Detection of Covid-19 Pneumonia via Chest X-Rays

BCF 1
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Current Situation ...

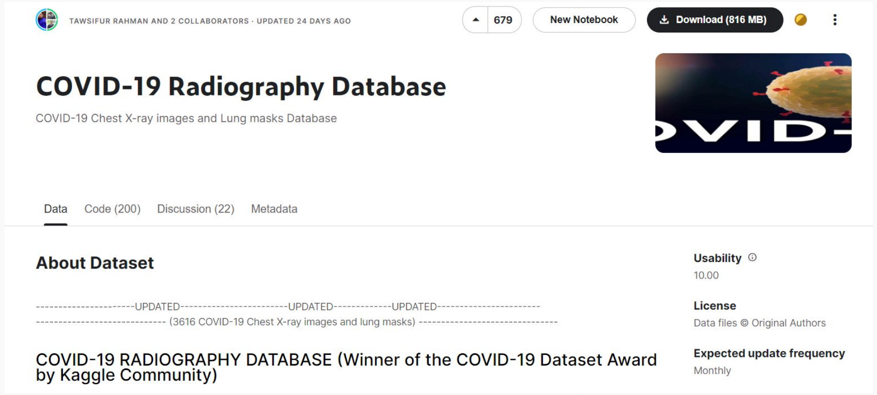
As COVID-19 becomes endemic, the **strain** on healthcare services worldwide **intensifies**, making it more difficult to **manage & detect** the serious complications of COVID-19.

We see the possibility of replacing the current, manual way of diagnosing pneumonia which is **unnecessarily exhausting limited resources** and **time-consuming** yet may not be highly effective due to the presence of **inevitable human errors**

How can we improve the efficiency of diagnosing normal, viral and covid-induced pneumonia in healthcare settings?

PROBLEM DEFINITION

COVID-19 Chest X-Ray Image Dataset


TAWSIFUR RAHMAN AND 2 COLLABORATORS · UPDATED 24 DAYS AGO

679 | New Notebook | Download (816 MB)

COVID-19 Radiography Database

COVID-19 Chest X-ray images and Lung masks Database

Data | Code (200) | Discussion (22) | Metadata

About Dataset

---------------------UPDATED----------------------UPDATED------------UPDATED----------------------

--------------------------- (3616 COVID-19 Chest X-ray images and lung masks) ------------------------------

COVID-19 RADIOGRAPHY DATABASE (Winner of the COVID-19 Dataset Award by Kaggle Community)

Usability
10.00

License
Data files © Original Authors

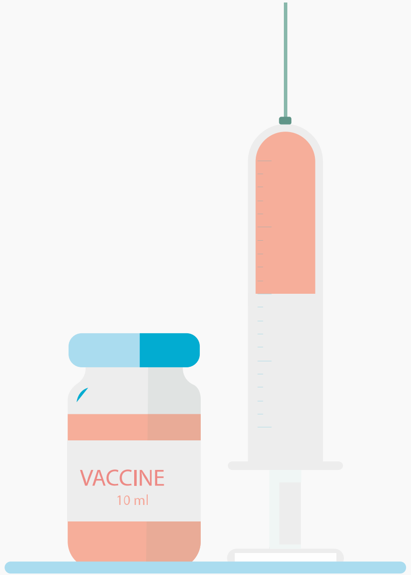
Expected update frequency
Monthly

- Found a dataset containing COVID-19 Chest X-Rays on Kaggle
- 21165 Chest X-Rays from 4 different categories
  - COVID_19
  - Normal
  - Lung Opacity
  - Viral Pneumonia

Our Solution...

To tackle this Multi-Class Classification Problem, we propose:

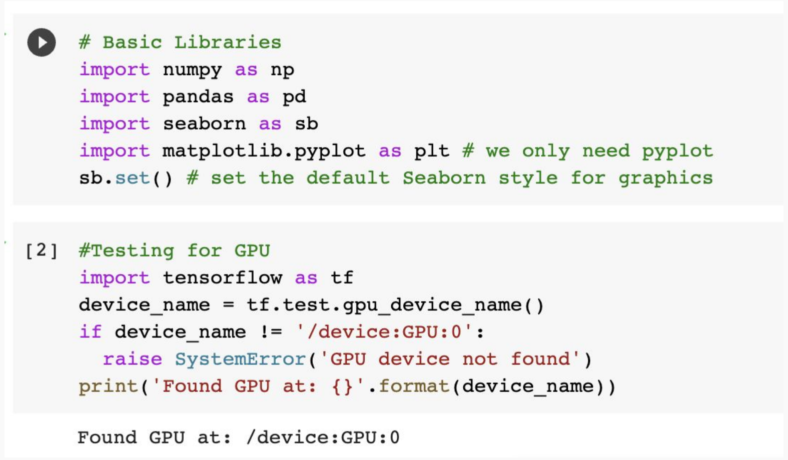
Image Classification model to classify Chest X-Ray images into 3 classes (normal, viral pneumonia and COVID-induced pneumonia)



Approach:

- Clean and use only relevant data
- Split into train, validation and test set
- Apply Transfer Learning

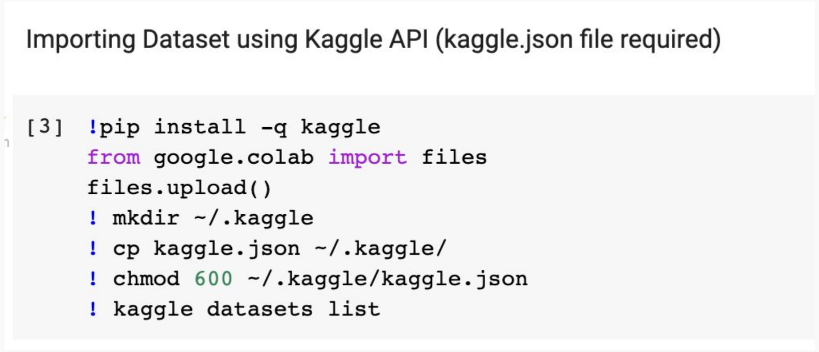
DATA PREPARATION



```
# Basic Libraries
import numpy as np
import pandas as pd
import seaborn as sb
import matplotlib.pyplot as plt # we only need pyplot
sb.set() # set the default Seaborn style for graphics
```

```
[2]  #Testing for GPU
     import tensorflow as tf
     device_name = tf.test.gpu_device_name()
     if device_name != '/device:GPU:0':
       raise SystemError('GPU device not found')
     print('Found GPU at: {}'.format(device_name))

     Found GPU at: /device:GPU:0
```

Import Essential Libraries for analysis and machine learning such as Tensorflow (NEW!)

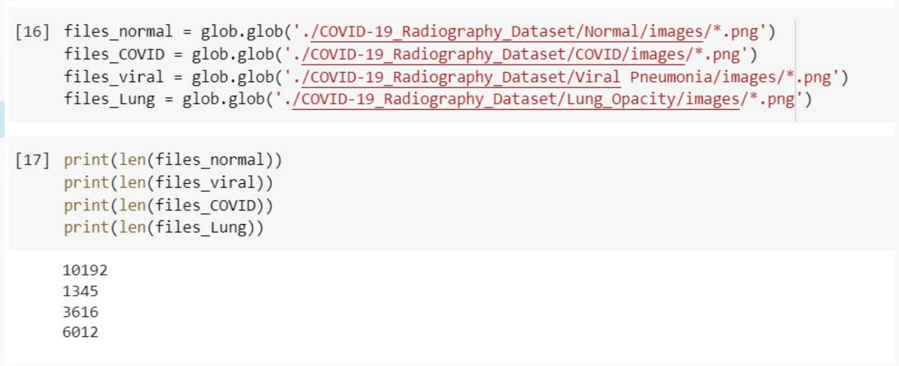


Importing Dataset using Kaggle API (kaggle.json file required)

```
[3]  !pip install -q kaggle
     from google.colab import files
     files.upload()
     ! mkdir ~/.kaggle
     ! cp kaggle.json ~/.kaggle/
     ! chmod 600 ~/.kaggle/kaggle.json
     ! kaggle datasets list
```

Imported Dataset using Kaggle API

DATA PREPARATION



```
[16] files_normal = glob.glob('./COVID-19_Radiography_Dataset/Normal/images/*.png')
     files_COVID = glob.glob('./COVID-19_Radiography_Dataset/COVID/images/*.png')
     files_viral = glob.glob('./COVID-19_Radiography_Dataset/Viral Pneumonia/images/*.png')
     files_Lung = glob.glob('./COVID-19_Radiography_Dataset/Lung_Opacity/images/*.png')
```

```
[17] print(len(files_normal))
     print(len(files_viral))
     print(len(files_COVID))
     print(len(files_Lung))
```

```
     10192
     1345
     3616
     6012
```

Lung Opacity

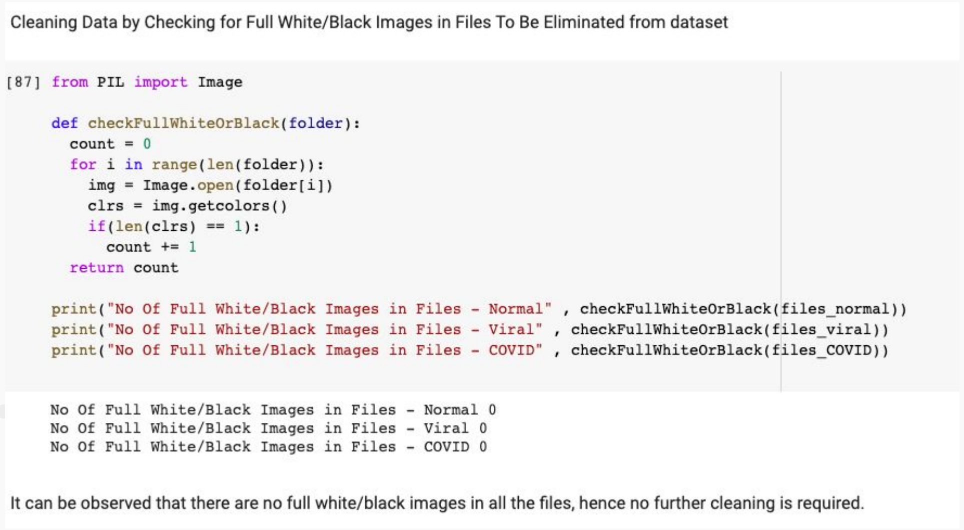
- 6012 images in dataset
- Contains a mix of Viral Pneumonia and other lung infections

Overlapping data could cause accuracy of classifier to decrease

Other lung infections are not relevant to our goal

Solution: Filter out the data

DATA PREPARATION...



Cleaning Data by Checking for Full White/Black Images in Files To Be Eliminated from dataset

```
[87] from PIL import Image

     def checkFullWhiteOrBlack(folder):
       count = 0
       for i in range(len(folder)):
         img = Image.open(folder[i])
         clrs = img.getcolors()
         if(len(clrs) == 1):
           count += 1
       return count

     print("No Of Full White/Black Images in Files - Normal" , checkFullWhiteOrBlack(files_normal))
     print("No Of Full White/Black Images in Files - Viral" , checkFullWhiteOrBlack(files_viral))
     print("No Of Full White/Black Images in Files - COVID" , checkFullWhiteOrBlack(files_COVID))
```

```
No Of Full White/Black Images in Files - Normal 0
No Of Full White/Black Images in Files - Viral 0
No Of Full White/Black Images in Files - COVID 0
```

It can be observed that there are no full white/black images in all the files, hence no further cleaning is required.

