Lung cancer detection : Classification of CT images using 3D CNN

Submited by Group 34

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***Abstract*—Lung Cancer is a malignant lung tumor originating from the uncontrolled growth of abnormal cells in the tissues of the lungs. Lung Cancer is one of the leading cause for cancer related deaths, also being one of the most commonly diagnosed cancer in the world. Ofcourse, the diagnosis of cancer is confirmed with other clinical tests which includes different sample examinations. However, for the people with high risk, CT scan stands as the better early detection method. But it is observed that for the same CT scan, when marked for potential lung nodules, they vary from radiologist to radiologist, where a radiologist goes through a CT scan and gets a 3D view of the lung by imagining. So, we're trying to leverage deep learning models to replace the work that is usually done by humans (radiologist). We train a model to predict the same, that will help detect and if present, locate maximum potential nodules, as with 3D-CNN technique we can train the model to extract and highlight required features in 3D. We're going with a different data set, with the intent of getting better results than what is previously achieved.**

***Index Terms*—CNN, Lung Nodule, CT Scan**

I. Introduction

The condition where Malignant unbalanced tumor which has uncontrollable growth, which progresses by invading the nearby healthy cells of lungs and sometimes to other organs is considered as lung cancer.

Lung Cancer is the most common cause of death from cancer with over 1.7 million deaths reported every year across the globe, leading to be the second most commonly diagnosed cancer across the globe with more than 2 million new cases arising every year. [1]. There isn't any exact cause for lung cancer, but there are some risk factors which may lead to lung cancer. The first on the list is Smoking, around 80% of the cases are due to direct Smoking or Secondhand Smoking. The other reasons may be due to exposure to harmful gases, like radon, diesel exhaust, and certain chemical emissions. In few cases even genetics play a role, by inheriting genes that lead to mutated cells which increases the chances of getting affected with cancer, and exposure to certain environments may lead to mutation of genes/cells which may lead to cancer [2].

When the cancer grows to an extent at which it blocks the airways, the people affected experience shortness of breath. This may worsen when the fluid starts accumulating in the region of affected lung, this condition is called pleural effusion. People can even develop a condition called hemoptysis, which causes bleeding in the air-way and coughing up blood. As any other cancer lung cancer also comes with severe pain in advanced stages. It is often observed that lung cancer spreads to other organs, such as Lymph nodes, Brain, Liver, Bone, Adrenaline Gland [3].

Though, the diagnosis of cancer is confirmed with other clinical tests which include different sample examinations. However, for the people with high risk, CT scan stands as the better early detection method due to its [4] asymptomaticity in the early stage and also for the diagnosed it helps in locating the cancerous nodules.

The survival rate for the diagnosed is about 57% when they are at stage I, whereas it is only 4% at stage IV. However only $\frac{1}{3}$ of the new cases are detected in stage I/II, it is expected that $\frac{2}{3}$ of the cases can be detected if screening is implemented [1]. Hence this model which uses low dose CT scans for screening has potential to save one's life and also to find the cancerous regions of the diagnosed.

With the help of Deep Neural Networks, which are effective in pattern recognition and image classification, cell growth region from the CT scans is obtained for diagnosis. According to [5] Convolution Neural Networks outperforms already existing DNN algorithms(APAC, Batch Normalisation maxout network, multi-column DNN, etc), as the only necessary information is passed on to further layers which increase the computation speed significantly.

In Computer Vision, CNN is designed to specifically learn the required important features and extract high-level features in deeper layers by applying different relevant filters.

In 2D CNN, the kernel(convolutional filter) convolves over the input(CT image) in two directions and gets a weighted-sum matrix of lower dimensions(feature map). Then the RELU activation function is used; after a certain value termed thresh-old, it is a linear function (x=y), else Zero. The max-pooling layer is next applied, which effectively decreases the dimension by extracting the maximum value from the window region. The last pooling layer's output is then delivered to the dense layer, which flattens it before sending it to the final connected layer.The last pooling output layer is then attached by the final connected layer, which has different activation functionality called softmax that generates probability distributions.These are the extracted features of the image, these are mapped to the final output i.e,malignant or benign.

