

COSC 6370 – FUNDAMENTALS OF MEDICAL IMAGING

**Topic: CT Lungs and Vessels Segmentation and Cancer
Detection**



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Abstract

One of the most important steps in contouring during radiation planning is accurate segmentation of medical pictures. The most used radiographic procedures for diagnosis, clinical research, and therapy planning are computed tomography (CT) scans. The division of an image into regions with equivalent qualities, such as brightness, contrast, color, texture, and gray level, is known as segmentation. In the case of medical pictures, segmentation, which splits the components of an image, is used to examine anatomical structure. Lung cancer is the second most prevalent cancer in the US. Additionally, it is the main cancer-related fatality factor. Lung cancer has a better chance of responding to treatment if it is discovered sooner, while it is still tiny, and before it has spread.

Introduction:

The imaging process known as computed tomography (CT) employs specialized x-ray equipment to produce in-depth images, or scans, of various body regions. Nearly every region of the body may be seen with a CT scan, which is also used to plan medical, surgical, or radiation treatments as well as detect diseases and injuries. A CT scan may provide cross-sectional pictures that can be rearranged in a variety of planes and even produce three-dimensional images that can be seen on a computer screen, reproduced on film, or transmitted to electronic devices. Lung segmentation, the technique of correctly differentiating the areas and limits of the lung field from surrounding thoracic tissue, is a crucial first step in pulmonary image processing for many clinical decision support systems. Following are our aims with this project:

Aim 1: CT data visualization with intensities and Hounsfield units. CT imaging can produce a 3D image of the body and can distinguish between variations in density. The Hounsfield scale is used to assess X-ray absorption. In contrast to MRI, which use a scale from 0 to 255 that is relative, it is critical to understand that the Hounsfield scale is an absolute scale. We intend to generate rich CT image scans by identifying the correct central intensity and clipping the optimum Hounsfield range. We will experiment with different levels and window values to understand the impact on the efficiency of the image.

Aim 2: Lung segmentation based on intensity values. This aim has multiple sub-aims that is needed to achieve the segmentation:

- We intend to calculate the pixel dimension to identify the real area and binarize the image.
- We then aim to find contours in the images. Simply said, a contour is a curve that connects all continuous points (along the boundary) that have the same hue or intensity. Contours are a helpful tool for object detection and recognition as well as form analysis.
- Our next plan would be to find the lung area from a set of possible contours. We want to make use of the areas identified in the contours and isolate the lungs.

Aim 3: Segment the main vessels and compute the vessels over lung area ratio. We plan to use the resulting image from the above methods and identify the vessels, denoise the image and get the lung area ration which is used to identify many diseases like alveolar hypoxia or thrombotic obstruction. The clinical diagnosis of pulmonary disorders depends on the ability to segment pulmonary vessels, which is difficult because of their complex nature.

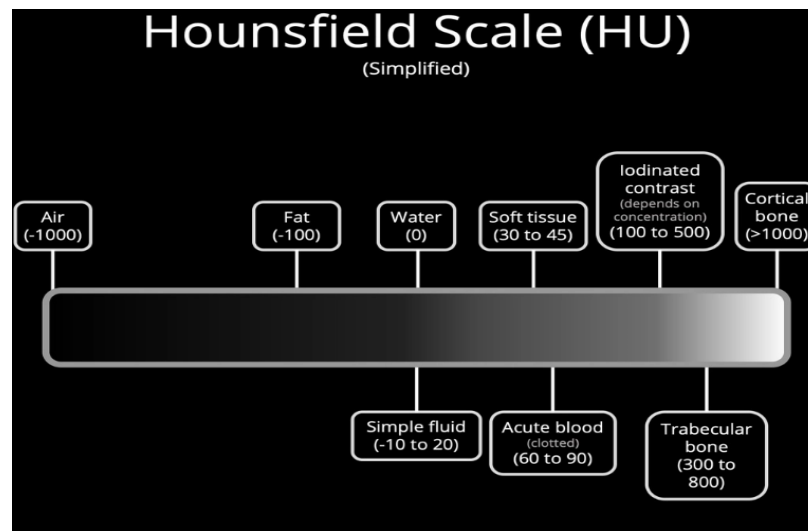
Aim 4: Train our model upon these obtained masked images that is information rich compared to the unaltered CT scan image and predict whether a tumor is present in the Lungs or not and display its type.

