An Approach for Lung Cancer Detection using Deep Learning

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Abstract: Lung malignant growth is a perilous sickness that taking human life quickly around the world. The passing of the individuals is expanding exponentially on account of lung malignant growth. So as to lessen the illness and spare a human's life, the mechanized framework is required. The motivation behind the lung malignant growth identification framework can identify and give dependable data to specialists and clinicians from the clinical picture. To limit this issue, numerous frameworks have been proposed by utilizing diverse picture preparing methods, AI, and profound learning strategies. A registered tomography (CT) imaging methodology is a proficient procedure for clinical screening utilized for lung disease location and analysis. Doctor and radiologist utilize the CT examine pictures to investigate, decipher and analyze the lung malignant growth from lung tissues. Be that as it may, much of the time, getting an exact determination result without utilizing the additional clinical device known as a PC Aid identification and Diagnosis (CAD) framework is monotonous work for some doctors. To get a precise outcome from PC supported analysis framework lung disease identification techniques are essential once. Machine learning algorithms such as support vector machines are often used to detect and classify tumors. But they are regularly restricted by the presumptions we make when we characterize highlights. This outcomes in decreased affectability. Nonetheless, profound learning could be perfect arrangement in light of the fact that these calculations can take in highlights from crude picture information. One test in actualizing these calculations is the shortage of named clinical picture information. While this is a confinement for all uses of profound learning, it is all the more so for clinical picture information in view of patient classification concerns. In this exploration we manufacture a convolutional neural system, train it, and have it distinguish lung cancer of the patient's lung CT scan and classification methodology. We have used a convolutional neural network and designed a 3D CNN model that has a 0.97% accuracy performance. Our model has a precision with 87.31 %, recall with 74.46 % and specificity with 97.68 %.

Keywords: Lung cancer, Cancer classification, Nodule detection, 3D CNN, Deep learning

1. INTRODUCTION

Lung malignant growth is one of the most well-known tumors, representing more than 225,000 cases, 150,000 passing's, and $12 billion in social insurance costs yearly in the U.S. [1]. It is additionally probably the deadliest disease; generally speaking, just 17% of individuals in the U.S. determined to have lung malignant growth endure five years after the determination, and the endurance rate is lower in creating nations. The phase of a malignant growth alludes to how broadly it has metastasized. Stages 1 and 2 allude to tumors limited to the lungs and last stages allude to malignant growths that have spread to different organs. Current diagnostic methods include biopsies and imaging, such as CT scans.

