COMPUTER VISION

Pneumonia Detection Challenge - Capstone Project

Final Report

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Introduction

Pneumonia is a disease in one or the two lungs. Microscopic organisms, infections, and growths cause it. The contamination causes aggravation in the air sacs in your lungs, which are called alveoli.

Pneumonia represents more than 15% of all passings of youngsters under 5 years of age universally. In 2015, 920,000 kids younger than 5 passed on from the sickness.

While normal, precisely diagnosing pneumonia is a difficult task. It requires a survey of a chest radiograph (CXR) by exceptionally prepared trained professionals and affirmation through clinical history, important bodily functions and lab tests.

Pneumonia generally appears as an area or area of expanded obscurity on CXR.

However, the diagnosis of pneumonia on CXR is complicated as a result of various circumstances in the lungs like liquid over-burden (pneumonic oedema), dying, volume misfortune (atelectasis or breakdown), cellular breakdown in the lungs, or post-radiation or surgical changes.

Outside of the lungs, fluid in the pleural space (pleural emanation) additionally shows up as increased opacity on CXR. When accessible, examination of CXRs of the patient taken at various times focuses and connection with clinical side effects and history are useful in making the diagnosis.

CXRs are the most generally performed symptomatic imaging study. Various factors, such as the patient's situating and profundity of motivation, can change the presence of the CXR, complicating interpretation further.

2. Summary of Problem Statement

Problem Statement:

Pneumonia detection using chest radiographs (X-rays) is a critical task in medical imaging, as early detection and diagnosis significantly improve patient outcomes. The task in this project involves designing a deep learning (DL) based algorithm to automatically detect pneumonia in medical images by identifying lung opacities on chest radiographs. The goal is to identify regions of the lungs that exhibit signs of pneumonia, which typically appear as white patches or areas of opacification in the image.

Problem Statement, Data and Finding

PROBLEM STATEMENT:

- The goal is to build an algorithm to detect a visual signal for pneumonia in medical images. Specifically, our algorithm needs to automatically locate lung opacities on chest radiographs which will help us detect Inflammation of the lungs in Pneumonia detection.
- In the dataset, some features are labelled as “Not Normal No Lung Opacity.” This extra third class indicates that while pneumonia was determined not to be present,

there was nonetheless some type of abnormality in the image. This finding may often mimic the appearance of true pneumonia.

Original link to the dataset: https://www.kaggle.com/c/rsna-pneumonia-detection-challenge/data.

Acknowledgements: https://www.kaggle.com/c/rsna-pneumonia-detection-challenge/overview/acknowledgements.

Dataset Description:

1. **File descriptions:**

stage_2_train_labels.csv

In **train labels,** the dataset is given the patient ID and the window (x min, y min, width, and height) containing evidence of pneumonia.

stage_2_train_images.zip

The directory containing 26000 training set raw image (DICOM) files

stage_2_test_images.zip

The directory containing 3000 testing set raw image (DICOM) files

stage_2_sample_submission.csv

A sample submission file in the correct format. Contains the patients' ID for the test set. Note that the sample submission contains one box per image, but there is no limit to the number of bounding boxes that can be assigned to a given image.

stage_2_detailed_class_info.csv

This file provides detailed information about the type of positive or negative class for each image.

2. Data fields:

1. Patient ID - A patient ID. Each patient ID corresponds to a unique image.
2. x - the upper-left x coordinate of the bounding box.
3. y - the upper-left y coordinate of the bounding box.

4. **width** - the width of the bounding box.
5. **height** - the height of the bounding box.
6. **Target** - the binary Target, indicating whether this sample has evidence of pneumonia.

The dataset for this challenge consists of medical images stored in the **DICOM format** (.dcm), which includes both pixel data and metadata. The dataset consists of annotated chest radiographs, divided into categories:

- **Not Normal No Lung Opacity**: Indicates abnormalities mimicking pneumonia.
- **Normal**: Images without abnormalities.
- **Lung Opacity (Pneumonia)**: Confirmed pneumonia cases.

- The dataset is divided into **training** and **testing** sets.
- Each image has an associated **annotation file** that includes bounding boxes marking areas of interest, specifically lung opacities.

Key features of the dataset:

- Images are stored as DICOM files.
- The images are labelled into three categories: **"Normal" "Lung Opacity," and "No Lung Opacity / Not Normal."**
- The bounding boxes indicate where opacities, which could be signs of pneumonia, are located within the radiographs.

Initial Findings

The data includes labelled abnormalities, creating a multi-class classification problem. Annotations guide the bounding box localization task, making it both a classification and object detection challenge.

EDA – Exploratory Data Analysis

Preprocessing Techniques

- Imported essential libraries (e.g., Pandas, NumPy, Seaborn, Matplotlib, and Pydicom for handling DICOM images).
- Mapped training/testing images to respective annotations and classes.

Exploratory Data Analysis (EDA)

DATASET INFORMATION:

```
[ ] df_Class_Train = pd.read_csv(Class_dir)
    print("Class Data Share " , df_Class_Train.shape);
```

```
Class Data Share  (30227, 2)
```

Total Class Data is 30,227

```
[ ] df_Class_Train.head()
```

	patientId	class
0	0004cfab-14fd-4e49-80ba-63a80b6bddd6	No Lung Opacity / Not Normal
1	00313ee0-9eaa-42f4-b0ab-c148ed3241cd	No Lung Opacity / Not Normal
2	00322d4d-1c29-4943-afc9-b6754be640eb	No Lung Opacity / Not Normal
3	003d8fa0-6bf1-40ed-b54c-ac657f8495c5	Normal
4	00436515-870c-4b36-a041-de91049b9ab4	Lung Opacity

Summary of Class data : 'stage_2_detailed_class_info.csv' :-

patientId - A patientId.
class - Have three values depending what is the current state of the patient's lung: 'No Lung Opacity / Not Normal', 'Normal' and 'Lung Opacity'.

The total class data is 30,227.

patientId - A patientId.

Class- Having three values depending upon what is the current state of the patient's lung.

: 'No Lung Opacity / Not Normal', 'Normal' and 'Lung Opacity'.

```
class_value_counts = df_Class_Train['class'].value_counts()
print(class_value_counts)
```

```
class
No Lung Opacity / Not Normal    11821
Lung Opacity                     9555
Normal                           8851
Name: count, dtype: int64
```

Summary of "Class" Data count:-

No Lung Opacity / Not Normal = 11,821

Lung Opacity = 9,555

Normal = 8,851

There are the following findings in class Data counts-

No Lung Opacity / Not Normal = 11,821

Lung Opacity = 9,555

Normal = 8,851

1.2 Import the data : "Labels" Data

```
[ ] df_Labels_Train = pd.read_csv(Label_dir)
    print(df_Labels_Train.shape)
```

```
(30227, 6)
```

```
[ ] df_Labels_Train.head()
```

	patientId	x	y	width	height	Target
0	0004cfab-14fd-4e49-80ba-63a80b6bddd6	NaN	NaN	NaN	NaN	0
1	00313ee0-9eaa-42f4-b0ab-c148ed3241cd	NaN	NaN	NaN	NaN	0
2	00322d4d-1c29-4943-afc9-b6754be640eb	NaN	NaN	NaN	NaN	0
3	003d8fa0-6bf1-40ed-b54c-ac657f8495c5	NaN	NaN	NaN	NaN	0
4	00436515-870c-4b36-a041-de91049b9ab4	264.0	152.0	213.0	379.0	1

Summary of "Labels" Data 'stage_2_train_labels.csv' :-

1. patientId - A patientId.
2. x - The x coordinate of the bounding box
3. y - The y coordinate of the bounding box
4. width - The width of the bounding box
5. height - The height of the bounding box
6. Target - The binary Target indicating whether this sample has evidence of pneumonia or not.

There are the following findings in Labels Data-

patientId - A patientId.

x - The x coordinate of the bounding box

y - The y coordinate of the bounding box

width - The width of the bounding box

height - The height of the bounding box

Target - The binary Target indicates whether this sample has evidence of pneumonia or not.

```
[ ]  target_value_counts = df_Labels_Train['Target'].value_counts();
     target_is_nan_or_blank = df_Labels_Train['Target'].isna() | (df_Labels_Train['Target'] == '');
     print(target_value_counts);
     print(target_is_nan_or_blank.sum());
```

```
Target
0    20672
1     9555
Name: count, dtype: int64
0
```

Summary of Lables Count

Total LAbelss 30,227

Target count with value 0 = 20,672

Target count with value 1 = 9,555

No Target with null or blank value

Below points complated as Step 1 with some basic observations

1. Data Import for "Class" and "Labels"
2. Shape
3. head and
4. Count summary

There are the following findings in Label count-

Total Labels are 30,227

Target count with value 0 = 20,672

Target count with value 1 = 9,555

No Target with a null or blank value

Below are points completed as Step 1 with some basic observations

1. Data Import for "Class" and "Labels"
2. Shape
3. head and
4. Count summary

1.3 Basic EDA on Import Class and Labels data

Merge Class and Lables data in single data frame so that we can map with images

```
[ ] # Merging class and Lables in one data frame
    df_Class_Labels_Merged=pd.merge( df_Labels_Train, df_Class_Train,on='patientId')
    df_Class_Labels_Merged.shape
```

```
(37629, 7)
```

Observation on Duplicate data:

When Merged "Class" and "Labels" dataframe, resultant dataframe has **37,629** records, which is more then **30,277** i.e original file has duplicate patient id

We need to remove duplicate , check count and merge again

Remove dupcoiate patientId from "Class" Data

```
[ ] print("Class Shape before/original dataframe :-" , df_Class_Train.shape);
    df_Class_Train_unique = df_Class_Train.drop_duplicates(subset='patientId');
    print("Class Shape after removing duplicate patientId in unique dataframe:-", df_Class_Train_unique.shape);
```

```
Class Shape before/original dataframe :- (30227, 2)
Class Shape after removing duplicate patientId in unique dataframe:- (26684, 2)
```

We need to remove duplicate , check count and merge again

Remove dupcoiate patientId from "Class" Data

```
[ ] print("Class Shape before/original dataframe :-" , df_Class_Train.shape);
    df_Class_Train_unique = df_Class_Train.drop_duplicates(subset='patientId');
    print("Class Shape after removing duplicate patientId in unique dataframe:-", df_Class_Train_unique.shape);
```

```
Class Shape before/original dataframe :- (30227, 2)
Class Shape after removing duplicate patientId in unique dataframe:- (26684, 2)
```

Remove dupcoiate patientId from "Labels" Data

```
[ ] print("Labels Shape before/original dataframe :-" , df_Labels_Train.shape);
    df_Labels_Train_unique = df_Labels_Train.drop_duplicates(subset='patientId');
    print("Label Shape after removing duplicate patientId in unique dataframe:-", df_Labels_Train_unique.shape);
```

```
Labels Shape before/original dataframe :- (30227, 6)
Label Shape after removing duplicate patientId in unique dataframe:- (26684, 6)
```

Now we have unique 26,684 records

Lets merge now

Merging unique data frames of "Class" and "Labels" which has unique patientId now

```
[ ] df_Class_Labels_Merged_unique=pd.merge( df_Labels_Train_unique, df_Class_Train_unique,on='patientId')
    df_Class_Labels_Merged_unique.shape
```

```
(26684, 7)
```

This merging looks good and merged dataframe also has 26,684

```
[ ] df_Class_Labels_Merged_unique.head(5)
```

	patientId	x	y	width	height	Target	class
0	0004cfab-14fd-4e49-80ba-63a80b6bddd6	NaN	NaN	NaN	NaN	0	No Lung Opacity / Not Normal
1	00313ee0-9eaa-42f4-b0ab-c148ed3241cd	NaN	NaN	NaN	NaN	0	No Lung Opacity / Not Normal
2	00322d4d-1c29-4943-afc9-b6754be640eb	NaN	NaN	NaN	NaN	0	No Lung Opacity / Not Normal
3	003d8fa0-6bf1-40ed-b54c-ac657f8495c5	NaN	NaN	NaN	NaN	0	Normal
4	00436515-870c-4b36-a041-de91049b9ab4	264.0	152.0	213.0	379.0	1	Lung Opacity

- After merging the class and Labels data frame,
- The resultant dataframe is 37,629 records which is more than 30,277 records.
- i.e. original file has duplicate records.
- Unique records are only 26,684.

This merging looks good and the merged dataframe also has 26,684.

Lets compare "class" value with "Target"

class column value count

```
[ ] class_value_counts_merged = df_Class_Labels_Merged_unique['class'].value_counts();
    print(class_value_counts_merged);
```

```
class
No Lung Opacity / Not Normal    11821
Normal                           8851
Lung Opacity                     6012
Name: count, dtype: int64
```

Target column value count

```
[ ] target_value_counts_merged = df_Class_Labels_Merged_unique['Target'].value_counts();
    print(target_value_counts_merged);
```

```
Target
0    20672
1     6012
Name: count, dtype: int64
```

class with Target value count

```
[ ] df_Class_Labels_Merged_unique.groupby('class')['Target'].unique()
```

```
class
Lung Opacity                    [1]
No Lung Opacity / Not Normal    [0]
Normal                          [0]
Name: Target, dtype: object
```

Conclusion on "class" and "Target" values:-

All class with "Lung Opacity" has target value [1]

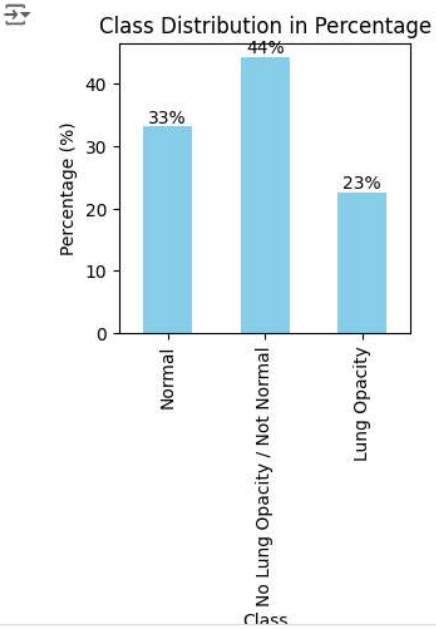
Both class with "Normal" OR "No Lung Opacity / Not Normal" has target value [0]

Conclusion on "class" and "Target" values:-

- All class with "Lung Opacity" has a target value [1].
- Both class with "Normal" OR "No Lung Opacity / Not Normal" has target value [0].