Methods and algorithms

X-ray beams are used in computed tomography (CT) to produce 3D pixel intensities of the human body. High-energy beams (electrons) are released when a cathode is heated; these electrons then release their energy as X-ray radiation. X-rays go through the tissues of the human body and land on a detector on the other side. Bones and other solid tissues will absorb radiation more strongly than soft tissues (i.e. fat).

We perceive X-rays as black, much like a black film, when they reach the detector and are not absorbed by the body (for example, in the air region inside the lungs). Contrarily, white is the colour used to represent dense tissues. CT imaging may produce a 3D image of the body and can discern between variations in density.

Radiologists analyze computed tomography (CT) images using **Hounsfield units (HU)**, a relative quantitative measure of radiance. During the CT reconstruction process, a grayscale image is created using radiation absorption/attenuation coefficients in tissue. Absorption or attenuation of an x-ray beam is proportional to the physical density of tissue. Hounsfield units, also known as CT units, are determined using a linear transformation of the initial linear attenuation coefficient of the X-ray beam, arbitrarily setting Hounsfield units (HU) to zero for distilled water and - for air. 1000 HU (at standard pressure and temperature). The maximum value for bone is 1000 and can be as high as 2000 for dense bones.



Bones are quite intense. The image is typically cropped to have a higher maximum range. For practical purposes, the maximum value might be 1000, for example. Visualization libraries operate on a [0, 255] scale. Visualizing the entire Hounsfield scale (from -1000 to 1000+) to 256 scales for medical diagnosis wouldn't be a good idea.

Window and Level is the name of an interactive tool for enhancing contrast that is typically included in image processing software. It is an increase in pixel contrast inside a specific window range. The centre point Level and the size of the range Window are the two parameters that specify the range. By selecting a window and a central intensity, or level, the Hounsfield range is clipped according to medical imaging convention.

Region/Tissue	Window	Level
brain	80	40
lungs	1500	-600
liver	150	30
Soft tissues	250	50
bone	1800	400

We will measure the actual area in mm² in addition to segmenting the lungs. To do that, we must ascertain the actual dimensions of the pixels. By dividing the width and height by the dpi, one can calculate the pixel dimensions. Lungs should fall within the [-1000, -300] Hounsfield unit range. To achieve this, we must binarize the numbers to 0 and 1 and trim the image range to [-1000, -300].

A contour in medical imaging is a collection of dots that identify a line or a region. Therefore, instead of receiving a full binary mask for each detected contour, we will just receive a collection of x and y values. The lung areas that are depicted in white are important to us. We have applied the marching squares technique, also known as **skimage.measure.find_contours()**, to find constant valued contours in a picture from **skimage** ().

Scikit-learn, also referred to as sklearn, is a Python library that is used to implement machine learning algorithms. Since it is an open-source library, using it is free. To improve the precision of the produced contours, array values are linearly interpolated in the **skimage.measure.find_contours** function. All other contours are closed, whereas those that cross the image edge are open. A specific instance of the marching cubes method is the marching squares algorithm.

Since we are just interested in the lungs, we must impose restrictions to keep out the undesirable areas. We used Scipy to first extract a convex polygon from the contour. We suppose that to depict the lungs, the contour must be a closed set and have a minimum volume of 2000 pixels. There could be more than three contours as a result, including or excluding the body contour. Having the largest volume of the contour that satisfies the previously described assumptions allows the body to be easily discarded in that situation.

The set of points must be transformed into a lung binary mask. We used the pillow Python library, which generates a binary image mask and draws a polygon. The lung contour masks that had already been discovered were then combined. The standard image processing package for the Python language is the Python Imaging Library (extension of PIL). It includes simple image processing capabilities that help with image creation, editing, and saving. 2011 saw the end of support for the Python Imaging Library, but a project called pillow forked the PIL project and added Python3.x support to it. PIL will be replaced going forward with Pillow, according to the announcement.

The number of nonzero elements is simply multiplied by the two-pixel dimensions of the respective image to get the necessary lung area in mm². Along with the image name, the lung regions are stored in a csv file. Finally, we changed the lung area's value from 1 to 255 in order to save the mask as nifty and display it on a nifty viewer. Additionally, we preserve the image with the initial CT slice's affine transformation so that it can be properly shown (aligned without any rotation conflicts).