Early detection of lung cancer (detection during the earlier stages) significantly improves the chances for survival, but it is also more difficult to detect early stages of lung cancer as there are fewer symptoms [1]. Lung malignant growth is one of the hazardous illnesses on the planet that taking human life quickly. The passing of the individuals is expanding exponentially in light of lung malignant growth. So as to diminish the illness, wrong understanding of the radiologist, and spare a human's life, the lung disease recognition and determination framework are required. As indicated by worldwide malignant growth insights report in 2012, around 1.83 million new lung disease cases has enlisted and over 1.5 million passing's are assessed [12], and as per the most recent World Health Organization information distributed in 2017 Lung Cancers Deaths in Ethiopia arrived at 1,584 or 0.25% of all out passing's [13]. Clinical imaging framework delivers a lot of clinical picture containing the applicable data identified with illnesses. The medical image is one of the interesting research fields in medical problem domains to detect and diagnosis numerous diseases. Medical image analysis is used to analyzing and solving medical problems by using different medical image analysis techniques to detect relevant and hidden information or knowledge from any medical images. There are various medical imaging modalities that used to screening the from our body, those are Computed Tomography (CT scan), Positron Emission Tomography (PET), mammography, X-ray, and Magnetic Resonance Image (MRI), ultrasound and so on, that used for early detection and diagnosis of disease [12]. Be that as it may, outstanding amongst other imaging procedure is Computed Tomography (CT check) imaging are effective for lung disease identification and conclusion since it can reveal each suspected and unsuspected lung malignant growth knobs from CT pictures [1]. Convolutional Neural Network (CNN) is an algorithm that most used and popular model in various research fields. CNN has been successfully applied to various research areas and has achieved state-of-the-art performance in video classification, natural language processing, image recognition and classification [2]. But there is still room for improvement on performance. We believe that enhancing the invariance of image features is a way to improve performance. We have used a convolutional neural network for classification due to the popularity of image and video classification, natural language processing and pattern recognition, etc. The principle favorable position of a convolutional neural system can extricate and recognize significance highlights from a given information naturally with no master control. It has a unique convolutional and pooling layer that perform boundary sharing tasks. This boundary sharing activity makes the convolutional neural system most famous Algorithms. As analyzed as completely associated ANN, weight partaking in Convolutional Neural Network (CNN) encouraging in learning an element paying little heed to its situation in the picture, alongside having the additional preferred position of diminished calculations. After convolution activity the Pooling activity is played out, this pooling activity is utilized to diminish the measurement and number of boundaries utilized in our model. This causes preparing time to abbreviate and diminish overfitting. The pooling layer activity comprises of max pooling and implies pooling. Mean pooling ascertains the normal neighborhood inside the component focuses, and max pooling and means pooling. Mean pooling figures the normal neighborhood inside the element focuses, and max pooling computes the area inside a limit of highlight focuses. The blunder of highlight extraction mostly originates from two viewpoints: the local size confinement brought about by the assessed fluctuation and convolution layer boundary evaluated mistake brought about by the mean deviation. Mean pooling can lessen the main mistake, holding more picture foundation data. Max pooling can decrease the subsequent mistake, holding more surface data. After the convolution layer and pooling layers, we ought to utilize completely associated layers. Our undertaking is a paired classification issue to recognize the nearness of lung malignancy in persistent CT sweeps of lungs with and without beginning phase lung disease. We expect to utilize strategies from PC vision and profound learning, especially 2D and 3D convolutional neural systems, to manufacture an exact classifier. An exact lung malignant growth classifier could accelerate and decrease expenses of lung disease screening, taking into account progressively across the board early location and improved endurance. The objective is to build a PC helped analysis (CAD) framework that takes as information persistent chest CT sweeps and yields whether the patient has lung malignancy [2]. In spite of the fact that this errand appears to be direct, it is really a needle in the sheaf issue. So as to decide if a patient has beginning phase malignant growth, the CAD framework would need to distinguish the nearness of a small knob (< 10 mm in measurement for beginning phase tumors) from a huge 3D lung CT filter (ordinarily around 200 mm × 400 mm × 400 mm). A case of a beginning phase lung malignant growth knob appeared in inside a 2D cut of a CT check is given in Fig. 1. Besides, a CT examine is filled with clamor from encompassing tissues, bone, air, so for the CAD frameworks search to be efficient, this commotion would first must be pre-prepared. Henceforth our classification pipeline is picture pre-handling, knob up-and-comer's location, and harm classification. In this paper, we apply a broad pre-handling methods to get the exact knobs so as to improve the exactness of discovery of lung disease. Besides, we play out a start to finish preparing of CNN without any preparation so as to understand the maximum capacity of the neural system for example to learn discriminative highlights. Broad trial assessments are performed on a dataset including lung knobs from in excess of 1390 low portion CT filters.

Figure 1. 2D CT scan slice containing a small (5mm) early stage lung cancer nodule

In this paper we have utilized two distinctive datasets (kaggle information science Bowel 2017 and Lung knob examination 2016), that is an assistance to build the exhibition of preparing of our model. In this undertaking, we are pre-prepared and portioned the knobs from a given dataset that will help the future postulation works and our model assessed by utilizing the precision measurements. Consequently our lung disease location framework pipeline comprises of pre-preparing, lung division, competitor knob division, knob identification, and order.

2. LITERATURE REVIEW

Recently, deep artificial neural networks have been applied in many applications in pattern recognition and machine learning, especially, Convolutional neural networks (CNNs) which is one class of models [3].