Class Distribution in Percentage.

```
[ ] class_counts = df_Class_Labels_Merged_unique['class'].value_counts().sort_index(ascending=False)
    class_percentages = (class_counts / class_counts.sum()) * 100

    # Plot the bar graph
    fig, ax = plt.subplots(figsize=(3, 3))
    class_percentages.plot(kind='bar', ax=ax ,color='skyblue')
    ax.set_ylabel('Percentage (%)')
    ax.set_xlabel('Class')
    ax.set_title('Class Distribution in Percentage')
    ax.bar_label(ax.containers[0], fmt='%.0f%%')  # Adding percentage labels on bars
    plt.show()
```



Conclusion: All Pneumonia cases are of class "Lung Opacity" and target value 1

1. 23 % data has Lung Opacity
2. 33+ 44= 77% data has no Lung Opacity its either Normal or No Lung Opacity

Map training and testing images to their annotations

```
#Step 3: Map training and testing images to its annotations.
train_bbox_df = pd.read_csv("/content/drive/MyDrive/Vishal_Notebook/rsna-pneumonia-detection-challenge/stage_2_train_labels.csv")

train_bbox_df.head()
```

	patientId	x	y	width	height	Target
0	0004cfab-14fd-4e49-80ba-63a80b6bddd6	NaN	NaN	NaN	NaN	0
1	00313ee0-9eaa-42f4-b0ab-c148ed3241cd	NaN	NaN	NaN	NaN	0
2	00322d4d-1c29-4943-afc9-b6754be640eb	NaN	NaN	NaN	NaN	0
3	003d8fa0-6bf1-40ed-b54c-ac657f8495c5	NaN	NaN	NaN	NaN	0
4	00436515-870c-4b36-a041-de91049b9ab4	264.0	152.0	213.0	379.0	1

```
train_bbox_df.shape
```

```
(30227, 6)
```

```
[ ] train_bbox_df[train_bbox_df.isnull().any(axis=1)].Target.value_counts()
```

Target	count
0	20672

dtype: int64

```
[ ] train_bbox_df[~train_bbox_df.isnull().any(axis=1)].Target.value_counts()
```

Target	count
1	9555

dtype: int64

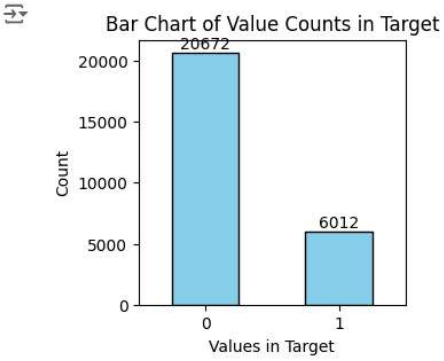
```
[ ] train_bbox_df.Target.value_counts()
```

Target	count
0	20672
1	9555

dtype: int64

Value count in Target.

```
# Get the count of unique values in 'Column1'
value_counts_merged_barchart = df_Class_Labels_Merged_unique['Target'].value_counts()

# Plot the bar chart
barChart_Target =value_counts_merged_barchart.plot(kind='bar', color='skyblue', edgecolor='black' ,figsize=(3, 3))

# Add labels and title
plt.xlabel('Values in Target')
plt.ylabel('Count')
plt.title('Bar Chart of Value Counts in Target')

# Add annotations on the bars
count=0
for i, count in enumerate(value_counts_merged_barchart):
    barChart_Target.text(i, count + 0.1, str(count), ha='center', va='bottom', fontsize=10)

plt.xticks(rotation=0)  # Rotate x-axis labels if needed
plt.show()
```




```
# Checking nulls in bounding box columns:
print('Number of nulls in bounding box columns of df_Class_Labels_Merged_unique : {}'.format(df_Class_Labels_Merged_unique[['x', 'y', 'width', 'height']].isnull().sum().to_dict()))
```

```
Number of nulls in bounding box columns of df_Class_Labels_Merged_unique : {'x': 20672, 'y': 20672, 'width': 20672, 'height': 20672}
```

Observation: All Target 0 has null bounding box

Number of nulls in bounding box columns 20,672 are equal to the number of 0's we have in the Target column.

Observation: All Target 0 has a null bounding box

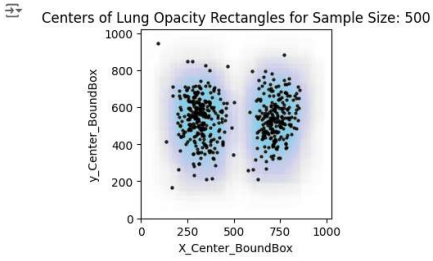
- The number of nulls in bounding box columns 20,672 is equal to the number of 0s we have in the Target column.

Bounding Box Distribution-

Bounding Box Distribution for Target = 1

We dont have bounding box for Target 0 we filter the data only for Target 1

```
[ ] sample_size_distribution=500
    fig, ax = plt.subplots(1, 1, figsize = (3,3));
    df_Target_1 = df_Class_Labels_Merged_unique[df_Class_Labels_Merged_unique['Target'] == 1];
    target_sample = df_Target_1.sample(sample_size_distribution);
    target_sample['X_Center_BoundBox'] = target_sample['x'] + target_sample['width'] / 2;
    target_sample['y_Center_BoundBox'] = target_sample['y'] + target_sample['height'] / 2;
    plt.title('Centers of Lung Opacity Rectangles for Sample Size: ' + str(sample_size_distribution));
    target_sample.plot.scatter(x = 'X_Center_BoundBox', y = 'y_Center_BoundBox', xlim = (0, 1024), ylim = (0, 1024), ax = ax, alpha = 0.8, marker = '.', color = 'black');

    for i, crt_sample in target_sample.iterrows():
        ax.add_patch(Rectangle(xy=(crt_sample['x'], crt_sample['y']),
                    width=crt_sample['width'],height=crt_sample['height'],alpha=3.5e-3, color="skyblue"))
```



Conclusion:

Centres for the bounding box are spread out evenly across the lungs. Though a large portion of the bounding box has its centres at the centres of the lung, some centres of the box are also located at the edges of the lung.

Read and print Train Data dicom images

Step 2: Map training and testing images to its classes. [4 points]

Digital Imaging and Communications in Medicine (DICOM) (.dcm) format is an international standard to transmit, store, retrieve, print, process, and display medical imaging information and it makes medical imaging information interoperable.
Lets check how many Annotaitons or element we have in images provided to us...

Read and print Train Data dicom images

```
[ ] print_new_lines(2);
    print('Number of images in Training images folders are: {}.'.format(len(os.listdir(Train_dicom_dir))));
    print_new_lines(2);
    print('Number of images in Test images folders are: {}.'.format(len(os.listdir(Test_dicom_dir))));
    print_new_lines(2);
```

```
Number of images in Training images folders are: 26684.


Number of images in Test images folders are: 12.
```

- The training images folder has **26,684** images
- unique patient IDs are also **26,684**
- Each of the unique patient IDs present in CSV files **corresponds** to an image present in the folder.

Randomely read one Train image and check the Metadata/Element/Annotation

```
[ ]  #Read first random file name
     for filename in os.listdir(Train_dicom_dir):
         if filename.lower().endswith(".dcm"):  # Check for .dcm extension
             first_dicom_file = filename
             break  # Stop after finding the first file

     # Read the first random DICOM file selected
     dicom_data = pydicom.dcmread(Train_dicom_dir + "\\"+ first_dicom_file)

     # Print all metadata in the DICOM file
     print_new_lines(1);
     print("DICOM Metadata Element Name list  :-")
     print_new_lines(1);
     #count in enumerate(value_counts_merged_barchart):
     for j, element in enumerate(dicom_data):
         print(f"{j} - {element.name}")
     print_new_lines(3);
     print('Metadata of the image consists of :-');
     print_new_lines(1);
     print(dicom_data);
     print_new_lines(2);
```

```
DICOM Metadata Element Name list  :-

0 - Specific Character Set
1 - SOP Class UID
2 - SOP Instance UID
3 - Study Date
4 - Study Time
5 - Accession Number
6 - Modality
7 - Conversion Type
8 - Referring Physician's Name
9 - Series Description
10 - Patient's Name
11 - Patient ID
12 - Patient's Birth Date
13 - Patient's Sex
14 - Patient's Age
15 - Body Part Examined
16 - View Position
17 - Study Instance UID
18 - Series Instance UID
19 - Study ID
20 - Series Number
21 - Instance Number
22 - Patient Orientation
23 - Samples per Pixel
24 - Photometric Interpretation
25 - Rows
26 - Columns
27 - Pixel Spacing
28 - Bits Allocated
29 - Bits Stored
30 - High Bit
31 - Pixel Representation
32 - Lossy Image Compression
33 - Lossy Image Compression Method
34 - Pixel Data
```

Observations –

- The file has 35 Elements (0 to 34) including Pixel Data, which is the image
- From the above sample we can see that the dicom file contains some of the information that can be used for further analysis such as sex, age, body part examined, view position and modality.
- The size of this image in Pixes data Rows and Columns elements is 1024 x 1024 (rows x columns).

Images From Dicom Dataset(Train and Test)-

```
[ ]  # Display the images from the DICOM datasets

     for i, dicom_data_train in enumerate(list_dicom_train_data_raw[:LimitCountToTest]):
         if 'PixelData' in dicom_data_train:
             # Extract pixel data (image) from the DICOM object
             image_train = dicom_data_train.pixel_array

             # Plot the image using matplotlib
             plt.figure(figsize=(2 ,2))
             plt.imshow(image_train, cmap='gray')
             plt.title(f"DICOM Train Image {i + 1} PatientName={list_dicom_train_data_raw[i].PatientName}" )
             plt.axis('off')  # Hide axes
             plt.show()
         else:
             print(f"File {i + 1} does not contain image data.")
```

DICOM Train Image 1 PatientName=0004cfab-14fd-4e49-80ba-63a80b6bddd6

DICOM Train Image 2 PatientName=000924cf-0f8d-42bd-9158-1af53881a557

DICOM Train Image 3 PatientName=000db696-cf54-4385-b10b-6b16fbb3f985

DICOM Train Image 4 PatientName=000fe35a-2649-43d4-b027-e67796d412e0

DICOM Train Image 5 PatientName=001031d9-f904-4a23-b3e5-2c088acd19c6

```
[ ]  # Display the images from the DICOM datasets

     for i, dicom_data_test in enumerate(dicom_datasets_test[:LimitCountToTest]):
         if 'PixelData' in dicom_data_test:
             # Extract pixel data (image) from the DICOM object
             image_test = dicom_data_test.pixel_array

             # Plot the image using matplotlib
             plt.figure(figsize=(2, 2))
             plt.imshow(image_test, cmap='gray')
             plt.title(f"DICOM test Image {i + 1} PatientName={dicom_datasets_test[i].PatientName}")
             plt.axis('off')  # Hide axes
             plt.show()
         else:
             print(f"File {i + 1} does not contain test image data.")
```

DICOM test Image 1 PatientName=0000a175-0e68-4ca4-b1af-167204a7e0bc

DICOM test Image 2 PatientName=000e3a7d-c0ca-4349-bb26-5af2d8993c3d

DICOM test Image 3 PatientName=00a221ac-da8f-4f61-8d4f-fc195143491d

DICOM test Image 4 PatientName=00ad18b7-06ee-4c4d-abca-14bdf814e8b2

DICOM test Image 5 PatientName=00af3668-1970-4f65-a292-525d2c5aed5c

Display images with Bounding Box-

Step 5: Display images with bounding box. [5 points]

```
df_Class_Labels_Images_Merged_unique[df_Class_Labels_Images_Merged_unique['Target']==1].iloc[:5]
```

	patientId	x	y	width	height	Target	class	path
4	00436515-870c-4b36-a041-de91049b9ab4	264.0	152.0	213.0	379.0	1	Lung Opacity	rsna-pneumonia-detection-challenge\stage_2_tra...
7	00704310-78a8-4b38-8475-49f4573b2dbb	323.0	577.0	160.0	104.0	1	Lung Opacity	rsna-pneumonia-detection-challenge\stage_2_tra...
12	00aecb01-a116-45a2-956c-08d2fa55433f	288.0	322.0	94.0	135.0	1	Lung Opacity	rsna-pneumonia-detection-challenge\stage_2_tra...
13	00c0b293-48e7-4e16-ac76-9269ba535a62	306.0	544.0	168.0	244.0	1	Lung Opacity	rsna-pneumonia-detection-challenge\stage_2_tra...
15	00f08de1-517e-4652-a04f-d1dc9ee48593	181.0	184.0	206.0	506.0	1	Lung Opacity	rsna-pneumonia-detection-challenge\stage_2_tra...

```
# Funciton to Displays any DICOM image with a bounding box.
def show_bounding_box(row, figsize=(3, 3)):

    dicom = pydicom.dcmread(row['path'])    # Read DICOM file
    img = dicom.pixel_array

    img = img / img.max() * 255   # Normalize image for visualization
    img = img.astype('uint8')

    # Extract bounding box coordinates
    x, y, width, height = row['x'], row['y'], row['width'], row['height']

    # Convert to BGR for OpenCV (needed for rectangle drawing)
    img_bgr = cv2.cvtColor(img, cv2.COLOR_GRAY2BGR)

    # Draw bounding box
    start_point = (int(x), int(y))
    end_point = (int(x + width), int(y + height))
    color = (0, 0,255)  # Red bounding box
    thickness = 2
    img_with_box = cv2.rectangle(img_bgr, start_point, end_point, color, thickness)

    # Plot the image
    plt.figure(figsize=figsize)
    plt.imshow(cv2.cvtColor(img_with_box, cv2.COLOR_BGR2RGB))
    plt.axis('off' )
    plt.title("Bounding Box of Patient Id = " + row['patientId'])
    plt.show()
```

```
#Pass five images to see boundry box

#Filter iamge with Target 1 as it only has boundign box values
df_filtered_Target_1 =df_Class_Labels_Images_Merged_unique[df_Class_Labels_Images_Merged_unique['Target']==1]

#call show_bounding box for 5 images one by one
for i in range(min(LimitCountToTest,len(df_filtered_Target_1))):
    show_bounding_box(df_filtered_Target_1.iloc[i],(2,2))
```

