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Lung Cancer Diagnosis using Prewitt & SVM as Hybrid Model

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Abstract:- The illness that claims the most lives is lung cancer. It begins with the tissues that are responsible for breathing. The majority of cancer patients have lung cancer, and the survival rate is the same for men and women. Lung cancer is most commonly brought on by smoking, however there are several industrial asbestos products that can harm our lungs and result in lung cancer. Lung cancer can fall into one of two types, the first of which is benign, which is thought to be caused by malignant cells but is less hazardous since it can be treated. It is the earliest stage of lung cancer and only affects a small number of tissues. The second type is malignant, which is serious and deadly and can kill a person. It is strongly advised to begin receiving therapies as soon as possible because it is the second and final stage of lung cancer, which is scarcely treatable. Numerous researchers have studied it and attempted to develop a way to identify it in its early stages, while cells are still in the benign state. Lung cancer may be accurately identified through image processing, which is a field of study. There are several methods for implementing it, but accuracy and false alarm rate are important. System should take false alarm rates very seriously and should have high, reliable accuracy. The shape of malignant cells and blood vessels are extracted using Prewitt edge detection in the suggested approach. The proposed approach employs Support Vector Machine (SVM) as well to identify normal and pathological cells so that it can decide right away which grade each one belongs to. The IQ-OTHNCCD dataset, which has a total of 1097 pictures for benign, malignant, and normal categories, was used to evaluate the proposed approach. Compared to previously implemented systems, the system maintained a high degree of accuracy.

Keywords:- *Lung Cancer, Prewitt Edge Detection, Support Vector Machine, Benign, Malignant, CT-Scan.*

I. INTRODUCTION

Lung cancer and its causes are topics that everyone is acquainted with. Smoking is one of the major reasons, although it is not the only one. People who are near smokers and who inhale their smoke run the risk of developing lung cancer. Inhaling asbestos, arsenic, soot, and other industrial pollutants are only a few of the many industrial sources of the same. If someone in the family has had lung cancer, it might also be a contributing factor. Lung cancer can also result from HIV infection, and those who have HIV infection may also be more likely to have tissue impairments [1]. However, they all have a few symptoms that may be identified by a medical checkup or an imaging equipment. Lung cancer may be detected at both phases using computerised tomography, sometimes known as a CT scan. Image processing can automate the procedure since human diagnosis takes a little amount of time. If a person wants a routine exam, an automated system that can scan for cancer and identify its stages or determine if it is normal or not must be used. The dataset called IQ-OTHNCCD has CT lung pictures that may be used for testing. Each dataset places a new challenge on the researchers to evaluate the effectiveness of their systems and make the necessary improvements for a better automated system.

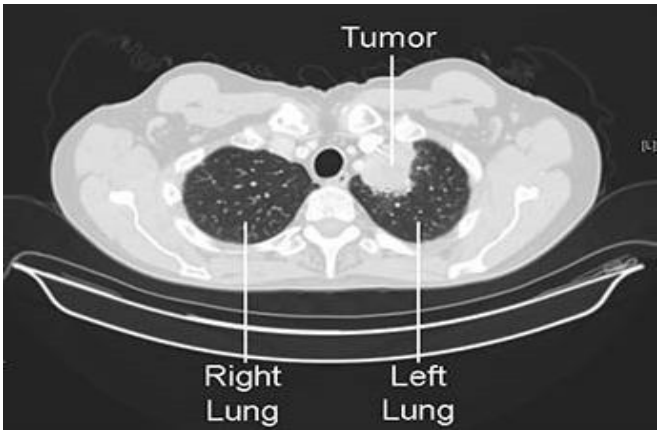

Fig 1 Lung CT Scan Image [1]

The lung's CT scan picture in Fig. 1 depicts damaged cells. Any imaging test can not prove that a person has lung cancer or any other disease, but it does provide a wealth of information that may be used to accurately predict any disease. An imaging system can be used to detect lung cancer at an early stage. Every illness has relatively few early signs, therefore it's important to identify it quickly in order to effectively treat it. Lung cancer is a terrible illness that may kill people, hence automatic diagnosis is a highly valuable tool [2]. Therefore, a lot of studies rely on machine learning techniques like CNN, RNN, ResNet, and others. However, all of them are highly deep neural networks that take more computing time to train and test the datasets since they need a lot of training samples. A network model should be lightweight and employ modest, clever filters in hidden layers so that precise, effective results may be obtained. There is a different strategy, called a classifier, which can categorise normal and pathological cells and make decisions in accordance with that classification. There are several classifiers available that may be used to do classification for improved results, including Navie Bayes, K-means clustering, SVM, and many others. However, SVM is regarded as the best classifier among them since it has a higher degree of prediction for categorising various cell patterning [3].

