

Thyroid Cancer Detection using Deep Learning

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Abstract: This research paper aims to detect thyroid cancer using ultrasound image of the thyroid. This is done by using CNN model of deep learning to classify whether the cancer is benign or malignant. This model uses image processing by deep learning using which we are measuring accuracy and loss values of convolutional neural network model and the performance of the algorithm is evaluated by accuracy score, loss and mean accuracy. Finally, we selected the K-fold cross-validation for cross-checking and better accuracy.

Keywords: Thyroid cancer, Deep learning, CNN, K-fold

I. INTRODUCTION

Early detection of thyroid cancer is very important so that the problems because of thyroid cancer can be avoided in the future.

When bodily cells transform (mutate) and proliferate out of control, cancer develops. When your body need more normal cells, they multiply until they are no longer required. The irregular cells that make up cancer develop even if your body doesn't require them to. The irregular cells in the majority of cancers develop into a lump or mass known as a tumor. A cancer cell's ability to infect adjacent tissues depends on how long it has been present in the body. They may even spread to various anatomical regions (metastasize).

The endocrine system includes the thyroid gland. Your body produces and uses hormones under its control. Your windpipe and the front of your neck are covered by it (trachea). It's above your collarbone and below your Adam's apple. Frequently, you cannot see or feel your thyroid.

Thyroid gland changes are often simple to see and feel. Nodules, which are lumps or bumps, are widespread. the most of them are not cancer (benign). They might not even require treatment. The spread of benign thyroid growths to other bodily organs is unlikely. Through the blood and lymphatic systems, malignant cells can enter adjacent tissues, spread out of control, and invade other regions of the body.

Early detection of thyroid cancer is very important so that the problems because of thyroid cancer can be avoided in the future. Outbreaks of thyroid cancer have increased by 3% - 7% almost every year.

In our proposed system we are using convolutional neural network and K-Fold algorithms. Our dataset contains images two different classes of cancer -benign and malignant. To remove noise from images we have applied augmentation (adjustment) technique such as brightness, zoom, rear, flip, etc.

Based on different values of epochs and other parameters we are measuring accuracy and loss values of convolution neural network model and the performance of the algorithm is evaluated by accuracy score, loss and mean accuracy.

In order to interpret data with a grid pattern, such as images, CNN is a type of deep learning model. CNN was created with the animal visual cortex in mind and is intended to learn spatial hierarchies of features automatically and adaptively from low to high level patterns. Convolution, pooling, and fully connected layers are the three types of layers (or "building blocks") that make up a standard CNN.

We apply a resampling method known as cross-validation to ensure that the model can successfully operate on unseen data. For greater accuracy and cross-validation, we choose the K-fold cross-validation. When compared to other techniques, K-Fold CV provides a model with less bias. In K- Fold CV, we have parameter 'k'.

The dataset will be split into how many folds depending on this parameter. Every fold has an equal probability of appearing in the training set (k-1) times, ensuring that every observation in the dataset is present and allowing the model to better understand the underlying data distribution. This makes sure model work under unseen environment as well with same level of accuracy and flexibility.

II. RELATED WORK

Of all solid malignant tumors, thyroid cancer incidence has been rising at the quickest rate. Thyroid cancer is now ranked as the seventh most frequent cancer in women and the fifteenth most common cancer in men globally due to its relatively high incidence, which is expected to continue to rise [21]. The medical profession and society are now very concerned about the study of thyroid cancer. It is difficult to make a thyroid cancer diagnosis until it is known how fast growing it is. Most thyroid tumors appear as thyroid nodules, which are usually found by chance during neck diagnostic imaging [23–25]. The gold standard test for identifying thyroid nodules is high-resolution ultrasound. Thyroid disease is generally diagnosed by visual inspection of ultrasound images. By giving ultrasound pictures, thyroid nodule imaging enhances thyroid disease diagnosis. Radiologists can report on the likelihood that thyroid nodules are malignant using a standardized grading system based on ultrasonographic features of thyroid nodules such as internal composition, echogenicity, calcification, margins, and size. When employing high-resolution ultrasound, the prevalence of thyroid nodules in a randomly chosen population is as high as 19–68%. It is crucial to distinguish between benign and malignant thyroid nodules since the majority of nodules are benign and the percentage of malignant nodules is very low (7–15%) [26].