Another methodology of CNNs was applied on ImageNet Classification in 2012 is called an outfit CNNs which beat the best outcomes which were well known in the PC vision network [4]. There has likewise been well known most recent examination in the zone of clinical imaging utilizing profound learning with promising outcomes. Suk et al. [5] proposed another inactive and shared component portrayal of neuro-imaging information of cerebrum utilizing Deep Boltzmann Machine (DBM) for AD/MCI determination. Wu et al. [6] grew profound component learning for deformable enrollment of mind MR pictures to improve picture enlistment by utilizing profound highlights. Xu et al. [7] introduced the adequacy of utilizing profound neural systems (DNNs) for highlight extraction in clinical picture examination as a directed methodology. Kumar et al. [8] proposed a CAD framework which utilizes profound highlights removed from an autoencoder to order lung knobs as either harmful or benevolent on LIDC database. In [9], Yaniv et al. introduced a framework for clinical utilization of chest pathology identification in x-beams which utilizes convolutional neural systems that are found out from a non-clinical file. That work demonstrated a blend of profound learning (Decaf) and PiCodes highlights accomplishes the best execution. The proposed mix introduced the possibility of distinguishing pathology in chest x-beam utilizing profound learning approaches dependent on nonmedical learning. The pre-owned database was made out of 93 pictures. They got a territory under bend (AUC) of 0.93 for Right Pleural Effusion identification, 0.89 for Enlarged heart discovery and 0.79 for classification among solid and irregular chest x-beam. In [10], Suna W. et al., executed three diverse profound learning calculations, Convolutional Neural Network (CNN), Deep Belief Networks (DBNs), Stacked Denoising Autoencoder (SDAE), and contrasted them and the customary picture include based CAD framework. The CNN engineering contains eight layers of convolutional and pooling layers, reciprocally. For the customary contrasted with calculation, there were around 35 extricated surface and morphological highlights. These highlights were taken care of to the bit based help vector machine (SVM) for preparing and classification. The came about precision for the CNN approach arrived at 0.7976 which was minimal higher than the customary SVM, with 0.7940. They utilized the Lung Image Database Consortium and Image Database Resource Initiative (LIDC/IDRI) open databases, with around 1018 lung cases. In [11], J. Tan et al. structured a system that recognized lung knobs, at that point decreased the bogus positive for the distinguished knobs dependent on deep neural system and Convolutional Neural Network. The CNN has four convolutional layers and four pooling layers. The filter was of profundity 32 and size 3.5. The utilized dataset was obtained from the LIDC-IDRI for around 85 patients. The came about affectability was of 0.82. The False positive decrease gotten by DNN was 0.329.

In [12], R. Golan proposed a structure that train the loads of the CNN by a back spread to recognize lung knobs in the CT picture sub-volumes. This framework accomplished affectability of 78.9% with 20 bogus positives, while 71.2% with 10 FPs for each sweep, on lung knobs that have been commented on by every one of the four radiologists Convolutional neural systems have accomplished better than Deep Belief Networks in current investigations on benchmark PC vision datasets. The CNNs have pulled in significant enthusiasm for AI since they have solid portrayal capacity in taking in valuable highlights from input information as of late. We additionally utilized the patient lung CT examine dataset with marked knobs from the Lung Nodule Analysis 2016 (LUNA16) Challenge [14] to prepare a U-Net for lung knob discovery. The LUNA16 dataset contains marked information for 888 patients, which we partitioned into a preparation set of size 710 and an approval set of size 178. For every patient, the information comprises of CT check information and a knob mark (rundown of knob focus directions and width). For every patient, the CT filter information comprises of a variable number of pictures (regularly around 100-400, each picture is a hub cut) of 512 × 512 pixels. LUNA16 information was utilized to prepare a U-Net for knob discovery, one of the stages in our classification pipeline. The issue is to precisely anticipate a patient's mark ('malignant growth' or 'no disease') in light of the patient's Kaggle lung CT check.

As we inspected, numerous lung malignant growth location framework and conclusion framework have been proposed to the assistance of radiologist and clinician to recognize and arranges the malady with the better outcome by utilizing various methodologies of picture handling, AI, and profound learning. Be that as it may, the profound learning procedures are the present status of-workmanship techniques for lung malignant growth location framework. We sum up these frameworks dependent on the techniques they embrace.

2.1 Image preparing approaches: Image handling method has an extraordinary job in clinical picture investigation and it makes the order forms progressively precise. Picture handling procedures have been extraordinarily investigated in knob characterization for lung CT pictures. Various examinations received division, morphological tasks, and shape channel approaches for better knob location [5]. By utilizing those methodologies a few analysts have proposed and actualize lung malignancy discovery framework with great precision. Neelima Singh et.al [6] has been proposed lung disease identification frameworks by utilizing picture handling strategies. The framework is utilized picture pre-handling, and after pre-preparing of a picture, a shrewd channel is utilized for Edge Detection. Super pixel Segmentation has been utilized for division, and Gabor channel is utilized for denoise the clinical pictures.

2.2 Machine learning Approach: Machine learning is contemplating techniques that enable PCs to take care of issues by gaining from encounters. The objective is to make scientific models that can be prepared to deliver valuable yields when taken care of info information. AI models are given encounters through preparing information and are tuned to deliver precise expectations for the preparation information by an advancement calculation [7]. As of late Machine learning strategies have assumed a significant job in the clinical field like clinical picture preparing, PC helped determination, picture understanding, picture enrollment, picture division, picture recovery, and examination. These methods made out of ordinary calculations without learning like Support Vector Machine (SVM), Neural Network (NN), and KNN, and so on. Suren Makajua et al. [8] proposed a model that identify the carcinogenic knob structure CT check picture by utilizing watershed division for identification. In this proposed framework Gaussian channel strategy is actualized in the pre-handling stages and utilizing SVM for characterization of the knob as Malignant or amiable. Qing. W et al. [9] proposed a framework that identifies little cell lung disease (SCLC) structure registered tomography (CT) filter pictures. The framework proposed a novel Neural-Network Based calculation, alludes to an entropy debasement strategy (EDM) and utilize the vectorized histogram as preparing inputs.