II. RELATED WORKS

Many studies have attempted to extract the lesion from lung imaging and have had fair success with a limited amount of false alarms. An enhanced deep neural network and ensemble classifier based lung cancer detection system was proposed by P. Mohamed Shakeel et al. [4]. System attempted to address the shortcomings of deep neural networks, which demand large amounts of memory to hold the system's weight model. However, deep learning is still necessary for deep neural networks to provide effective results. The system also employs ensemble classifiers like GAWA, ACO, PSOMS, and HSOGR, which integrate the results from four classifiers. But compared to other classifiers, SVM is far more advanced and effective. SVM has a good prediction rate and can handle both linear and nonlinear data. The best classifier for any illness linked to image processing is considered to be SVM. In the sphere of medical science, accuracy is crucial since a false alarm rate with a serious patient might result in the loss of a human life. EK-Mean Clustering is the foundation of the approach presented by P.B. Sangamithaa et al. [5]. This methodology divides the ROI first, followed by exams for impairment detection that look at the illness. Given that lung growth CT images have some features, such as variability in cancer appearance and ambiguous cancer limits, even with a few newly developed lung growth divisions and improving cancer division techniques, which are still fascinating. The growth division approach for CT images, which was developed to address this problem, separates non-upgrading lung tumours from lung tissues that had previously been clustered. Using a median filter and morphological operation as its foundation, Selin Uzelaltinbulat et al. [6] created a system. The work comprises unique image processing tools that, when gradually integrated into the system, successfully achieved the required goals. The division framework goes through several steps before achieving its ultimate goal, which is to segment the lung development. The first step is picture pre-processing, where several enhancement techniques are used to improve and lower noise in photos. The subsequent stage is when the various components in the photos are divided into sections to define the cancer region. Since each image's development has unique dim levels, the stage edge was chosen in this case in a way that ensures the correct selection of all pictures. Various systems in the area of automated lung cancer diagnosis were examined by G. Niranjana et al. [7]. After evaluating several studies on the approaches for dividing lung lesions, it has been shown that adding an edge to various CT scans separates the lung region from non- ROI. The most effective and least complicated lung division strategy is staggered thresholding. It produces better results for lesion division than other division methods. Lesion characteristics are determined by the lesion's form and surface components. The component-based technique was deemed to be superior for categorization in light of the discussion above. A ResNet-based system was proposed by Zirong Li et al. [8]. The author of this work described a method for utilising ResNet to identify density in a chest picture. The RCNN architecture has been shown to be a little quicker and to be able to provide results more efficiently. Component extraction, which involves taking a section of the network and using RESNET to demonstrate improved execution, has also been found to be more effective. Whether the picture depicts a malignant or healthy lung has been determined. It has been demonstrated that it performs better than Alexnet and contains slightly more convolutional layers than Alexnet. The issue with this article is that it uses chest X-rays rather than lung CT scan pictures. Lung cancer cannot be accurately diagnosed with an X-ray picture. The lung cancer's malignant region cannot be seen on an X-ray. As opposed to X-ray pictures, it is preferable to utilise CT scan images since they may generate a high degree of precision. A system based on the Gaussian Filter, Median Filter, and Watershed Segmentation was proposed by Suren Makaju et al. [9]. The suggested model is inaccurate and fails to identify the cells that are impacted by cancer. The suggested framework uses watershed division to identify the cancerous lesion from the lung CT scan picture and classifies the cancer cells as malignant or benign. The proposed model has a precision of 92%, which is greater than that of previous models, while the classifier has a precision of 86.6%. Overall, the suggested framework is better than the best model now in use, although it doesn't classify diseases into stages like cancer's stages I, II, III, and IV. Therefore, carrying out the arrangement in phases should be achievable as future degree development. Likewise, proper pre-processing and excellent noise removal may increase accuracy even more. A method based on DenseNet and Adaptive Boosting was suggested by SHANCHEN PANG et al. [10] et al. With the use of computations from DenseNet and AdaBoost, the author of this study created a model of lung cancer CT scans. In order to improve the model's capacity for conjecture and prevent clustering findings from being biassed, interpretation and transformation procedures are added to the initial dataset.