Stepwise Implementation and obtained outputs

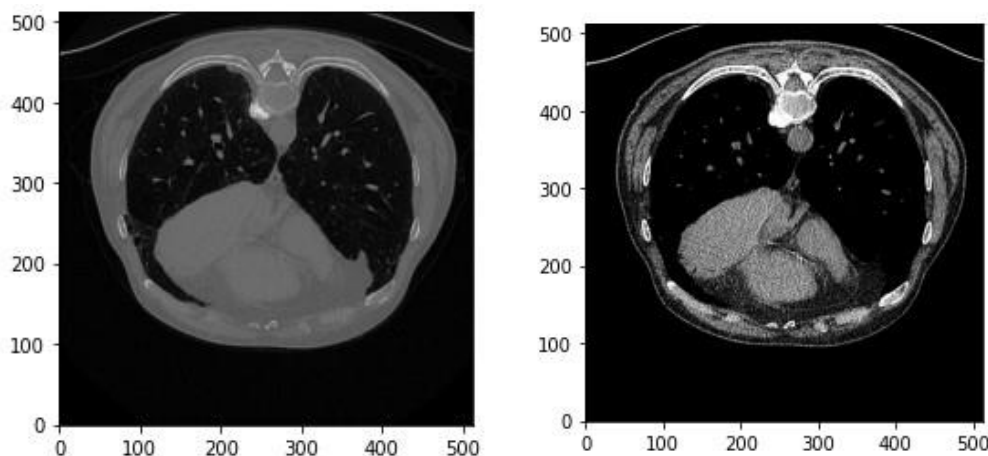
Our method deals with the usage of what is called the Housenfield range to segment the lungs and vessels from the sliced CT scan images. Firstly, it does not deal with segmentation using labels. It uses imaging techniques to first isolate the bone, tissue, and other contents in scan. Then we binarize the image using intensity thresholding with reference to the Housendfield range. We will then perform various operations upon the image that would give us the required information to train the model to classify a tumor's presence.

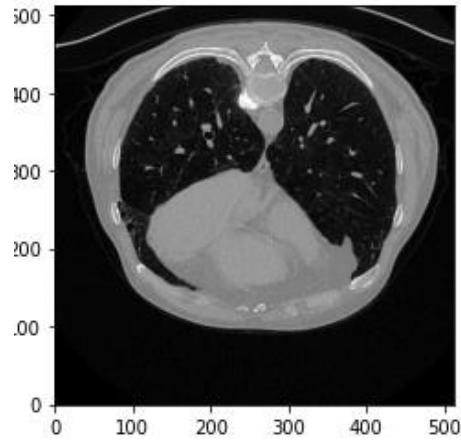
Step 1: Firstly, we slice the Housendfield range by choosing a central intensity called level and window using the formula given below: -