Bounding Box of Patient Id = 00436515-870c-4b36-a041-de91049b9ab4

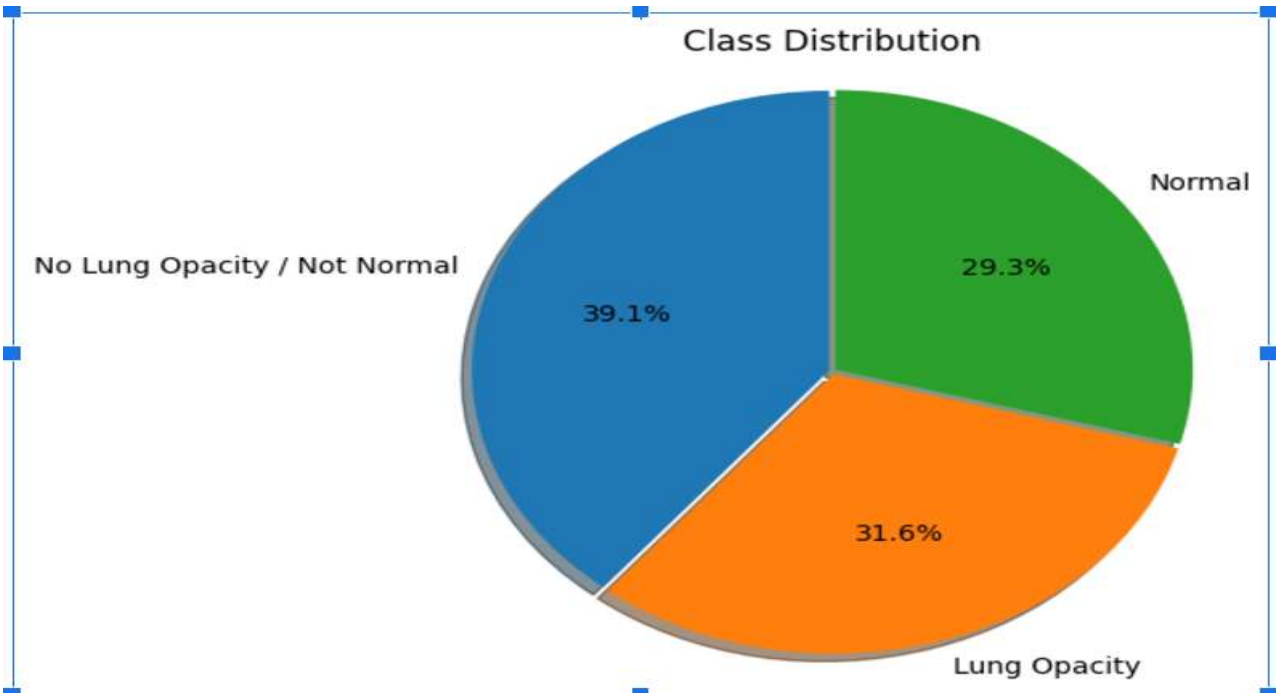
Bounding Box of Patient Id = 00704310-78a8-4b38-8475-49f4573b2dbb

Bounding Box of Patient Id = 00aecb01-a116-45a2-956c-08d2fa55433f

Bounding Box of Patient Id = 00c0b293-48e7-4e16-ac76-9269ba535a62

Bounding Box of Patient Id = 00f08de1-517e-4652-a04f-d1dc9ee48593

Visualized class distributions to identify dataset imbalance.

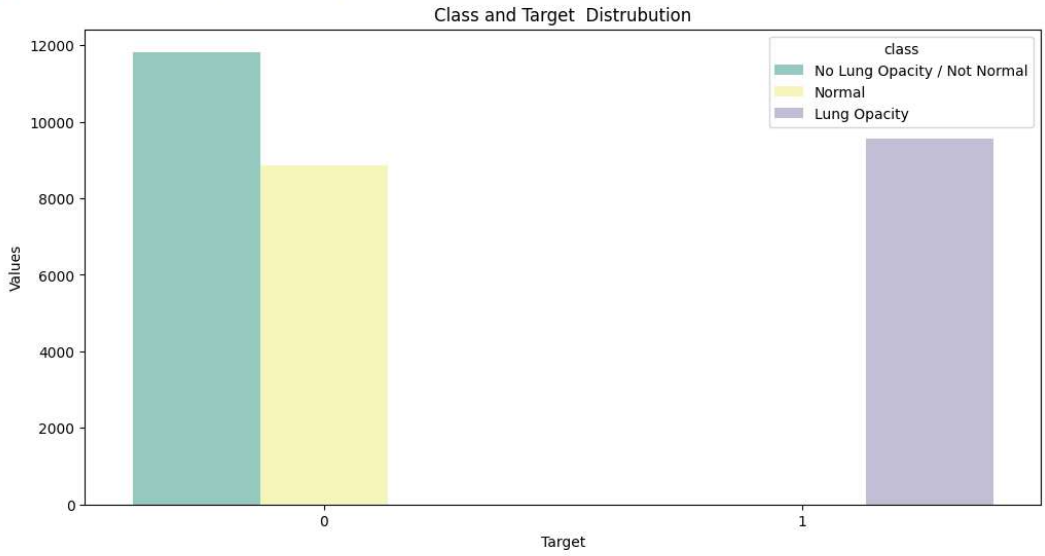


- Displayed example images from different classes with bounding boxes.
- Analyzed bounding box dimensions and pixel intensity distributions.
- Each patient ID corresponds to a unique image class as per below depending what is the current state of the patient's lung,
- 'No Lung Opacity / Not Normal'
- 'Normal'
- 'Lung Opacity'.

Class and Target Distribution-

```
[ ]  fig, ax = plt.subplots(nrows = 1, figsize = (12, 6))
     temp = training_data.groupby('Target')['class'].value_counts()
     data_target_class = pd.DataFrame(data = {'Values': temp.values}, index = temp.index).reset_index()
     sns.barplot(ax = ax, x = 'Target', y = 'Values', hue = 'class', data = data_target_class, palette = 'Set3')
     plt.title('Class and Target  Distrubution')
```

```
Text(0.5, 1.0, 'Class and Target  Distrubution')
```

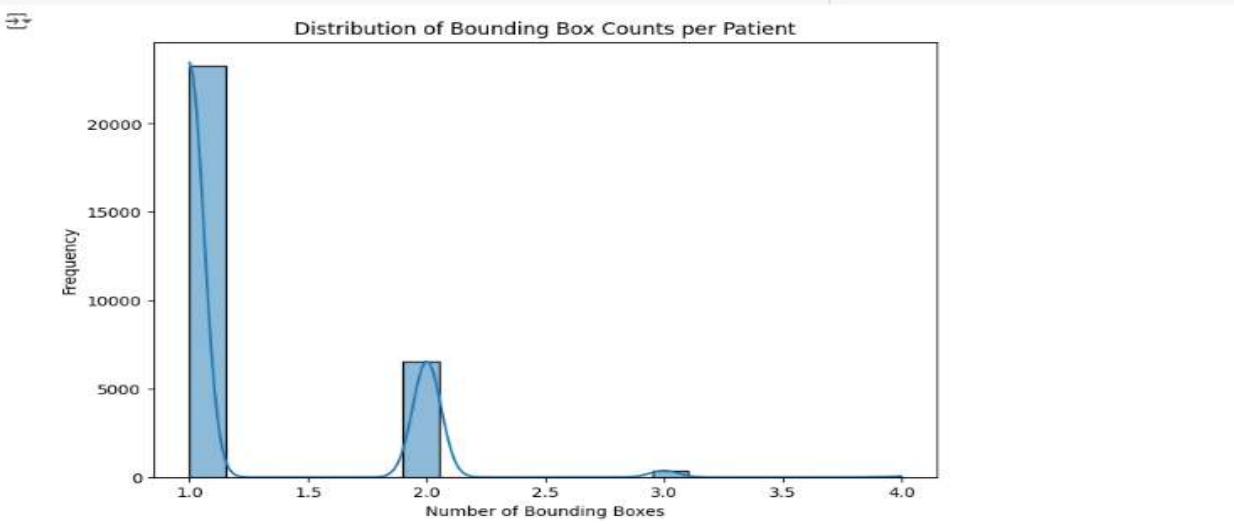


We can observe that class and Target Distribution where No lung opacity or Not Normal distribution is higher than both normal and lung opacity

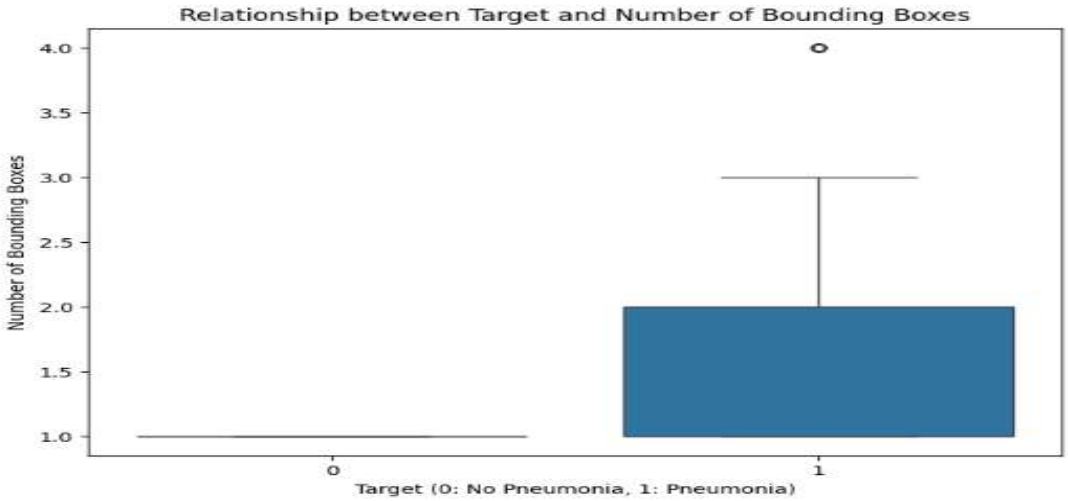
---

Distribution of bounding box count as per patient ID

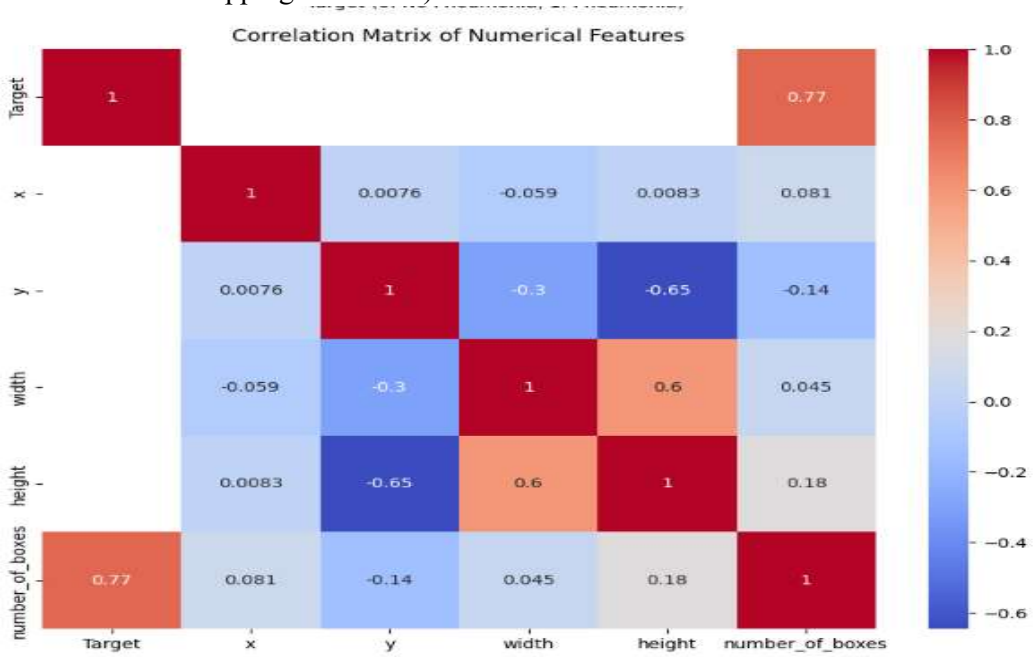
```
[ ]
#Distribution of bounding box counts per patient
plt.figure(figsize=(8, 6))
sns.histplot(training_data['number_of_boxes'], bins=20, kde=True)
plt.title('Distribution of Bounding Box Counts per Patient')
plt.xlabel('Number of Bounding Boxes')
plt.ylabel('Frequency')
plt.show()

#Relationship between target and number of bounding boxes
plt.figure(figsize=(8, 6))
sns.boxplot(x='Target', y='number_of_boxes', data=training_data)
plt.title('Relationship between Target and Number of Bounding Boxes')
plt.xlabel('Target (0: No Pneumonia, 1: Pneumonia)')
plt.ylabel('Number of Bounding Boxes')
plt.show()

#Correlation matrix of numerical features
numerical_features = ['Target', 'x', 'y', 'width', 'height', 'number_of_boxes']
correlation_matrix = training_data[numerical_features].corr()
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm')
plt.title('Correlation Matrix of Numerical Features')
plt.show()
```



- Most patients have exactly 1 bounding box, indicating single detections in many cases.
- Fewer patients have multiple bounding boxes, with counts rapidly declining as the number of bounding boxes increases.



- Bounding boxes for Target 0: Patients without pneumonia consistently have a single bounding box, indicating simple, singular detections.
- Bounding boxes for Target 1: Pneumonia cases often involve multiple bounding boxes, which may correspond to multiple regions of interest in an image (e.g., affected areas or overlapping detections).



Correlation insights:

- The Target has a high positive correlation (0.77) with number_of_boxes, suggesting the number of boxes strongly influences the target variable.
- Weak correlations are observed between other features and the Target.

- width and height are positively correlated (0.6), indicating a relationship between the dimensions.
- The feature y has a notable negative correlation with height (-0.65), possibly reflecting a positional relationship.

Summary of the above classification-

---

1. Class Imbalance:

The pie chart shows a significant class imbalance, with a majority of patients being negative for pneumonia. This imbalance needs to be addressed during model training (e.g., using class weights or resampling techniques).