In [1] it is stated how common thyroid diseases are now-a-days and how data mining techniques can be used to predict such diseases. Humans frequently get thyroid diseases. Today, more women than males suffer from thyroid illness. Thyroid illness comes in two different forms: hypothyroid and hyperthyroid. These illnesses have a wide range of side effects on the human body, including stress, weight increase, and weight reduction. Physicians can treat patients properly if this sickness is discovered at an earlier stage. Many illnesses may now be predicted thanks to data mining. One of the most important techniques in data mining is classification. This learning is monitored. Predefined data sets are classified using it. Health care data are both increasing in bulk and complexity at an exponential rate. The primary purposes of data mining in healthcare organizations are decision-making, illness diagnosis, and improving patient care. In this study, data mining is used to forecast hypothyroid illness. The hypothyroid study's dataset was downloaded from the UCI repository. The classification of this thyroid condition is challenging. To improve accuracy, an experimental investigation is conducted utilizing linear discriminant analysis (LDA). CART, REP Tree, J48, and other data mining classification algorithms are only a few examples. In order to get superior classification results, the study as a whole recommends using hybrid models rather than any one model.

In paper [2] author tries to describe how health conditions can vary greatly from healthy to very ill. This study suggests using a graph-based algorithm to predict risk in order to categorize a situation that is gradually growing and where the majority of the data is unlabeled. The construction of an effective iterative algorithm includes a demonstration of convergence. The usefulness and efficiency of our technology are demonstrated through extensive tests using datasets from both real health examinations and artificial datasets.

Author in paper [3] determines how Thyroid Data can be Predicted using Data Classification Algorithm. The principal and largest gland in the endocrine system, according to this statement, is the thyroid gland. The hypothyroid dataset is subjected to the data mining approach in order to identify the positive and negative cases across the board. To improve therapy, decision-making, and illness diagnosis, datasets are categorized. In this study, the random forest method from data mining is used to predict hypothyroid disease. Comparing the random forest with LDA method leads to better accuracy, precision, recall, and F-measure. Future research focuses on verifying several illness datasets concurrently, including those for heart disease, diabetes, and other conditions.

In [4], author uses Optimal feature-based multi-kernel SVM approach for thyroid disease classification. The author attempts to classify thyroid data using a kernel-based classifier approach and the best feature selection. For the purpose of classifying data using "multi kernel support vector machines," they developed classification models and a group presentation. The suggested model's uniqueness and goal was feature selection; it was utilised to improve grey wolf optimization to increase the performance of the classifying process. The irrelevant elements from the unique dataset served as the basis for this best feature selection, which also increased the model's performance computationally. However, in longer run, using SVM can cause some issues as well. After training and evaluating accuracy, SVM linear encountered a hardware processing capacity issue when classifying the data.

According to earlier research, binary classification tasks were the most often performed. Machine learning techniques have been used relatively often in these research to differentiate between hypothyroidism and hyperthyroidism. By blending linear discriminant analysis (LDA), k-nearest neighbors (KNN), and adaptive neuro-fuzzy inference system, for example, [7] have suggested a hybrid decision support system for detecting thyroid illness and have achieved an accuracy of 98.5%. [9] also utilized LDA, and according to this research, the classification accuracy rates for

hypothyroidism and hyperthyroidism were 99.62%. Similar to how random forest (RF), support vector machine (SVM), and KNN were each used independently, the RF technique yielding accuracy rates of 98.5% [11].