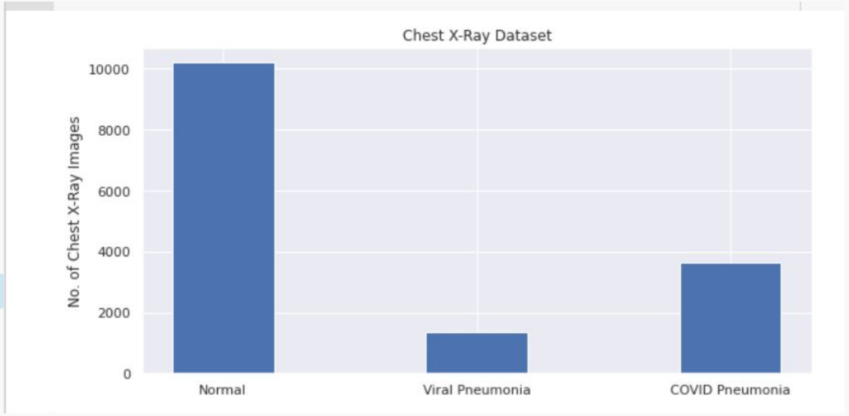
Checking for Blank Images

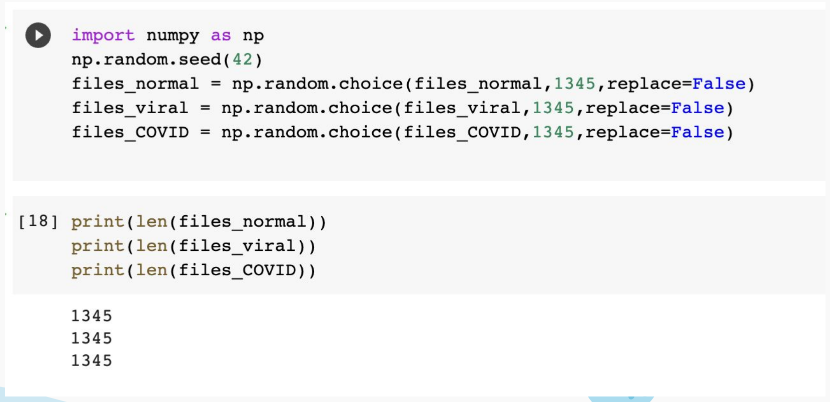
- There may be full black or white images within the files
- This would interfere with the accuracy of the classifier and the parameters used in it

Solution: Check and filter out blank images

- But upon checking, we found no blank images
- Did not filter out any image

DATA PREPARATION





```
import numpy as np
np.random.seed(42)
files_normal = np.random.choice(files_normal,1345,replace=False)
files_viral = np.random.choice(files_viral,1345,replace=False)
files_COVID = np.random.choice(files_COVID,1345,replace=False)
```

```
[18] print(len(files_normal))
     print(len(files_viral))
     print(len(files_COVID))

     1345
     1345
     1345
```

Data Imbalance

- 10192 Normal X-Rays
- 1345 Viral Pneumonia X-Rays
- 3616 COVID Pneumonia X-Rays

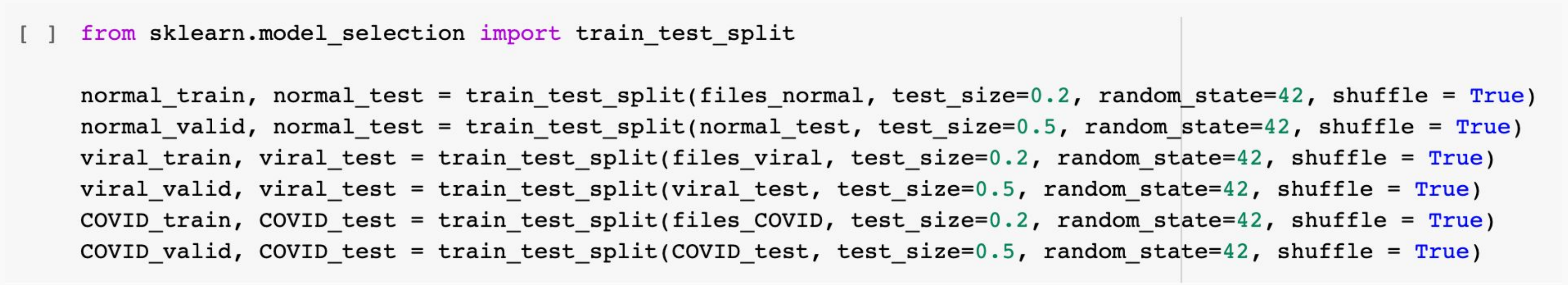
Highly Skewed to Normal Dataset

Solution: Undersampling (NEW!)

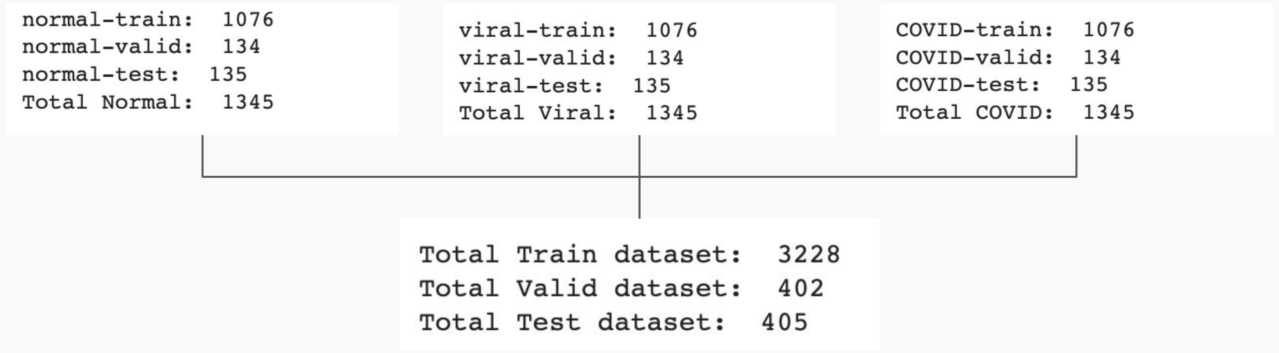
- Use class with lowest number of datapoints as base
- Randomly pick data from other classes

Balances out the number of chest x-ray images for each category

Train Test Split



```
[ ] from sklearn.model_selection import train_test_split

    normal_train, normal_test = train_test_split(files_normal, test_size=0.2, random_state=42, shuffle = True)
    normal_valid, normal_test = train_test_split(normal_test, test_size=0.5, random_state=42, shuffle = True)
    viral_train, viral_test = train_test_split(files_viral, test_size=0.2, random_state=42, shuffle = True)
    viral_valid, viral_test = train_test_split(viral_test, test_size=0.5, random_state=42, shuffle = True)
    COVID_train, COVID_test = train_test_split(files_COVID, test_size=0.2, random_state=42, shuffle = True)
    COVID_valid, COVID_test = train_test_split(COVID_test, test_size=0.5, random_state=42, shuffle = True)
```

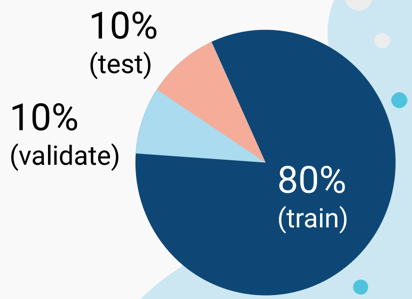


```
normal-train:  1076
normal-valid:  134
normal-test:  135
Total Normal:  1345
```

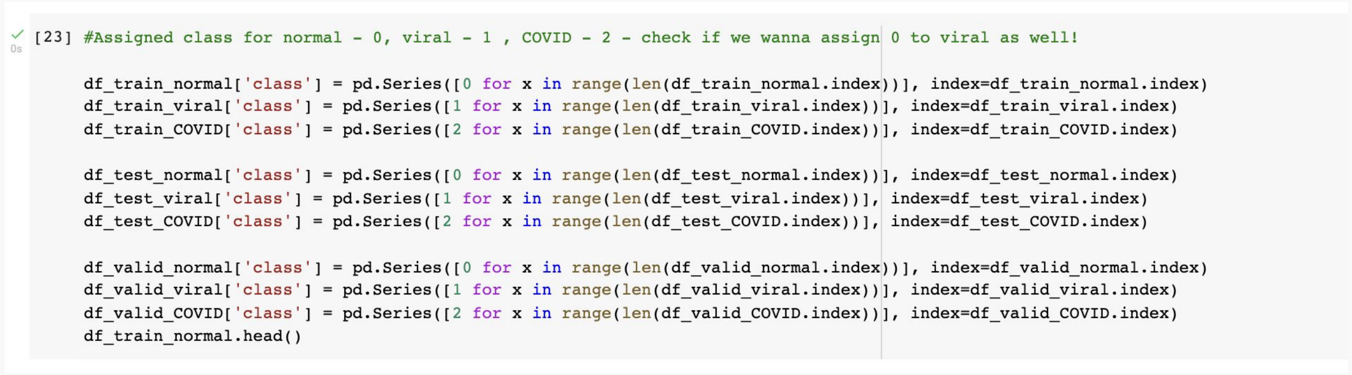
```
viral-train:  1076
viral-valid:  134
viral-test:  135
Total Viral:  1345
```

```
COVID-train:  1076
COVID-valid:  134
COVID-test:  135
Total COVID:  1345
```

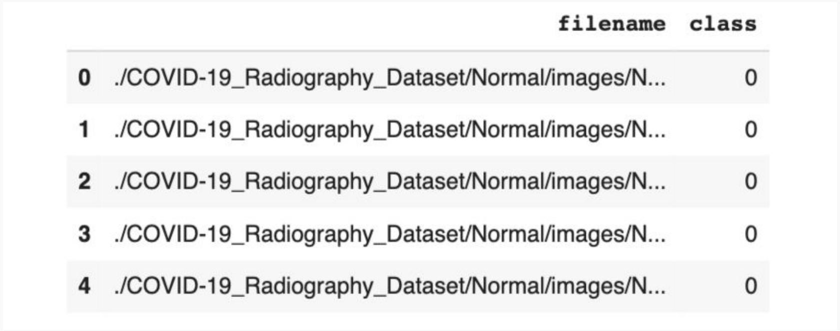
```
Total Train dataset:  3228
Total Valid dataset:  402
Total Test dataset:  405
```