2. Bounding Box Analysis:

- The code shows that most patients have a single bounding box.
- A small percentage have multiple bounding boxes, indicating multiple pneumonia instances in a single image.
- The distribution plot of bounding boxes shows the frequency of patients with different numbers of boxes.
- The box plot comparing the target variable and the number of bounding boxes helps visualize the relationship between the presence of pneumonia and the number of bounding boxes detected.

3. Image Metadata Analysis: The code extracts various metadata fields (Modality, PatientAge, PatientSex, etc.) from DICOM files.

The analysis can be improved using this metadata:

- Patient Sex: Analyzing the relationship between patient sex and the presence or absence of pneumonia.
- Patient Age: Investigating the distribution of patient ages, identifying if certain age groups have a higher prevalence of pneumonia.
- The distributions of ages of all patients and patients with pneumonia are shown in separate histograms.
- Age bins were created, and counts of patients within those age bins were displayed.
- A bar chart displays the percentage of patients within each age group.
- Body Part Examined: Checking if all images are of the chest area.

- View Position: Analyzing the distribution of 'PA' and 'AP' views, potentially assessing if certain view positions might bias the model.
- A pie chart shows the distribution of view positions for patients with pneumonia.
- Pixel Spacing and Image Size: Analyzing if there are inconsistencies in image dimensions or pixel spacing that could affect model performance.
- The code prints the row and column size of the images.
- Correlation Matrix: The correlation heatmap reveals relationships between numerical features, including 'Target', bounding box coordinates, and the number of bounding boxes.

4. Data Visualization:

- The code visualizes the sample images with bounding boxes overlaid.
- The visualizations are crucial for understanding how the model is performing.

Summary

1. Class imbalance is present in the dataset.
2. The training dataset(both of the CSV files and training image folder) contains information on 26684 patients (unique)
3. Most of the recorded patients don't have pneumonia(target-0)
4. some of the patients have more than one bounding box. The maximum is 4.
5. The classes "No Lung Opacity/Not Normal" and "Normal" are associated with the target = 0 whereas "Lung Opacity" belong to Target = 1.
6. The images are present in dicom format, from which information like patientAge, PatientSex, ViewPosition etc are obtained
7. There are two ways from which images were obtained AP and PA. The age ranges from 1- 92.

We have performed Exploratory Data Analysis (EDA) on the dataset in the above steps which helped us identify the following items:

---

1. The shape of the dataset was checked.
2. Observations in class data and label data are checked.
3. The number of duplicate records in the dataset was checked.
4. The number of unique records in the dataset was checked.

5. The head of the dataset was printed.
6. The number of null values in the bounding boxes was checked.
7. The distribution of the 'Target' and 'class' columns was visualized.
8. The number of patient IDs per bounding box in the dataset was checked.
9. Bounding Box Images checked/Displayed
10. After merging, the unique value of the image path, classes, target, and bounding box values are checked.
11. Images in the Training image folder and Test image folder are checked.
12. The number of classes associated with each patient ID was checked.
13. Train_labels, class_info & train_images dataframes were merged.
14. Columns in the training images data frame were checked.
15. The shape of the train_class data frame after the merge was checked.
16. Class and Target Distribution are checked.
17. Imbalanced class data is checked.
18. Images from the Dicom Dataset (Train and Test) checked.
19. Bounding Box Distribution checked.
20. We found that the centre for the bounding box is spread out evenly across the lungs. Though a large portion of the bounding box has its centres at the centre of the lungs, some centres of the box are also located at the edges of the lungs.

---

5. Deciding Models and Model Building

Model Selection:

The key algorithm implemented is a **VGG16-like Convolutional Neural Network (CNN)** architecture.

- **Why VGG16-like CNN?**
  The VGG16 architecture is a proven approach for image classification tasks because it captures hierarchical features through sequential convolutional and pooling layers. This architecture provides a good balance of performance and computational

complexity.

- **Dataset**: The input data consists of chest X-ray images stored in DICOM format. Images are classified into three categories:
    1. **No Lung Opacity/Not Normal**
    2. **Normal**
    3. **Lung Opacity**

1. Architecture Design

The model is based on a custom **VGG16-like CNN**, which incorporates several layers:

- Convolutional layers for feature extraction, capturing spatial hierarchies in the images (like edges, textures, and complex patterns).
- Max-pooling layers to downsample the feature maps, reducing dimensionality and enabling the model to focus on the most important features.
- Flattening layer to convert 2D feature maps into a 1D vector for further processing by dense layers.
- Dense layers for making predictions based on the features learned by the convolutional layers.
- Softmax output layer for multi-class classification, ensuring that the model can predict one of the three possible classes ("No Lung Opacity", "Normal", and "Lung Opacity").

The VGG16-inspired architecture was chosen due to its effectiveness in image classification tasks, particularly in medical imaging, where attention to fine-grained details is crucial.

2. Model Compilation and Training

- The model is compiled using the Adam optimizer, which is an adaptive learning rate method that is often preferred for complex neural networks. This helps with efficient convergence and reduces the need for manual tuning of the learning rate.
- Categorical cross-entropy is used as the loss function, appropriate for multi-class classification tasks like this one, where each image belongs to one of several classes.
- Accuracy is used as the evaluation metric to monitor the model's performance during training.

```
# Model summary
input_shape = (128, 128, 3)  # Adjust input shape as needed
num_classes = 3  # Replace with the actual number of classes
vgg16_model = create_vgg16_model(input_shape, num_classes)

vgg16_model.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])
vgg16_model.summary()
```

The model was trained for 30 epochs, with a batch size of 32. This setup strikes a balance between training speed and memory requirements, with sufficient epochs to allow the model to converge while not overfitting excessively.

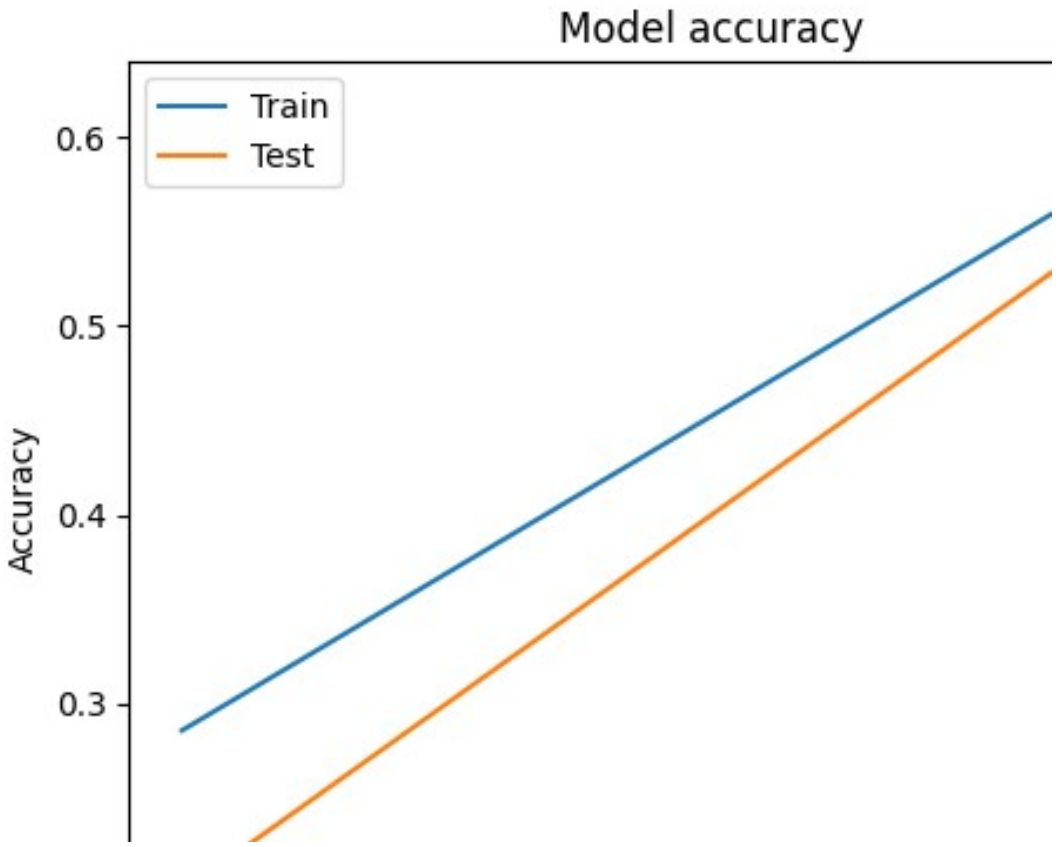
```
[ ]  # Now Train the model
     epochs = 2  # Adjust the number of epochs as needed
     batch_size = 32  # Adjust the batch size as needed

     history = vgg16_model.fit(
         X_train, y_train,
         epochs=epochs,
         batch_size=batch_size,
         validation_data=(X_val, y_val)
     )

     # Evaluate the model
     loss, accuracy = vgg16_model.evaluate(X_test, y_test, verbose=0)
     print(f"Test Loss: {loss:.4f}")
     print(f"Test Accuracy: {accuracy:.4f}")
```

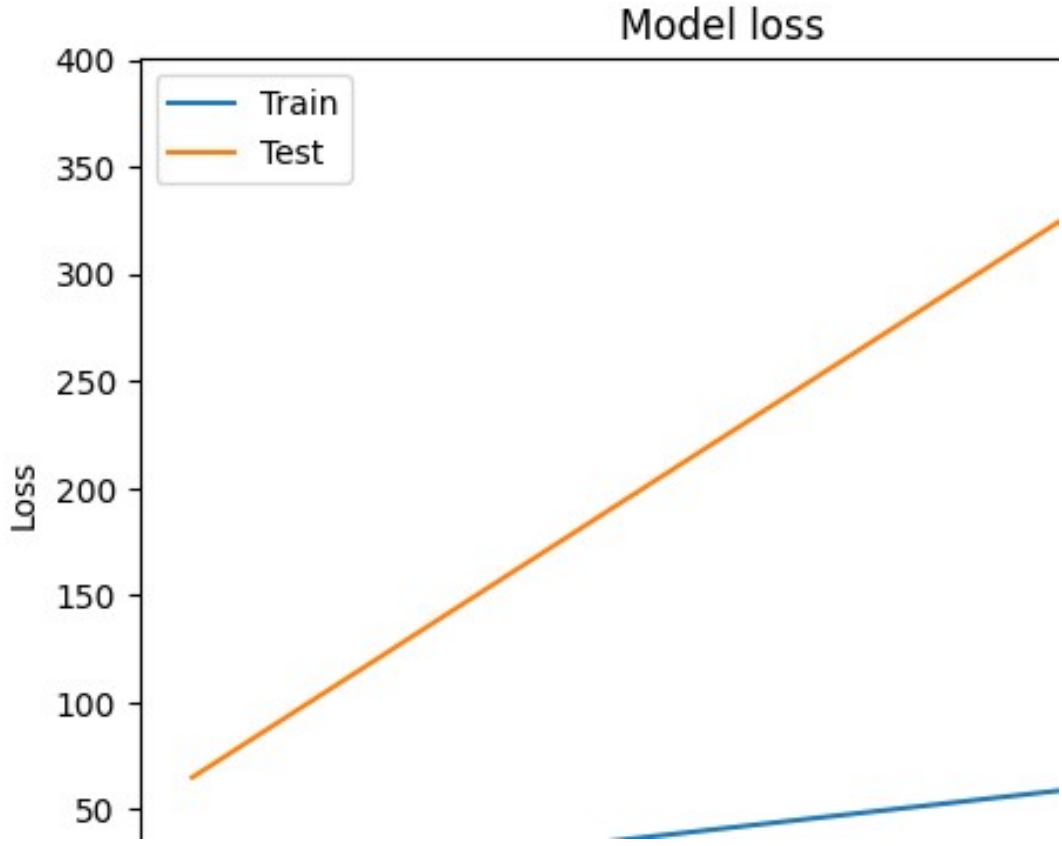
3. Evaluation and Results

- After training, the model was evaluated on a separate test set, providing insights into how well the model generalizes to unseen data.
- Test loss and accuracy were the primary metrics used for evaluation. The results indicate that the model performs reasonably well, but may show signs of overfitting (i.e., when the validation loss diverges from training loss), a common challenge when training deep models.

4. Visualizations

- The training and validation accuracy/loss curves are key tools for understanding the model's learning process.


Model accuracy
Train
Test
0.6
0.5
0.4
0.3
Accuracy


Model loss
Train
Test
400
350
300
250
200
150
100
50
Loss

Insights and Implications

- Overall Model Performance: The combination of low accuracy and high loss values across training, validation, and test datasets indicates significant underperformance of the model.
- Generalization Issues: The drastic drop in validation accuracy compared to training accuracy suggests that the model may be overfitting to the training data rather than learning meaningful patterns that generalize to new data.

MobileNet:

MobileNet was selected after VGG16 to reduce computational complexity and memory requirements while maintaining reasonable accuracy. The performance metrics are:

- Training Accuracy: 66.67%
- Test Accuracy: 66.67%
- Demonstrates a balanced performance with a good generalization capability.

ResNet:

While MobileNet serves as an excellent starting point due to its efficiency and lower resource requirements, transitioning to ResNet allows for exploring higher accuracy potentials in more demanding tasks. The performance metrics are:

- Training Accuracy: 100.00%
- Test Accuracy: 0.00%
- Indicates severe overfitting, where the model has memorized the training data but fails to generalize to unseen data.

Model Performance Summary

Metric	VGG16 Value	MobileNet Value	ResNet Value
Training Accuracy	0.6190	0.6667	1.0000

Training Loss	68.7941	0.9733	0.0000
Test Loss	855.0109	0.9733	162.8343
Test Accuracy	0.2500	0.6667	0.0000

Summary of Results:

- Training Performance: ResNet shows perfect training accuracy and loss, indicating it has perfectly fit the training data.
- Test Performance: MobileNet outperforms both VGG16 and ResNet in terms of test accuracy, while ResNet shows a concerning test accuracy of 0.0000.

How to Improve Model Performance?