When compared to thyroid issue diagnosis, thyroid cancer detection is another challenging topic for researchers to explore. Due to a rise in thyroid cancer cases, differentiating benign and malignant thyroid nodules is a challenging study area. Machine learning algorithms have been widely used by researchers to extract different aspects from ultrasound pictures for thyroid cancer screening. The size, echogenicity, microcalcifications, border, form, contour, and vascularity of thyroid nodules are the characteristics that are most frequently utilized to categorize thyroid nodules using ultrasound imaging [14]. According to [8], who used a Bayesian classifier and evaluated 49 nodules, the area under the curve was 0.851. The extreme learning machine (ELM) was used with 203 nodules utilizing ultrasound pictures in addition to the Bayesian classifier and attained an accuracy of 87.72% [16].

The quantity of medical pictures is crucial to the deep learning-based medical diagnostic system. The performance of the deep learning algorithm may be guaranteed by having enough data. Thyroid nodule image data, however, is extremely scarce and costly in the field of medical image processing. When classifying thyroid nodules using deep learning, the lack of data has become a difficult issue.

A deep neural networks classification model based on image enhancement technology is suggested in this study as a solution to this issue. We can now fully utilize the little image data thanks to the development of image enhancing technologies. The clinical relevance of the computer-aided diagnosis system would be significantly determined by the accuracy, precision, and value of loss during model propagation.

III. PROCESS FLOW DIAGRAMS

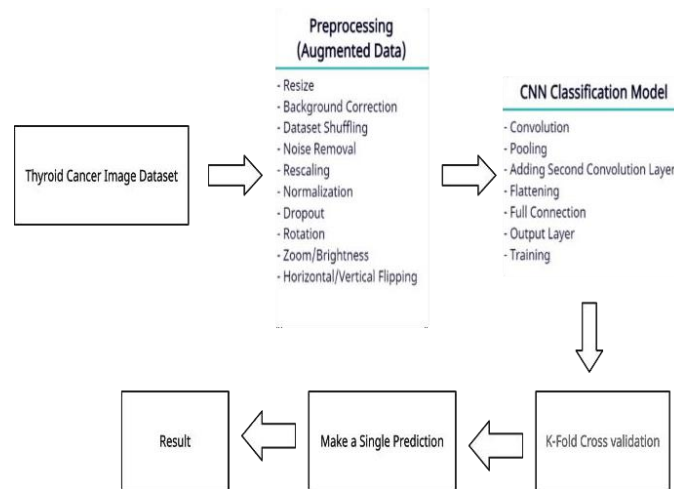


Fig. 1 Architecture Diagram of the Model

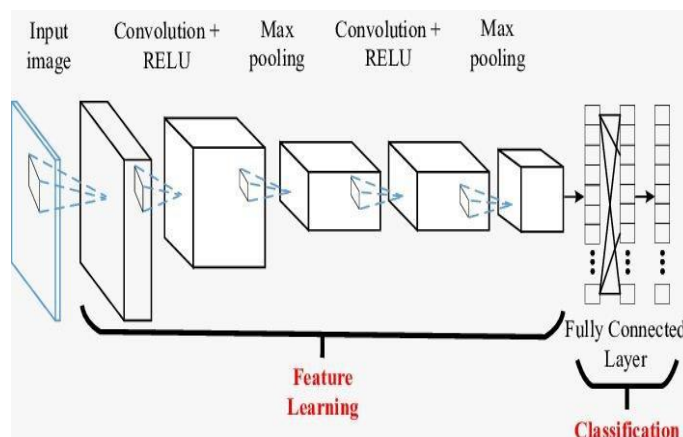


Fig. 2 Working of a Convolutional Neural Network

IV. METHODOLOGY

To implement Fig. 1 in Section III ----

The present study aims to explore the potential use of the metaverse in the fields of virtual shopping and collaborative shopping. The data set images were divided into two categories—benign and malignant. The data set had 293 ultrasound exams in total. The images obtained from the data collection needed to be enhanced and pre-processed. It was necessary to resize, scale, and filter each image to the same distance. Picture pre-processing was followed by segmentation, which entailed the binarization of the image. This is done through data augmentation.

