In [237]:
```
import xml.etree.ElementTree as ET
import pandas as pd
import numpy as np
import cv2
import matplotlib.pyplot as plt
#from tqdm.notebook import tqdm
import os
import re
import seaborn as sns
from tqdm import tqdm_notebook as tqdm
import warnings
warnings.filterwarnings('ignore')
from collections import defaultdict
#import tensorflow as tf
```

Loading Data

In [16]:
```
!gdown "https://drive.google.com/drive/u/0/my-drive"
```

```
/usr/local/lib/python2.7/dist-packages/gdown/parse_url.py:31: UserWarning: You
specified Google Drive Link but it is not the correct link to download the fil
e. Maybe you should try: https://drive.google.com/uc?id=None (https://drive.goo
gle.com/uc?id=None)
  .format(url='https://drive.google.com/uc?id={}'.format(file_id))
Downloading...
From: https://drive.google.com/drive/u/0/my-drive (https://drive.google.com/dri
ve/u/0/my-drive)
To: /content/my-drive
62.0kB [00:00, 1.99MB/s]
```

In [19]:
```
import shutil
shutil.unpack_archive("/content/NLMCXR_png.tgz","/content/NLMCXR_png")
```

In [ ]:
```
shutil.unpack_archive("/content/ecgen-radiology.zip")
```

In [ ]:
```
columns = ["image_id", "caption", "comparison", "indication", "findings", "i
df = pd.DataFrame(columns = columns)
```

In [20]:
```
len(os.listdir("/content/NLMCXR_png/"))
```

Out[20]: 7471

Extracting data from XML files

In [ ]:
```
for file in tqdm(os.listdir("ecgen-radiology/")):
    if file.endswith(".xml"):
        k = "ecgen-radiology/"
        path = k + file
        mytree = ET.parse(path)# parsing xml report
        comparision = mytree.find(".//AbstractText[@Label='COMPARISON']").te
        indication = mytree.find(".//AbstractText[@Label='INDICATION']").tex
        findings = mytree.find(".//AbstractText[@Label='FINDINGS']").text #
        impression = mytree.find(".//AbstractText[@Label='IMPRESSION']").tex

        mytree = ET.parse(path)
        for x in mytree.findall("parentImage"):
            image_id = x.attrib['id']+".png"
            filename = 'NLMCXR_png/' + image_id
            image = cv2.imread(filename) # reading image

            height, width, channels = image.shape
            caption = '' if x.find('caption').text is None else x.find('capt

            df = df.append(pd.Series([image_id, caption, comparision, indica
                                                        index = columns), i
```

```
HBox(children=(FloatProgress(value=0.0, max=3956.0), HTML(value='')))
```

In [ ]:
```
df.shape
```

Out[64]:
```
(7470, 8)
```

In [ ]:
```
1 df
```

Out[65]:

	image_id	caption	comparison	indication	findings	impression
0	CXR1082_IM-0058-1001.png	Chest x-XXXX XXXX and lateral performed on XXX...	Chest x-XXXX XXXX and lateral from XXXX.	XXXX year old female with abdominal pain.	Stable cardiomegaly. Stable tortuosity of the ...	Stable cardiomegaly with clear lungs.
1	CXR473_IM-2101-1001.png	PA and lateral chest.	None	preop for XXXX	None	Heart size normal. Lungs clear.
2	CXR473_IM-2101-1002.png	PA and lateral chest.	None	preop for XXXX	None	Heart size normal. Lungs clear.
3	CXR1883_IM-0572-1001.png	Xray Chest PA and Lateral	None.	XXXX onset of right-sided weakness for one XXXX.	Frontal and lateral views of the chest show no...	No acute or active cardiac, pulmonary or pleur...
4	CXR1883_IM-0572-2001.png	Xray Chest PA and Lateral	None.	XXXX onset of right-sided weakness for one XXXX.	Frontal and lateral views of the chest show no...	No acute or active cardiac, pulmonary or pleur...
...	...	...	...	...	...	...
7465	CXR2421_IM-0965-2001.png	CHEST 2V FRONTAL/LATERAL	None	Dyspnea	The heart is enlarged. The left subclavian ICD...	Stable moderate to marked cardiomegaly.
7466	CXR3165_IM-1490-1001.png	Chest x-XXXX, 2 views, XXXX, XXXX XXXX PM	XXXX	Dyspnea	Normal and stable cardiomediastinal contours. ...	Mildly improved XXXX XXXX opacities, which may...
7467	CXR3165_IM-1490-13013.png	Chest x-XXXX, 2 views, XXXX, XXXX XXXX PM	XXXX	Dyspnea	Normal and stable cardiomediastinal contours. ...	Mildly improved XXXX XXXX opacities, which may...
7468	CXR1108_IM-0075-1001.png	Xray Chest PA and Lateral	None.	SHORTNESS OF BREATH;	The lungs are clear and hyperinflated. Heart s...	Hyperinflated lungs. No acute cardiopulmonary ...
7469	CXR1108_IM-0075-2001.png	Xray Chest PA and Lateral	None.	SHORTNESS OF BREATH;	The lungs are clear and hyperinflated. Heart s...	Hyperinflated lungs. No acute cardiopulmonary ...