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DenseNet is then developed to handle the lung cancer datasets and characterise the gathered data at that point. Finally, adaboost computation is used to categorise findings in order to improve execution yet further. Results from the test indicate that the model performs a little bit better, and the test's precision was 89.85%. Here, data has been transformed to improve system performance. However, the densely linked network of DenseNet may make it more difficult and negatively impact the effectiveness of computing. Alexnet CNN is the foundation of the method developed by Aman Agarwal et al. [11]. In this study, the author sought to identify the cancer's malignant component using an image from a lung CT scan as input. Here, the network has been trained using diverse lung malignant pattern shapes and sizes from CT scanned pictures. It has been put into place based on the categorization procedure, which determines whether it is malignant or benign. Additionally, the cancer region is being extracted from the picture utilising different thresholding techniques, specific morphological methods, and Alexnet for the final classification. Here, the system's classification of malignant and non-cancerous pictures resulted in an accuracy rate of 96%. The performance of the system or network is weak since Alexnet is not a particularly deep model or network and may have trouble extracting the image's features.

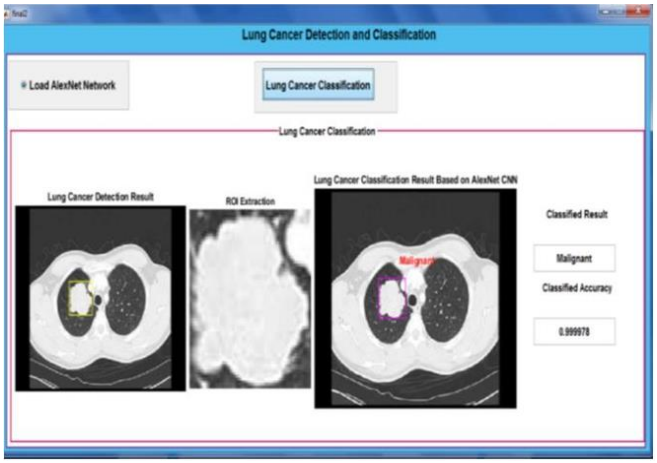

Fig 2 GUI of Alexnet based System [6]

An Entropy Degrading-based system was proposed by Qing Wu et al. [12]. In this review, the author put out a method for detecting SCLC for the early diagnosis of malignant cancer using EDM AI calculations and vectorized histogram elements. Although it demonstrates that EDM has a logically excellent forecast, there is still much need for improvement before the computation can be applied in a clinical setting. The primary goal of this study is to develop a clinical dynamic framework that will enable radiologists to predict lung cancer detection from SCLC with processed tomography (CT) imaging with ease.

III. IMPLEMENTATION DETAILS

Prewitt edge detection and Support Vector Machine are the foundations of the proposed system. The suggested approach has the ability to identify lung cancer automatically while grading it as benign or malignant.

Prewitt edge detection is a technology that can be used to extract the edge of any object and analyse its form. The different blood veins shown in a CT lung picture must be covered up or erased in order to categorise the lesion region. The pre-processing of a picture aids in image enhancement and classifies the different region. To make damaged areas more visible and to determine the density of infected cells, Prewitt edge detection is helpful. Similar cells can be grouped or clustered together using SVM to be classified according to patterns. A non-linear SVM that can classify non-linear data is used in this system: polynomial SVM. Because the structure of a lung CT picture is quite complex, it is preferable to employ a non-linear classifier to provide accurate accuracy. Therefore, the system employs a hybrid model that combines Prewitt Edge Detection and Support Vector Machine.