Encoding Classes in Data ...



```
[23] #Assigned class for normal - 0, viral - 1 , COVID - 2 - check if we wanna assign 0 to viral as well!

     df_train_normal['class'] = pd.Series([0 for x in range(len(df_train_normal.index))], index=df_train_normal.index)
     df_train_viral['class'] = pd.Series([1 for x in range(len(df_train_viral.index))], index=df_train_viral.index)
     df_train_COVID['class'] = pd.Series([2 for x in range(len(df_train_COVID.index))], index=df_train_COVID.index)

     df_test_normal['class'] = pd.Series([0 for x in range(len(df_test_normal.index))], index=df_test_normal.index)
     df_test_viral['class'] = pd.Series([1 for x in range(len(df_test_viral.index))], index=df_test_viral.index)
     df_test_COVID['class'] = pd.Series([2 for x in range(len(df_test_COVID.index))], index=df_test_COVID.index)

     df_valid_normal['class'] = pd.Series([0 for x in range(len(df_valid_normal.index))], index=df_valid_normal.index)
     df_valid_viral['class'] = pd.Series([1 for x in range(len(df_valid_viral.index))], index=df_valid_viral.index)
     df_valid_COVID['class'] = pd.Series([2 for x in range(len(df_valid_COVID.index))], index=df_valid_COVID.index)
     df_train_normal.head()
```



	filename	class
0	./COVID-19_Radiography_Dataset/Normal/images/N...	0
1	./COVID-19_Radiography_Dataset/Normal/images/N...	0
2	./COVID-19_Radiography_Dataset/Normal/images/N...	0
3	./COVID-19_Radiography_Dataset/Normal/images/N...	0
4	./COVID-19_Radiography_Dataset/Normal/images/N...	0

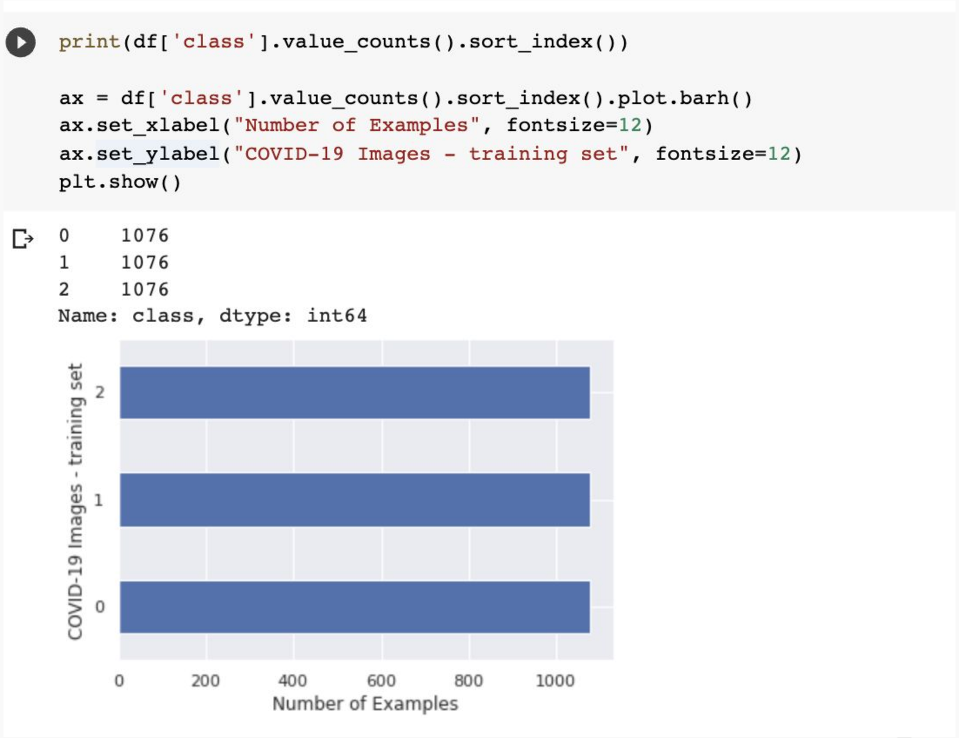
0 - Normal

1 - Viral Pneumonia

2 - COVID Pneumonia

Exploratory Data Analysis

Inspecting the distribution of classes in the train dataset

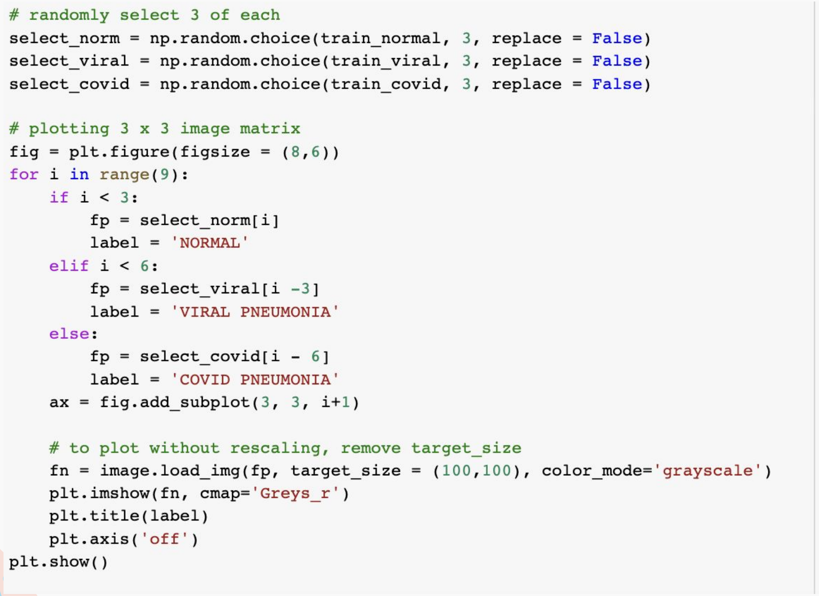


```
print(df['class'].value_counts().sort_index())

ax = df['class'].value_counts().sort_index().plot.barh()
ax.set_xlabel("Number of Examples", fontsize=12)
ax.set_ylabel("COVID-19 Images - training set", fontsize=12)
plt.show()
```

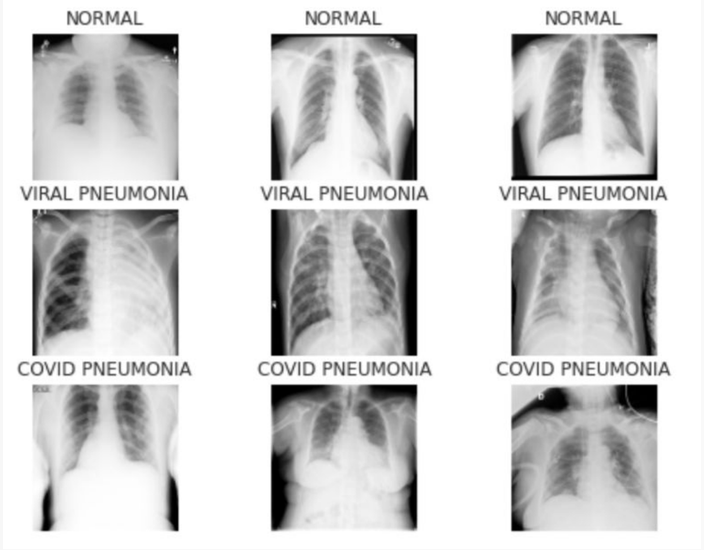
```
0     1076
1     1076
2     1076
Name: class, dtype: int64
```

Exploratory Data Analysis

Raw Observations Of Image Data



```
# randomly select 3 of each
select_norm = np.random.choice(train_normal, 3, replace = False)
select_viral = np.random.choice(train_viral, 3, replace = False)
select_covid = np.random.choice(train_covid, 3, replace = False)

# plotting 3 x 3 image matrix
fig = plt.figure(figsize = (8,6))
for i in range(9):
    if i < 3:
        fp = select_norm[i]
        label = 'NORMAL'
    elif i < 6:
        fp = select_viral[i -3]
        label = 'VIRAL PNEUMONIA'
    else:
        fp = select_covid[i - 6]
        label = 'COVID PNEUMONIA'
    ax = fig.add_subplot(3, 3, i+1)

    # to plot without rescaling, remove target_size
    fn = image.load_img(fp, target_size = (100,100), color_mode='grayscale')
    plt.imshow(fn, cmap='Greys_r')
    plt.title(label)
    plt.axis('off')
plt.show()
```



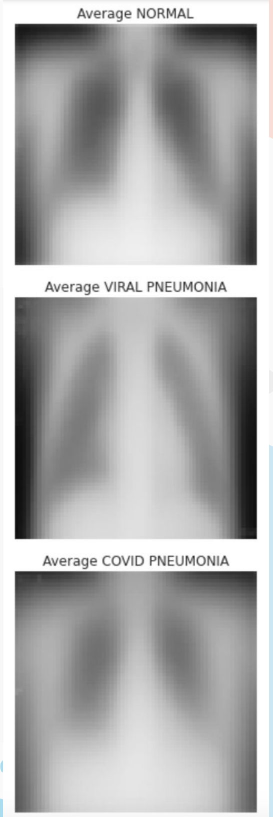
Exploratory Data Analysis ...

Average Comparison Of Image Data(NEW!)

Converting Images to Matrix → Finding the average image for each class

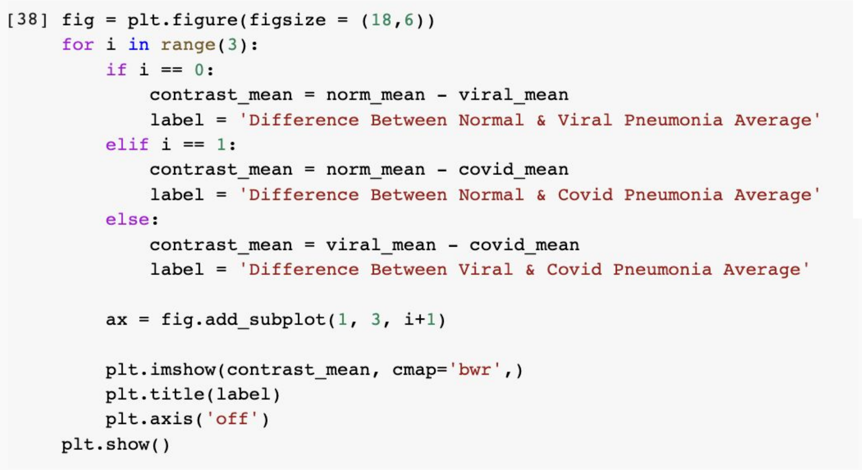
```python
def img2np(list_of_filename, size = (64, 64)):
    # iterating through each file
    for fn in list_of_filename:
        fp = fn
        current_image = image.load_img(fp, target_size = size,
                                       color_mode = 'grayscale
        # covert image to a matrix
        img_ts = image.img_to_array(current_image)
        # turn that into a vector / 1D array
        img_ts = [img_ts.ravel()]
        try:
            # concatenate different images
            full_mat = np.concatenate((full_mat, img_ts))
        except UnboundLocalError:
            # if not assigned yet, assign one
            full_mat = img_ts
    return full_mat

# run it on our folders
normal_images = img2np(train_normal)
viral_images = img2np(train_viral)
covid_images = img2np(train_covid)
```

```python
def find_mean_img(full_mat, title, size = (64, 64)):
    # calculate the average
    mean_img = np.mean(full_mat, axis = 0)
    # reshape it back to a matrix
    mean_img = mean_img.reshape(size)
    plt.imshow(mean_img, vmin=0, vmax=255, cmap='Greys_r')
    plt.title(f'Average {title}')
    plt.axis('off')
    plt.show()
    return mean_img

norm_mean = find_mean_img(normal_images, 'NORMAL')
viral_mean = find_mean_img(viral_images, 'VIRAL PNEUMONIA')
covid_mean = find_mean_img(covid_images, 'COVID PNEUMONIA')
```

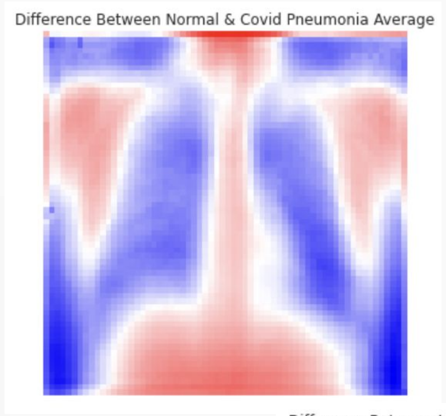


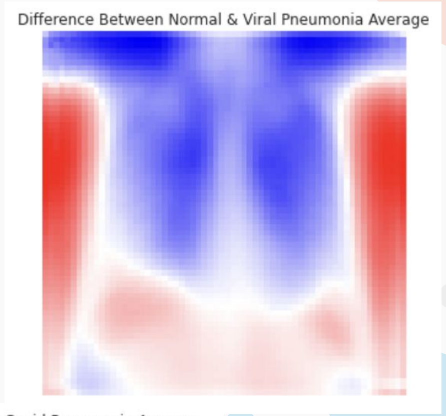
Exploratory Data Analysis ...