$$max=level+window/2$$

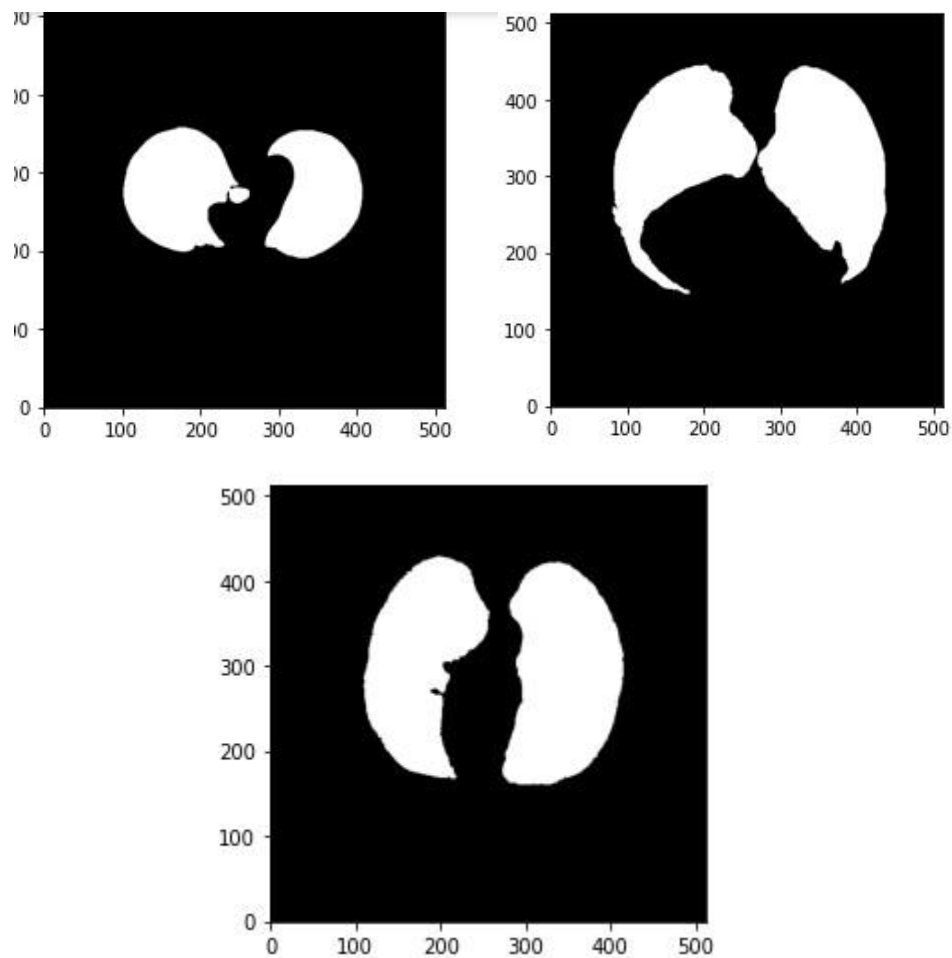
$$min = level - window/2$$

We will be using the standard reference table for the values of level and window of each region/tissue for the CT scan image.





Step 2: Then, we start to find the area of the given input image and binarize it to observe the densities of the regions and tissues and compare it with the Housendfield range. We expect lungs to be in the Housendfield unit range of $[-1000, -300]$. So, we need to clip the image range to $[-1000, -300]$ and binarize the values to 0 and 1.



Step 3: We then visualize the contours that are isolated from the lung area so that the vessels can be segmented from the lung region effectively in the coming steps. We use the marching squares method for this contour isolation step.

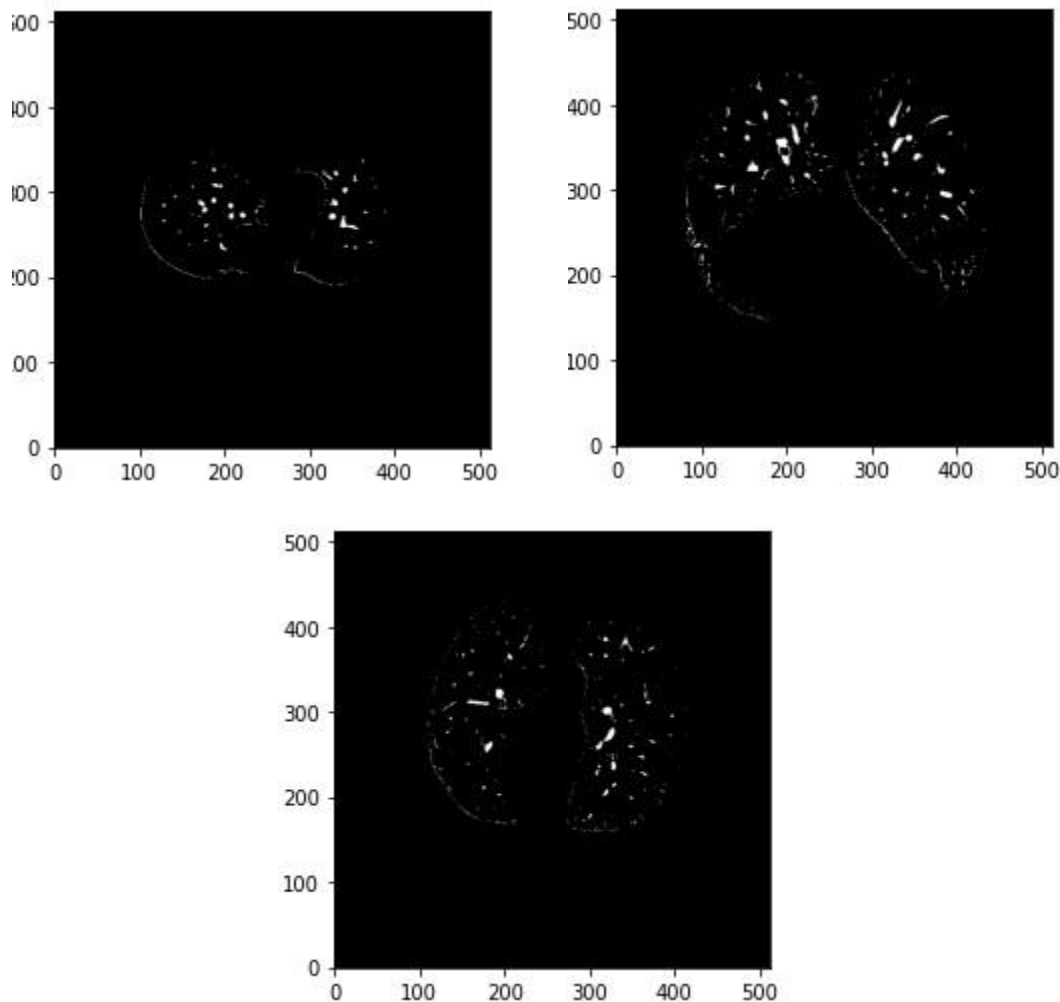
Step 4: We then need to isolate the lung area in the CT scan. We do this by extracting a polygon shape that obeys these constraints:

The lungs must have a closed set shape (always true)

To depict the lungs, the contour must have a minimum volume of 2000 pixels.

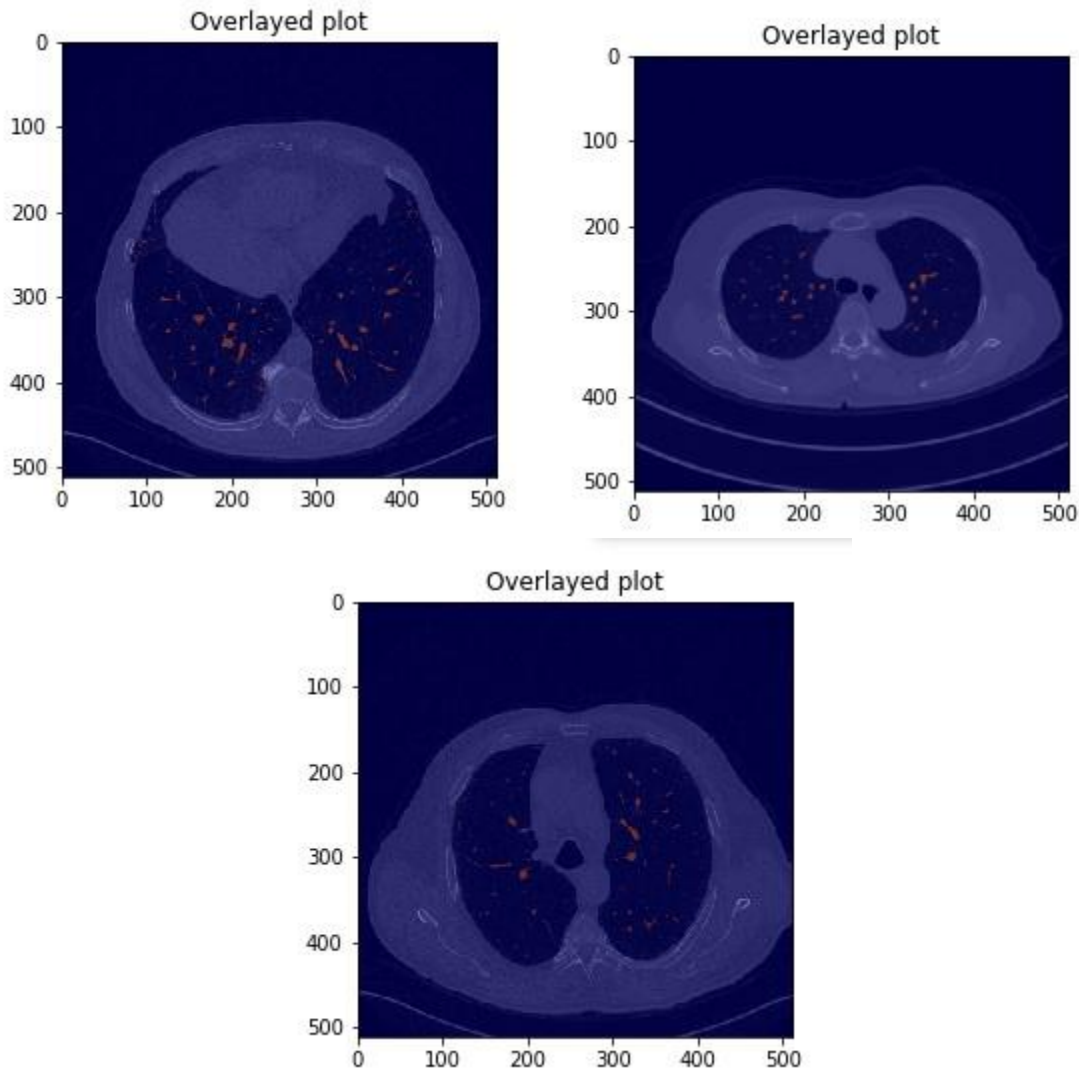
This might contain or exclude the body contour, resulting in more than three contours. When this occurs, the body is simply eliminated since it has the biggest volume of the shape that meets the pre-defined assumptions.