A. Prewitt Edge Detection

Edges can be extracted by their kernel using the Prewitt edge detection technique. The relevant pixels are compared to extract the edges in this case. Prewitt edge detection uses a kernel that must be combined with the input image matrix and has specific requirements, including that the mask's opposite sign or negative value be present and that the sum of the values in the kernel be zero. According to the needsof the system, the weight of the edge that is to be extracted depends on the kernel value. Two kernels must be processed, one for vertical edge detection and the other for horizontal edge detection. Horizontal kernel can be represented as;

$$G_x = \begin{matrix} -1 & 0 & 1 \\ [-1 & 0 & 1] \\ -1 & 0 & 1 \end{matrix}$$

$$I = \begin{bmatrix} J_{11} & J_{12} & J_{13} & J_{14} & J_{15} & J_{16} \\ J_{21} & J_{22} & J_{23} & J_{24} & J_{25} & J_{26} \\ J_{31} & J_{32} & J_{33} & J_{34} & J_{35} & J_{36} \\ J_{41} & J_{42} & J_{43} & J_{44} & J_{45} & J_{46} \\ J_{51} & J_{52} & J_{53} & J_{54} & J_{55} & J_{56} \\ [J_{61} & J_{62} & J_{63} & J_{64} & J_{65} & J_{66}] \end{bmatrix}$$

$$I_n = G_x \times I$$

Where Gx is the horizontal kernel mask for prewitt edge detection and I is the input matrix.

$$I = \begin{bmatrix} J_{11} \times (-1) & J_{12} \times 0 & J_{13} \times 1 & J_{14} & J_{15} & J_{16} \\ J_{21} \times (-1) & J_{22} \times 0 & J_{23} \times 1 & J_{24} & J_{25} & J_{26} \\ J_{31} \times (-1) & J_{32} \times 0 & J_{33} \times 1 & J_{34} & J_{35} & J_{36} \\ J_{41} & J_{42} & J_{43} & J_{44} & J_{45} & J_{46} \\ J_{51} & J_{52} & J_{53} & J_{54} & J_{55} & J_{56} \\ [J_{61} & J_{62} & J_{63} & J_{64} & J_{65} & J_{66}] \end{bmatrix}$$

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$$I_i = [J_{11} \times (-1) + J_{12} \times 0 + J_{13} \times 1] + [J_{21} \times (-1) + J_{22} \times 0 + J_{23} \times 1] + [J_{31} \times (-1) + J_{32} \times 0 + J_{33} \times 1]$$

$$G_y = \begin{bmatrix} -1 & -1 & -1 \\ 0 & 0 & 0 \\ 1 & 1 & 1 \end{bmatrix}$$

$$I = \begin{bmatrix} K_{11} & K_{12} & K_{13} & K_{14} & K_{15} & K_{16} \\ K_{21} & K_{22} & K_{23} & K_{24} & K_{25} & K_{26} \\ K_{31} & K_{32} & K_{33} & K_{34} & K_{35} & K_{36} \\ K_{41} & K_{42} & K_{43} & K_{44} & K_{45} & K_{46} \\ K_{51} & K_{52} & K_{53} & K_{54} & K_{55} & K_{56} \\ K_{61} & K_{62} & K_{63} & K_{64} & K_{65} & K_{66} \end{bmatrix}$$

$$I_m = G_y \times I$$

Where Gy is the vertical kernel mask for prewitt edge detection and I is the input matrix.

$$I = \begin{bmatrix} K_{11} \times (-1) & K_{12} \times (-1) & K_{13} \times (-1) & K_{14} & K_{15} & K_{16} \\ K_{21} \times 0 & K_{22} \times 0 & K_{23} \times 0 & K_{24} & K_{25} & K_{26} \\ K_{31} \times 1 & K_{32} \times 1 & K_{33} \times 1 & K_{34} & K_{35} & K_{36} \\ K_{41} & K_{42} & K_{43} & K_{44} & K_{45} & K_{46} \\ K_{51} & K_{52} & K_{53} & K_{54} & K_{55} & K_{56} \\ K_{61} & K_{62} & K_{63} & K_{64} & K_{65} & K_{66} \end{bmatrix}$$

$$I_j = [K_{11} \times (-1) + K_{12} \times (-1) + K_{13} \times (-1)] + [K_{21} \times 0 + K_{22} \times 0 + K_{23} \times 0] + [K_{31} \times 1 + {}_{32} \times 1 + K_{33} \times 1]$$