In 3D CNN the entire architecture is the same where the input and kernels are in 3D and the features are now extracted in 3D fashion. The kernel convolves over the dataset in 3 directions. The output feature map is also a 3D matrix.

II. Problem Statement

It is observed that for the same CT scan, when marked for potential lung nodules, they vary from radiologist to radiologist, where a radiologist goes through a CT scan and gets a 3D view of the lung by imagining. So, this paper aims to leverage deep learning models to replace the work that is usually done by humans (Radiologist). The paper aims to train a model to predict the same, that will help detect and if present, locate maximum potential nodules, as with 3D-CNN technique we can train the model to extract and highlight required features in 3D.

III. Literature Review

A. Yung Su et al. [6]

They build an optimised faster RCNN framework where the following information is deduced, which helps in easy understanding of model and key points from the paper

1) Approach: Optimised faster R-CNN

2) Classification: Due to deep learning's high performance and extensive feature extraction, the Faster R-CNN-Classic detection algorithm is utilized for classification, and the ZF model and VGG(excellent feature extraction network) 16 model are employed as feature extractors.

3) Evaluation metrics: Average Precision(AP) and Precision-Recall graph

4) Pros: Optimised Faster R-CNN model used showed more AP.

5) Cons/Future Scope: As it is a Small and old data set model training can be improved with other bigger and new datasets. Benign small nodules are not marked in this dataset, which have potential to turn into malignant. And also 3D CNN can be used for better detection

6) Dataset used: LIDC-IDRI data set

B. Prasad Dutande et al. [7]

They used a combination of both 2D and 3D CNN

1) Approach: 2D-3D cascaded CNN

2) Segmentation: SquEx-UNet is used, which is an improvised version of UNet that extracts fine-grained information to segment nodules.

3) Classification: Nodule detection is accomplished using a 2D-3D cascaded CNN. In addition, 3D-NodNet distinguishes between nodules and non-nodule volumetric cubes, as MIP failed to achieve superior segmentation.

4) Metrics for evaluation: For nodule segmentation, Dice-Coefficient metrics is 0.80 . The identification of nodules has a sensitivity of 90.1

5) Pros: Used the standard CAD segmentation and classification methods, such as the first 2D patch based CNN for segmentation, 3D CNN for nodule classification, and a cascaded segmentation and classification pipeline for detection, which resulted in efficiently segmented nodules.

6) Drawbacks/Future Scope: The uneven shape of nodules requires more exact segmentation. Coughing, dyspnea, bronchitis, rust-colored sputum, body weight loss, pneumonia, and swelling of feet are all physiological indicators which indeed improves the efficacy and potency of CNNs involved in the earlier stages of the cancer.

7) Dataset used: Indian Lung CT image dataset(ILCID) independent dataset not available online LNDb dataset accessible only for participants.

C. Eali Stephen Neal Joshua et al. [8]

They used GradCAM for better reliability on the model

1) Methodology: For visual assistance, they used 3D AlexNet with Grad-CAM (gradient weighted class activation mapping).

2) Classification: The following architecture was used to classify nodules as malignant or benign using an improvised 3D AlexNet with lightweight design.

3) Evaluation metrics: On this dataset, the evaluation criteria were Classification Accuracy of 97.17 %. Other metrics used are Area Under Curve(AUC) of Receiver Operator Characteristic (ROC).

4) Advantages: They claimed that this was the initial research to employ 3D AlexNet to classify lung flaws.The use of GradCAM increases the model's credibility among radiologists. GradCAM's visual insights assist us in determining where and why the model is failing. We can solve the problem and get better outcomes by modifying the architecture.

5) Drawbacks/Future Scope: They intend to use Capsule Neural Network, which employs class equivalence for storing and emulate the human visual system,and is also better than CNN when working with smaller datasets.

6) Dataset used: Luna 16

D. Aryan Mobiny et al. [9]

They used Fast Capsnet, which is a different DL model from traditional state-of-art approach CNN, which outperformed CNN when the training dataset is low. Usually CNNs require large datasets for better performance.

1) Approach: Custom made 3D CapsNet where there is change in dynamic routing process which dramatically increased the speed of computation by 3 times

2) Evaluation metrics: Precision, Recall rate, Error rate

3) Pros: Training is done efficiently when the size of the dataset is small, which is the case for most of the tasks which are based on medical image analysis.