2.3 Deep learning Approach: Machine learning is calculations are constrained in preparing the regular pictures in their crude structure, tedious, in light of master information and requires a great deal of time for tuning the highlights. Because of this restriction AI is overpowering by profound learning strategies. Profound learning is taken care of with crude information, programmed highlights student and quick. These calculations attempt to become familiar with various degrees of deliberation, portrayal, and data consequently from a huge arrangement of pictures that display the ideal conduct of information. Profound learning based calculations indicated promising execution just as speed in various areas like discourse acknowledgment, text acknowledgment, lips perusing, PC helped determination, face acknowledgment, medicate revelation. Presently a day profound learning calculation has got extraordinary enthusiasm for every single field and particularly in clinical picture examination because of the portrayal of numerous degrees of deliberation and extraction of highlights from huge dataset naturally. This framework was attempting to analyze the outcomes dependent on their highlights including handmade highlights (Bag of frequencies and ordered lists), profound learning highlights and utilize them two by linking. The outcome shows the promising outcomes yet it needs a room of progress for both high quality highlights. The Combined outcomes were gotten by connecting the element vectors (carefully assembled and profound learning), however the extraordinary difference in size prompted lower precision than anticipated.

Allison et al. [1] are to build up a Deep Learning for Categorization of Lung Cancer CT Images. The framework has been available outfit techniques for Convolutional Neural Network (CNN) utilizing numerous pre-preparing strategies to improving the exactness of the framework. This framework utilizes both un-smoothing and smoothing pictures in isolated systems to improve the grouping. The outcome anticipated by utilizing the two systems in a consolidated way by applying casting a ballot frameworks as opposed to utilizing normal qualities. The smoothing system utilizes Gaussian channel techniques to the testing and preparing pictures to make a second smoothed preparing testing set.

Rotem et al [11] have been proposed Lung Nodule Detection in CT Images utilizing Deep Convolutional Neural Networks. The framework was proposed by utilizing the exposure accessible Lung Image Database Consortium (LIDC) and Image Database Resource Initiative (IDRI) database, which comprises of CT examine pictures with various shape and size, and the framework utilizes a profound Convolutional Neural Network (CNN), which is prepared, utilizing the back-proliferation calculation to remove lung knobs in sub volumes of CT pictures. The framework has a 78.9% affectability (True positive rate) with 20 False Positives (FPs) per examine.

This proposed system has been achieved the result without using any segmentation methods and any FPS reduction process.

Albert C. et al [5] has been proposed Deep Convolutional neural networks for lung cancer detection system. This system has used a linear classifier as a baseline, a vanilla 3D CNN, and a Google net-based 3D CNN. Each classifier uses weighted softmax cross-entropy loss (weight for a label is the inverse of the frequency of the label in the training set) and Adam Optimizer, and the CNNs use ReLU activation and dropout after each convolutional layer during training. Hongtao et al.[4] Has proposed an automated pulmonary nodule detection in CT images using deep convolutional neural networks. Wafaa A. et al [12] has proposed Lung Cancer Detection and Classification with 3D Convolutional Neural Network (3D-CNN). Prajwal R. et al [3] has proposed Convolutional Neural Networks for Lung Cancer Screening in Computed Tomography (CT) Scans.

Emre Dandil [13] has been proposed a computer-aid pipeline for automatic lung cancer classification on Computed Tomography (CT) scan. The system used a private dataset that consists of 47 CT scans from 47 different patients. This proposed pipeline has composed on four stages: (1) Image pre-processing stage, in this stage, CT scan images are enhanced, and lung volume are extracted from the image, (2) Nodule detection stage. (3) Feature computation stage that used to extract features from lung image, and Principal Component Analysis (PCA) is used for feature reduction. The final stage is classification, in this stage the system, in this stage, the system has been used Probabilistic Neural Network (PNN) that used for benign and malign nodules.

3. PROPOSED METHODOLOGY

In our proposed system has five stages as shown below in figure 1. The basic idea is to leverage the information given from LUNA 16 dataset to predict the nodule Locations in the Kaggle dataset. Since we use two datasets, a pre-processing step ensures that they are in the same field. The segmentation of lung tissues on chest images is an important step to reduce the search space. The two steps are common for both the LUNA and Kaggle datasets. Next, detection and segmentation of lung nodules from the available search space. This is achieved by using LUNA dataset, as it provides us with cancerous regions in the lungs. This is then fed to the Kaggle dataset to locate cancerous regions. Finally, the classification of the detected nodules into malignant and benign is the final step. The details of each step are discussed below. This pipeline include data collection, image pre-processing, lung segmentation (including nodule segmentation) and classification (CNN model that classify whether the patients have cancer or non-cancer) pipelines of our lung cancer detection model that include data collection, image pre-processing, lung segmentation (including nodule segmentation) and classification (CNN model that classify whether the patients have cancer or non-cancer).