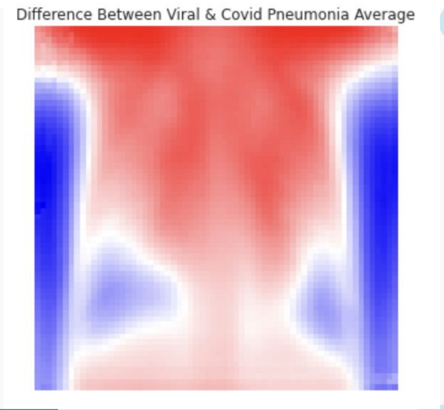
Contrast between Average Images Of Normal, Viral Pneumonia and Covid Pneumonia(NEW!)



```
[38] fig = plt.figure(figsize = (18,6))
     for i in range(3):
         if i == 0:
             contrast_mean = norm_mean - viral_mean
             label = 'Difference Between Normal & Viral Pneumonia Average'
         elif i == 1:
             contrast_mean = norm_mean - covid_mean
             label = 'Difference Between Normal & Covid Pneumonia Average'
         else:
             contrast_mean = viral_mean - covid_mean
             label = 'Difference Between Viral & Covid Pneumonia Average'

         ax = fig.add_subplot(1, 3, i+1)

         plt.imshow(contrast_mean, cmap='bwr',)
         plt.title(label)
         plt.axis('off')
     plt.show()
```

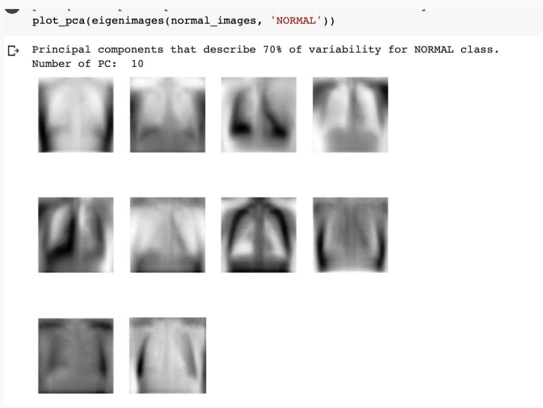






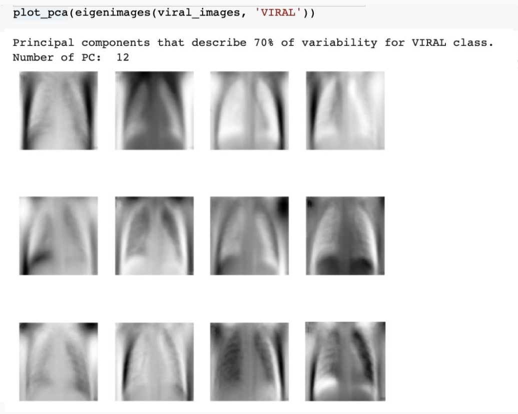
Exploratory Data Analysis ...

Eigenimages from Principal Component Analysis (PCA) (NEW!)



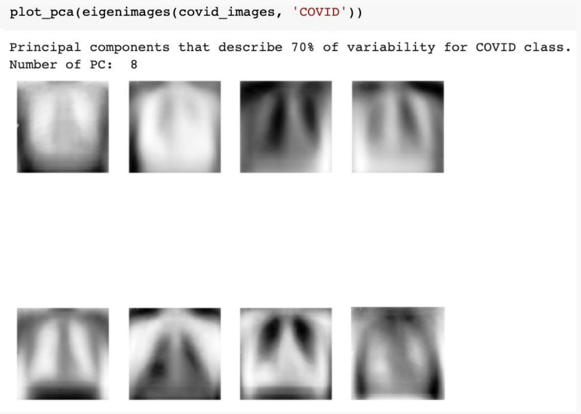
```
plot_pca(eigenimages(normal_images, 'NORMAL'))
```

```
Principal components that describe 70% of variability for NORMAL class.
Number of PC:  10
```



```
plot_pca(eigenimages(viral_images, 'VIRAL'))
```

```
Principal components that describe 70% of variability for VIRAL class.
Number of PC:  12
```



```
plot_pca(eigenimages(covid_images, 'COVID'))
```

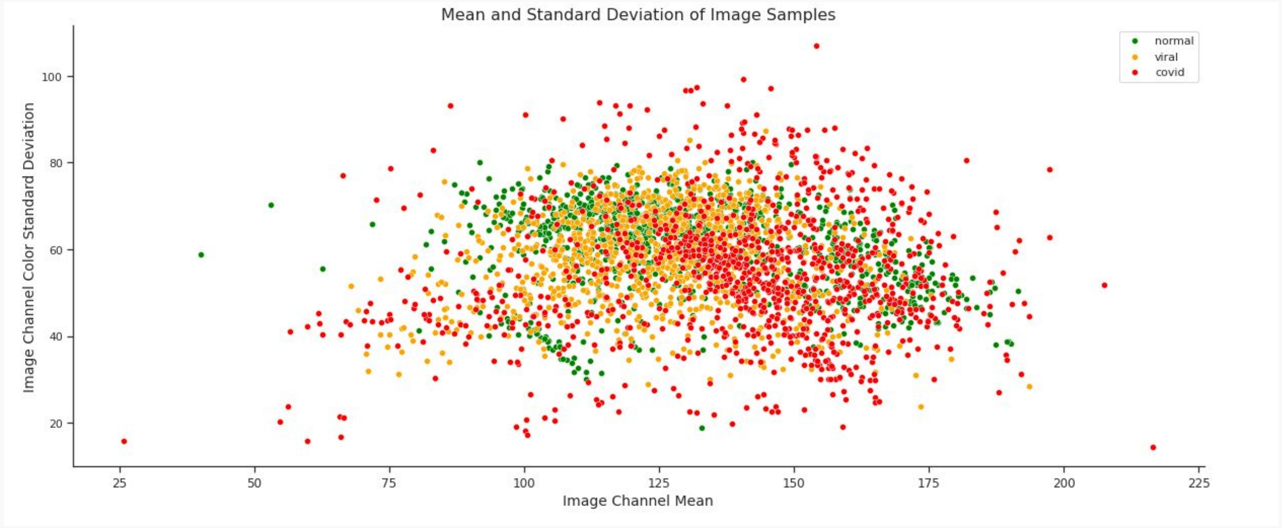
```
Principal components that describe 70% of variability for COVID class.
Number of PC:  8
```

Dimension reduction technique — Principal Component Analysis (PCA)

- Visualize the components that best describes each class.
- Eigenimages — Plotted from matrix shaped by components from PCA
  - Principal components that describe 70% of variability for each class.

Exploratory Data Analysis

Image Value Distribution (NEW!)



3 clusters — Normal, Viral, Covid

Normal:
- Mean - 100 to 150
- Standard Deviation - 60 to 70

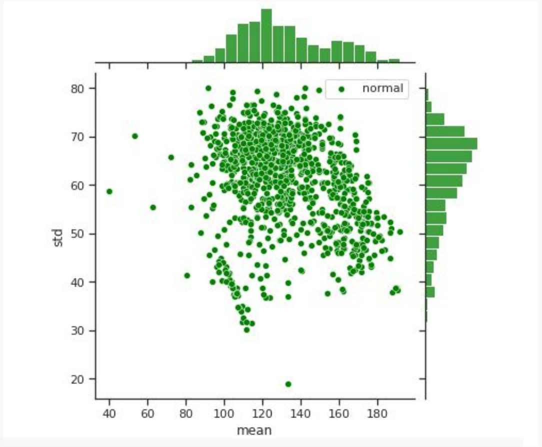
Viral:
- Mean - 100 to 150
- Standard Deviation - 50 to 80

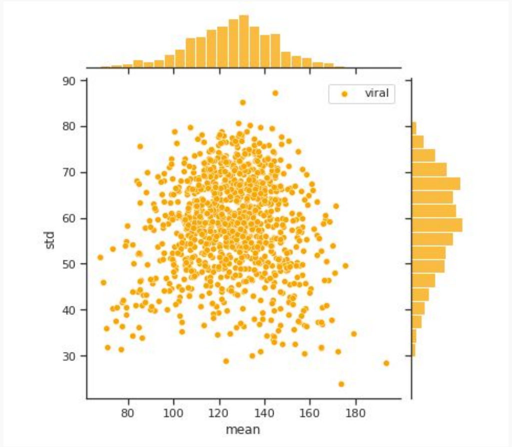
Covid:
- Mean - 125 to 175
- Standard Deviation - 40 to 60

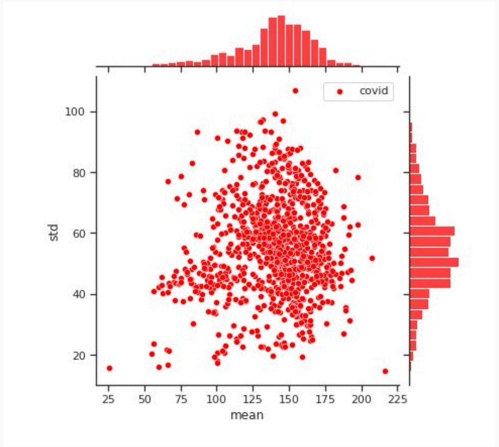
Exploratory Data Analysis

black - rgb(0,0,0)
White - rgb(255,255,255)

Image Value Distribution (NEW!)