Step 5: Saving the lung area in the image and combining all the masks that isolate the contours along with the binary mask is done so that the vessels are highlighted. Then we create binary mask using the contours found in the previous step and merge them together to isolate and visualize the vessels clearly. Since we have the lung area, and the vessel area is calculated in this step we can find the vessel over lung area ratio for obtaining an output as shown in the images below.



Step 6: Then, we do element-wise multiplication between the CT image and the lung mask to get only the lungs. We assign the resulting zeros from the element-wise multiplication to -1000 (AIR in HU) and then maintain only the intensities greater than -500 as vessels.

Step 7: Finally, to analyze and improve the segmentation's result we avoid some parts of contours that are not needed. To do that we create a denoising function that considers the distance of the mask to all the contour points. If it is below 0.1, we set the pixel value to 0 and as a result exclude them from the detected vessels.



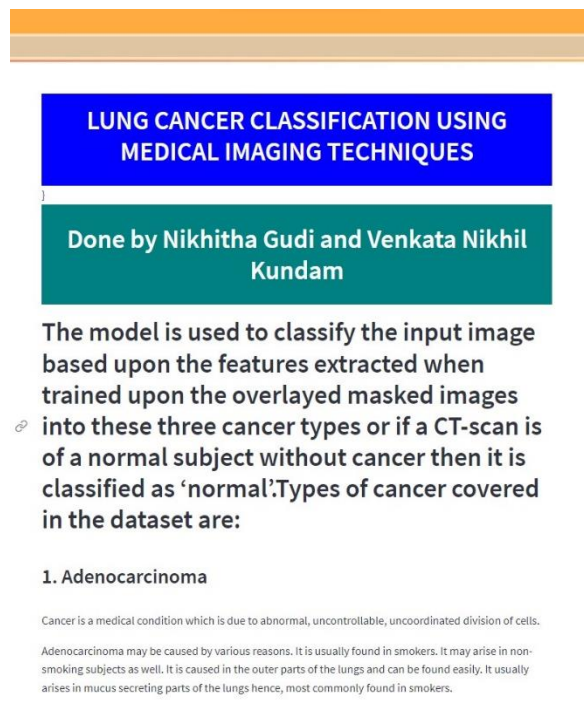
Implementation of our classification model

- We then train our model upon this dataset of masked images that is information rich compared to the unaltered CT scan image and predict whether a tumor is present in the Lungs or not. We have obtained substantially improved performance in the normal classification model that provides an accuracy of 92% with minimal loss.