7470 rows × 8 columns

In [ ]:
```
1 df[df['image_id']=='CXR1_1_IM-0001-3001.png']
```

Out[66]:

	image_id	caption	comparison	indication	findings	impression	height	width
6086	CXR1_1_IM-0001-3001.png	Xray Chest PA and Lateral	None.	Positive TB test	The cardiac silhouette and mediastinum size ar...	Normal chest x-XXXX.	624	512

In [ ]:
```
1 df.shape
```

Out[53]: (7470, 8)

In [ ]:
```
1 def absolute_path(x):
2     '''Makes the path absolute '''
3     x = 'NLMCXR_png/'+ x
4     return x
5
6 df['Image_path'] = df['image_id'].apply(lambda x : absolute_path(x)) # makin
```

In [ ]:
```
1 df.head(5)
```

Out[69]:

	image_id	caption	comparison	indication	findings	impression	height	width	
0	CXR1082_IM-0058-1001.png	Chest x-XXXX XXXX and lateral performed on XXX...	Chest x-XXXX XXXX and lateral from XXXX.	XXXX year old female with abdominal pain.	Stable cardiomegaly. Stable tortuosity of the ...	Stable cardiomegaly with clear lungs.	624	512	NLM
1	CXR473_IM-2101-1001.png	PA and lateral chest.	None	preop for XXXX	None	Heart size normal. Lungs clear.	510	512	NLM
2	CXR473_IM-2101-1002.png	PA and lateral chest.	None	preop for XXXX	None	Heart size normal. Lungs clear.	601	512	NLM
3	CXR1883_IM-0572-1001.png	Xray Chest PA and Lateral	None.	XXXX onset of right-sided weakness for one XXXX.	Frontal and lateral views of the chest show no...	No acute or active cardiac, pulmonary or pleur...	502	512	NLM
4	CXR1883_IM-0572-2001.png	Xray Chest PA and Lateral	None.	XXXX onset of right-sided weakness for one XXXX.	Frontal and lateral views of the chest show no...	No acute or active cardiac, pulmonary or pleur...	512	512	NLM

In [ ]:

```
count = 1
fig = plt.figure(figsize=(15,35))

for filename in df['Image_path'].values[95:100]:
    findings = list(df["findings"].loc[df["Image_path"] == filename].values)
    img = cv2.imread(filename)
    ax = fig.add_subplot(5, 2 , count , xticks=[], yticks=[])
    ax.imshow(img)
    count += 1
    ax = fig.add_subplot(5 ,2 ,count)
    plt.axis('off')
    ax.plot()
    ax.set_xlim(0,1)
    ax.set_ylim(0, len(findings))
    for i, f in enumerate(findings):
        ax.text(0,i,f,fontsize=20)
    count += 1
plt.show()
```

No focal lung consolidation. Heart size and pulmonary vascularity are within normal limits. No pneumothorax or pleural effusion. Osseous structures are grossly intact.

No focal lung consolidation. Heart size and pulmonary vascularity are within normal limits. No pneumothorax or pleural effusion. Osseous structures are grossly intact.

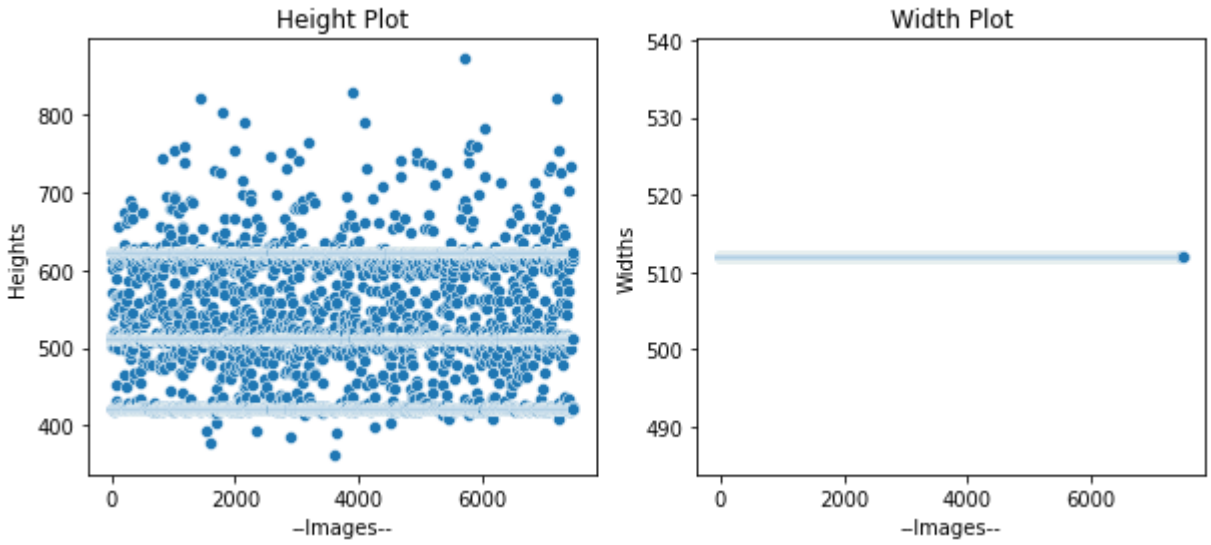
The heart and lungs have XXXX XXXX in the interval. Both lungs are clear and expanded. Heart and mediastinum normal. No change right anterior soft tissue surgical clips. Configuration of breast shadows on the PA view suggests prior right lumpectomy.