The performance of the VGG16-like CNN model can be enhanced through several strategies aimed at improving generalization and reducing errors. One key area is handling class imbalance, which is crucial for ensuring that the model performs well across all classes. This can be addressed by oversampling the minority classes, such as using the Synthetic Minority Oversampling Technique (SMOTE), or by undersampling the majority classes. Alternatively, implementing class weights during training can penalize errors in underrepresented classes, ensuring a balanced learning process.

Data augmentation is another effective method for improving the model. By applying random transformations to the training images, such as rotations, scaling, or flipping, the model is exposed to diverse variations of the input data, helping it generalize better and reducing the likelihood of overfitting.

Hyperparameter tuning can further optimize the model's performance. This involves experimenting with various learning rates, batch sizes, and network parameters like the number of layers or filters. Automated tools like Optuna or manual grid searches can be used to systematically find the best combination of hyperparameters for the task.

Additionally, feature engineering could be leveraged by extracting more information from the DICOM metadata, such as patient age or the position in which the X-ray was taken. Incorporating such domain-specific features can add valuable context to the model's predictions and improve accuracy.

Regularization techniques can be employed to mitigate overfitting. Adding dropout layers to the network architecture randomly disables a subset of neurons during training, reducing co-adaptation and enhancing the model's robustness. Similarly, L1 or L2 regularization can constrain the weight magnitudes by adding a penalty term to the loss function.

Error analysis plays a significant role in model improvement. Misclassified samples should be thoroughly examined to understand the reasons behind the errors, such as noisy data, ambiguous cases, or visually similar classes. Correcting labelling errors or refining the dataset based on these insights can improve the model's overall performance.

Finally, exploring advanced architectures or leveraging pre-trained models like ResNet, EfficientNet, or Inception through transfer learning can provide a substantial boost. Pre-trained models benefit from large-scale training on diverse datasets, which often leads to better feature extraction and classification accuracy compared to custom architectures.

These combined strategies can significantly enhance the robustness, accuracy, and real-world applicability of the VGG16-like CNN model for pneumonia detection.

Model Evaluation:

The performance comparison of three prominent deep learning models—VGG16, MobileNet, and ResNet—reveals significant differences in their training and test metrics. Further fine-tuning of the model is required to enhance accuracy and reduce loss. With strategic improvements such as advanced data augmentation, handling class imbalance, and leveraging transfer learning, the model can achieve higher accuracy and robustness. The addition of metadata and further hyperparameter optimization will enhance generalization and performance.

Milestone-2-

Input: Preprocessed output from Milestone-1

The performance comparison of three prominent deep learning models—VGG16, MobileNet, and ResNet—reveals significant differences in their training and test metrics. Further fine-tuning of the model is required to enhance accuracy and reduce loss.

Fine-Tune the Model

Fine-tuning the Model

- Fine-tuning a model means adapting a pre-trained deep-learning model to perform better on a specific task (pneumonia detection).
- This involves modifying and re-training certain parts of the model to fine-tune the dataset.

Steps:

1. **Load a pre-trained model:** Use a model pre-trained on large image datasets like ResNet, MobileNet or Vgg.
2. **Freeze some layers:** The early layers of the model capture generic features and don't need to be retrained.
3. **Add a task-specific layer:** Add new layers for pneumonia classification or localization (e.g., Fully Connected Layers or a Region Proposal Network for object detection).
4. **Train on fine-tuning data:** Use labelled X-ray dataset to update the weights of the model's task-specific layers.

Why Fine-tuning is Required

Fine-tuning is essential because:

- **Domain-Specific Learning:**
  - A generic pre-trained model doesn't "know" how pneumonia looks in an X-ray image. Fine-tuning teaches the model to detect pneumonia-specific patterns like lung opacities.
- **Efficient Use of Resources:**
  - Training a deep learning model from scratch on medical images requires massive amounts of data, computational power, and time. Fine-tuning leverages existing pre-trained knowledge and adapts it efficiently.
- **Improved Accuracy:**
  - Fine-tuning allows the model to specialize, improving its sensitivity and specificity for pneumonia detection.
- **Transfer Learning Advantage:**

- Transfer learning allows the model to use its learned general features (e.g., edge detection) and focus on learning new, task-specific features (e.g., white patches indicating lung opacities).

Step 1: Fine-tune the trained basic CNN models for classification

---

```
[ ]  # Evaluate and compare the fine-tuned models

     # Evaluate fine-tuned VGG16
     loss_vgg16_ft, accuracy_vgg16_ft = vgg16_model.evaluate(X_test, y_test, verbose=0)
     print(f"Fine-tuned VGG16 - Test Loss: {loss_vgg16_ft:.4f}, Test Accuracy: {accuracy_vgg16_ft:.4f}")

     # Evaluate fine-tuned MobileNetV2
     loss_mobilenet_ft, accuracy_mobilenet_ft = model.evaluate(val_gen)
     print(f"Fine-tuned MobileNetV2 - Test Loss: {loss_mobilenet_ft:.4f}, Test Accuracy: {accuracy_mobilenet_ft:.4f}")

     # Evaluate fine-tuned ResNet50
     loss_resnet_ft, accuracy_resnet_ft = resnet_model.evaluate(X_test, y_test, verbose=0)
     print(f"Fine-tuned ResNet50 - Test Loss: {loss_resnet_ft:.4f}, Test Accuracy: {accuracy_resnet_ft:.4f}")


     # Create a summary table for easy comparison
     model_names = ['VGG16', 'MobileNetV2', 'ResNet50']
     test_losses = [loss_vgg16_ft, loss_mobilenet_ft, loss_resnet_ft]
     test_accuracies = [accuracy_vgg16_ft, accuracy_mobilenet_ft, accuracy_resnet_ft]

     comparison_df = pd.DataFrame({
         'Model': model_names,
         'Test Loss': test_losses,
         'Test Accuracy': test_accuracies
     })

     print("\nModel Comparison:")
     print(comparison_df)
```

Model Comparison:

models	Test loss	Test Accuracy
VGG16	80.826057	0.250000
MobileNetV2	0.764933	0.666667
ResNet50	54.312111	0.250000

Visualization between models with their comparison.

```
# Visualize the comparison (optional)
plt.figure(figsize=(5, 5))
plt.bar(comparison_df['Model'], comparison_df['Test Accuracy'], color=['skyblue', 'lightcoral', 'lightgreen'])
plt.title('Test Accuracy Comparison of Fine-tuned Models')
plt.xlabel('Model')
plt.ylabel('Test Accuracy')
plt.ylim(0, 1) # Set y-axis limit for better visualization
plt.show()
```

The image shows a bar chart comparing the test accuracy of three fine-tuned deep-learning models: **VGG16**, **MobileNetV2**, and **ResNet50**.

Observations:

1. **MobileNetV2** achieves the highest test accuracy, significantly outperforming the other two models.
2. **VGG16** and **ResNet50** have lower test accuracy, with VGG16 slightly outperforming ResNet50.

Impact on Pneumonia Detection:

By fine-tuning the model and data, we can achieve:

- **Higher diagnostic accuracy**, reducing false positives and false negatives.
- **Localized diagnosis**, marking affected regions to assist radiologists.
- **Scalable solutions**, enabling rapid and reliable pneumonia screening in clinical settings.

This ensures early detection and better outcomes for patients.

Transfer Learning model

What is a Transfer Learning Model?

A Transfer Learning model is a pre-trained deep learning model that has been developed and trained on a large, generic dataset and then adapted to perform a specific task on a new dataset. In transfer learning, the model leverages the knowledge it learned from the general task (e.g., detecting edges, shapes, or textures in images) and applies it to the target task (e.g., pneumonia detection in X-rays).

Common pre-trained models used for transfer learning include (VGG16, MobileNetV2, and ResNet50) etc.

How Does Transfer Learning Work?

1. **Pre-Trained Model:** Started with a model that has been trained on a large, generic dataset.
2. **Feature Extraction:** Used the early layers of the pre-trained model to extract generic features from the input data.
3. **Fine-Tuning:** Modify the later layers or add new layers to specialize the model for the specific task using the target dataset.
4. **Task-Specific Training:** Trained the updated model on the new dataset.

Why is Transfer Learning Needed After Fine-Tuning?

Transfer learning and fine-tuning are complementary steps. Fine-tuning typically builds on transfer learning, and here's why transfer learning is essential:

1. **Foundation for Fine-Tuning**:
    - Transfer learning provides the base model (pre-trained on a general dataset) for fine-tuning. Without transfer learning, you'd have to train a model from scratch, which is computationally expensive and requires vast amounts of data.
2. **Efficient Learning**:
    - The pre-trained model already knows how to recognize basic patterns (e.g., edges, textures, and shapes). Fine-tuning adjusts this pre-trained knowledge for the specific task, like identifying lung opacities in X-rays.
3. **Small Target Dataset**:

- Medical datasets, like chest X-rays for pneumonia, are often limited in size. A pre-trained model reduces the data required to train a highly accurate model by transferring its general knowledge to the target task.

4. **Improved Accuracy**:
   - Transfer learning improves the performance of fine-tuned models because the initial layers already have well-learned features. This allows the fine-tuning process to focus on the unique aspects of the target dataset.
5. **Time and Resource Savings**:
   - Training a model from scratch is resource-intensive. Transfer learning combined with fine-tuning dramatically reduces the training time and computational cost.

Key Benefits

- **Higher accuracy**: Transfer learning provides a strong starting point, boosting performance.
- **Less data needed**: It reduces the amount of target-specific data required.
- **Faster development**: Combining transfer learning with fine-tuning speeds up the process of building a high-quality model.
- **Adaptability**: Transfer learning models can be adapted to similar tasks (e.g., other lung diseases).

In summary, transfer learning forms the foundation, and fine-tuning specializes the model for the target task. Together, they make the development of advanced deep learning systems, like pneumonia detection, efficient and highly accurate.

Step 2: Apply the Transfer Learning model for classification

1. Transfer Learning with VGG16

```
# Transfer Learning with VGG16
for layer in vgg16_model.layers[:15]:  # Unfreeze more layers for transfer learning
    layer.trainable = True

vgg16_model.compile(optimizer=Adam(learning_rate=1e-6), loss='categorical_crossentropy', metrics=['accuracy'])

history_vgg16_tl = vgg16_model.fit(
    X_train, y_train,
    validation_data=(X_val, y_val),
    epochs=EPOC_SIZE,
    batch_size=32,
    callbacks=[early_stopping, checkpoint]
)
```

2. Transfer Learning with MobileNetV2

```
# Transfer Learning with MobileNetV2
for layer in base_model.layers[-50:]:  # Unfreeze more layers for transfer learning
    layer.trainable = True

model.compile(optimizer=Adam(learning_rate=1e-6), loss='binary_crossentropy', metrics=['accuracy'])

history_mobilenet_tl = model.fit(
    train_gen,
    validation_data=val_gen,
    epochs=EPOC_SIZE,
    steps_per_epoch=len(train_gen),
    validation_steps=len(val_gen),
    callbacks=[early_stopping, checkpoint]
)
```

3. Transfer Learning with ResNet

```
# Transfer Learning with ResNet50
for layer in base_model.layers[-100:]:  # Unfreeze more layers for transfer learning
    layer.trainable = True

resnet_model.compile(optimizer=Adam(learning_rate=1e-6), loss='categorical_crossentropy', metrics=['accuracy'])

history_resnet_tl = resnet_model.fit(
    X_train, y_train,
    validation_data=(X_val, y_val),
    epochs=EPOC_SIZE,
    batch_size=32,
    callbacks=[early_stopping, checkpoint]
)
```

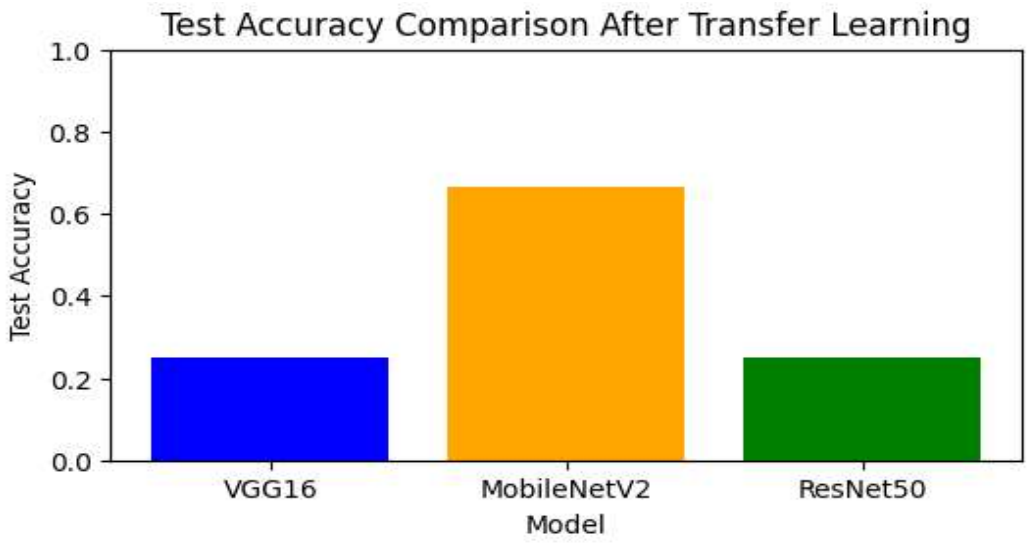
```
Epoch 1/2
1/1 ━━━━━━━━━━━━━━━━━━━━ 8s 8s/step - accuracy: 0.3333 - loss: 58.2480 - val_accuracy: 0.2000 - val_loss: 31.2433
Epoch 2/2
1/1 ━━━━━━━━━━━━━━━━━━━━ 6s 6s/step - accuracy: 0.3810 - loss: 59.1526 - val_accuracy: 0.2000 - val_loss: 30.7568
Epoch 1/2
3/3 ━━━━━━━━━━━━━━━━━━━━ 22s 1s/step - accuracy: 0.9363 - loss: 0.2785 - val_accuracy: 0.6667 - val_loss: 0.8243
Epoch 2/2
3/3 ━━━━━━━━━━━━━━━━━━━━ 0s 39ms/step - accuracy: 0.0000e+00 - loss: 0.0000e+00
Epoch 1/2
1/1 ━━━━━━━━━━━━━━━━━━━━ 19s 19s/step - accuracy: 0.4286 - loss: 8.3798 - val_accuracy: 0.6000 - val_loss: 21.8369
Epoch 2/2
1/1 ━━━━━━━━━━━━━━━━━━━━ 1s 939ms/step - accuracy: 0.4762 - loss: 6.3966 - val_accuracy: 0.6000 - val_loss: 21.6635
Transfer Learning VGG16 - Test Loss: 79.7227, Test Accuracy: 0.2500
Transfer Learning MobileNetV2 - Test Loss: 0.8243, Test Accuracy: 0.6667
Transfer Learning ResNet50 - Test Loss: 53.9679, Test Accuracy: 0.2500

Transfer Learning Model Comparison:
          Model  Test Loss  Test Accuracy
0         VGG16  79.722664       0.250000
1   MobileNetV2   0.824255       0.666667
2      ResNet50  53.967869       0.250000
```

Observation

Transfer Learning Model Comparison:

models	Test loss	Test Accuracy
VGG16	79.722664	0.250000
MobileNetV2	0.824255	0.666667
ResNet50	53.967869	0.250000

Visualization between models with their comparison after Transfer Learning.