Normal:

- 100 to 150
- Majority: 120 to 125

Viral:

- 105 to 145
- Majority: 130 to 135

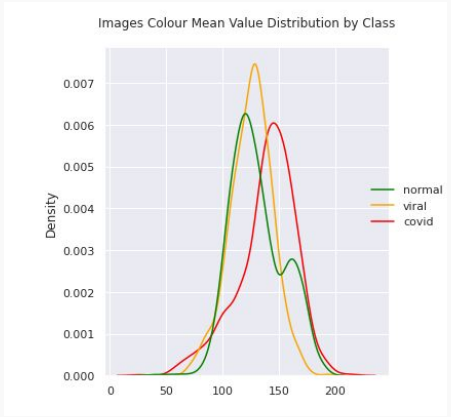
Covid:

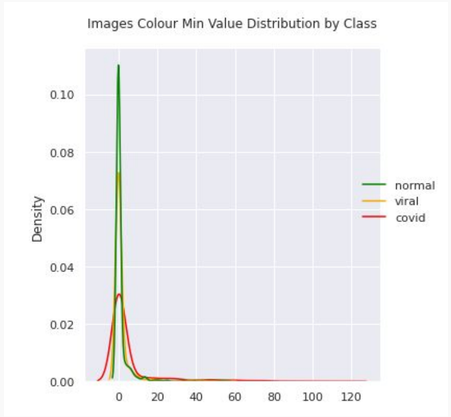
- 125 to 175
- Majority: 145 to 150

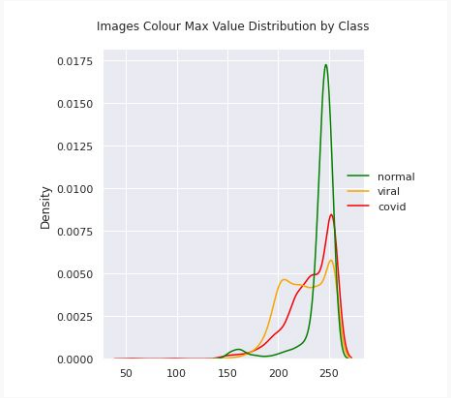
Exploratory Data Analysis

Image Value Distribution – Pixel Density plots **(NEW!)**

black - rgb(0,0,0)
White - rgb(255,255,255)







Mean Values:

- Normal: 120
- Viral: 130
- Covid: 145

Min Values:

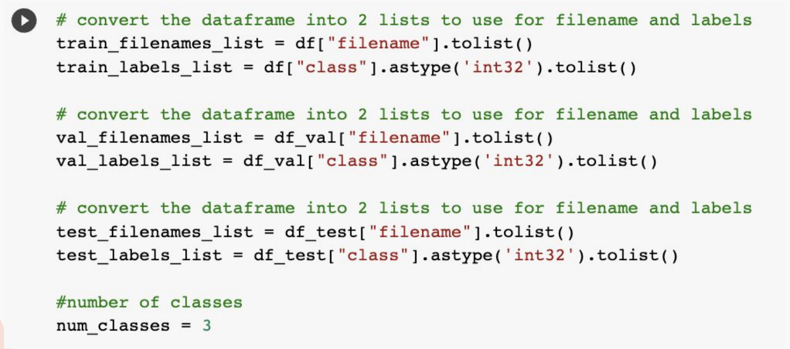
- Normal: 0
- Viral: 0
- Covid: 0

Max Values:

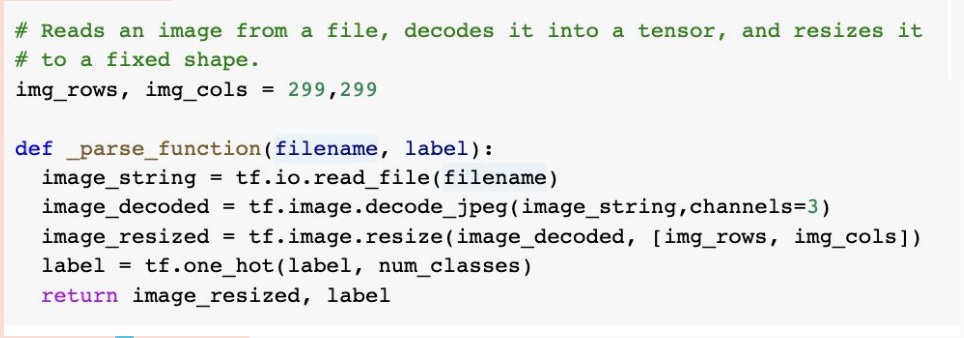
- Normal: 245
- Viral: 200 to 250
- Covid: 230 to 250

Machine Learning . . .

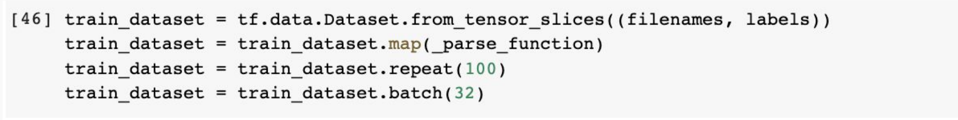
Preparation of Pipeline to Load images



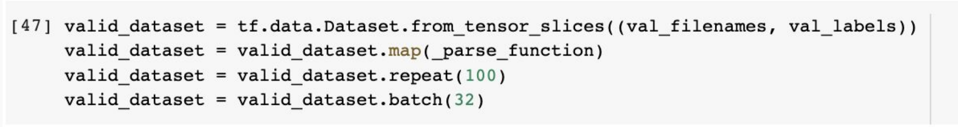
```
# convert the dataframe into 2 lists to use for filename and labels
train_filenames_list = df["filename"].tolist()
train_labels_list = df["class"].astype('int32').tolist()

# convert the dataframe into 2 lists to use for filename and labels
val_filenames_list = df_val["filename"].tolist()
val_labels_list = df_val["class"].astype('int32').tolist()

# convert the dataframe into 2 lists to use for filename and labels
test_filenames_list = df_test["filename"].tolist()
test_labels_list = df_test["class"].astype('int32').tolist()

#number of classes
num_classes = 3
```



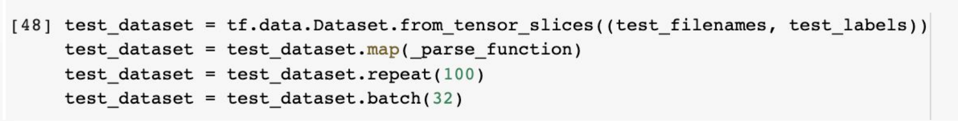
```
# Reads an image from a file, decodes it into a tensor, and resizes it
# to a fixed shape.
img_rows, img_cols = 299,299

def _parse_function(filename, label):
  image_string = tf.io.read_file(filename)
  image_decoded = tf.image.decode_jpeg(image_string,channels=3)
  image_resized = tf.image.resize(image_decoded, [img_rows, img_cols])
  label = tf.one_hot(label, num_classes)
  return image_resized, label
```



```
[46] train_dataset = tf.data.Dataset.from_tensor_slices((filenames, labels))
     train_dataset = train_dataset.map(_parse_function)
     train_dataset = train_dataset.repeat(100)
     train_dataset = train_dataset.batch(32)
```

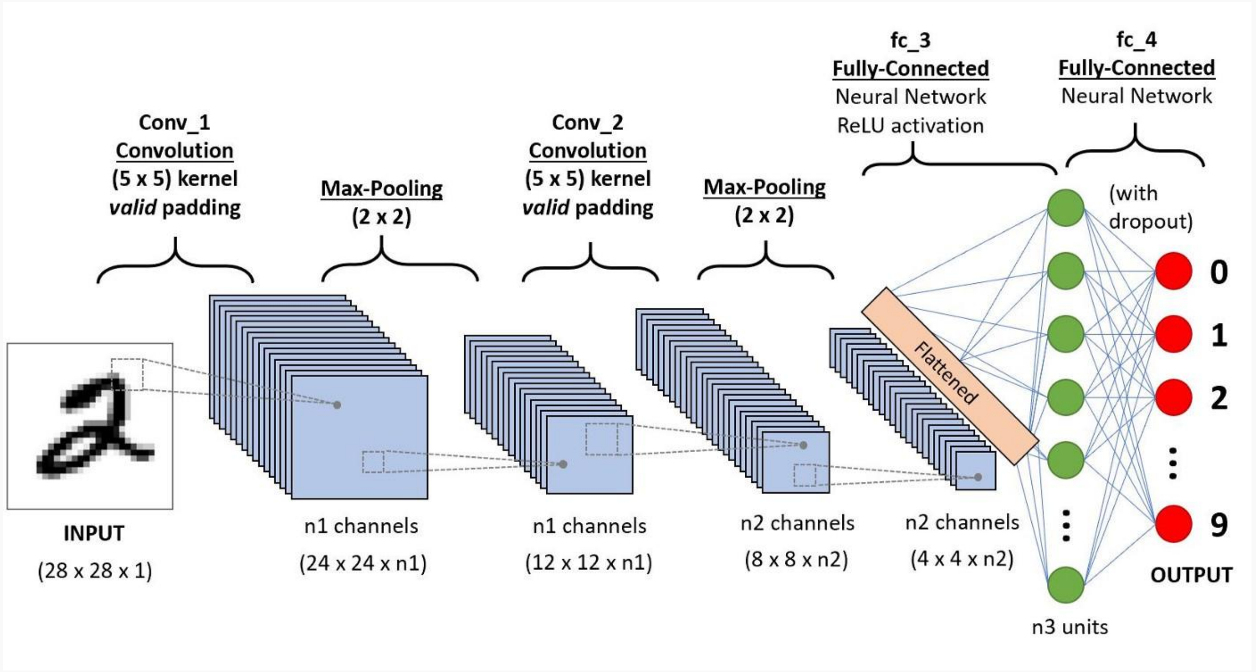


```
[47] valid_dataset = tf.data.Dataset.from_tensor_slices((val_filenames, val_labels))
     valid_dataset = valid_dataset.map(_parse_function)
     valid_dataset = valid_dataset.repeat(100)
     valid_dataset = valid_dataset.batch(32)
```

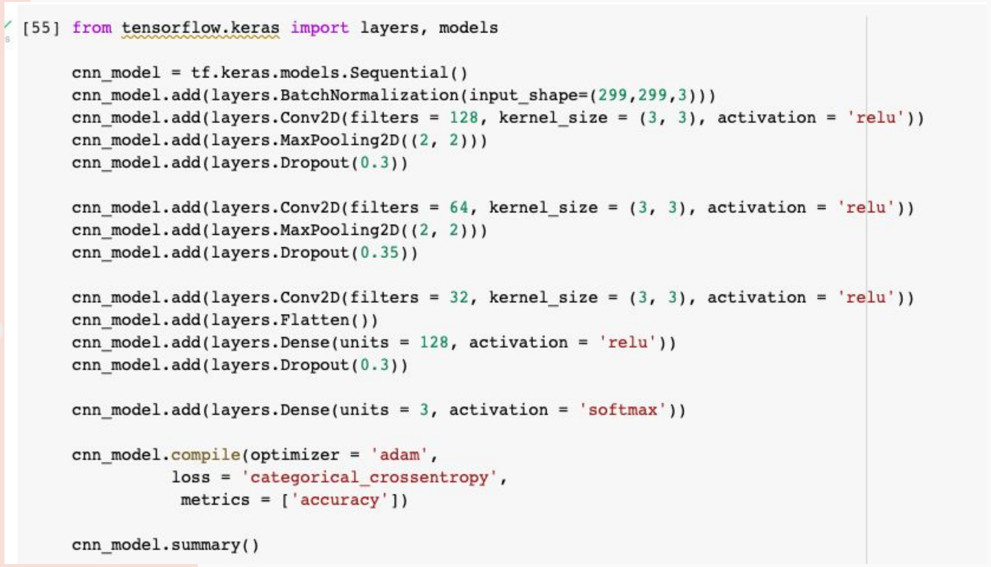


```
[48] test_dataset = tf.data.Dataset.from_tensor_slices((test_filenames, test_labels))
     test_dataset = test_dataset.map(_parse_function)
     test_dataset = test_dataset.repeat(100)
     test_dataset = test_dataset.batch(32)
```

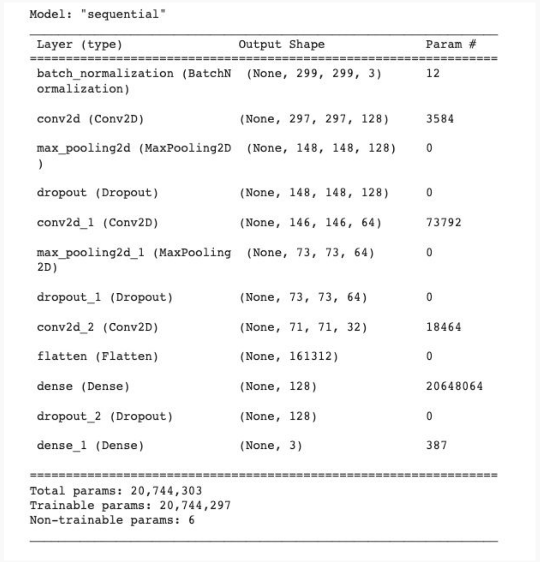
Convolutional Neural Networks (CNN) (NEW!)