The heart and lungs have XXXX XXXX in the interval. Both lungs are clear and expanded. Heart and mediastinum normal. No change right anterior soft tissue surgical clips. Configuration of breast shadows on the PA view suggests prior right lumpectomy.

Negative for cardiac enlargement or vascular congestion. Minimal subsegmental atelectasis at the left base otherwise negative for focal confluent airspace disease. The visualized bony structures are intact. There are minimal degenerative disc changes of the mid/lower thoracic spine. No pneumothorax.

In [ ]:
```
plt.figure(figsize=(10,4))
plt.subplot(121)
plt.title('Height Plot')
plt.ylabel('Heights')
plt.xlabel('--Images--')
sns.scatterplot(range(len(df.height.values)), df.height.values)
plt.subplot(122)
plt.title('Width Plot')
plt.ylabel('Widths')
plt.xlabel('--Images--')
sns.scatterplot(range(len(df.width.values)), df.width.values)
```

Out[71]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7ff023da0550>
```



In [ ]:
```
# number of missing values
df.isnull().sum()
```

Out[72]:
```
image_id         0
caption          0
comparison    1157
indication     159
findings       997
impression      52
height           0
width            0
Image_path       0
dtype: int64
```

In [ ]:
```
1 data = df[['image_id','findings','height','width','Image_path']]
```

In [ ]:
```
1 data.shape
```

Out[74]:
```
(7470, 5)
```

In [ ]:
```
1 data.isnull().sum()
```

Out[75]:
```
image_id        0
findings      997
height          0
width           0
Image_path      0
dtype: int64
```

In [ ]:
```
1 data = data.dropna(axis=0) # drop all missing value rows
```

In [ ]:
```
1 data.shape
```

Out[77]:
```
(6473, 5)
```

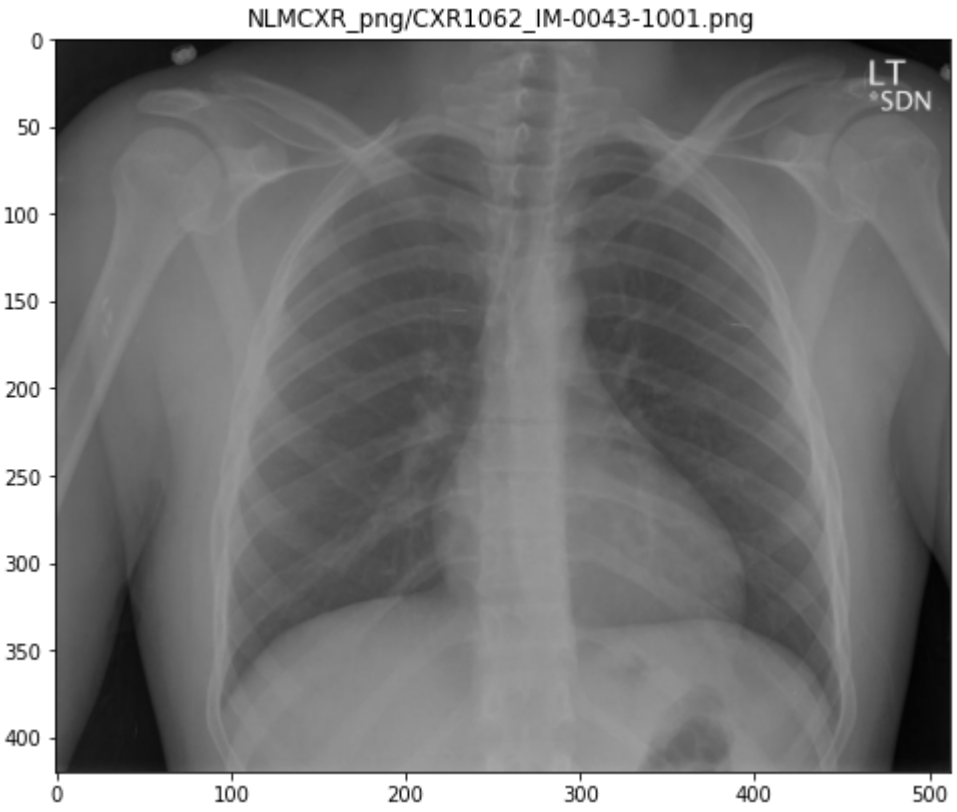
In [ ]:
```
1 data.isnull().sum()
```

Out[78]:
```
image_id      0
findings      0
height        0
width         0
Image_path    0
dtype: int64
```

In [ ]:
```
plt.figure(figsize=(8,7))
img = cv2.imread(data['Image_path'].values[5])
plt.imshow(img)
plt.title(data['Image_path'].values[5])