Then Images are passed through a CNN training model. One of CNN's key strengths is that it trains its classifiers using simple techniques, which enables it to learn the properties of the target object. Convolution, pooling, and fully connected layers are the three types of layers (or "building blocks") that make up a standard CNN. Convolution and pooling layers do feature extraction, whereas a fully connected layer translates the retrieved features into the output, such as classification. Then K-fold cross validation is used. K-fold Cross-validation, which divides the dataset into K folds, is used to assess the model's performance when faced with fresh data. K denotes how many groups the data sample is divided into. For instance, if the k-value is 5, we may refer to this as a 5-fold cross-validation. At some point throughout the procedure, every fold is utilized as a testing set.

(b) To implement Fig. 2 in Section III:

When the Ultrasound of Thyroid cancer patients from dataset are fed into the training model, model captures the features of all ultrasound images and using the knowledge that images are classified as benign or malignant, model is trained. All images go through the convolutional neural network's different layers for assessment.

Convolution, pooling, and fully connected layers are the three types of layers (or "building blocks") that make up a standard CNN. Convolution and pooling layers do feature extraction, whereas a fully connected layer translates the retrieved features into the output, such as classification. In CNN, which is made up of a stack of mathematical operations, such as convolution, a specific kind of linear operation, a convolution layer plays a crucial part. This layer creates a dot product between two matrices, one of which is the kernel—a collection of learnable parameters—and the other of which is the bound area of the receptive field.

Then, by generating a summary statistic from the surrounding outputs, the pooling layer substitutes for the network's output at certain points. This helps in lowering the representation's spatial size, which lowers the amount of computation and weights needed. The pooling operation is processed on every slice of the representation individually. The translation invariance that is provided by pooling ensures that an item may be recognized wherever it appears in the frame. Following that, the Fully Connected layer aids in mapping the representation between the input and output. When the model is fully trained using all 187 training images, model can estimate that whether the test images and the user's input image is benign or malignant. This helps user to know the level of threat they have with the thyroid cancer in their body.

V. EXPERIMENTS

A. Dataset

Ultrasound images to be fed into the convolutional neural network for training are classified as Benign and Malignant.

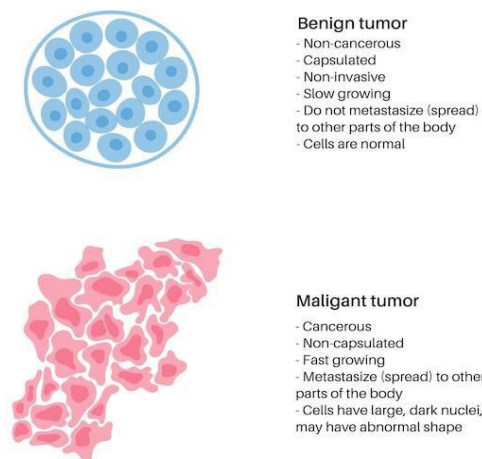


Fig. 3 Benign vs Malignant Cancer

The database is taken from the ITCIC (International thyroid cancer Image Collaboration) Archive. Contains 133 images of malignant tumors and 160 images of benign tumors. All images have been converted to low resolution (64x64x3) RGB. Then Data augmentation and pre-processing is done to all the images.

During preprocessing we have passed resizing, Rescaling, Shuffling, Dropout, Zoom/Brightness adjustment, Rotation, Background correction, horizontal flipping, etc. parameters So that we can convert our image data into augmented image data which will help our CNN model to learn for low- resolution images.

To remove noise from images we have applied augmentation (adjustment) technique such as brightness, zoom, rear, flip, etc. Using augmentation technique, we are making dataset clearer and generating new dataset from existing dataset.