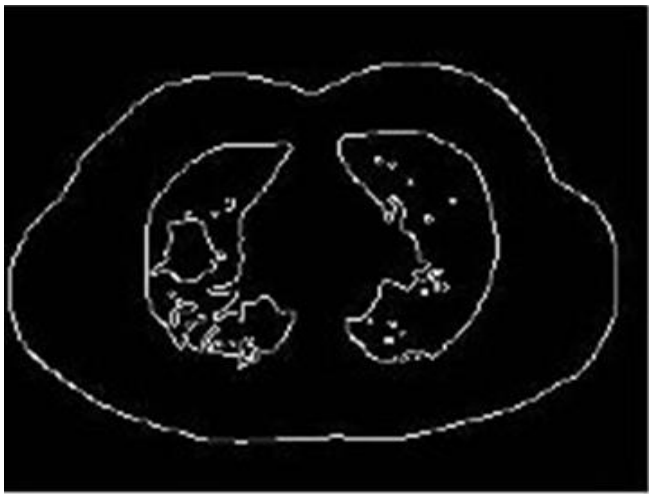

Fig 3 Prewitt Edge Detection of CT Lung Image

$$G = \sqrt{I_n^2 + I_m^2}$$

Where In and Im are the resultant matrix of horizontal kernel and vertical kernel respectively. G is the gradient magnitude of the both the kernels.

B. Support Vector Machine

Support Vector Machine is method of classifying data on the basis of their patterns or appearance. SVM is considered as the most robust prediction technique that can classify data with more preciseness. Here system uses non linear SVM to deal with the non linear data. Most of the medical data belongs to the non-linear classes because of complex structure of blood vessels. Fig. 6 shows the separation of data with hyperplane.

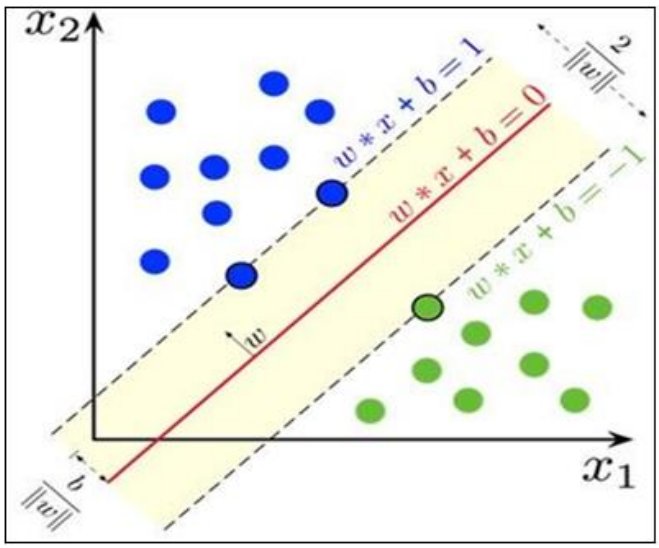

Fig 4 SVM for Two Sample Classes [11]

Every hyperplane can be written as;

$$w * x + b = 1$$
$$w * x + b = 0$$
$$w * x + b = -1$$

Where w is the normal vector, b is the bias, x is the data points. If data point is on the hyperplane then it would be;

$w * x - b = 0$ otherwise it would be either negative or positive. It is required to know that which data points are closer or nearer to the hyperplane.

$$h(x_i) = \begin{cases} +1 \; if \; w.x + b \geq 0 \\ -1 \; if \; w.x + b < 0 \end{cases}$$

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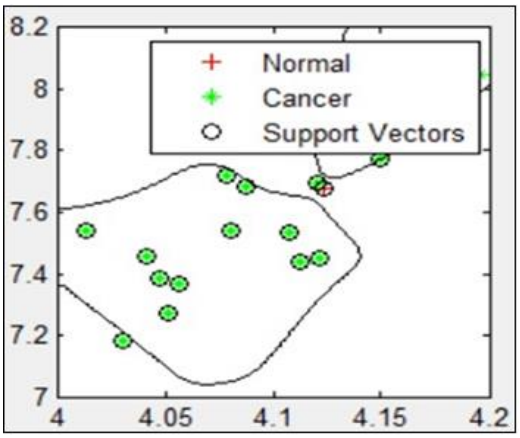