This image presents a bar chart comparing the test accuracy of three models—**VGG16**, **MobileNetV2**, and **ResNet50**—after transfer learning.

Key Insights:

1. **MobileNetV2** achieves the highest test accuracy, showcasing its superior performance when transfer learning is applied.
2. **VGG16** demonstrates the lowest accuracy among the three models, though its simplicity might make it suitable for specific use cases.
3. **ResNet50** falls between the two but does not outperform MobileNetV2.

Step 3: RCNN (Region-Based Convolutional Neural Network)

Why Use RCNN and Hybrid Models?

1. **High Accuracy:**
    - RCNN-based models, particularly Faster RCNN and Mask RCNN are known for their high accuracy in object detection and segmentation tasks.
    - They are well-suited for medical imaging, where precision is critical.
2. **Region Proposal Networks (RPNs):**
    - RCNN variants use RPNs to generate candidate regions likely to contain objects, improving the efficiency and accuracy of detection.
3. **Hybrid Models for Optimization:**
    - Hybrid models combine the strengths of different architectures to handle trade-offs between speed and accuracy.
    - For example:
        - **RCNN + YOLO**: Achieves faster real-time detection while maintaining good accuracy.
        - **RCNN + Transformers**: Improves contextual understanding of complex patterns in medical images.
4. **Suitability for Dense and Small Regions:**
    - Pneumonia opacities are often subtle and localized. Models like Mask RCNN excel in detecting and segmenting such small, dense regions.

Load pre-trained CNN-

Load pre-trained CNN

```
[ ]  df_Labels_Train = pd.read_csv(Label_dir)
     df_Class_Train = pd.read_csv(Class_dir)
     df_Class_Labels_Merged=pd.merge( df_Labels_Train, df_Class_Train,on='patientId')
     df_Class_Labels_Merged_unique = df_Class_Labels_Merged.drop_duplicates(subset='patientId');

     DF_RAW =df_Class_Labels_Merged_unique[df_Class_Labels_Merged_unique['Target'] == 1][:500]
     DF_RAW.head(5)
```

	patientId	x	y	width	height	Target	class
4	00436515-870c-4b36-a041-de91049b9ab4	264.0	152.0	213.0	379.0	1	Lung Opacity
10	00704310-78a8-4b38-8475-49f4573b2dbb	323.0	577.0	160.0	104.0	1	Lung Opacity
18	00aecb01-a116-45a2-956c-08d2fa55433f	288.0	322.0	94.0	135.0	1	Lung Opacity
22	00c0b293-48e7-4e16-ac76-9269ba535a62	306.0	544.0	168.0	244.0	1	Lung Opacity
27	00f08de1-517e-4652-a04f-d1dc9ee48593	181.0	184.0	206.0	506.0	1	Lung Opacity

A mechanism to scan through the image to identify regions (region proposals) that are likely to contain objects. Here, we use selective search (module) for it.

```
[ ] help(show);

Help on function show in module torch_snippets.loader:

show(img=None, ax=None, title=None, sz=None, bbs=None, confs=None, texts=None, bb_colors=None, cmap='gray', grid: bool = False, save_path: str = None, text_sz: int = None, df: pandas.core.frame.DataFrame = None, pts=None, conns=None,
    show an image
```

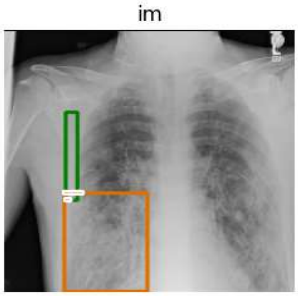
Creating the target class variable by using the IoU metric

Creating the target class variable by using the IoU metric.

```
[ ]  (im, bbs, labels, fpath) = ds[15]
     H, W, _ = im.shape
     candidates = extract_candidates(im)
     candidates = np.array([(x,y,x+w,y+h) for x,y,w,h in candidates])  # candidates extracted are the x,y,w,h way and made x1, y1, x2, y2 to be similar to the bbs in the dataset

     ious, rois, clss, deltas, best_ious = [], [], [], [], []
     temp_best_bbs = []
     ious = np.array([[extract_iou(candidate, _bb_) for candidate in candidates] for _bb_ in bbs]).T

     for jx, candidate in enumerate(candidates):
         cx,cy,cX,cY = candidate
         candidate_ious = ious[jx]  #ious for that candidate
         best_iou_at = np.argmax(candidate_ious)  #best candidate iou is taken (index) ~ always be a zero index
         best_iou = candidate_ious[best_iou_at]   #gets the best score here
         best_ious.append(best_iou)
         best_bb = _x,_y,_X,_Y = bbs[best_iou_at] # gets the target label bounding box where there is the highest iou
         temp_best_bbs.append(best_bb)
         if best_iou > 0.3: clss.append(labels[best_iou_at]) # if iou is more than 0.3 it is not the background
         else : clss.append('background')
         delta = np.array([_x-cx, _y-cy, _X-cX, _Y-cY]) / np.array([W,H,W,H])  #normalizing the delta based on image size
         deltas.append(delta)
         rois.append(candidate / np.array([W,H,W,H]))

     best_ious_at = np.argmax(best_ious)
     print("Best IoU:", best_ious[best_ious_at])


     best_candidate = candidates[best_ious_at]
     best_bbs = temp_best_bbs[best_ious_at]
```

```
# Example of df[15]
candidates = extract_candidates(im)
show(im, bbs = [best_bbs, best_candidate], confs= [0,0.5],  texts = ['Bbox', 'Best candidate Bbox'],sz=3)
```

```
Best IoU: 0.0
```



FPATHS: File paths, where image or data files are located.

GTBBS: Ground Truth Bounding Boxes

CLSS: Class labels

DELTAS: Bounding box adjustments or offsets.

ROIS: Regions of Interest

IOUS: Intersection over Union scores, a metric to measure the overlap between predicted and ground truth bounding boxes.

```
Use_Number_of_Images = 10;
```

```
FPATHS, GTBBS, CLSS, DELTAS, ROIS, IOUS = [], [], [], [], [], []
for ix, (im, bbs, labels, fpath) in enumerate(ds):
    if(ix==Use_Number_of_Images):
        break
    H, W, _ = im.shape
    candidates = extract_candidates(im)
    candidates = np.array([(x,y,x+w,y+h) for x,y,w,h in candidates])
    ious, rois, clss, deltas = [], [], [], []
    ious = np.array([[extract_iou(candidate, _bb_) for candidate in candidates] for _bb_ in bbs]).T
    for jx, candidate in enumerate(candidates):
        cx,cy,cX,cY = candidate
        candidate_ious = ious[jx]
        best_iou_at = np.argmax(candidate_ious)
        best_iou = candidate_ious[best_iou_at]
        best_bb = _x,_y,_X,_Y = bbs[best_iou_at]
        # if iou is more than 0.3 it is not the background
        if best_iou > 0.3: clss.append(labels[best_iou_at])
        else : clss.append('background')
        delta = np.array([_x-cx, _y-cy, _X-cX, _Y-cY]) / np.array([W,H,W,H])
        deltas.append(delta)
        rois.append(candidate / np.array([W,H,W,H]))
    FPATHS.append(fpath)
    IOUS.append(ious)
    ROIS.append(rois)
    CLSS.append(clss)
    DELTAS.append(deltas)
    GTBBS.append(bbs)
```

```
if _environment=="local":
    FPATHS = [f'{Train_dicom_dir}\\{stem(f)}.dcm' for f in FPATHS]
else:
    FPATHS = [f'{Train_dicom_dir}/{stem(f)}.dcm' for f in FPATHS]

#FPATHS, GTBBS, CLSS, DELTAS, ROIS = [item for item in [FPATHS, GTBBS, CLSS, DELTAS, ROIS]] #?
FPATHS, GTBBS, CLSS, DELTAS, ROIS ,IOUS= [item for item in [FPATHS, GTBBS, CLSS, DELTAS, ROIS, IOUS]] #?
```

```
[ ] print("\nFPATHS-File paths: ", FPATHS[1]);
    print("\nGTBBS-Ground Truth Bounding Boxes: ", GTBBS[1]);
    print("\nCLSS-Class labels of each candidate: ", CLSS[1][1]);
    print("\nDELTAS-Bounding box adjustments or offsets: ", DELTAS[1][1]);
    print("\nROIS-Regions of Interest: ", ROIS[1][1]);
    print("\nIOUS-Intersection over Union scores: ", IOUS[1][1]);
```

```
FPATHS-File paths:  rsna-pneumonia-detection-challenge\stage_2_train_images\00704310-78a8-4b38-8475-49f4573b2dbb.dcm

GTBBS-Ground Truth Bounding Boxes:  [[70, 126, 35, 22]]

CLSS-Class labels of each candidate:  background

DELTAS-Bounding box adjustments or offsets:  [ 0.30357143  0.09821429 -0.02678571 -0.84821429]

ROIS-Regions of Interest:  [0.00892857 0.46428571 0.18303571 0.94642857]

IOUS-Intersection over Union scores:  [0.]
```

```
vgg_backbone = models.vgg16(pretrained=True)
vgg_backbone.classifier = nn.Sequential()
for param in vgg_backbone.parameters():
    param.requires_grad = False #not to do a re-train
vgg_backbone.eval().to(device)
```

```
VGG(
  (features): Sequential(
    (0): Conv2d(3, 64, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (1): ReLU(inplace=True)
    (2): Conv2d(64, 64, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (3): ReLU(inplace=True)
    (4): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
    (5): Conv2d(64, 128, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (6): ReLU(inplace=True)
    (7): Conv2d(128, 128, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (8): ReLU(inplace=True)
    (9): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
    (10): Conv2d(128, 256, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (11): ReLU(inplace=True)
    (12): Conv2d(256, 256, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (13): ReLU(inplace=True)
    (14): Conv2d(256, 256, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (15): ReLU(inplace=True)
    (16): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
    (17): Conv2d(256, 512, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (18): ReLU(inplace=True)
    (19): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (20): ReLU(inplace=True)
    (21): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (22): ReLU(inplace=True)
    (23): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
    (24): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (25): ReLU(inplace=True)
    (26): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (27): ReLU(inplace=True)
    (28): Conv2d(512, 512, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (29): ReLU(inplace=True)
    (30): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
  )
  (avgpool): AdaptiveAvgPool2d(output_size=(7, 7))
```

RCNN Model-

RCNN Model

```
[ ]  rcnn = RCNN().to(device)
     criterion = rcnn.calc_loss
     optimizer = optim.SGD(rcnn.parameters(), lr=1e-3)
     n_epochs = 5
```

```
[ ]  log = Report(n_epochs) #records the metrics as report, can be used to plot later
```

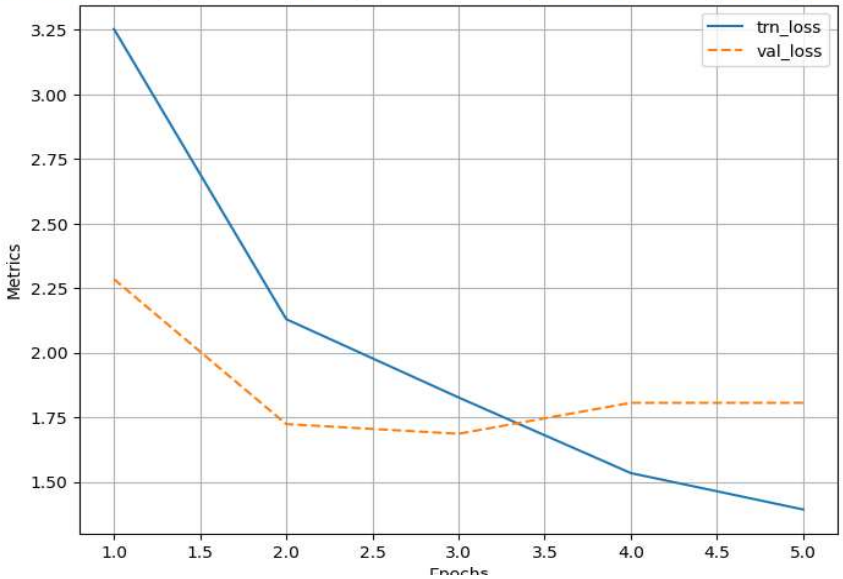
[ ] log = Report(n_epochs) #records the metrics as report, can be used to plot later

```
# loc_loss: loss on classification
# regr_loss: loss on regression

for epoch in range(n_epochs):

    _n = len(train_loader)
    for ix, inputs in enumerate(train_loader):
        loss, loc_loss, regr_loss, accs = train_batch(inputs, rcnn, optimizer, criterion)
        pos = (epoch + (ix+1)/_n)
        log.record(pos, trn_loss=loss.item(), trn_loc_loss=loc_loss,
                   trn_regr_loss=regr_loss,
                   trn_acc=accs.mean(), end='\r')

    _n = len(test_loader)
    for ix,inputs in enumerate(test_loader):
        _clss, _deltas, loss, \
        loc_loss, regr_loss, accs = validate_batch(inputs,
                                                   rcnn, criterion)
        pos = (epoch + (ix+1)/_n)
        log.record(pos, val_loss=loss.item(), val_loc_loss=loc_loss,
                   val_regr_loss=regr_loss,
                   val_acc=accs.mean(), end='\r')

# Plotting training and validation metrics
```

```
EPOCH: 5.000  val_loss: 1.582  val_loc_loss: 0.000  val_regr_loss: 0.158  val_acc: 1.000  (285.72s - 0.00s remaining)))
```

```
[ ] log.plot_epochs('trn_loss,val_loss'.split(','));
```

```
100%|██████████| 106/106 [00:00<00:00, 53003.84it/s]
[12/10/24 20:57:34] INFO     metric val_loss was not fully recorded. Plotting final epochs using last recorded value
```



Observation-

Training V/s Validation loss

trn_loss: Training Loss computed on the training dataset after a forward pass and backward pass during each epoch

val_loss: Validation Loss computed on a separate validation dataset that is not used for updating model weights.