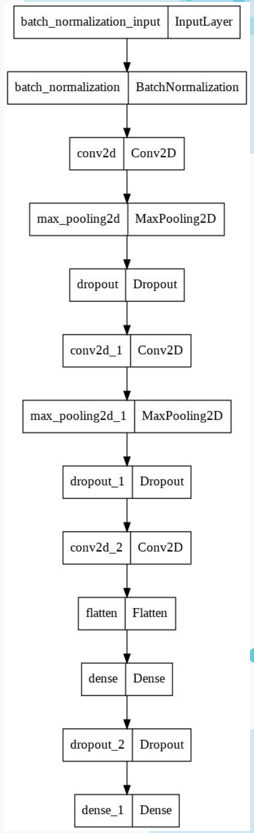
Convolutional Neural Networks (CNN) (NEW!)



```
[55] from tensorflow.keras import layers, models

     cnn_model = tf.keras.models.Sequential()
     cnn_model.add(layers.BatchNormalization(input_shape=(299,299,3)))
     cnn_model.add(layers.Conv2D(filters = 128, kernel_size = (3, 3), activation = 'relu'))
     cnn_model.add(layers.MaxPooling2D((2, 2)))
     cnn_model.add(layers.Dropout(0.3))

     cnn_model.add(layers.Conv2D(filters = 64, kernel_size = (3, 3), activation = 'relu'))
     cnn_model.add(layers.MaxPooling2D((2, 2)))
     cnn_model.add(layers.Dropout(0.35))

     cnn_model.add(layers.Conv2D(filters = 32, kernel_size = (3, 3), activation = 'relu'))
     cnn_model.add(layers.Flatten())
     cnn_model.add(layers.Dense(units = 128, activation = 'relu'))
     cnn_model.add(layers.Dropout(0.3))

     cnn_model.add(layers.Dense(units = 3, activation = 'softmax'))

     cnn_model.compile(optimizer = 'adam',
               loss = 'categorical_crossentropy',
                metrics = ['accuracy'])

     cnn_model.summary()
```

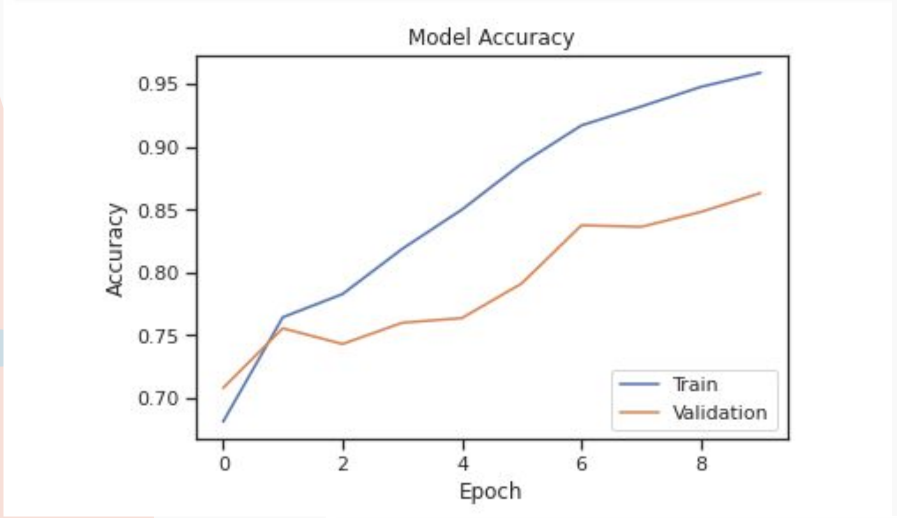


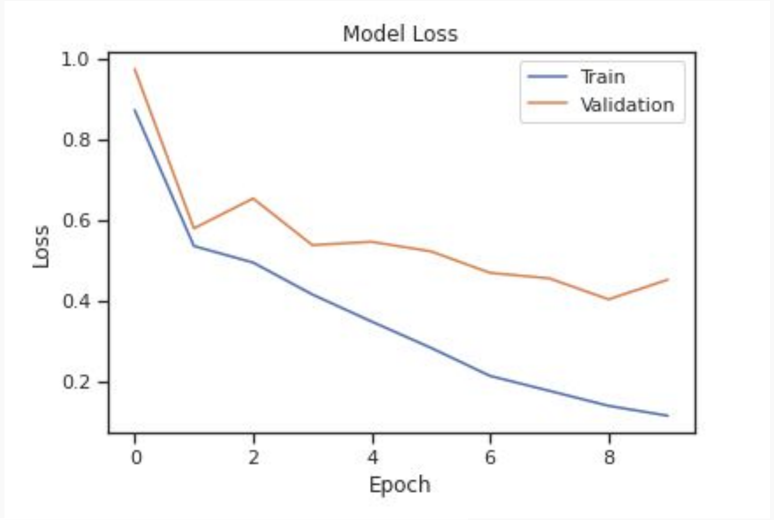
```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 batch_normalization (BatchN  (None, 299, 299, 3)      12
 ormalization)

 conv2d (Conv2D)             (None, 297, 297, 128)     3584

 max_pooling2d (MaxPooling2D  (None, 148, 148, 128)    0
 )

 dropout (Dropout)           (None, 148, 148, 128)     0

 conv2d_1 (Conv2D)           (None, 146, 146, 64)      73792

 max_pooling2d_1 (MaxPooling  (None, 73, 73, 64)       0
 2D)

 dropout_1 (Dropout)         (None, 73, 73, 64)        0

 conv2d_2 (Conv2D)           (None, 71, 71, 32)        18464

 flatten (Flatten)           (None, 161312)            0

 dense (Dense)               (None, 128)               20648064

 dropout_2 (Dropout)         (None, 128)               0

 dense_1 (Dense)             (None, 3)                 387

=================================================================
Total params: 20,744,303
Trainable params: 20,744,297
Non-trainable params: 6
_________________________________________________________________
```



Convolutional Neural Networks (CNN) (NEW!)

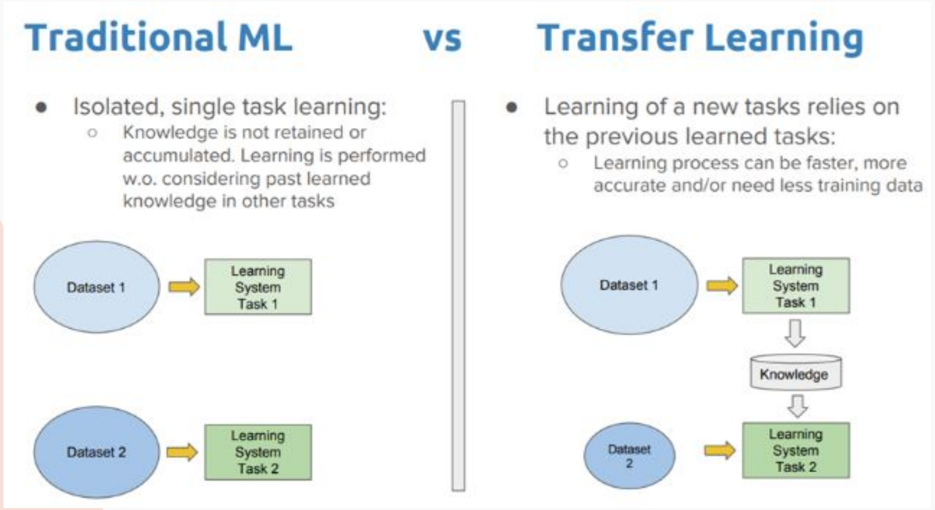
```
[59] plot_loss_acc(history_cnn)
```





```
[60] metrics = cnn_model.evaluate(test_dataset,steps=50)
     print("model accuracy:",metrics[1])

     50/50 [==============================] - 7s 144ms/step - loss: 0.3920 - accuracy: 0.8475
     model accuracy: 0.8475000262260437
```

Transfer Learning(NEW!)



Traditional ML vs Transfer Learning

- Isolated, single task learning:
  - Knowledge is not retained or accumulated. Learning is performed w.o. considering past learned knowledge in other tasks

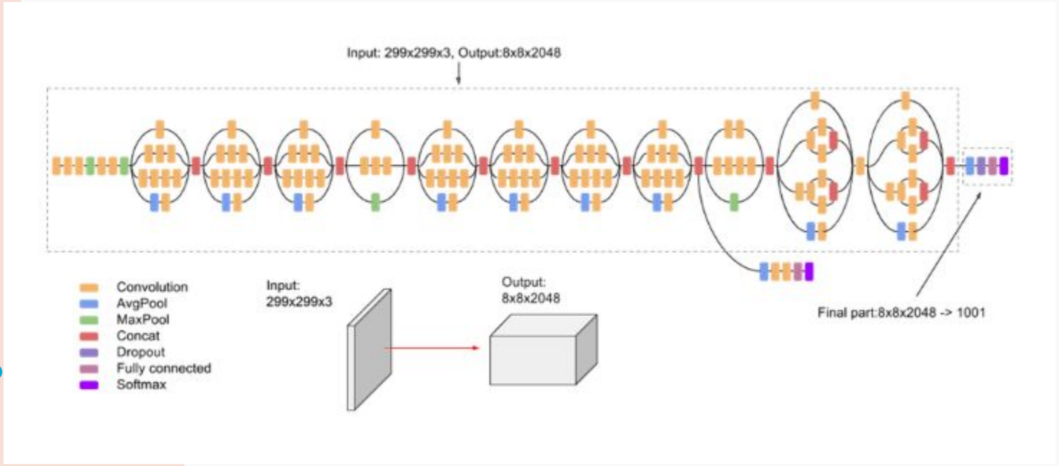
- Learning of a new tasks relies on the previous learned tasks:
  - Learning process can be faster, more accurate and/or need less training data

Key Strengths Over Traditional ML models

- Don't require training from **scratch**
- **Computationally less expensive** and efficient to achieve better results
- Achieve **optimal performance faster** as they leverage knowledge from previously trained models that already understand the features

Transfer Learning(NEW!)