data['findings'].values[5]
```

Out[79]: 'XXXX XXXX and lateral chest examination was obtained. The heart silhouette is normal in size and contour. Aortic XXXX appear unremarkable. Lungs demonstrate no acute findings. There is no effusion or pneumothorax. No displaced rib fracture visualized.'



In [ ]:
```
1 data.Image_path
```

Out[81]:
```
0        NLMCXR_png/CXR1082_IM-0058-1001.png
3        NLMCXR_png/CXR1883_IM-0572-1001.png
4        NLMCXR_png/CXR1883_IM-0572-2001.png
5        NLMCXR_png/CXR2431_IM-0973-1001.png
6        NLMCXR_png/CXR2431_IM-0973-2001.png
                        ...
7465     NLMCXR_png/CXR2421_IM-0965-2001.png
7466     NLMCXR_png/CXR3165_IM-1490-1001.png
7467    NLMCXR_png/CXR3165_IM-1490-13013.png
7468     NLMCXR_png/CXR1108_IM-0075-1001.png
7469     NLMCXR_png/CXR1108_IM-0075-2001.png
Name: Image_path, Length: 6473, dtype: object
```

In [ ]:
```
1  images = {}
2  findings = {}
3
4  for img,fin in data[['Image_path','findings']].values:
5      a = img.split('.')
6      file_type = a[-1]
7      a = a[0].split('-')
8      a.pop(len(a)-1)
9      a = ('-'.join(e for e in a))
10     if a not in images.keys():
11         images[a] = 1
12         findings[a] = fin
13     else:
14         images[a] += 1
15         findings[a] = fin
```

In [ ]:
```
1 images['NLMCXR_png/CXR1001_IM-0004'],findings['NLMCXR_png/CXR1001_IM-0004']
```

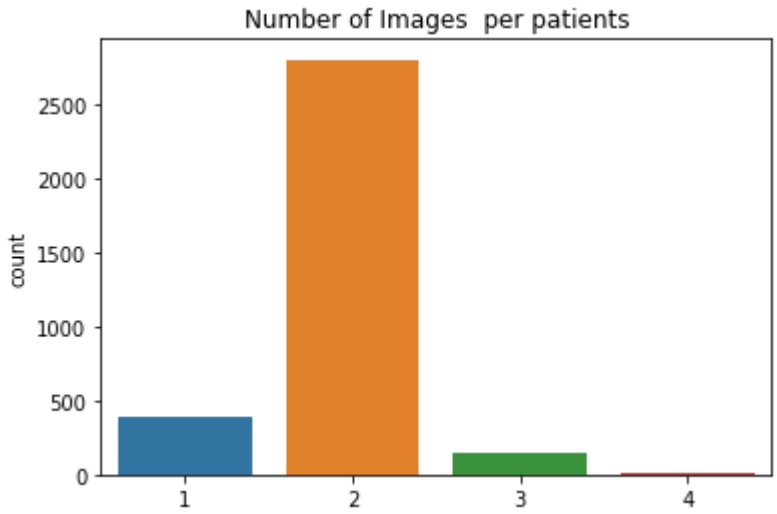
Out[83]:
```
(2,
 'Interstitial markings are diffusely prominent throughout both lungs. Heart si
ze is normal. Pulmonary XXXX normal.')
```

In [ ]:
```
1 print('Total Number of Unique_IDs :', len(images.keys()))
```

```
Total Number of Unique_IDs : 3350
```

In [ ]:
```
plt.title('Number of Images  per patients')
sns.countplot(list(images.values()))
```

Out[86]: <matplotlib.axes._subplots.AxesSubplot at 0x7ff02fbd7128>



In [ ]:
```
def train_test_split(data):
    persons = list(data.keys())
    persons_train = persons[:2500]
    persons_cv = persons[2500:3000]
    persons_test = persons[3000:3350]
    return persons_train, persons_cv, persons_test

images_train, images_cv, images_test = train_test_split(images)
```

In [ ]:
```
def combining_images(image_set):