4) Cons/Future Scope: It is observed that when the data set is large both CapsNet and CNN perform nearly the same. In future they are planning to use Unsupervised learning of CapsNet.

5) Dataset used: In the paper it is mentioned that the dataset used has 266scans from General Electric and Siemens Scanners, but we couldn't find it online and there is no reference found for the dataset.

IV. Design

A. 3D CNN

Convolutional Neural Network (ConvNet/CNN) is a Deep Learning technique in computer vision which takes in an input image, assign readable weights and biases to several objects in the image, and can also differentiate one from another. Using the appropriate filters,it is capable of effectively capturing Spatial Characters (coordinates, intensity, gradient,and so on) in the image, Due to the less involvement of the parameters and reused weights involved, the CNN architecture performs better when attaching an image dataset.That is, the neural network may be trained for better understanding of the image's complexities.

The main notion is that it has these convolution and pooling layers, and that the input (picture) passes through these layers before being transferred to a fully connected layer, exactly like any other neural network, through which the final output is obtained.

The architecture's structure is made up of the layers listed below:

1) Convolution layer: The layers where filters are applied to the raw image are known as convolutional layers. This layer contains filters that will construct a feature map that summarises features in the input image, making it a key component of feature extraction.

A filter is a type of matrix with a user-specified size (here 3x3x3) that we move across the input in a 3D form. A value is calculated for each point on the image using a convolution operation based on the filter.

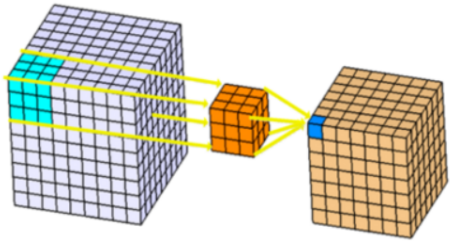

Fig. 1. 3D Kernel(source: internet)

2) Activation Layer: This is a supplementary step to the convolution layer where the nonlinearity of the image features is increased so that during the feature learning process in the convolution layer it learns better and gives better results for the new data.

rectified linear function, $f(x) = max(0, x)$

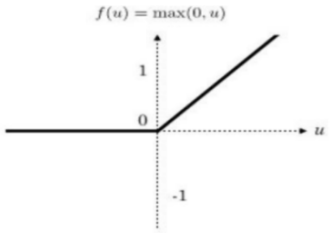

Fig. 2. ReLU Activaion Layer(source: internet)

3) Pooling Layer: Pooling Layer: This pooling layer is of the Max-Pooling kind. In this the dimensions are downed for the detection of features in the feature maps,Leading to the network's computational cost and the number of parameters to learn are reduced. The features accomodated in the region of the feature map caused by a convolution neural network layer indeed adds up to the pooling layer.

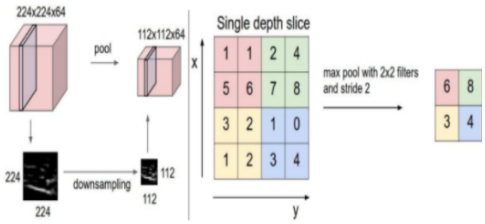

Fig. 3. Max-Pooling Layer(source: internet)

4) Fully Connected Layer: A fully-connected layer allows you to learn non-linear combinations of the needed attributes for a low cost.

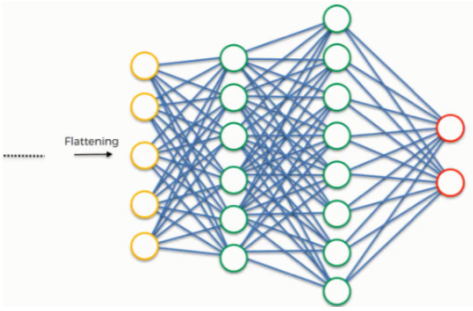

Fig. 4. Fully Connected Layer(source: internet)

B. Dataset

The Cancer Imaging Archive(TCIA) hosts archived data of several clinical images related to various cancers. There

are images of different modality MRI, digital histopathology, CT, etc. This is called the Cancer Imaging Programme(CIP) initiated by the National Cancer Institute, where we can submit the data and all the data is made publicly available to aid the researchers all over the world. The cancer datasets obtained are shown in Fig 5.