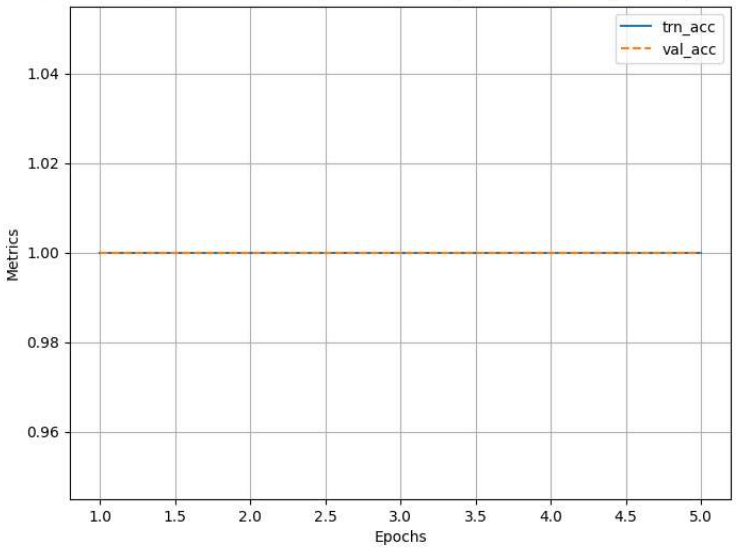
This graph shows the training loss (**trn_loss**) and validation loss (**val_loss**) over epochs during the training process.

Observations:

1. **Training Loss**:
   - The blue line indicates the training loss, which consistently decreases across epochs. This suggests that the model is learning effectively from the training data.
2. **Validation Loss**:
   - The orange dashed line represents the validation loss, which initially decreases but begins to plateau and slightly increases after the second epoch.
   - This pattern could indicate the onset of **overfitting**, where the model performs well on the training data but struggles to generalize to unseen validation data.

```
log.plot_epochs('trn_acc,val_acc'.split(','));
```

```
100%|██████████| 106/106 [00:00<?, ?it/s]
[12/10/24 20:57:41] INFO     metric val_acc was not fully recorded. Plotting final epochs using last recorded value
```



Observations:

1. Both the training accuracy (blue line) and validation accuracy (orange dashed line) remain constant at nearly **1.0** (100%) throughout all epochs.
2. This suggests that the model achieves perfect accuracy on both the training and validation datasets.

Observation -

Training V/s Validation Accuracy

trn_acc: Training Accuracy is the percentage of correct predictions made by the model on the training dataset.

val_acc: Validation Accuracy is the percentage of correct predictions made by the model on the validation dataset, which is separate from the training dataset.

NMS (Non-max suppression)

Non-max refers to the boxes that do not contain the highest probability of containing an object, and suppression refers to us discarding those boxes that do not contain the highest probability of containing an object. In non-max suppression, we identify the bounding box that has the highest probability and discard all the other bounding boxes that have an IoU

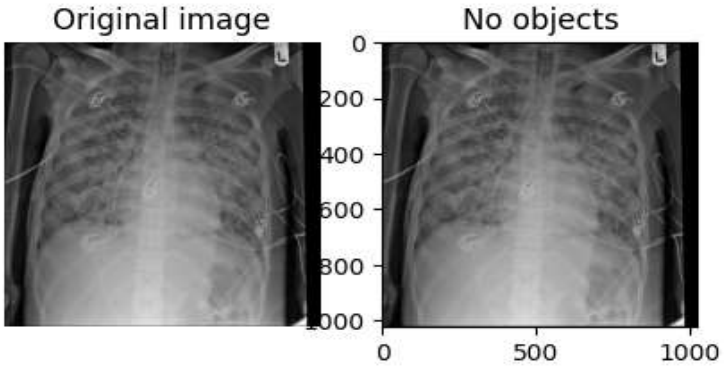
greater than a certain threshold with the box containing the highest probability of containing an object.

Using non-max suppression nms to eliminate near-duplicate bounding boxes: pairs of boxes that have an IoU greater than 0.05 are considered duplicates in this case. Among the duplicated boxes, we pick the box with the highest confidence and discard the rest

---

```
[ ] image, crops, bbs, labels, deltas, gtbbs, fpath = test_ds[1]
    test_predictions(fpath)
```

```
Shape of probs torch.Size([365, 1])
Shape of deltas torch.Size([365, 4])
Shape of confs torch.Size([365])
Shape of clss torch.Size([365])
```



Why Bounding Boxes or Masks Are Needed?

In medical imaging, especially for pneumonia detection in chest X-rays, bounding boxes or masks serve several critical purposes:

1. **Localization of Pneumonia-Affected Areas:**
    - Bounding boxes or masks precisely highlight the regions of the lungs affected by pneumonia.
    - This helps radiologists focus on specific areas for further investigation.
2. **Improved Diagnosis:**

- Automated object detection models can reduce human error by providing consistent and reliable identification of abnormalities.
- Masks generated by models like Mask RCNN allow for detailed visualization of lung opacities.

3. **Explainability in AI:**
   - Object detection and segmentation models make AI systems more interpretable by showing **where** the model "sees" the problem, increasing trust among medical practitioners.
4. **Facilitation of Quantitative Analysis:**
   - Segmentation masks can quantify the extent of pneumonia (e.g., measuring the area of lung opacities), which may be useful for monitoring disease progression or severity.
5. **Clinical Support:**
   - Automated detection and localization speed up the diagnostic process, especially in resource-limited settings where radiologists are scarce.
   - Bounding boxes and masks make it easier to detect cases that might otherwise be missed, enabling early intervention.

RCNN Conclusion

Using RCNN and hybrid-based models for object detection and segmentation in pneumonia detection ensures **precise, interpretable, and reliable diagnosis**. The bounding boxes or masks provide valuable visual cues that aid medical professionals in making informed decisions. These methods play a critical role in advancing AI-assisted healthcare by improving diagnostic efficiency and accuracy, especially in detecting subtle and complex patterns in medical images.

Hybrid RCNN(FASTER RCNN)

Using a Small dataset and image folders of 20 files

Using 20 images for Faster RCCN in _20 folder

```
seed = 42
num_classes = 2
batch_size = 2
train_img_size = 256
origin_img_size = 1024
scale_factor = train_img_size / origin_img_size
np.random.seed(seed)
rcnn_losses = ["loss_objectness", "loss_box_reg", "loss_rpn_box_reg"]
```

```
if _environment=="local":
    TRAIN_DIR = "stage_2_train_images_20"
    TEST_DIR = "stage_2_test_images_20"
    ROOT_DIR = "rsna-pneumonia-detection-challenge"
    LABELS_FILE = "stage_2_train_labels_20.csv"
    SUBMISSION_FILE = "stage_2_train_labels_20.csv" # stage_2_sample_submission.cs
if _environment=="colab":
    TRAIN_DIR = "stage_2_train_images_20"
```

Train /Test split from the small sample for Faster RCNN

Let's split our training dataset into training and validation sets. We leave a third of training samples for validation.

```
train_imgs = os.listdir(os.path.join(ROOT_DIR, TRAIN_DIR))
test_imgs =  [patienId + ".dcm" for patienId in pd.read_csv(os.path.join(ROOT_DIR, SUBMISSION_FILE
```

```
from sklearn.model_selection import train_test_split

train_imgs, valid_imgs = train_test_split(train_imgs, test_size=0.33, random_state=seed)

print(f"Number of training samples: {len(train_imgs)}")
print(f"Number of validation samples: {len(valid_imgs)}")
```

Reading the file with 20 records and correspondig folder with 20 images only and o

Re-scaling the image and deriving X1, Y1 and Area

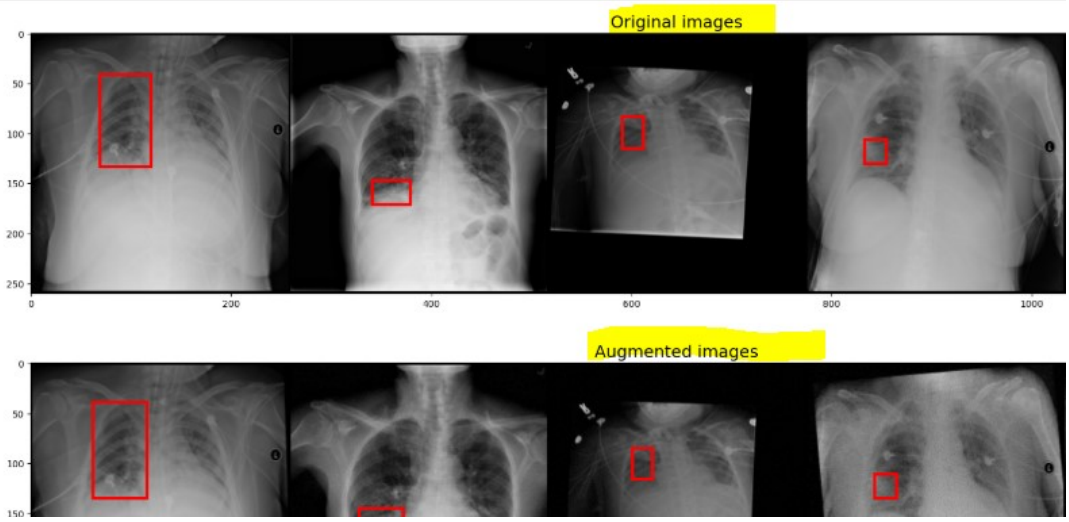
Our model require box coordinates in format X0, X1. We also multiply bounding box coordinates with scale_factor since we wil
size 256 instead of their original size 1024. R-CNN also require area of bounding box as input.

```
isna_count = len(train_label_df[train_label_df.Target == 0]) # number of images without bounding
train_label_df = train_label_df[train_label_df.Target == 1]
train_label_df.rename(columns={"x": "X0", "y": "Y0"}, inplace=True)
train_label_df["X1"] = train_label_df["X0"] + train_label_df["width"]
train_label_df["Y1"] = train_label_df["Y0"] + train_label_df["height"]
train_label_df[["X0", "X1", "Y0", "Y1"]] = train_label_df[["X0", "X1", "Y0", "Y1"]] * scale_facto
train_label_df["area"] = train_label_df["width"] * scale_factor * train_label_df["height"] * scal
train_label_df.drop(["width", "height"], axis=1, inplace=True)
train_label_df.head()
```

	patientId	X0	Y0	Target	X1	Y1	area
0	00436515-870c-4b36-a041-de91049b9ab4	66.00	38.00	1	119.25	132.75	5045.4375
1	00704310-78a8-4b38-8475-49f4573b2dbb	80.75	144.25	1	120.75	170.25	1040.0000

Augmented the images for Faster RCNN and display the images

```
augmented_batch = sample_batch[:5] + [process_batch(i, sample) for i, sample in enumerate(sample_b
plot_samples(augmented_batch, titles=["Original images", "Augmented images"], fig_size=(20, 10), n
del sample_batch, augmented_batch
```



Defining Faster RCNN Model

Faster RCMM Model

We will fine-tune a model trained on COCO dataset. For this purpose we have to replace model classifier with a new one adap
exploit Resnet50 as backbone. We incorporate our model into PyTorch lightning module. This way we can easily train and vali

In [145]:
```
import pytorch_lightning as pl
from torchvision.ops import nms
from torchvision.models.detection.faster_rcnn import FastRCNNPredictor


class LitRCNN(pl.LightningModule):
    def __init__(self, num_classes):
        super().__init__()

        model = torchvision.models.detection.fasterrcnn_resnet50_fpn(pretrained=True)
        in_features = model.roi_heads.box_predictor.cls_score.in_features
        model.roi_heads.box_predictor = FastRCNNPredictor(in_features, num_classes)

        self.model = model

    def forward(self, x):
        self.model.eval()

        outputs =  self.model(x)

```

Defined Metrix callback

]:
```
from pytorch_lightning import Callback
from pytorch_lightning.callbacks import ModelCheckpoint


class MetricsCallback(Callback):
    """PyTorch Lightning metric callback."""

    def __init__(self, metrics):
        super().__init__()
        self.metrics = metrics
        self.training = {}
        self.validations = {}

    def on_train_epoch_end(self, trainer, pl_module):
        self.training[trainer.current_epoch] = {metric: trainer.callback_metrics

    def on_validation_end(self, trainer, pl_module):
        self.validations[trainer.current_epoch] = {metric: trainer.callback_metr


checkpoint_callback = ModelCheckpoint(dirpath='checkpoints',
                                      filename='{epoch}-{val_loss:.4f}',
                                      every_n_epochs=1,
```