    image_per_person = defaultdict(list)  # creating a list of dictionary to
                                          #corresponding to a person_id
    for pid in image_set:
        for img in data['Image_path'].values:
            if pid in img:
                image_per_person[pid].append(img)
            else:
                continue
    return image_per_person
```

In [ ]:
```
img_per_person_train = combining_images(images_train)
img_per_person_cv = combining_images(images_cv)
img_per_person_test = combining_images(images_test)
```

In [ ]:
```
img_per_person_train['NLMCXR_png/CXR1001_IM-0004']
```

Out[95]:
```
['NLMCXR_png/CXR1001_IM-0004-1001.png', 'NLMCXR_png/CXR1001_IM-0004-1002.png']
```

In [ ]:
```
def load_image(file):
    img = cv2.imread(file)
    return img
```

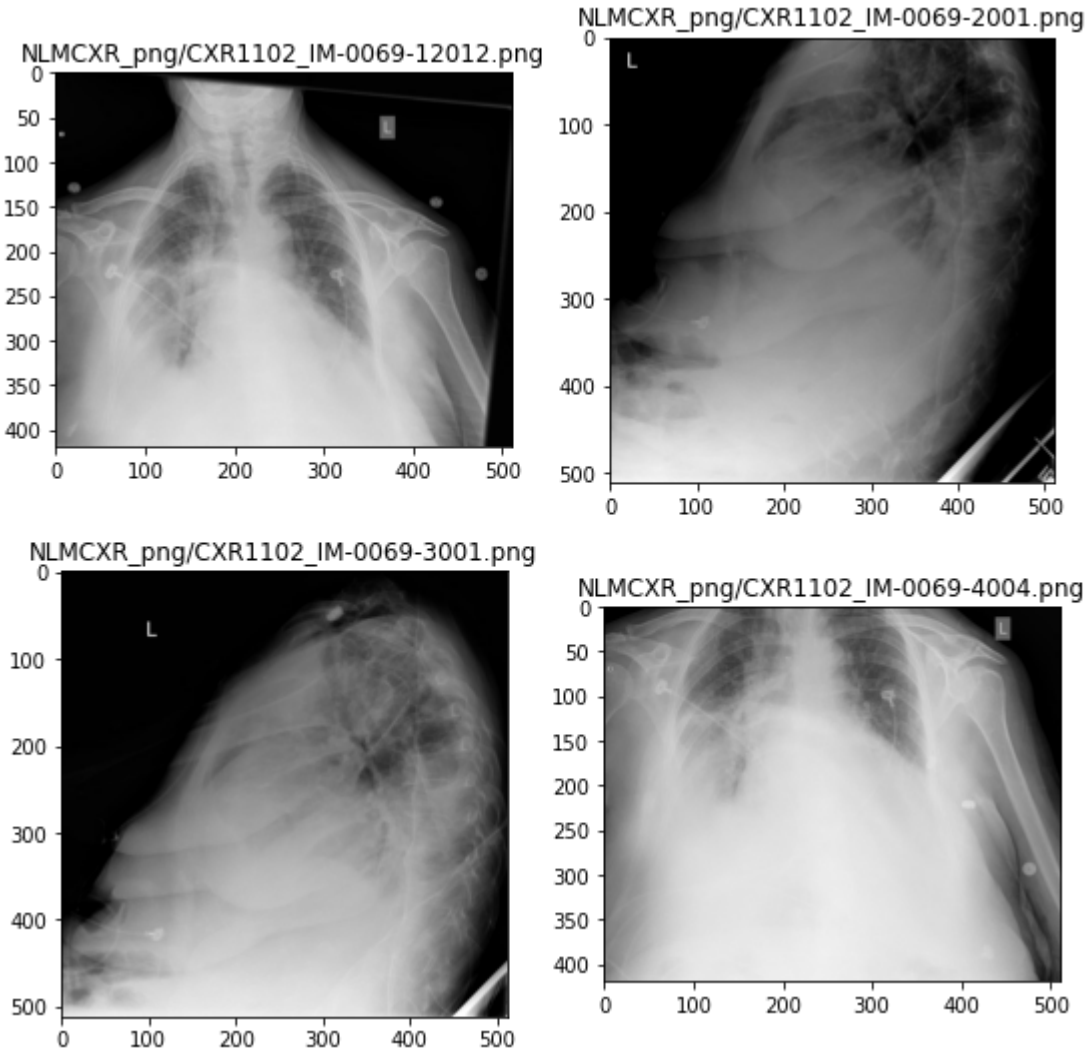
In [ ]:
```
# just checking the ID which has 4 images
for k,v in images.items():
    if v == 4:
        print(k)
        break

```

```
NLMCXR_png/CXR1102_IM-0069
```

In [ ]:
```
plt.figure(figsize=(9,9))
plt.subplot(221)
plt.imshow(load_image('NLMCXR_png/CXR1102_IM-0069-12012.png'))
plt.title('NLMCXR_png/CXR1102_IM-0069-12012.png')
plt.subplot(222)
plt.imshow(load_image('NLMCXR_png/CXR1102_IM-0069-2001.png'))
plt.title('NLMCXR_png/CXR1102_IM-0069-2001.png')
plt.subplot(223)
plt.imshow(load_image('NLMCXR_png/CXR1102_IM-0069-3001.png'))
plt.title('NLMCXR_png/CXR1102_IM-0069-3001.png')
plt.subplot(224)
plt.imshow(load_image('NLMCXR_png/CXR1102_IM-0069-4004.png'))
plt.title('NLMCXR_png/CXR1102_IM-0069-4004.png')
```

Out[98]: Text(0.5, 1.0, 'NLMCXR_png/CXR1102_IM-0069-4004.png')



2 side view and 2 front view images for the same ID

Sample chest scans of a person(4 images)

Now, we have multiple chest scans to produce a single report. Some person_ids have 1, some have 2 and the highest is 4. So we can take pairs of those images as input. If it has only one image, then it can be replicated.

Data Preperation

In [ ]:

```
import itertools

def create_data(image_per_person):
    # new dataset
    person_id, image1, image2, report = [],[],[],[]
    for pid, imgs in image_per_person.items():   #contains pid and the image

        if len(imgs) == 1:
            image1.append(imgs[0])
            image2.append(imgs[0])
            person_id.append(pid)
            report.append(findings[pid])
        else:
            num = 0
            a = itertools.combinations(imgs, 2)
            for i in a:
                image1.append(i[0])
                image2.append(i[1])
                person_id.append(pid + '_' + str(num))
                report.append(findings[pid])
                num += 1
    data = pd.DataFrame()
    data['Person_id'] = person_id
    data['Image1'] = image1
    data['Image2'] = image2
    data['Report'] = report

    return data
```

In [ ]:
```
train = create_data(img_per_person_train)
test = create_data(img_per_person_test)
cv = create_data(img_per_person_cv)
```

In [ ]:
```
train.head()
```

Out[101]:

	Person_id	Image1	Image2	Report
0	NLMCXR_png/CXR1082_IM-0058	NLMCXR_png/CXR1082_IM-0058-1001.png	NLMCXR_png/CXR1082_IM-0058-1001.png	Stable cardiomegaly. Stable tortuosity of the ...
1	NLMCXR_png/CXR1883_IM-0572_0	NLMCXR_png/CXR1883_IM-0572-1001.png	NLMCXR_png/CXR1883_IM-0572-2001.png	Frontal and lateral views of the chest show no...
2	NLMCXR_png/CXR2431_IM-0973_0	NLMCXR_png/CXR2431_IM-0973-1001.png	NLMCXR_png/CXR2431_IM-0973-2001.png	Lungs are clear. No focal airspace consolidati...
3	NLMCXR_png/CXR1062_IM-0043	NLMCXR_png/CXR1062_IM-0043-1001.png	NLMCXR_png/CXR1062_IM-0043-1001.png	XXXX XXXX and lateral chest examination was ob...
4	NLMCXR_png/CXR224_IM-0837_0	NLMCXR_png/CXR224_IM-0837-1001.png	NLMCXR_png/CXR224_IM-0837-2001.png	Clear lungs. Normal heart. No pneumothorax. No...

In [ ]:
```
train.to_csv('train.csv')
test.to_csv('test.csv')
cv.to_csv('cv.csv')
```

Preporcessing text data

In [ ]:

```
def lowercase(text):
    '''Converts to lowercase'''
    new_text = []
    for line in text:
        new_text.append(line.lower())
    return new_text

def decontractions(text):
    '''Performs decontractions in the doc'''
    new_text = []
    for phrase in text:
        phrase = re.sub(r"won't", "will not", phrase)
        phrase = re.sub(r"can\'t", "can not", phrase)
        phrase = re.sub(r"couldn\'t", "could not", phrase)
        phrase = re.sub(r"shouldn\'t", "should not", phrase)
        phrase = re.sub(r"wouldn\'t", "would not", phrase)
        # general
        phrase = re.sub(r"n\'t", " not", phrase)
        phrase = re.sub(r"\'re", " are", phrase)
        phrase = re.sub(r"\'s", " is", phrase)
        phrase = re.sub(r"\'d", " would", phrase)
        phrase = re.sub(r"\'ll", " will", phrase)
        phrase = re.sub(r"\'t", " not", phrase)
        phrase = re.sub(r"\'ve", " have", phrase)
        phrase = re.sub(r"\'m", " am", phrase)
        phrase = re.sub(r"\*+", "abuse", phrase)
        new_text.append(phrase)

    return new_text

def rem_punctuations(text):
    '''Removes punctuations'''
    punctuations = '''!()-[]{};:'"\,<>/?@#$%^&*~''' # full stop is not remov
    new_text = []
    for line in text:
        for char in line:
            if char in punctuations:
                line = line.replace(char, "")
        new_text.append(' '.join(e for e in line.split()))
    return new_text

def rem_numbers(text):
    '''Removes numbers and irrelevant text like xxxx*'''
    new_text = []
    for line in text:
        temp = re.sub(r'x*','',line)
        new_text.append(re.sub(r'\d','',temp))
    return new_text

def words_filter(text):
    '''Removes words less than 2 characters except no and ct'''
    new_text = []
    for line in text:
        temp = line.split()
        temp2 = []
        for word in temp:
```