LungCT-Diagnosis	Lung Cancer	Lung	Human	61
NSCLC-Radiomics-Genomics	Lung Cancer	Lung	Human	89
SPIE-AAPM Lung CT Challenge	Lung Cancer	Lung	Human	70
RIDER Lung CT	Lung Cancer	Chest	Human	32
QIN LUNG CT	Non-small Cell Lung Cancer	Lung	Human	47
LIDC-IDRI	Lung Cancer	Chest	Human	1010

Fig. 5. Lung Cancer Database

LIDC/IDRI dataset is the largest among the available datasets. In LIDC/IDRI dataset the data structure is like, each folder has a CT scan of a patient wherein the images are of format dicom and there is a xml(Fig.6) file which has all the annotations.

Fig. 6. Sample XML file

All the other datasets present in Fig 5 variations of the LIDC/IDRI dataset where the metadata is altered for easy usability for a specific challenge.The data variety used in our base paper is SPIE-AAPM Challenge dataset which has only 70 scans.

After going through the many papers we came to the conclusion that CNN requires large datasets for better results, hence we are going to use the LUNA16 Challenge dataset where there are 888 scans, which are again derived from the LIDC/IDRI dataset but the structure varies. Instead of XML files they have CSV files for annotations again for easy usability.

The data format is as follows: there are 10 zip files containing CT pictures and annotations. The 'annotations V2.csv' file has an expanded list of candidate locations for the 'false positive reduction' track, while the 'candidates V2.csv' file contains the annotations used as a reference standard for the 'nodule detection' track.

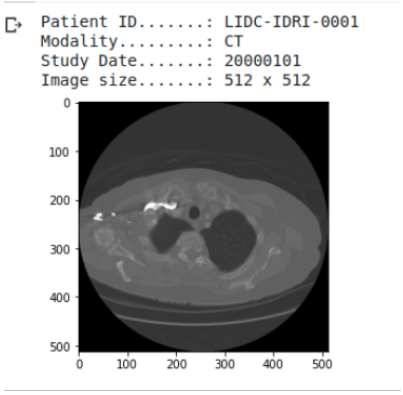

Fig. 7. CT Scan from the dataset (screen snap from google Colab)

C. Data Preprocessing

1) Conversion to Hounsfield Unit: It is a dimensionless standardized unit that helps radiologists in the interpretation of CT scans. It is a relative quantitative measure of radio intensity. At STP distilled water has 0 HU and air has -1000 HU. At first, the DICOM files are sorted by the instance number. And then the pixel array arrays are converted to Hounsfield Unit(HU) with the Rescale Slope and Rescale Intercept values from the metadata of DICOM by using the below equation.

$$HU = (P * S) + I$$

Where, P - Pixel value, S - Rescale slope, I - Rescale Intercept

2) Extract the nodule mask:

(a) The image is thresholded: Out of different attenuation values of Hounsfield Units, to segment the lung portion threshold value of -420 HU is chosen. A segmentation mask is used which assigns 1 for the pixel values less than -420 HU and 2 otherwise(the area of our interest).

(b) Removing the pixels with air above the patient tray: The connected region, i.e region where the adjacent pixel values are the same, are labeled with different values, other than regions with 0 as value. Then pixels with values same as value at (0,0,0) of the mask are assigned with value 2. As observed the air above the tray and below the tray where the person lies down for CT scan is separated, they get different labels, i.e, air above gets labelled as 2 and whereas below as 1.

(c) Fill the lung area: In this step a duplicate is created where all the pixel values are subtracted by 1, and again the step 'b' is performed, i.e., marking the connected region. Then pixels excluding which are, maximum number of connected pixels, are set to 1(i.e, region inside

the lung). This results in an image where the mask has the lung area as 1, and the rest as 2.

(d) Removing air below the tray and air pockets: Now step 'b' is again performed by inverting the binary mask obtained after subtracting 1 from the pixels as in step 'b', and then the maximum connected region(i.e, lung region now) remains as it is and the rest is set to 0. And the duplicate in the step 'c' which has not undergone operations of step 'c' is taken and the above operations are performed.