Trained the Model using only two Epocs

Training the model model_LiteRCNN

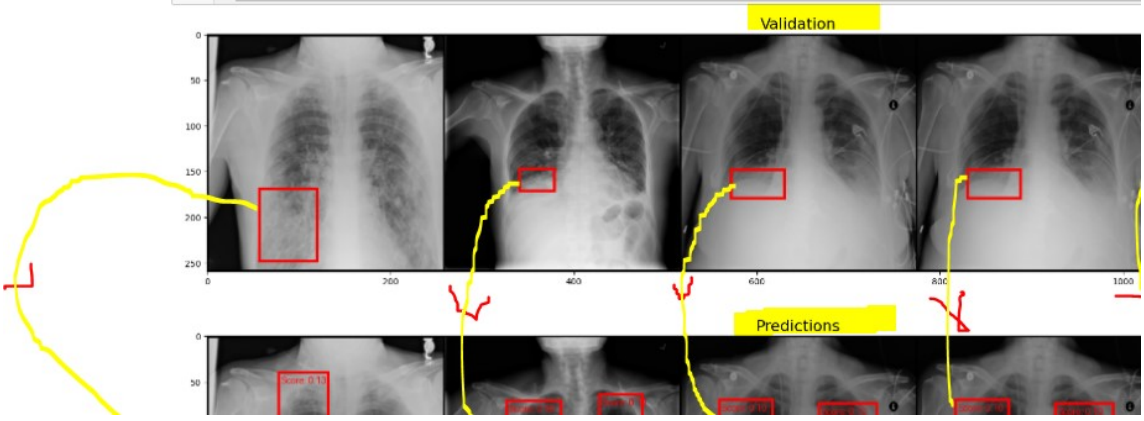
```
7]:  1 device = "gpu" if torch.cuda.is_available() else "cpu"
     2 trainer = pl.Trainer(accelerator=device, max_epochs=2, callbacks=callbacks)
     3 trainer.fit(model=model, train_dataloaders=train_loader, val_dataloaders=valid_loader)
```

```
GPU available: False, used: False
TPU available: False, using: 0 TPU cores
HPU available: False, using: 0 HPUs

  | Name  | Type       | Params | Mode
-------------------------------------------
0 | model | FasterRCNN | 41.3 M | train
-------------------------------------------
41.1 M    Trainable params
222 K     Non-trainable params
41.3 M    Total params
165.197   Total estimated model params size (MB)
189       Modules in train mode
0         Modules in eval mode
```

Display the prediction by FasterRCNN

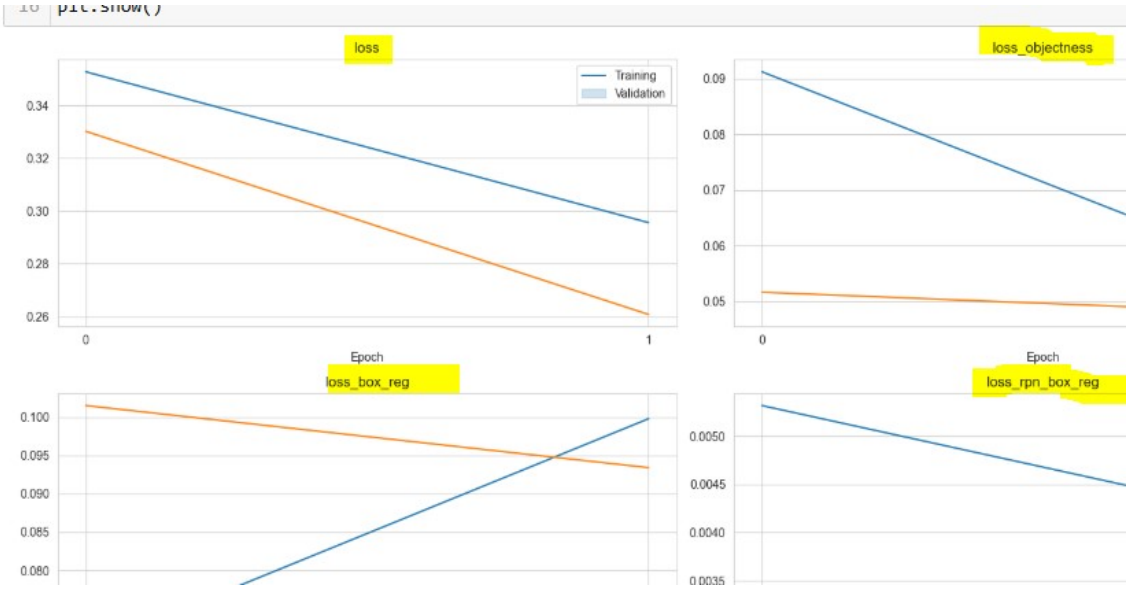
Evaluation or validaiton of Model (We used only 20 input sample if we use full sample , resu more better. ¶

```
[149]:  1 sample_batch_idx = np.random.choice(len(valid_imgs), size=5)
        2 sample_batch = read_images(np.array(valid_ds.img_names)[sample_batch_idx], train_label_df, (trair
        3
        4 preds = model([valid_ds[i][0] for i in sample_batch_idx])
        5 for i, pred in enumerate(preds):
        6     sample_batch.append((sample_batch[i][0],
        7                          torch.tensor(pred["boxes"], dtype=torch.int32),
        8                          pred["scores"]))
        9
       10 plot_samples(sample_batch, titles=["Validation", "Predictions"], fig_size=(20, 10), n_rows=2)
```



If you observe the Validation and Prediction, you will see all Validation boundary boxes have equivalent Prediction boxes, which means even though we took only 20 images our Model was able to predict the infected area and create a slightly bigger boundary box, which is a very positive result from our model and non of actual infection is missing.

Different loss in two EPOCHS, if we run for 10 or 20 EPOCS, we will get an improved result



Display the Submission or Predict Bounding box and Save it to Submission_outFile_20.csv

val_loss_rpn_box_reg 0.002800

In [153]:

```
preds = trainer.predict(model, test_loader)

outputs = []
for batch_pred in preds:
    for sample_pred in batch_pred:
        scores, boxes = sample_pred["scores"], sample_pred["boxes"]
        if len(scores) == 0:
            outputs.append(np.nan)
        else:
            label = ""
            boxes = boxes / scale_factor
            for score, box in zip(scores, boxes):
                label += f"{score:.2f} {box[0]:.1f} {box[1]:.1f} {(box[2]-box[0]):.1f} {(box[3]-bo
            outputs.append(label.strip())

submission = pd.read_csv(os.path.join(ROOT_DIR, SUBMISSION_FILE))
submission.PredictionString = outputs
submission.to_csv("submission_Outfile_20.csv", header=True, index=False)
submission
```

Predicting DataLoader 0: 100%

Out[153]:

	patientId	x	y	width	height	Target
0	00436515-870c-4b36-a041-de91049b9ab4	264	152	213	379	1
1	00704310-78a8-4b38-8475-49f4573b2dbb	323	577	160	104	1
2	00aecb01-a116-45a2-956c-08d2fa55433f	288	322	94	135	1
3	00c0b293-48e7-4e16-ac76-9269ba535a62	306	544	168	244	1
4	00f08de1-517e-4652-a04f-d1dc9ee48593	181	184	206	506	1
5	0100515c-5204-4f31-98e0-f35e4b00004a	703	416	84	77	1
6	010ccb9f-6d46-4380-af11-84f87397a1b8	652	437	161	293	1
7	012a5620-d082-4bb8-9b3b-e72d8938000c	133	613	275	275	1
8	0174c4bb-28f5-41e3-a13f-a396badc18bd	155	182	273	501	1
9	019d950b-dd38-4cf3-a686-527a75728be6	229	318	250	301	1
10	01a6eaa6-222f-4ea8-9874-bbd89dc1a1ce	141	306	225	327	1
11	01a7353d-25bb-4ff8-916b-f50dd541dccf	214	582	239	133	1
12	01adfd2f-7bc7-4cef-ab68-a0992752b620	225	415	98	101	1
13	01b9e362-4950-40f5-88fa-7557ac2a45bb	366	289	208	527	1
14	01be392f-a46d-4aef-a57e-9cd1a80dd47e	535	626	177	240	1

Faster RCNN Conclusion:-

In Milestone 2, first, we used RCNN to find the Bounding box, IOC and max region then did a prediction and compared the prediction with actual validation. For Hybrid, we used Faster RCNN and created a model. Trained and validated the Model. For both RCNN and Faster RCNN we used a subset of data as using 30K images takes a lot of time and resources for execution.

Pickel the Mode

Save the RCNN Model for future use:-

RCNN Modle Pickel

```
In [139]:  1  torch.save(rcnn, 'rcnn_model.pth')
```

Save the FAster RCNN Model for future use:-

Faster RCNN Pickle

```
In [164]:  1  # Save the model
           2  torch.save(model, 'fasterrcnn_model
```

Implications

---

1. **Impact on Business:**
    - **Cost Savings:** Hospitals and diagnostic centres can save costs by reducing dependency on manual labour and speeding up diagnostic workflows.
    - **Improved Service Delivery:** Faster and more accurate diagnosis enhances patient satisfaction and trust.
    - **Revenue Opportunities:** The solution can be commercialized as a SaaS (Software as a Service) or integrated into existing radiology platforms.
2. **Recommendations:**
    - **Confidence Levels:**
        - High confidence in the system's ability to assist radiologists in diagnosing pneumonia effectively.
        - Moderate confidence in complete automation without human oversight due to potential edge cases and ethical considerations.
    - **Recommended Actions:**
        - Integrate the solution with PACS (Picture Archiving and Communication Systems) for seamless deployment in hospitals.
        - Conduct further clinical validation with diverse datasets to improve generalizability.

Limitations

The limitations can be divided into three categories —**Data-Related**, **Model-Related**, and **Clinical and Ethical**. These encompass the main challenges faced in developing and deploying a deep-learning model for pneumonia detection using chest X-rays.

1. Data-Related Limitations

These limitations are primarily concerned with the availability, quality, and diversity of the data used for training and testing the model.

- **Limited Annotated Data**: Lack of sufficient labelled data, especially expert annotations, can hinder model training and performance.
- **Imbalanced Datasets**: The scarcity of pneumonia cases compared to normal cases can lead to bias toward predicting healthy results.
- **Diverse Imaging Techniques**: Variations in X-ray devices, protocols, and patient positioning can introduce inconsistencies in the dataset.
- **Presence of Artifacts**: X-rays can contain motion blur, exposure issues, or overlaid medical devices, which can confuse the model.

- **Demographic Differences**: Variability in patient demographics (age, gender, ethnicity) can impact how pneumonia appears in X-rays, affecting the model's ability to generalize across different groups.
- **Geographic Variability**: Pneumonia's presentation can differ regionally (e.g., bacterial vs. viral), potentially affecting model generalization.

2. Model-Related Limitations

These limitations are associated with the deep learning model itself, including its performance, robustness, and adaptability in real-world scenarios.

- **False Positives and False Negatives**: The model may misclassify healthy regions as pneumonia (false positives) or miss pneumonia in some cases (false negatives).
- **Complexity of Pneumonia Presentation**: Subtle or early-stage pneumonia may be difficult for the model to detect, leading to missed cases or incorrect diagnoses.
- **Other Lung Conditions**: The model may confuse pneumonia with other lung conditions that present similarly in X-rays (e.g., tuberculosis, lung cancer).
- **Generalization Across Populations**: The model may not perform well across diverse populations or regions due to differences in disease presentation.
- **Dependency on X-ray Quality**: The model may struggle to perform accurately on poor-quality or low-resolution X-ray images, limiting its robustness.
- **Model Updating**: Continuously updating the model to handle new data or evolving pneumonia types may be computationally expensive and challenging.

3. Clinical and Ethical Limitations

These limitations involve practical concerns around the deployment and use of the model in a healthcare setting, including trust, regulation, and ethical issues.

- **Trustworthiness**: Deep learning models are often seen as "black-box" systems, which can make it difficult for clinicians to trust their predictions without understanding how they concluded.
- **Model Reliability**: Healthcare professionals may be hesitant to rely on AI-based systems, particularly in critical cases where human expertise is traditionally trusted.

- **Regulatory and Medical Approval**: Obtaining regulatory approvals (e.g., FDA) for clinical use is time-consuming and requires proving the model's safety and effectiveness.
- **Bias and Equity**: Models may inadvertently exacerbate health disparities if trained on data that is not diverse or representative of all patient groups, leading to unequal healthcare outcomes.

4. Real-World Challenges

- **Interpretability Issues:** Clinicians may require transparent explanations for model decisions, which can be difficult with deep learning models.
- **Regulatory and Ethical Hurdles:** Approval from medical regulatory bodies (e.g., FDA) and ethical concerns about deploying AI without human oversight.

5. System Constraints

- **Computational Requirements:** Real-time inference in hospitals with limited computational resources can be challenging.

Enhancing the Solution

1. **Data Improvements:**
    - Collect a larger, more diverse dataset with annotations for pneumonia and other lung conditions.
    - Perform data augmentation to simulate variations and enhance model robustness.
2. **Model Enhancements:**
    - Use ensemble models combining RCNN with other architectures for better accuracy and generalizability.
    - Implement interpretability tools like Grad-CAM or SHAP to visualize and explain predictions.
3. **System Optimization:**

- Optimize the model for edge devices using techniques like quantization or pruning for deployment in low-resource settings.

4. **Clinical Integration:**
    - Collaborate with radiologists for feedback and iterative improvements.
    - Conduct prospective clinical trials to validate performance in real-world scenarios.

While a deep learning model for pneumonia detection in chest radiographs holds promise, it faces challenges related to data quality, model generalization, interpretability, and its ability to handle diverse and complex clinical cases. To mitigate these limitations, it is crucial to have high-quality, diverse datasets, as well as transparent, explainable models that can be trusted and understood by healthcare professionals.

Closing Reflection

---

1. Learnings:

- Importance of Domain Knowledge: Collaborating with medical experts is essential for understanding the nuances of pneumonia detection.
- Value of Iteration: Model performance improves significantly with iterative training and testing cycles, using diverse and realistic datasets.
- Need for Interpretability: Making AI predictions interpretable is critical for building trust among users.

2. What to Do Differently Next Time:

- Focus more on data diversity early in the project to reduce bias and improve model robustness.
- Allocate more resources to interpretability tools and user-friendly interfaces for clinicians.

- Involve end-users (radiologists) earlier in the design process to align the solution with practical needs.

By reflecting on these aspects, future projects can achieve greater accuracy, usability, and real-world impact.

Conclusion

This project explored the effectiveness of transfer learning for pneumonia detection using chest X-ray images. Three pre-trained CNN architectures (VGG16, MobileNetV2, and ResNet50) were fine-tuned and evaluated against a baseline model. The results indicate that transfer learning significantly improved the classification performance of all three models compared to their initial fine-tuning, achieving higher test accuracies.

First, we used RCNN to find the Bounding box, IOC and max region, then made a prediction and compared the prediction with actual validation. For Hybrid, we used Faster RCNN and created a model. Trained and validated the model. For both RCNN and Faster RCNN we used a subset of data as using 30K images takes a lot of time and resources for execution.

As Faster RCNN is an improved version of RCNN and takes fewer resources and instead of Selective Search uses Region based approach, **we recommend Faster RCNN** for this research and prediction.