```
            if  len(word) <=2 and word != 'no' and word != 'ct':
                continue
            else:
                temp2.append(word)
        new_text.append(' '.join(e for e in temp2))
    return new_text

def multiple_fullstops(text):
    ''' Removes multiple full stops from the text'''
    new_text = []
    for line in text:
        new_text.append(re.sub(r'\.\.+', '.', line))
    return new_text

def fullstops(text):
    new_text = []
    for line in text:
        new_text.append(re.sub('\.', ' .', line))
    return new_text

def multiple_spaces(text):
    new_text = []
    for line in text:
        new_text.append(' '.join(e for e in line.split()))
    return new_text

def separting_startg_words(text):
    new_text = []
    for line in text:
        temp = []
        words = line.split()
        for i in words:
            if i.startswith('.') == False:
                temp.append(i)
            else:
                w = i.replace('.','. ')
                temp.append(w)
        new_text.append(' '.join(e for e in temp))
    return new_text

def rem_apostrophes(text):
    new_text = []
    for line in text:
        new_text.append(re.sub("'",'',line))
    return new_text
```

In [ ]:
```
def text_preprocessing(text):
    '''Combines all the preprocess functions'''
    new_text = lowercase(text)
    new_text = decontractions(new_text)
    new_text = rem_punctuations(new_text)
    new_text = rem_numbers(new_text)
    new_text = words_filter(new_text)
    new_text = multiple_fullstops(new_text)
    new_text = fullstops(new_text)
    new_text = multiple_spaces(new_text)
    new_text = separting_startg_words(new_text)
    new_text = rem_apostrophes(new_text)
    return new_text
```

In [ ]:
```
train['Report'] = text_preprocessing(train['Report'])
test['Report'] = text_preprocessing(test['Report'])
cv['Report'] = text_preprocessing(cv['Report'])
```

In [ ]:
```
1 train
```

Out[106]:

	Person_id	Image1	Image2	Re
0	NLMCXR_png/CXR1082_IM-0058	NLMCXR_png/CXR1082_IM-0058-1001.png	NLMCXR_png/CXR1082_IM-0058-1001.png	s cardiomeg stable tortu th
1	NLMCXR_png/CXR1883_IM-0572_0	NLMCXR_png/CXR1883_IM-0572-1001.png	NLMCXR_png/CXR1883_IM-0572-2001.png	frontal and la views the c show nor
2	NLMCXR_png/CXR2431_IM-0973_0	NLMCXR_png/CXR2431_IM-0973-1001.png	NLMCXR_png/CXR2431_IM-0973-2001.png	lungs are c no focal airs consol
3	NLMCXR_png/CXR1062_IM-0043	NLMCXR_png/CXR1062_IM-0043-1001.png	NLMCXR_png/CXR1062_IM-0043-1001.png	and lateral c eamination obtainec
4	NLMCXR_png/CXR224_IM-0837_0	NLMCXR_png/CXR224_IM-0837-1001.png	NLMCXR_png/CXR224_IM-0837-2001.png	clear lu normal hear pneumotho
...	...	...	...	
2759	NLMCXR_png/CXR2725_IM-1186_0	NLMCXR_png/CXR2725_IM-1186-1001.png	NLMCXR_png/CXR2725_IM-1186-2001.png	cardiac medias contour within
2760	NLMCXR_png/CXR728_IM-2287_0	NLMCXR_png/CXR728_IM-2287-1001.png	NLMCXR_png/CXR728_IM-2287-2001.png	the int diameter nc has devel
2761	NLMCXR_png/CXR943_IM-2439_0	NLMCXR_png/CXR943_IM-2439-3003.png	NLMCXR_png/CXR943_IM-2439-5005.png	heart cardiomedias silhouette
2762	NLMCXR_png/CXR3379_IM-1627_0	NLMCXR_png/CXR3379_IM-1627-1001.png	NLMCXR_png/CXR3379_IM-1627-2001.png	no pneumot large pl effusion . bo
2763	NLMCXR_png/CXR2565_IM-1068_0	NLMCXR_png/CXR2565_IM-1068-1002.png	NLMCXR_png/CXR2565_IM-1068-1003.png	the heart nc size . the tortuou

2764 rows × 4 columns

In [ ]:
```
1 train.to_csv('processed_train.csv')
2 test.to_csv('processed_test.csv')
3 cv.to_csv('processed_cv.csv')
```

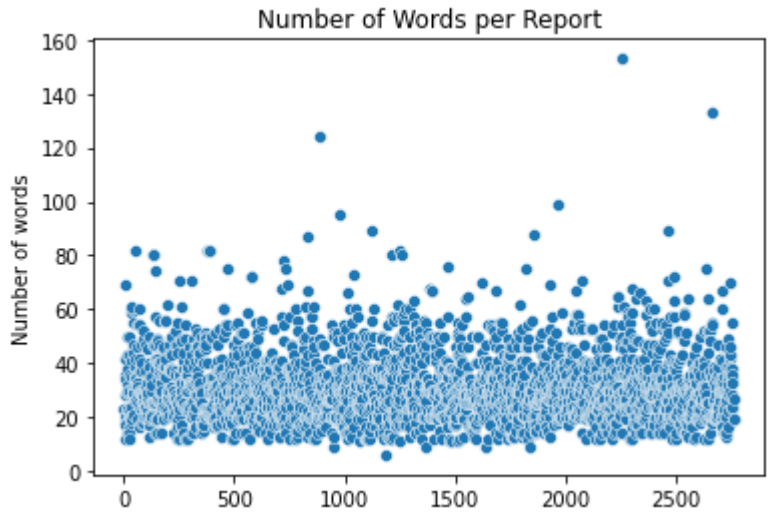
In [ ]:
```
1 l = [len(e.split()) for e in train['Report'].values]  # Number of words in e
```

In [ ]:
```
print('maximum word in a report is :',max(l))
```