(e) Obtaining Nodule Mask: Finally after having the two masks, one having the operation to fill the lung area and the other without, the former mask is subtracted from the latter mask, resulting in a mask with only nodules.

3) Applying the nodule mask to the original image: Now on multiplying the mask obtained so far with the original image. As a result, only the nodules from the original image are retained.

4) Crop, Rescale and Resize the Image::

(a) Cropping: The image is a 3D image, with dimensions ranging from 512x512x200 to 512x512x400 for each patient. To accommodate all of them into the CNN model, the slice count must be uniform, therefore 50 slices to the left and 50 slices to the right are taken from the nodule location given in the annotation, for a total of 100 slices.

(b) Rescaling the Image: Using the Spline Interpolation method, all nodule pictures are rescaled to uniform spacing of (1,1,1) using the DICOM image parameters (using slice thickness, pixel spacing). Following this stage, all of the data will have the same resolution.

(c) Resizing the Image: To reduce the computational cost the nodule image obtained by above steps, which is of dimension 512x512x100, is now reduced to 100x100x100 using Bilinear Interpolation method.

D. Model

Constructing the CNN model: After preprocessing the dataset then the 3D CNN model is built where The first convolution layer has 64 filters of size 3*3*3, followed by the batch normalisation layer and then activation function ReLU layer. These 3 set of layers are repeated again. A MaxPool layer of size 2*2*2 is then added after these layers. We then added 4 sets of the above mentioned 3 layers (convolution, batch normalisation, relu) to increase the sophistication. These are then followed by a MaxPool layer and a Adaptive average pooling layer which marks the end of the convolution architecture. Flattened layer is used to flatten the output from the above layers in order to further pass it into a artificial neural network.

A fully connected layer of 64 nodes(neurons) is used, followed by a ReLU activation function and the last fully connected layer with two nodes are added.

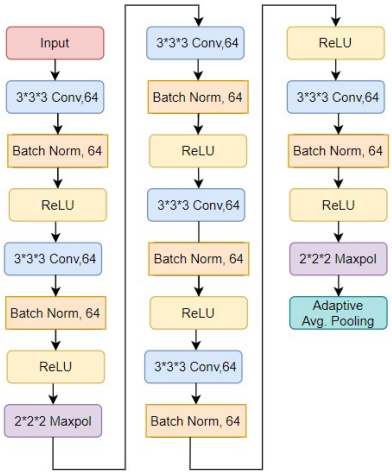

Fig. 8. Proposed design - CNN architecture (used draw.io tool)

E. Evaluation

Now the data is split into training set and testing set in 68% and 32% respectively. Then performed training and testing of the model using the below evaluation metrics.

The performance of the model is examined by various metrics such as,

(a) Testing Accuracy, it is the ratio of correctly identified instances with total number of instances

(b) Precision, to measure what proportion of positive identifications was actually correct

$$Precision = \frac{TP}{TP + FP}$$

(c) Recall is the measure of what proportion of actual positives was identified correctly

$$Recall = \frac{TP}{TP + FN}$$

(d) Kappa Score [10], it is the measure of agreement between a pair of variables, here it is used during testing between observed accuracy and predicted accuracy.

$$Precision = \frac{p_o - p_e}{1 - p_e}$$

(e) F-Score [11], it is the harmonic mean between precision and recall which is a measure of model accuracy. This is usually used with the models which have binary outputs, here it is malignant or benign.

$$F - Score = 2 * \frac{Precession * Recall}{Precession + Recall}$$

V. Work Done

We have read the papers published by others on this topic, and got familiar with their models and techniques used to preprocess, segmentation and classification. We decided to build the model of [12] and then built it over this model further.

Explored different datasets and decided to use the LUNA-16 dataset. Gone thoroughly through the [12] and understood the methodologies and implementation. Familiarised with the-oritical concepts of 3D CNN and related concepts(evaluation metrics, segmentation techniques, GradCAM, etc.) discussed in the cited papers in the literature section.

A. work done II

Retrieved data from the [13] and uploaded to the google drive to access from Google Colab Notebook. Then performed the following pre-processing operations.

(a) Loading the DICOM files using required python library pydicom.