Fig 5 Non Linear SVM Classification

Figure 7 illustrates the non-linear separation of data using SVM, with the aberrant cells shown by the green circle. It is necessary to keep the classification's balance between maximisation and loss. The suggested system's flowchart, shown in Fig. 8, initially loads the dataset picture as input data. The pre-processing module was then started in order to improve the photos' visibility. One of them, the histogram, is in charge of balancing the system's brightness and contrast. Once visibility rises, Prewitt Edge Detection may be activated to pull the lesion's edge and the blood vessels from the input picture. After the edge has been removed, the system will smooth the picture to make the lesion more visible. Once features have been extracted and chosen, SVM classification may begin to categorise the data points. The system then determines the retrieved lesion's entropy. It determines the lesion's density for subsequent comparison with the cutoff value. Threshold value is the relative value at which a choice can be made. As there are three types of lung cancer, the first is malignant, and entropy must be more than or equal to the higher threshold value to be classified as such. The second kind is benign; a healthy lung picture can be taken into consideration if the entropy is larger than the lower threshold value but less than the higher threshold value. As a result, the method also assigns a lung cancer grade based on the density of the lesion.

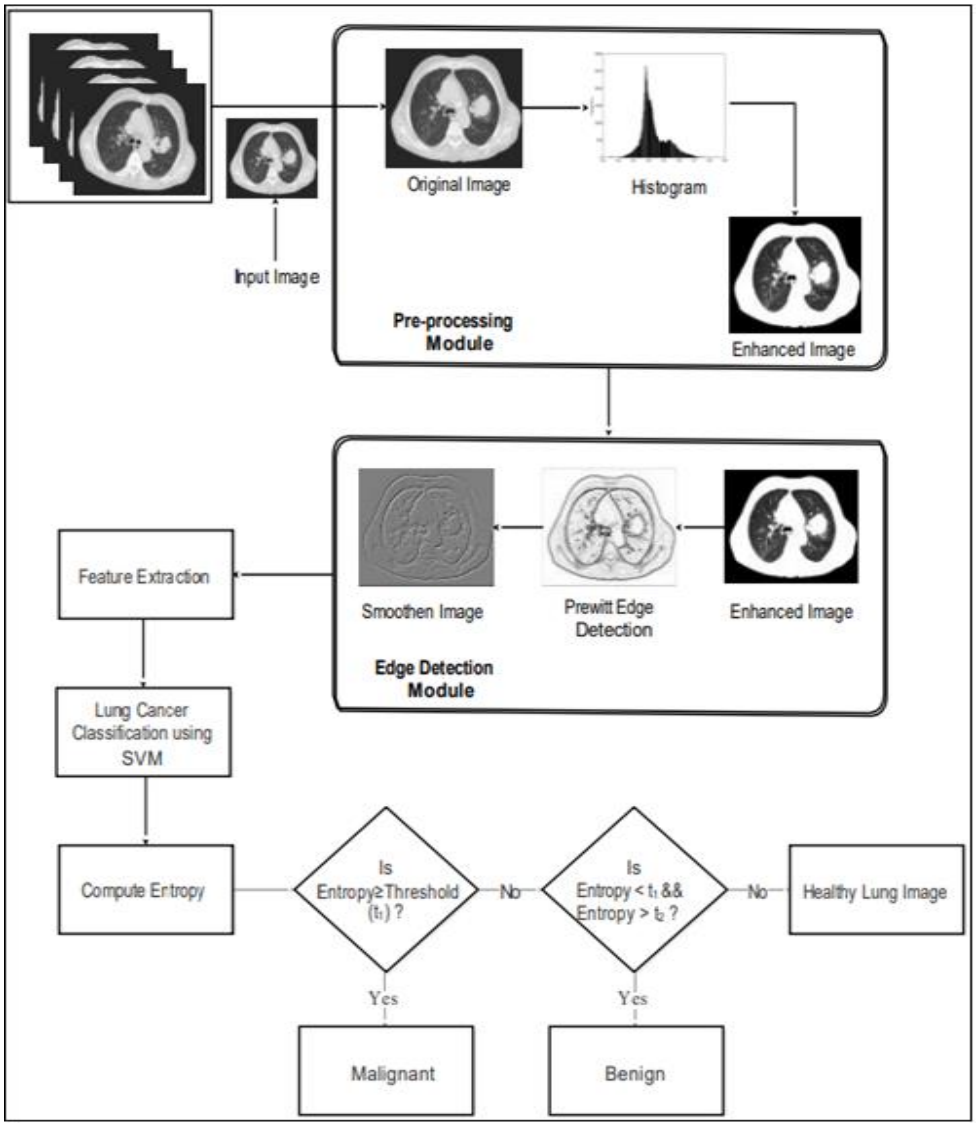