Pre-trained model Used : Inception V3



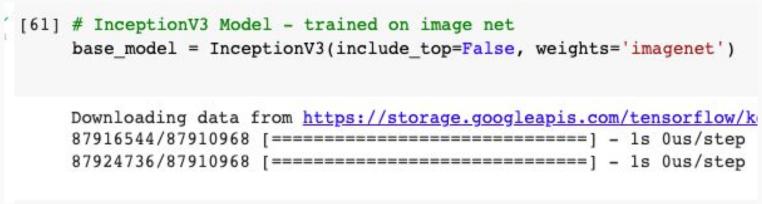
Key aspects:

- Good accuracy
- Low parameters

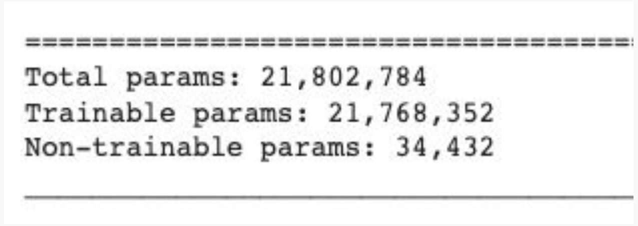
Feasible to deploy this **lightweight** model in **healthcare** settings

Transfer Learning ...

1. Creating a base model from InceptionV3

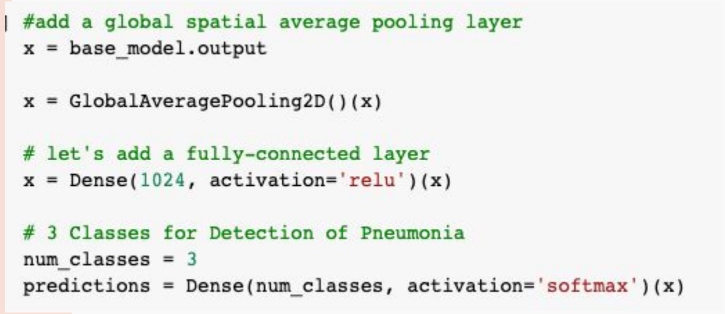


```
[61] # InceptionV3 Model - trained on image net
     base_model = InceptionV3(include_top=False, weights='imagenet')

     Downloading data from https://storage.googleapis.com/tensorflow/k
     87916544/87910968 [==============================] - 1s 0us/step
     87924736/87910968 [==============================] - 1s 0us/step
```



```
==========================================
Total params: 21,802,784
Trainable params: 21,768,352
Non-trainable params: 34,432
```

2. Creating a simple classification head so that we can train it



```
#add a global spatial average pooling layer
x = base_model.output

x = GlobalAveragePooling2D()(x)

# let's add a fully-connected layer
x = Dense(1024, activation='relu')(x)

# 3 Classes for Detection of Pneumonia
num_classes = 3
predictions = Dense(num_classes, activation='softmax')(x)
```

Transfer Learning ...

3. Freezing convolutional base layers except BatchNorm, to use as a feature extractor

```
# Creating the model that we will train
model = Model(inputs=base_model.input, outputs=predictions)
```

```
# Freeze the InceptionV3 layers except the BatchNorm
for layer in base_model.layers:
    if 'batch' in layer.name:
      print(layer.name)
      layer.trainable = True
    else:
      layer.trainable = False
```

4. Selecting an Optimizer - **The Adam Optimization algorithm**

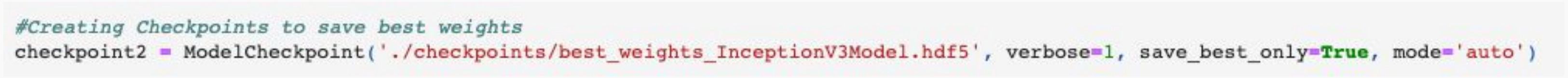
```
# tf.keras optimizer
opt = tf.keras.optimizers.Adam(lr)
```

5. Compiling The Model with Loss Function

```
# compile the model
model.compile(optimizer= opt, loss='categorical_crossentropy',metrics=['accuracy'])
```

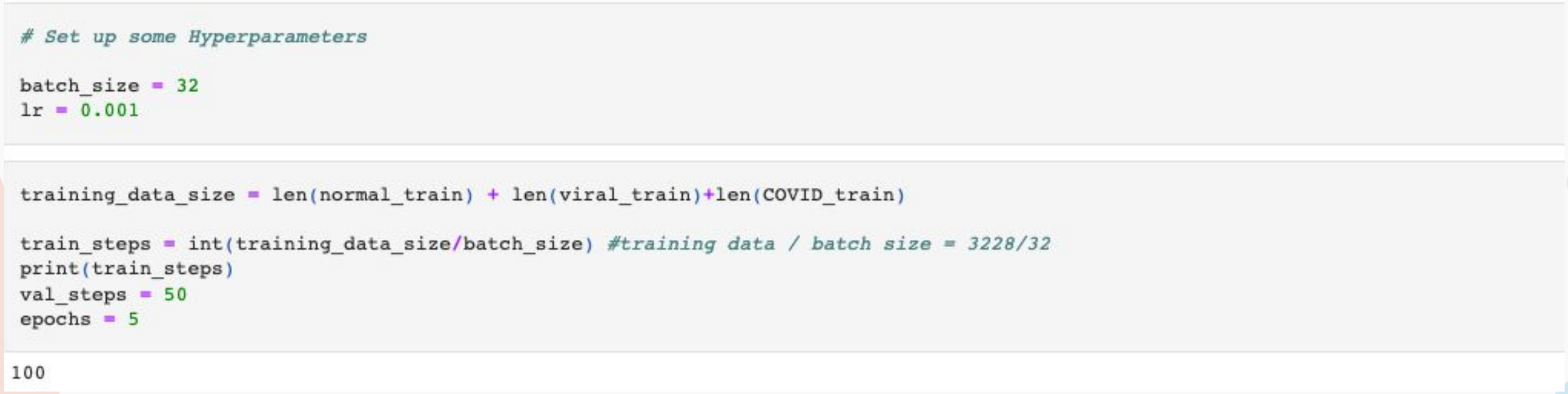
Transfer Learning ...

6. Creating Checkpoints To Save Best Weights



```
#Creating Checkpoints to save best weights
checkpoint2 = ModelCheckpoint('./checkpoints/best_weights_InceptionV3Model.hdf5', verbose=1, save_best_only=True, mode='auto')
```

7. Setting up some hyperparameters



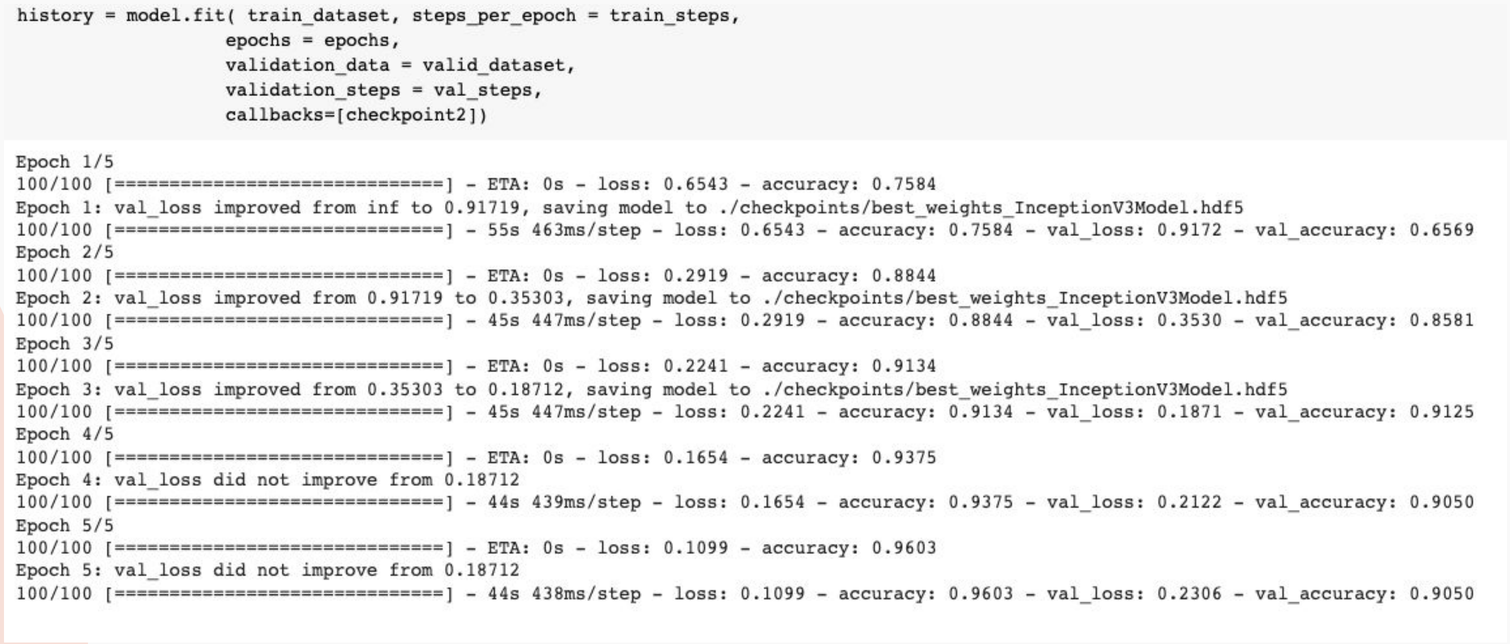
```
# Set up some Hyperparameters

batch_size = 32
lr = 0.001
```

```
training_data_size = len(normal_train) + len(viral_train)+len(COVID_train)

train_steps = int(training_data_size/batch_size) #training data / batch size = 3228/32
print(train_steps)
val_steps = 50
epochs = 5
```

```
100
```

Transfer Learning ...

Fitting the model

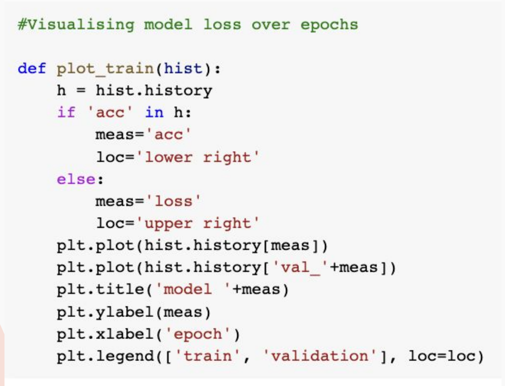


```
history = model.fit( train_dataset, steps_per_epoch = train_steps,
                     epochs = epochs,
                     validation_data = valid_dataset,
                     validation_steps = val_steps,
                     callbacks=[checkpoint2])
```

