	0.967050	0.892628	0.618697	0.105372
<b>final_model</b>	0.113301	0.986782	0.449658	0.911859	0.336356	0.074924

**NOTES:** From the `compare_df` you can see the testing data accuracy scored highest with this model. You can also see in both training and test data pneumonia recall score is the same. This is important because we want to avoid false negatives slipping by without immediate attention called to them. While it is not the highest of all the models it is important they match because we want a reliable model that is outputting similar results on unseen data as it does on testing data. As noted above, from the `metrics_df` you can see there is still a very high accuracy with both train and test data, ~98.7% and ~91.2% respectively. Additionally, the differences between training and test, loss and accuracy are the lowest in this final model. Remember, this is the `reduce_nodes` model and the only difference is the amount of data that has been used to train the model. This demonstrates the potential for this model to improve with more available data to learn with.

## Next Steps

While this model has the lowest difference between training and test, loss and accuracy there is still a slight difference. In future iteration, increasing the lambda coefficient in the L2 regularization may further decrease these differences. Additional methods may also be to reduce the kernel nodes even further, or decrease the dropout p value.

As we have seen, the more data available to train the model, the better it performs. One option to increase data, while maintaining equal distribution of classes, is instead of down sampling the pneumonia class to match that of the normal class, we can up sample the normal class using data augmentation to match the number of pneumonia cases. This will result in 2534 more "NORMAL" images and increase the total number of training images from 2698 to 7766.

# Recommendations

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My recommendation is that GE Healthcare have built into the CCS machines software the ability to not only flag cases of concern for immediate review, but also have the radiologist either confirm or reject the models predictions. This collaborative approach gives further opportunities for the model to learn and improve performance, and also provides a direct actionable way to improve clinical outcomes and elevate patient experience. This could even potentially mean a CCS machine could learn the proclivities of the particular office or medical practice that it is located in.

An additional recommendation would be to push software updates to existing machines, providing ongoing improvements of predictions. This would be particularly useful for small rural locations who don't have a high volume of patients. If they can get updates, and improve, due to the images being collected from clinics in more densely populated urban locations then you are giving every doctor's office around the globe a reason to want this technology for their own practice no matter how big or small they are.

These recommendations will make these CCS units more marketable to a larger range of businesses. The more CCS machines learning from new cases, the better these AI predictions can get. And the better the predictions, the more justification to bring this technology into every medical practice.

## Thank You

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Let's work together,

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