3.1 Data Source: In this section, we discuss the data and the architecture of the network that we have designed for tumour classification. We begin this section with details about the data, and the steps in converting it into a suitable form for the CNN. A. Data The database used is obtained from Lung Image Database Consortium (LIDC) [10]. This is a lung nodule classification database containing the scans of a total of 888 patients. Each patients' CT scan in turn is comprising of around 200 dicom/jpg format images. All dicom/jpg format images are, at first, obtained as 512x512 grayscale images. Since the overall size of the CT scan becomes very large, this is scaled down to a 128x128 grayscale image. Each image is then normalized by dividing this grayscale image pixel value by 255 (this is done so that the computations stay within finite values, otherwise error terms, etc. very quickly become unbounded). Next, each of the grayscale images are concatenated linearly to create a volume in HDF5 format. Further, this 2D array is zero padded to equalize the third dimension, i.e., the number of images in each CT scan provided for one patient. For conversion to HDF5 format, the 2D array is reshaped into an array of (1, 500, 128, 128). The conversion process is done using a python script. HDF5 contains two inputs: one being the data and the other being the label. The data are the 3D array and the label is another dimension to specify the class of the CT scan which in our case is 0 for benign and 1 for malignant. The sequence of operations for the preparation of the data are shown in Figure 1.

3.2 Creating an image database

The pictures were arranged as .mhd and .raw files. The header information is contained in .mhd records and multi-dimensional picture information is put away in .crude documents. I utilized SimpleITK library to peruse the .mhd files. Every CT filter has measurements of 512 x 512 x n, where n is the quantity of hub examines. There are around 200 pictures in every CT examine.

There were a sum of 551065 explanations. Of the considerable number of comments gave, 1351 were marked as knobs, rest were named negative. So there huge class irregularity. The easy method to manage it to under example the larger part class and enlarge the minority class through pivoting pictures.

We might prepare the CNN on all the pixels, yet that would build the computational expense and preparing time. So all things being equal I simply chose to trim the pictures around the directions gave in the explanations. The explanation were given in Cartesian directions. So they must be changed over to voxel organizes. Additionally the picture power was characterized in Hounsfield scale. So it must be rescaled for picture handling purposes.

The content underneath would create 50 x 50 grayscale pictures for preparing, testing and approving a CNN.

While the content above under-tested the negative class with the end goal that each 1 of every 6 pictures had a knob. The informational collection is still endlessly imbalanced for preparing. I chose to enlarge my preparation set by pivoting pictures. The content beneath does only that. So for an original image, my script would create these two images:

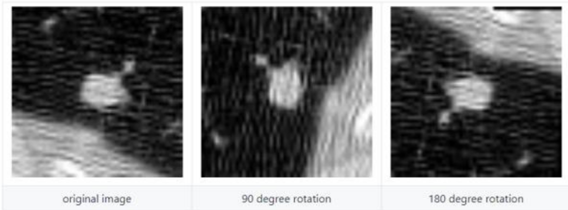

Figure 2. Augmentation of original image

A. Convolutional Neural Network: A CNN is a neural network architecture that efficiently exploits the spatial correlation of the input data. Moreover, weight sharing in CNN facilitates in learning a feature regardless of its position in the image, along with having the added advantage of reduced computations as compared to a fully connected ANN. The convolution layer of a CNN produces a feature map by convolving different sub regions of the image with a learned kernel (learned during the training process). Further, non-linear activation functions such as a sigmoid, tanh or rectified linear (ReLu) can also be applied. The ReLu layer is also known to improve the convergence properties when the error is low, leading to stagnation in the traditional sigmoid activation function [4]. Another method for reducing computations is the pooling layer, where a region of the image/feature map is chosen and the maximum among them is chosen as the representative pixel. Hence, a 2x2 or 3x3 grid can be reduced to a single scalar value. Average values can also be used for pooling, but in either case, the net effect is a large reduction in the sample size. More details about kernel size, feature maps, stride and other parameters related to a convolutional layer can be found in [4]. Additionally, traditional fully connected layer can also be used in conjunction with the convolutional layers, and are usually used towards the output stage, as in [4].