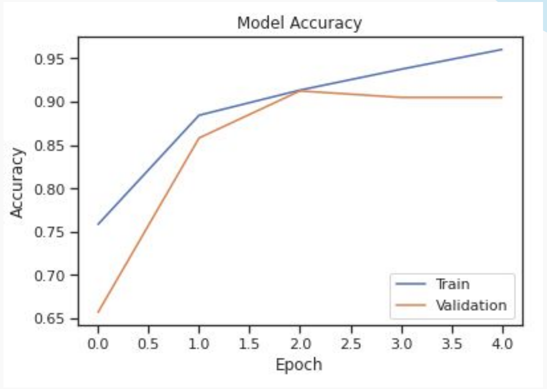
```
Epoch 1/5
100/100 [==============================] - ETA: 0s - loss: 0.6543 - accuracy: 0.7584
Epoch 1: val_loss improved from inf to 0.91719, saving model to ./checkpoints/best_weights_InceptionV3Model.hdf5
100/100 [==============================] - 55s 463ms/step - loss: 0.6543 - accuracy: 0.7584 - val_loss: 0.9172 - val_accuracy: 0.6569
Epoch 2/5
100/100 [==============================] - ETA: 0s - loss: 0.2919 - accuracy: 0.8844
Epoch 2: val_loss improved from 0.91719 to 0.35303, saving model to ./checkpoints/best_weights_InceptionV3Model.hdf5
100/100 [==============================] - 45s 447ms/step - loss: 0.2919 - accuracy: 0.8844 - val_loss: 0.3530 - val_accuracy: 0.8581
Epoch 3/5
100/100 [==============================] - ETA: 0s - loss: 0.2241 - accuracy: 0.9134
Epoch 3: val_loss improved from 0.35303 to 0.18712, saving model to ./checkpoints/best_weights_InceptionV3Model.hdf5
100/100 [==============================] - 45s 447ms/step - loss: 0.2241 - accuracy: 0.9134 - val_loss: 0.1871 - val_accuracy: 0.9125
Epoch 4/5
100/100 [==============================] - ETA: 0s - loss: 0.1654 - accuracy: 0.9375
Epoch 4: val_loss did not improve from 0.18712
100/100 [==============================] - 44s 439ms/step - loss: 0.1654 - accuracy: 0.9375 - val_loss: 0.2122 - val_accuracy: 0.9050
Epoch 5/5
100/100 [==============================] - ETA: 0s - loss: 0.1099 - accuracy: 0.9603
Epoch 5: val_loss did not improve from 0.18712
100/100 [==============================] - 44s 438ms/step - loss: 0.1099 - accuracy: 0.9603 - val_loss: 0.2306 - val_accuracy: 0.9050
```

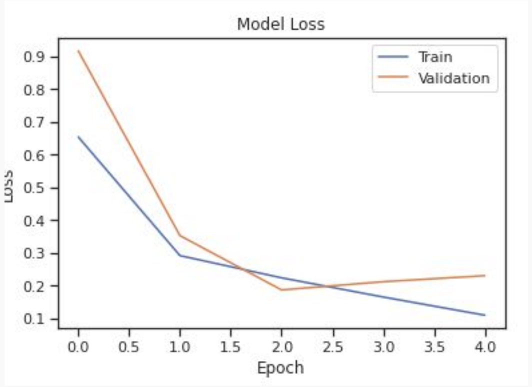
Transfer Learning ...

Visualising Loss Over Epochs



```
#Visualising model loss over epochs

def plot_train(hist):
    h = hist.history
    if 'acc' in h:
        meas='acc'
        loc='lower right'
    else:
        meas='loss'
        loc='upper right'
    plt.plot(hist.history[meas])
    plt.plot(hist.history['val_'+meas])
    plt.title('model '+meas)
    plt.ylabel(meas)
    plt.xlabel('epoch')
    plt.legend(['train', 'validation'], loc=loc)
```

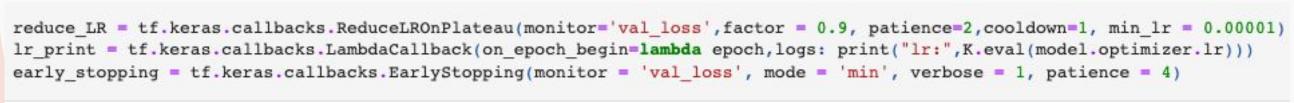




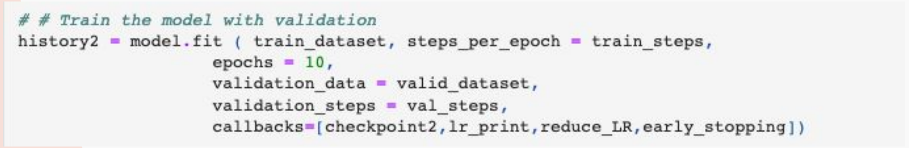
Increase in Validation Accuracy
Drop in Validation Loss

Transfer Learning ...

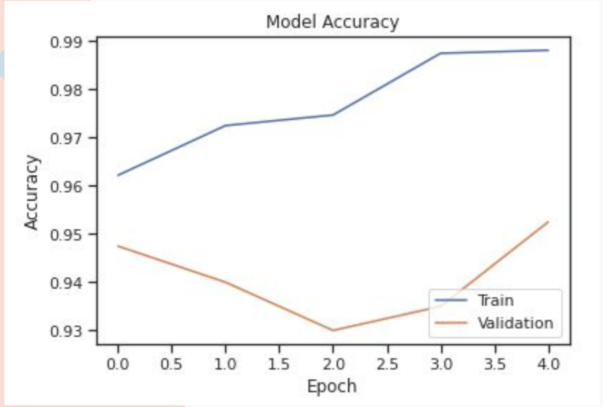
Further training for more epochs using more callbacks for optimisation in training process

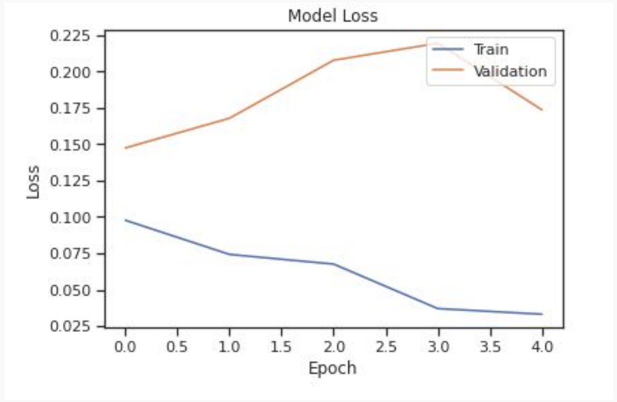


```
reduce_LR = tf.keras.callbacks.ReduceLROnPlateau(monitor='val_loss',factor = 0.9, patience=2,cooldown=1, min_lr = 0.00001)
lr_print = tf.keras.callbacks.LambdaCallback(on_epoch_begin=lambda epoch,logs: print("lr:",K.eval(model.optimizer.lr)))
early_stopping = tf.keras.callbacks.EarlyStopping(monitor = 'val_loss', mode = 'min', verbose = 1, patience = 4)
```



```
# # Train the model with validation
history2 = model.fit ( train_dataset, steps_per_epoch = train_steps,
                       epochs = 10,
                       validation_data = valid_dataset,
                       validation_steps = val_steps,
                       callbacks=[checkpoint2,lr_print,reduce_LR,early_stopping])
```





Some improvement in validation accuracy

- **Some signs of overfitting**

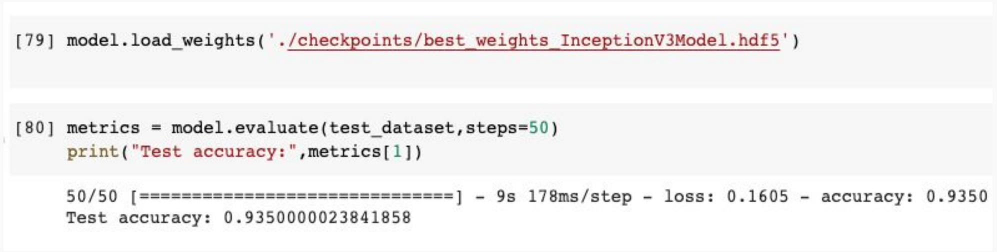
Outcomes . . .

Evaluating model with best weights:

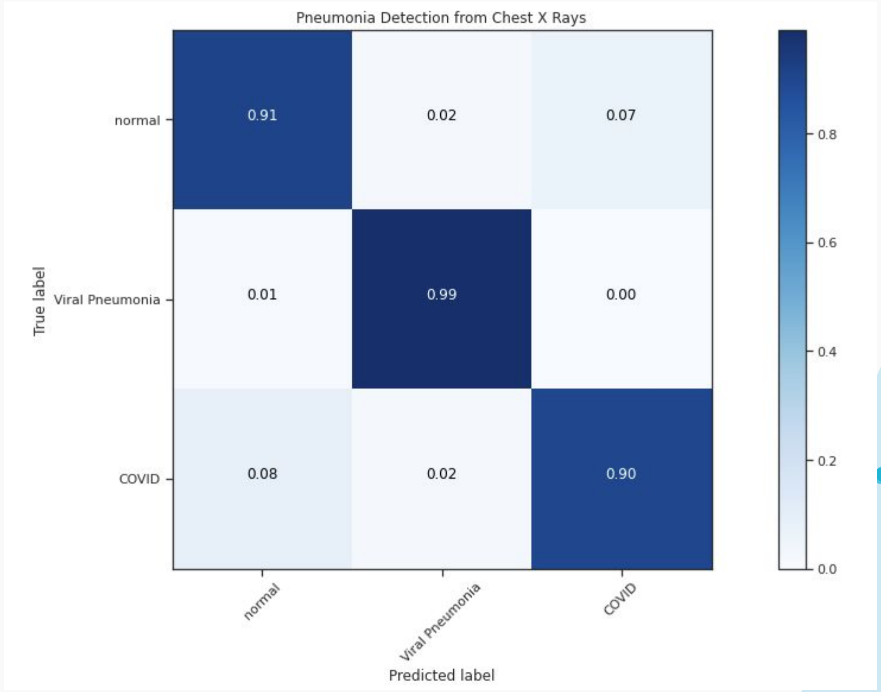
- Test Accuracy: 0.9350000023841858
- Outstanding accuracy of 93.5%.

Confusion Matrix:

- Our model has a **significantly high true positives** seen from 0.91(normal), 0.99(viral) and 0.90(COVID)
- There is a relatively significant chance of classifying **viral pneumonia** (0.01) and **COVID X-Rays** (0.08) as **normal** (0.09)
- The chances of wrongly classifying **COVID as viral pneumonia** (0.02) is **higher** than classifying **viral pneumonia as COVID** (0.00)



```
[79] model.load_weights('./checkpoints/best_weights_InceptionV3Model.hdf5')

[80] metrics = model.evaluate(test_dataset,steps=50)
     print("Test accuracy:",metrics[1])

     50/50 [==============================] - 9s 178ms/step - loss: 0.1605 - accuracy: 0.9350
     Test accuracy: 0.9350000023841858
```



Outcomes ...

Solving our problem:

Our model can be used in real life scenarios with **its high accuracy**, and **scalability**, and can be easily deployed onto **web applications** for healthcare professionals to use to accurately distinguish between Normal, Viral Pneumonia and COVID Cases, enabling **faster diagnosis and treatment** of viral and COVID-19 cases.

In the future, we can easily modify our model for other medical use cases (e.g detection of other lung infections like tuberculosis)

Improvements and further Modifications ...

Improving dataset:

- Image Augmentation — Genetic Algorithm, Keras ImageDataGenerator
- Adopt oversampling
- Adding on more X-Ray images to classes with less data

Other Pre-trained models:

- VGG16, ResNet

Other factors:

- Symptoms of COVID and viral pneumonia
- Other forms of Medical Diagnosis Images (e.g Brain CT scans)

What Have We Learned . . .

Exploratory Data Analysis

- Pixel Matrix analysis
- Eigenimages from Principal Component Analysis (PCA)
- Image Value Distributions

Machine Learning

- Convolutional Neural Networks (CNN)
- Transfer Learning
    - Tensorflow and Keras
    - Pre-trained Model - InceptionV3
    - Optimisers - Adam Optimisation Algorithm
    - Checkpoints, Callbacks

THANK YOU

Stay safe &
remember to mask up indoors!