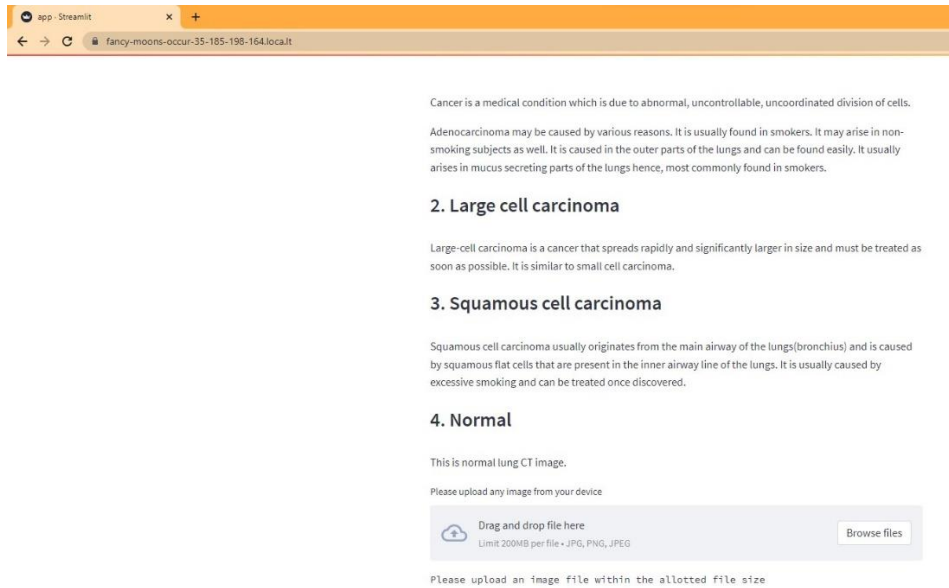
- Before we dive into the technical details it is important to discuss the types of cancer that can be classified by the model. Namely we are dealing with 3 types of cancer:
- **Large-cell carcinoma** is a cancer that spreads rapidly and significantly larger in size and must be treated as soon as possible. It is similar to small cell carcinoma.
- **Squamous cell carcinoma** usually originates from the main airway of the lungs(bronchus) and is caused by squamous flat cells that are present in the inner airway line of the lungs. It is usually caused by excessive smoking and can be treated once discovered.
- **Adenocarcinoma** may be caused by various reasons. It is usually found in smokers. It may arise in non-smoking subjects as well. It is caused in the outer parts of the lungs and can be found easily. It usually arises in mucus secreting parts of the lungs hence, most found in smokers.
- The model is used to classify the input image based upon the features extracted when trained upon the overlayed masked images into these three cancer types or if a CT-scan is of a normal subject without cancer then it is classified as '**normal**'.
- We created a sequential ImageNet neural network model to recognize the features with ReLU and sigmoid as the activation functions. Pooling technique helped us to calculate the probability value for each class of the image and choose the class with highest one.

User Interface for using the model for Classification

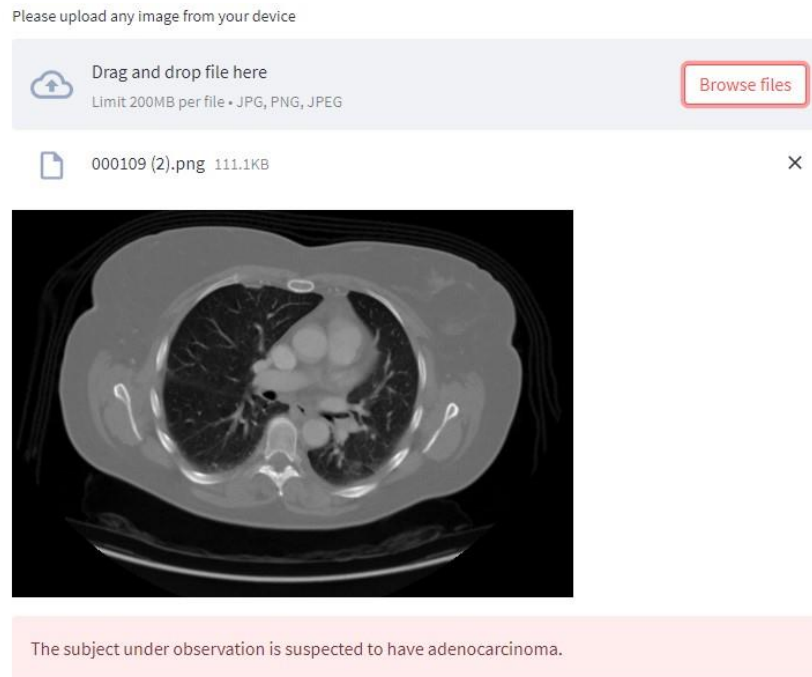
We have created a user interface using streamlit in Google collab that allows the user to travel to a website that gives him/her the ability to upload an image and know what kind of cancer is in the uploaded CT-scan image. You can follow the instructions in the collab file to use this web app. Here are the obtained outputs.