B. Proposed Convolutional Neural Network Architecture: We are proposing CNNA which is based on the layers that are used in a CNN, along with appropriate values for network parameters. CNNA contains two convolution layers immediately after the input layer, followed by a pooling layer, a dropout layer and a fully connected layer. Each convolution layer is in turn followed by a rectified linear output layer and the pooling layer is followed by a Dropout layer. The architecture is shown in Figure 2, and the layers are explained briefly:

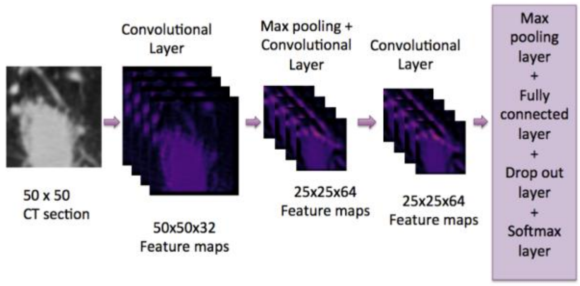

Figure 3. Architecture of proposed Convolutional Neural Network

4. EVOLUTION OF MODEL

Evaluation will be performed using various metrics like classification accuracy, precision, recall, F1-score. The F1 score reaches its best value as it tends to 1. We will compare and contrast the scores across our experiments to present conclusive evidence on which method gives the best results for detection of lung cancer using LUNA16 datasets.

The evaluation of the experiments are carried out using the following metrics:

True Positive (TP): A true positive is an outcome where the model correctly predicts the positive class.

True Negative (TN): A true negative is an outcome where the model correctly predicts the negative class.

False Positive (FP): A false positive is an outcome where the model incorrectly predicts the positive class.

False Negative (FN): A false negative is an outcome where the model incorrectly predicts the negative class.

Precision: The precision for a class is the number of true positives (i.e. the number of items correctly labeled as belonging to the positive class) divided by the total number of elements labeled as belonging to the positive class (i.e. the sum of true positives and false positives, which are items incorrectly labeled as belonging to the class).

$$\text{Precision} = \frac{TP}{(TP + FP)}$$

High precision means that an algorithm returned substantially more relevant results than irrelevant ones.

Recall: Recall is defined as the number of true positives divided by the total number of elements that actually belong to the positive class (i.e. the sum of true positives and false negatives, which are items which were not labeled as belonging to the positive class but should have been).

$$\text{Recall} = \frac{TP}{(TP + FN)}$$

High recall means that an algorithm returned most of the relevant results.

F-score: The F-beta score can be interpreted as a weighted harmonic mean of the precision and recall, where an F-beta score reaches its best value at 1 and worst score at 0.

$$F1 = \frac{2 \times (\text{Precision} \times \text{Recall})}{(\text{Precision} + \text{Recall})}$$

Support: The support is the number of occurrences of each class.

Accuracy: Model accuracy in terms of classification models can be defined as the ratio of correctly classified samples to the total number of samples:

$$\text{Accuracy} = \frac{(TP + TN)}{(TP + TN + FP + FN)}$$

4.1 Training the model

Because the data required to train a CNN is very large, it is often desirable to train the model in batches. Loading all the training data into memory is not always possible because you need enough memory to handle it and the features too. So we decided to load all the images into a hdfs dataset using h5py library.

Once I had the training data in a hdfs dataset, I trained the model.

C:\Users\acer 1\Anaconda3\LungCancerDetection\LungCancerDetection \src\models>python train.py

Training Step: 3706 | total loss: ←[1m←[32m0.08919←[0m←[0m | time: 21.141s

| Adam | epoch: 068 | loss: 0.08919 - acc: 0.9725 -- iter: 2016/5187

Training Step: 3707 | total loss: ←[1m←[32m0.09602←[0m←[0m | time: 22.219s

| Adam | epoch: 068 | loss: 0.09602 - acc: 0.9711 -- iter: 2112/5187

Training Step: 3708 | total loss: ←[1m←[32m0.09550←[0m←[0m | time: 23.313s

| Adam | epoch: 068 | loss: 0.09550 - acc: 0.9709 -- iter: 2208/5187

Training Step: 3709 | total loss: ←[1m←[32m0.10294←[0m←[0m | time: 24.391s

Training Step: 3846 | total loss: ←[1m←[32m0.11025←[0m←[0m | time: 53.860s

| Adam | epoch: 070 | loss: 0.11025 - acc: 0.9604 -- iter: 4896/5187

Training Step: 3847 | total loss: ←[1m←[32m0.10804←[0m←[0m | time: 54.969s

| Adam | epoch: 070 | loss: 0.10804 - acc: 0.9602 -- iter: 4992/5187

Training Step: 3848 | total loss: ←[1m←[32m0.10717←[0m←[0m | time: 56.079s

| Adam | epoch: 070 | loss: 0.10717 - acc: 0.9589 -- iter: 5088/5187

Training Step: 3849 | total loss: ←[1m←[32m0.10561←[0m←[0m | time: 57.204s

| Adam | epoch: 070 | loss: 0.10561 - acc: 0.9610 -- iter: 5184/5187

Training Step: 3850 | total loss: ←[1m←[32m0.10302←[0m←[0m | time: 61.813s

| Adam | epoch: 070 | loss: 0.10302 - acc: 0.9628 | val_loss: 0.21534 - val_acc:

0.9298 -- iter: 5187/5187

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Network trained and saved as nodule3-classifier.tfl!

The training took a couple of hours on my laptop. As the filters are of low resolution (5x5), it would be more useful to visualize features maps generated. So if I pass through this image through the first convolutional layer (50 x 50 x 32), it generates a feature map that looks like this:

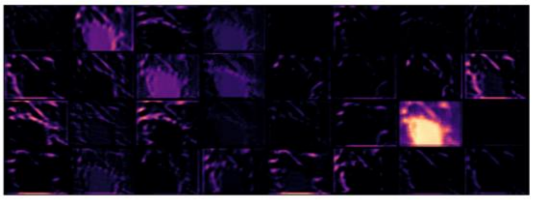

Figure 4. First Convolutional layer

The max pooling layer following the first layer down sampled the feature map by 2. So when the down sampled feature map is passed into the second convolutional layer of 64 5x5 filters, the resulting feature map is:

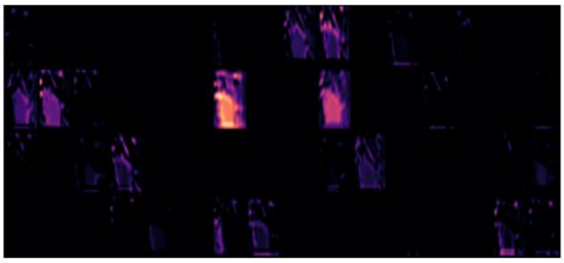

Figure 5. Second Convolutional layer

The feature map generated by the third convolutional layer containing 64 3x3 filters is:

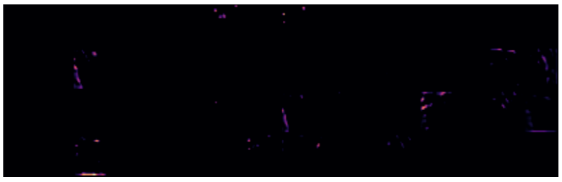

Figure 6. Third Convolutional layer

5. RESULT AND DISCUSSION

For the creation of our proposed model, we have used the Caffe deep learning framework developed by the Berkeley Vision and Learning Center [11]. The framework provides for the creation of deep networks by choosing appropriate layers and specifying the preceding and succeeding layers in the design. The inputs to the framework can be in the HDF5 format, which is particularly suitable for the representation of 3D data, such as a CT scan. The steps in preparing the data are explained in the previous section, and are the same for each CT scan. Hence, we have one HDF5 file representing all the CT scans of a patient, and each HDF5 file has the data along with the label. This label is used in both the training and testing phase

Batch sizes are also variable, and can be set by the user. For large batch sizes, the learning process is significantly slow (requires a few days) and often terminates due to insufficient memory availability. We have used a batch size of 20 for most experiments. The training of the network is run for 1000 iterations. After every 100 iterations the network is tested for accuracy. Initial learning rate is set to 0.001 and for every 100 iteration the learning rate drops by a factor gamma=0.1

Results:

5.1 Testing data

I tested my CNN model on 1622 images. I had an validation accuracy of 97.22 %. My model has a precision of 87.31 % and recall of 74.46 %. The model has a specificity of 97.68 %.

From the confusion matrix, we can conclude that out of 1622 CT scan images of different patients 1305 were detected as true positive which means they have cancer, 35 were detected as false positive which means the model predict that these patient having a cancer but they don't have cancer. The false positive is also known as type 1 error. A total of 69 patient have detected as false negative that means they don't have cancer but actually they have cancer. This type of error is also called as type 2 error. Out of 1622 CT scan of different patient 213 were detected as true negative which means these patient don't have cancer and the model predict that these patient don't have cancer.