Fig 6 Flowchart of Proposed System

Let it be more tangible with the proposed algorithm and the steps involved in the algorithm.

IV. EXPERIMENTAL RESULT

Four metrics—True Positive (TP), False Positive (FP), True Negative (TN), and False Negative (FN)—are used to measure the success of an experiment. True Positive refers to cases in which a system correctly identified an image as either malignant or benign, whereas True Negative refers to situations in which a system incorrectly identified an image as either benign or malignant. False Negative indicates that an image belongs to the malignant or benign group but that the system diagnosed it as normal. False Positive means that an image has zero grade level and the system diagnoses it as either malignant or benign. In the IQ-OTHNCCD benchmark, there are a total of 416 photos from the normal class, 120 images from the benign class, and 561 images altogether that belong to the malignant class.

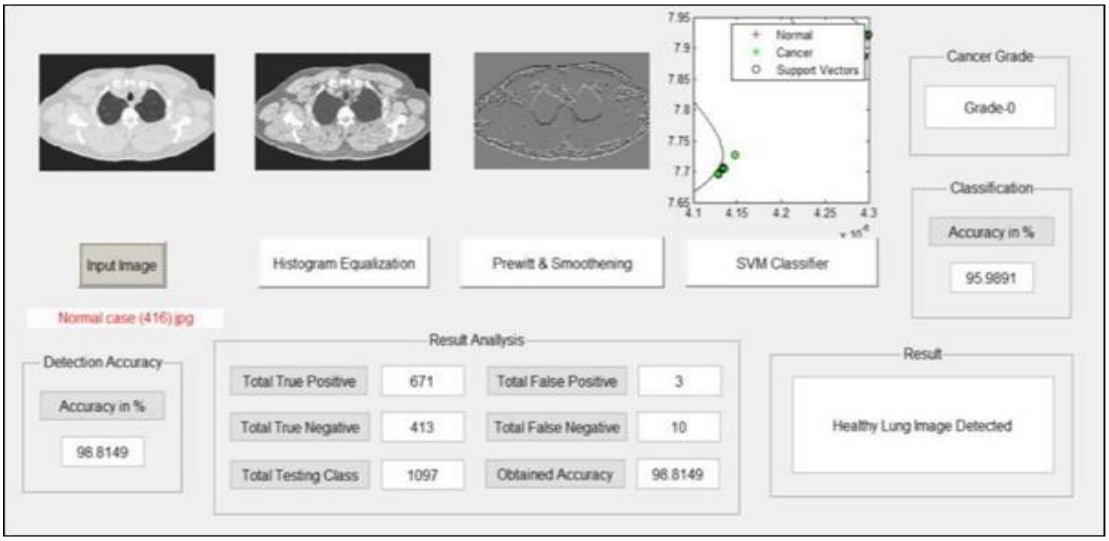

Fig 7 GUI of Proposed System

Table 1 Proposed Algorithm

Prewitt Kernel & SVM Algorithm

Initialization
Input: Set of Image $I=(i_1, i_2, i_3, \ldots\ldots i_n)$
Output: Entropy
Step 1: Input image
Step 2: Apply histogram equalization
Step 3: Apply Prewitt
G_x & G_y are gradient mask kernels derived from horizontally and vertically resp.

$$G_x = \begin{bmatrix} +1 & 0 & -1 \\ +1 & 0 & -1 \\ +1 & 0 & -1 \end{bmatrix} * I, \quad G_y = \begin{bmatrix} +1 & +1 & +1 \\ 0 & 0 & 0 \\ -1 & -1 & -1 \end{bmatrix} * I$$