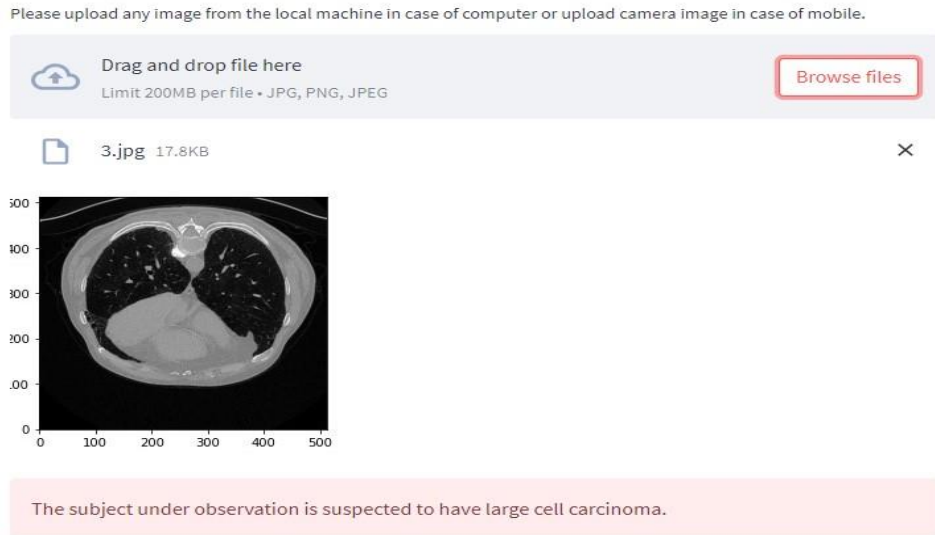
Screenshot 1: Intro page to the web application UI



Screenshot 2: Enables the User to upload image for classification



Screenshot 3: Classification done by model (Adenocarcinoma)



Screenshot 4: Classification done by model (Large cell carcinoma)

Conclusion and Future Scope for Improvements

- Usually, models are trained upon the labels and unaltered images (CT scan for lung cancer detection). This turns into a complete dependency on the neural network that lacks proper information or training. However, using these techniques and the Housendfield range in CT scan images (discussed in class) we tried to segment the images based upon the density values of the tissue, bone and lungs first.
- Creating a final mask using matrix operations (discussed in class) aggregated in the above steps to only extract the required information (vessels and lung area) and feeding it into our classification model to recognize the tumor turned out to yield far more beneficial results, than completely depending on the model by using labels and unaltered images only. It is unnecessary computational load on the model and depending completely on the deep learning model is not an optimal approach in this case.
- We have implemented this model based on masked images and created a UI to enable the user to check how the model works with custom input as well.
- Though regular classification methods for lung cancer detection based on unaltered CT scans yield impressive results in terms of accuracy, when the training process occurs it is difficult to interpret how the model is learning.
- These techniques that we have used helped us picture how a model can extract prominent features from the masked images, detect the cancer accurately and reduce the computational cost while increasing user interpretability of the learning process.
- This solution can further be developed in aspects like adding an extra neural network to automate the whole process of image processing and training methods based on custom datasets provided by the user in the User interface. This solution can also be used to generate complex models that can detect tumors in highly noisy CT-scan images.

References

- 1.) [D.Rudyanto, SjoerdKerkstra \(2014\) Comparing algorithms for automated vessel segmentation in computed tomography scans of the lung: the VESSEL12 study](#)
- 2.) [luimer, A. Schilham, M. Prokop and B. van Ginneken\(2006\), "Computer analysis of computed tomography scans of the lung: a survey](#)
- 3.) [What is Lung Cancer? And What are it's types – American Cancer Society](#)
- 4.) [E.J.Limkin, R.Sun, L.Dercle, E.I.Zacharaki, C.Robert, S.Reuzé, A.Schernberg, N.Paragios, E.Deutsch, C.Ferté \(2017\) Promises and challenges for the implementation of computational medical imaging \(radiomics\) in oncology](#)
- 5.) [Introduction to medical image processing with Python: CT lung and vessel](#)
- 6.) [Satrajit Basu; Lawrence O. Hall; Dmitry B. Goldgof; Yuhua Gu; Virendra Kumar; Jung Choi; Robert J. Gillies; \(2011\) Developing a classifier model for lung tumors in CT-scan imagesTBD](#)
- 7.) [Using Streamlit for User Interface](#)
- 8.) [Lung-Cancer Detection model architecure using Python](#)

Github Repository Link - https://github.com/kundamnikhil/COSC_6370_Final_Project