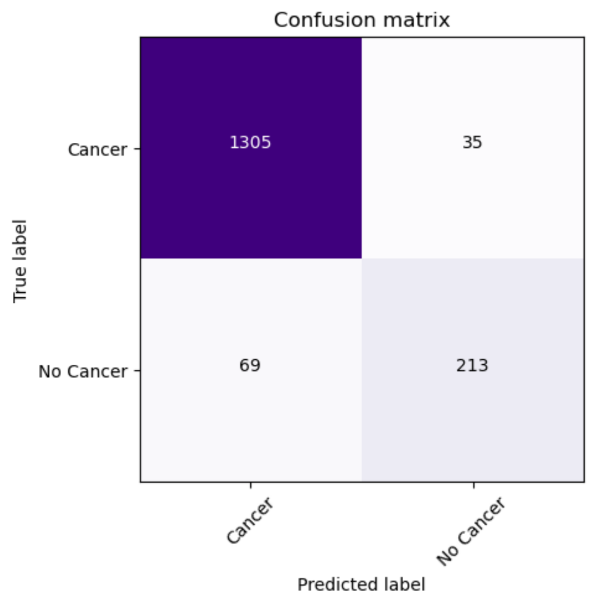

Figure 7. Confusion Matrix with True label and Predicted label

The visualization model shows enhanced visualization of lung cancer detection.

C:\Users\acer1\Anaconda3\LungCancerDetection\LungCancerDetection\src\models>python visualize_model.py

Instructions for updating:

Use standard file APIs to check for files with this prefix.

[[1. 0.]]

(5, 5, 1, 32)

The weighted convolutional neural network 0 is:

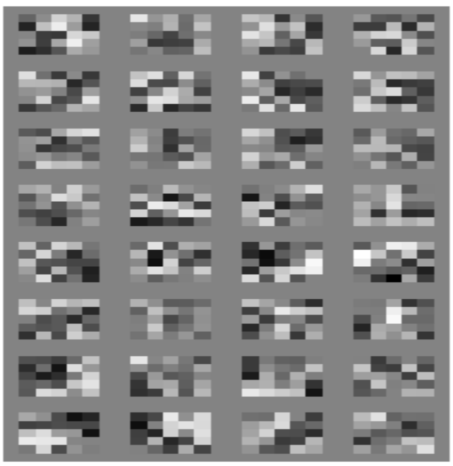

Figure 11. Weighted Convolutional Neural Network

5.2 ROC and AUC: ROC and AUC curves are important evaluation metrics for calculating the performance of any classification model. These definitions and jargons are pretty common in the Machine learning community and are encountered by each one of us when we start to learn about classification models. However, most of the times they are not completely understood or rather misunderstood and their real essence cannot be utilized. Under the hood, these are very simple calculation parameters which just needs a little demystification.

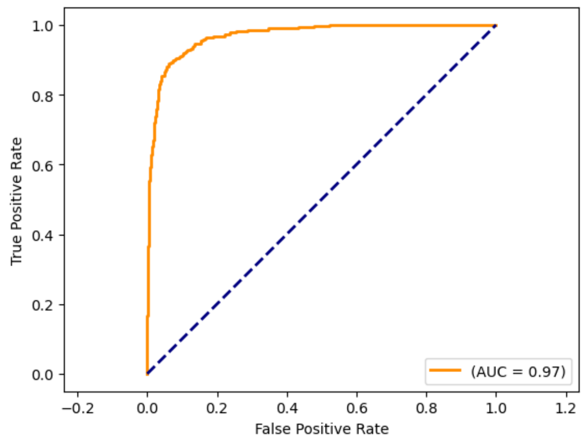

Figure 12. Accuracy obtained by our CNNA model

6. CONCLUSION

The accuracy of classification of the CT scans is calculated for the developed deep convolutional neural network (CNN) architecture to detect nodules in patients of lung cancer and detect the interest points using U-Net architecture. This step is a pre-processing step for CNN. The deep CNN models performed the best on the test set. While we achieve state-of-the-art performance AUC of 0.97, precision of 0.87 and recall of 0.74. The model has a specificity of 0.97. We perform well considering that we use less labeled data than most state-of-the-art CAD systems. As an interesting observation, the first layer is a pre-processing layer for segmentation using different techniques. Threshold, Watershed, and U-Net are used to identify the nodules of patients. The network can be trained end-to-end from raw image patches. Its main requirement is the availability of training database, but otherwise no assumptions are made about the objects of interest or underlying image modality. In the future, it could be possible to extend our current model to not only determine whether or not the patient has cancer, but also determine the exact location of the cancerous nodules. The most immediate future work is to use Watershed segmentation as the initial lung segmentation. Other opportunities for improvement include making the network deeper, and more extensive hyper parameter tuning. Also, we saved our model parameters at best accuracy, but perhaps we could have saved at other metrics, such as F1. Other future work include extending our models to 3D images for other cancers. The advantage of not requiring too much labeled data specific to our cancer is it could make it generalizable to other cancers.

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