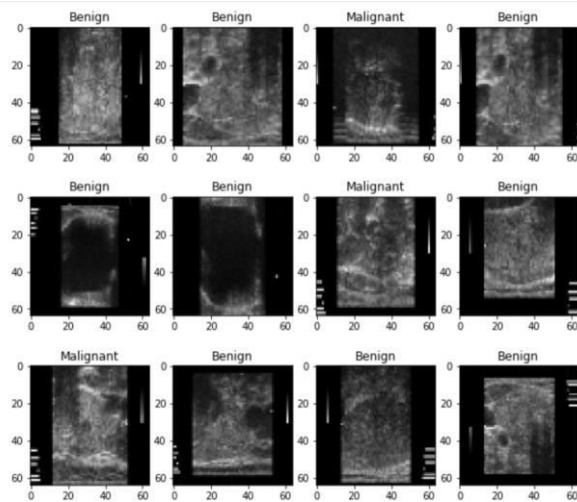


Fig. 4 Dataset Sample after pre-processing

B. Evaluation Metrics

Using 90 images of Ultrasound of benign cancer and 97 images of Malignant cancer, a convolutional neural network is trained. Based on different values of epochs and other parameters we are measuring accuracy and loss values of convolutional neural network model and performance of the algorithm is evaluated by accuracy score, loss and mean accuracy.

The accuracy of the model improves and the loss lowers as the number of epochs rises. Using values of loss and accuracy, data is tabulated and plotted in graphs to show the flow of model.

After model is fully trained using all images in dataset, test data is used to check accuracy. Test data in dataset consists of 70 ultrasounds of benign cancer and 38 images of malignant cancer. Each image after testing is classified as Benign and malignant based on the model, and then compared with original labeled classification to check the accuracy of the model.

VI. RESULT

Based on different values of epochs and other parameters we are measuring accuracy and loss values of convolutional neural network model and performance of the algorithm is evaluated by accuracy score, loss and mean accuracy.

TABLE 1
Results for different Values of Epochs

Epoch	Neurons	Accuracy	Loss	Val- loss	Val/ Accuracy
25	128	86.35	29.68	35.79	82.27
50	128	89.55	21.44	31.98	84.85
75	200	91.65	18.85	35.69	85.15
100	200	95.62	11.92	34.79	85.61

As value of number of Epochs go from 25 to 100, the overall accuracy of the model increases from 86.35% to 95.62.

The Loss of model decreases from 29.68 to 11.92. Accuracy and loss in the keras model for validation data may vary with different scenarios when we train the model. Loss should typically decrease and accuracy should increase as each period increases. This means model is learning the features instead of just cramming values.

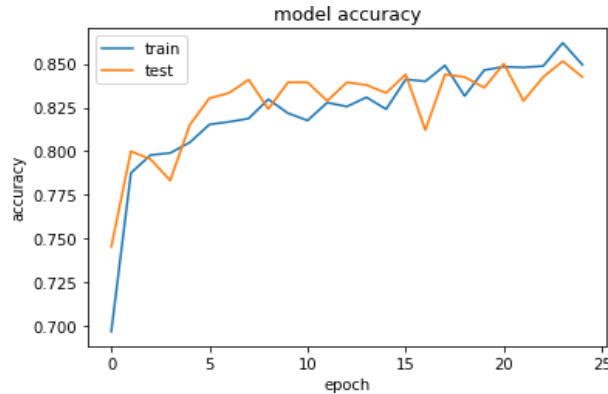


Fig. 5 Graph showing Accuracy vs Epoch for Total Epoch value =25

The first epoch train accuracy in plot 5 is 0.6387, while the last epoch train accuracy is 0.8474. The best/highest train accuracy, 0.8717, is provided by epoch 24, which is reached in that epoch. The graphic shows that the train's accuracy rises during the course of the 25 epochs. All 25 epochs show a modest difference between the val accuracy and the train accuracy. The maximum val accuracy value is 0.8515 for epoch 24. Val accuracy is 0.8424 as of the most recent era.