```
maximum word in a report is : 153
```

In [ ]:
```
plt.title('Number of Words per Report')
sns.scatterplot(range(train.shape[0]), l)
plt.ylabel('Number of words')
```

Out[111]:
```
Text(0, 0.5, 'Number of words')
```



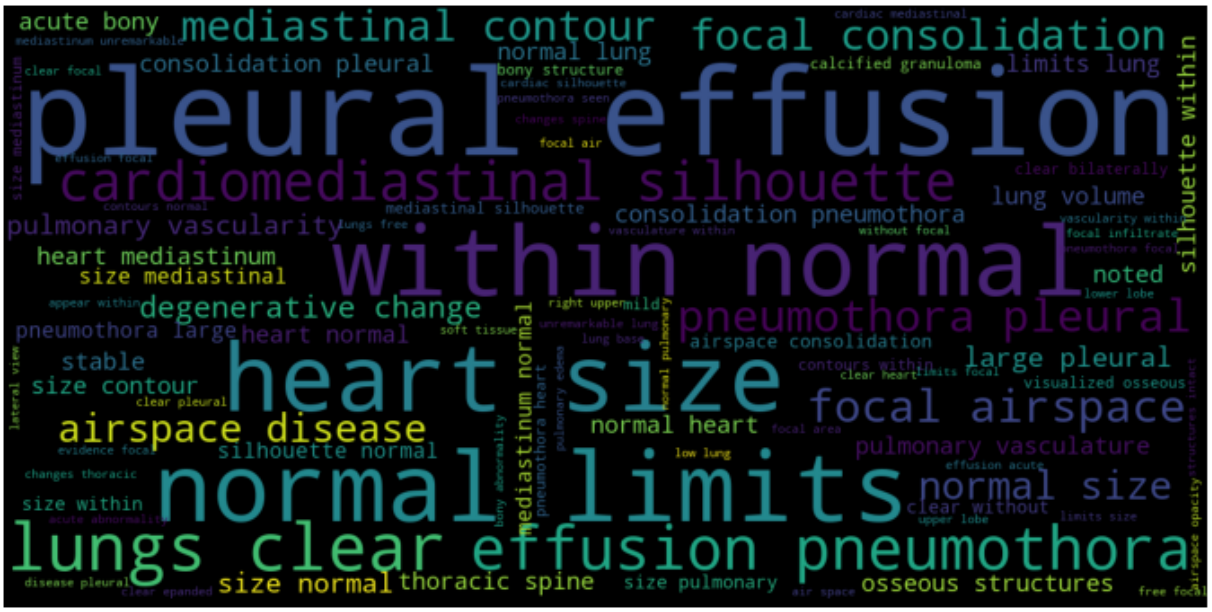
Most of the reports contain word count below 100

In [ ]:
```
from wordcloud import WordCloud
def show_wordcloud(data, title = None):
    wordcloud = WordCloud(background_color='black',max_words=800,max_font_si

    fig = plt.figure(1, figsize=(12, 15))
    plt.axis('off')
    if title:
        fig.suptitle(title, fontsize=20)
        fig.subplots_adjust(top=2.3)

    plt.imshow(wordcloud)
    plt.show()

show_wordcloud(train['Report'])
```



In [ ]:
```
countword = train['Report'].str.split().apply(len).value_counts()
countword[:].plot(kind='bar',figsize=(20,5) , title = 'Words for each findin
```

Out[120]: <matplotlib.axes._subplots.AxesSubplot at 0x7ff022586358>

In [ ]:
```
def remodelling(x):
    '''adds start and end tokens to a sentence '''
    return 'startseq' + ' ' + x + ' ' + 'endseq'
```

In [ ]:
```
train['Report'] = train['Report'].apply(lambda x : remodelling(x))
test['Report'] = test['Report'].apply(lambda x : remodelling(x))
cv['Report'] = cv['Report'].apply(lambda x : remodelling(x))
```

Exporting final dataset to csv file

In [ ]:
```
# save the cleaned data(STRUCTURED DATA)
train.to_csv('Final_Train_Data.csv', index=False)
test.to_csv('Final_Test_Data.csv', index=False)
cv.to_csv('Final_CV_Data.csv', index=False)
```