Gradient absolute magnitude can be computed by combining both the derivates that have been calculated horizontally and vertically.

$$G = \sqrt{G_x^2 + G_y^2}$$

Compute G^{-1} for inversing the matrix to smoothen the image for better visibility
Step 4: Collect data points from prewitt affected matrix as vectors w_i.
Step 5: Calculate the margin

$$w * x + b = 1$$
$$w * x + b = 0$$
$$w * x + b = -1$$
$$h(x_i) = \begin{cases} +1 \; if \; w.x + b \geq 0 \\ -1 \; if \; w.x + b < 0 \end{cases}$$

Step 6: Compute loss function
Step 7: Calculate Entropy of the cluster
Step 8: if $E \geq T_1$ then
Malignant;
elseif $E < T_1$ && $E > T_2$ then
Benign;
else
Normal;
end else
end if
Step 9: End

The suggested system's Graphical User Interface (GUI) is shown in Fig. 9, where all results are computed automatically and displayed in accordance with them.

Table 2 Experimental Results

Terms	**Proposed**
Total Testing Class	1097
True Positive	671
True Negative	413
False Positive	3
False Negative	10
Specificity in %	99.28
Precision in %	99.55
Accuracy in %	98.81
F1 Score in %	99.04
Recall in %	98.53

The abbreviation can be consider as Region Growing (RG), Global Threshold (GT), Fuzzy c-means (FCM), Canny method (CM), Sobel method (SM), Watershed approach (WSA), Improved deep neural network (IDNN) and Prewitt Method (PM).

Table 3 Result Comparison

Methods	**Accuracyin %**	**Specificityin %**	**Precisionin %**	**Recallin %**	**F1- Score in %**
RG [4]	72.3	86.5	87.3	84.6	83.8
GT [4]	84.3	97.2	87.9	87.5	82.5
FCM [4]	89.0	95.1	87.5	86.9	87.2
CM [4]	87.8	90.0	86.9	87.7	87.3
SM [4]	88.2	94.1	87.2	88.4	87.0
WSA [4]	83.5	87.8	88.0	89.1	89.4
IDNN [4]	96.2	98.4	97.4	98.0	98.4
PM	**98.81**	**99.28**	**99.55**	**98.53**	**99.04**

Table 2 represents the result obtained for all metrices and table 3 shows the result comparison with improved deep neural network and ensemble classifier.

Table 4 Proposed Classification Result

Terms	**Proposed**
Total Testing Class	1097
True Positive	640
True Negative	413
False Positive	3
False Negative	41
Specificity in %	99.28
Precision in %	99.53
Accuracy in %	95.99
F1 Score in %	96.68
Recall in %	93.97

Table 4 shows the proposed classification result based on three grades such as malignant, benign and normal.

Table 5 Classification Result Comparison

Methods	**Precisionin %**	**Recallin %**	***F*1- Score in %**	**Accuracyin %**
Naıve Bayes [4]	76.9	76.4	74.8	75.5
IBK [4]	80.3	78.3	78.8	79.9
J48 [4]	80.6	79.2	80.4	80.8
Random Forest [4]	81.3	80.4	81.3	82.7
JRip [4]	90.9	90.7	90.7	90.4
Rough Set Classifier [4]	91.4	91.8	91.8	91.9
Ensemble Classifier [4]	93.6	**94.4**	94.4	94.4
SVM Classifier	**99.53**	93.97	**96.68**	**95.99**

Table 5 Represents the Proposed Classification Result and Compare with the Previous System.

V. CONCLUSION & FUTURE SCOPE

The proposed method is based on Prewitt Edge Detection and Support Vector Machine, where Prewitt improves lesion visibility by extracting its edges and SVM categorises abnormal and normal cells so that decisions can be made efficiently and accurately on the basis of that information. System is somewhat more efficient across the board and produced better results than the ensemble classifier and upgraded deep neural network. The suggested classification method may identify normal and abnormal cells and determine whether a picture or illness falls within the benign or malignant category. The categorization outcome outperforms the prior model as well. The system performed better in tests using the IQ-OTHNCCD benchmark. In the future, several benchmarks including a variety of images or data can be used to evaluate a system. Certain contemporary pre-processing techniques can improve accuracy.

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