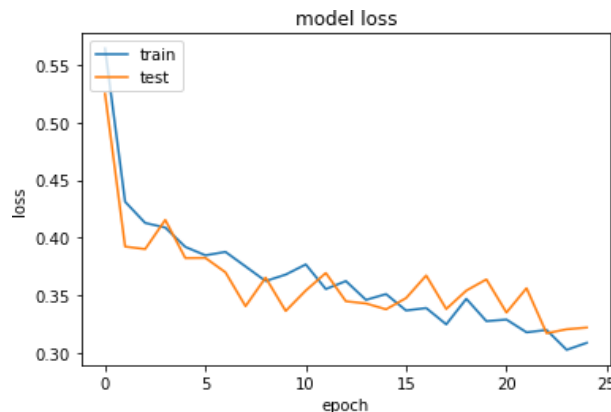


Fig. 6 Graph showing Loss vs Epoch for Total Epoch value =25\

In figure 6, the train loss for the first and last epochs is 0.6248 and 0.3209, respectively. In epoch 24, the smallest train loss of 0.2933 is achieved. The train loss plot appears to be declining throughout the course of all 25 epochs. All 25 epochs show a modest difference between the train loss and the val loss. Val loss as of end most Epoch is 0.3222. The loss curves help us detect any difficulties that may result in an underfit or an overfit model by providing a better understanding of how learning performance changes over the number of epochs.

The accuracy of the model improves and the loss lowers as the number of epochs rises. A model's loss value indicates how well or poorly it performs after each optimization cycle. Usually with every epoch increasing, loss should be going lower and accuracy should be going higher. This means model is learning the features instead of just cramming values. CNNs are primarily used for image classification and recognition. The specialty of a CNN is its convolutional ability.

Also, val_accuracy indicates the accuracy of the predictions of a randomly separated validation set after each training period. High and increasing val_accuracy means the model is not in overfitting conditions and is working properly.

We must divide the data set into three sets—Training, Testing, and Validation—in order to do this K-Fold Cross Validation, which is difficult due to the little amount of data. Throughout the whole procedure, training and testing would be executed precisely once for each set (fold). It aids in preventing overfitting. We are aware that the highest

performance accuracy is achieved when a model is trained utilizing all of the data in a single brief run. We can design a generalized model by avoiding this using k-fold cross-validation.

Now For K-Fold Cross validation, Value of K taken is 10. We are dividing the provided dataset into 10 folds and executing the Train and Test on each fold. One-fold is used for testing during each run, while the remaining folds are used for training and advancing through iterations.

TABLE 2
Results for different Values of Epochs for K=10

Epoch	Neurons	K-fold Split	Mean - accuracy (%)	Standard Deviation (%)
25	128	10	85	24.09
50	128	10	77.5	21.10
75	200	10	65.83	21.87
100	200	10	78.33	25.60

For K=10, one-fold is considered for testing while rest 9 folds are considered for training. Then the Model is run for different values of Epochs and Accuracy is noted. Mean accuracy and standard deviation are calculated to see how model works under different circumstances and conditions. If the standard deviation is too high, it could mean model is just cramming values instead of evaluating the dataset. This way data can be cross validated and reassured the model is working well under different conditions.

Here we can see for Epoch value 25, using the whole dataset the accuracy was 86.35, while using K fold cross validation the mean accuracy is 85%. This shows even with a whole different environment and dataset, model is still efficient and works perfectly fine.

VII. CONCLUSION

In conclusion we can Use Convolutional neural network to detect thyroid cancer in the ultrasound image and state how dangerous the cancer is for the patients' health. If the cancer is estimated to be benign, then the risk on patient's health is not lethal and is curable, whereas if the cancer is estimated to be malignant, immediate steps needs to be taken to stop the fast-growing cancer cells in thyroid.

CNNs are useful in settings in which some spatially invariant patterns in the input are expected, such as images or sequential data. In thyroid cancer ultrasound images, there are spatially invariant patterns, making CNN efficient model to estimate the classification of cancer. We also concluded using K-fold cross validation that the model is trained and is working properly. We see that model is able to give almost same accuracy even with different dataset as in K-fold cross validation.

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