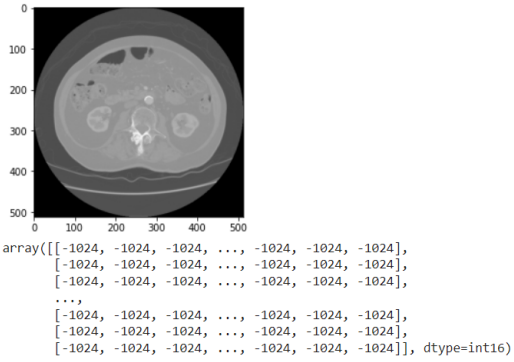

Fig. 9. Loaded Scan(screen snap from google Colab)

(b) Tranforming pixel data to Houndfield Units, the conversion is done using the below formula

$$HU = (P * S) + I$$

Where, P - Pixel value, S - Rescale slope, I - Rescale Intercept the Rescale slope and the Rescale Intercept are taken from the dicom file attributes and the obtained new image is stored in a new 3D array

(c) The images are re-scaled to uniform spacing of (1,1,1), by the parameters(using slice thickness, pixel spacing) of the DICOM image, with the Interpolation method

(d) 3D plotting: Matplot library is used to plot CT scan for 3D visualisation of the same for better understanding as shown in fig.13.

(e) Extracting the nodule mask steps: Threshold value of -420 HU is chosen. Pixels with air above the patient tray are removed, filled this with 1's in the binary image. Air below the tray and air pockets is removed. Only the largest air pocket is kept and final segmented nodules is obtained at the end.

B. work done III (Model training and testing)

We have built a 3D CNN Model using the PyTorch framework and fed the model with 60 training scans and 14 test scans. Model's architecture has been improvised further to accommodate more sophistication, hence increasing the efficiency of the model for better prediction on the test data set. Train scans have equal split between malign and benign (30 malign and 30 benign) scans and so is the case with test data too.

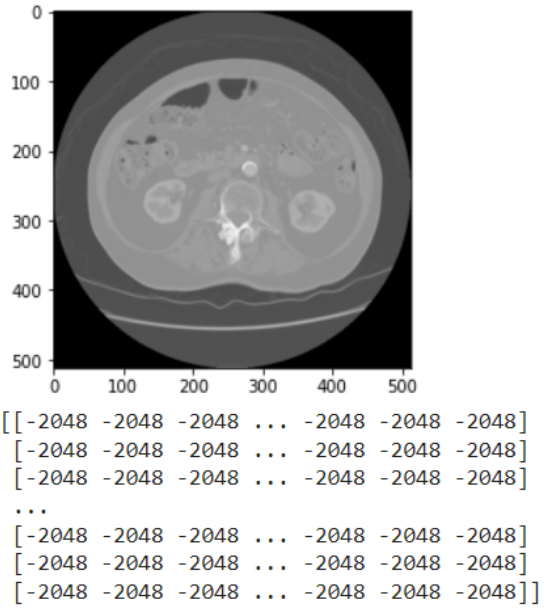

Fig. 10. After conversion to Hounsfield Units (screen snap from google Colab)

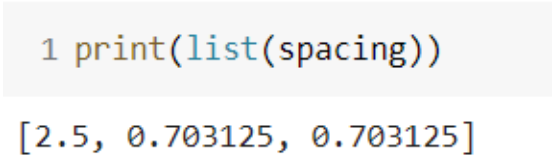

Fig. 11. Intital Spacing

Fig. 12. Spacing after Rescaling

VI. Work Plan

1. We would like to filter the data (which is currently skewed) and use more data (equal split between malign and benign) to feed our model and try every other possible way to improve the test accuracy of our model.
2. We would like to extend the architecture and work on segmentation in order to further enhance our knowledge around this and see if we could integrate it in our present model.

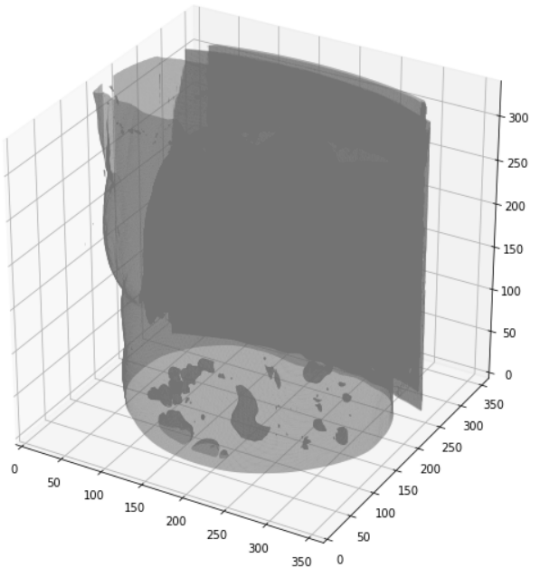

Fig. 13. 3D view of the CT Scan (screen snap from google Colab)

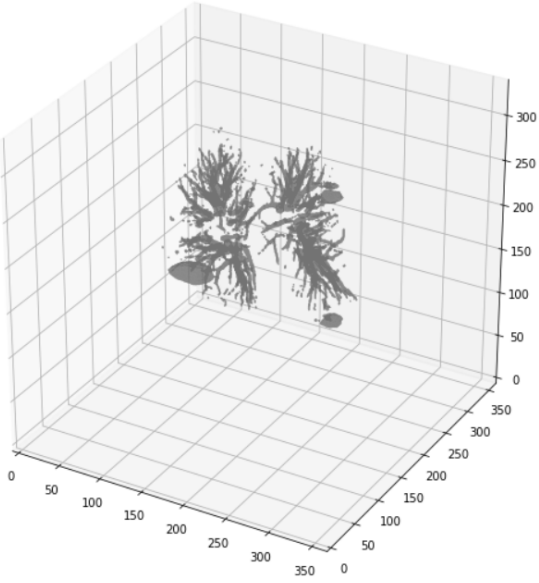

Fig. 14. Segmented Lung Nodule Image (screen snap from google Colab)

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```
class Net(nn.Module):
    def __init__(self):
        super(Net, self).__init__()
        self.conv1 = nn.Conv3d(1, 64, kernel_size=3, padding=1)
        self.bn1 = nn.BatchNorm3d(64)
        self.relu1 = nn.ReLU()
        self.conv2 = nn.Conv3d(64, 64, kernel_size=3, padding=1)
        self.bn2 = nn.BatchNorm3d(64)
        self.relu2 = nn.ReLU()
        self.conv3 = nn.Conv3d(64, 64, kernel_size=3, padding=1)
        self.bn3 = nn.BatchNorm3d(64)
        self.relu3 = nn.ReLU()
        self.pool1 = nn.MaxPool3d(kernel_size=2, stride=2, padding=0)
        self.conv4 = nn.Conv3d(64, 64, kernel_size=3, padding=1)
        self.bn4 = nn.BatchNorm3d(64)
        self.relu4 = nn.ReLU()
        self.conv5 = nn.Conv3d(64, 64, kernel_size=3, padding=1)
        self.bn5 = nn.BatchNorm3d(64)
        self.relu5 = nn.ReLU()
        self.conv6 = nn.Conv3d(64, 64, kernel_size=3, padding=1)
        self.bn6 = nn.BatchNorm3d(64)
        self.relu6 = nn.ReLU()
        self.conv7 = nn.Conv3d(64, 64, kernel_size=3, padding=1)
        self.bn7 = nn.BatchNorm3d(64)
        self.relu7 = nn.ReLU()
        self.pool2 = nn.MaxPool3d(kernel_size=2, stride=2, padding=0)
```

Fig. 15. convolution layers and pooling layers(screensnap from colab)

```
def forward(self, x):
    out = self.relu1(self.bn1(self.conv1(x)))
    out = self.relu2(self.bn2(self.conv2(out)))
    out = self.pool1(self.relu3(self.bn3(self.conv3(out))))
    out = self.relu4(self.bn4(self.conv4(out)))
    out = self.relu5(self.bn5(self.conv5(out)))
    out = self.relu6(self.bn6(self.conv6(out)))
    out = self.pool2(self.relu7(self.bn7(self.conv7(out))))
```

Fig. 16. forward function that defines the network structure (screensnap from colab)

```
Accuracy :  0.8928571428571429
Recall :  0.7857142857142857
Precession :  1.0
F-Score :  0.88
Kappa Score :  0.7857142857142858
```

Fig. 17. Evaluation metrics (screensnap from colab)

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