An AI-Powered Diagnostic Model for Detection of Lung and Liver Cancer

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Abstract. One in six deaths worldwide is due to cancer, which makes it the second most common cause of mortality globally. Breast, lung, liver, prostate, and pancreatic cancers are the leading cancers in the world. Because of their aggressive nature and late discovery at advanced stages, lung and liver cancers are one of the leading causes of cancer-related deaths. Malignant cells are generally detected and classified by medical images and laboratory tests. These activities are time-consuming and require a large team. Developing a method is essential to detecting malignant states at the earliest possible stage. Deep-learning methods are one option for supporting doctors in cancer testing. In this paper, a predictive screening method based on deep learning is proposed to detect various cancers, such as lung and liver. Deep learning for cancer detection may enable more cancer types to be diagnosed in a quicker manner. This looks into deep learning algorithms to classify images with malignancy features. A median filter is initially applied as a pre-processing step to the acquired images of different cancers. Then, the thresholding technique is used to segment the obtained pre- processed im-ages for the purpose of detecting tumors. The GLCM is used for feature extraction. The Convolutional Neural Network classifier identifies a tumor and classifies it as benign or malignant. Lastly, a number of measures are calculated and contrasted with the outcomes of earlier methods, including PSNR, accuracy, specificity, sensitivity, and MSE.

Keywords: Cancer · Deep Learning · Conventional Neural Network · DenseNet · Tumor · Screening

1 Introduction

Cancer is an extremely dangerous disease that is spreading all over the world. It is a condition in which the body develops malignant or tumorous growths as a result of unchecked cell division in specific tissues [1]. A collection of linked disorders is called cancer. Multiple body tissues begin to divide uncontrollably and spread around cells in all forms of cancer. Almost any area in human part, which is made up of trillions of cells, can become the site of cancer. When the body needs new tissues, human tissues often divide and expand, cells die and are replaced by new ones when they age or sustain injury.

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But this well-ordered mechanism disintegrates when cancerous growth appears. As cells become more and more aberrant, older or smashed cells function when they are supposed to perish, and new cells emerge if they aren′t required. These additional cells have the ability to divide endlessly, giving rise to growths known as tumors. Malignant tumors have the ability to invade or spread to neighboring cells. These tumors can produce a multitude of cancerous tissues that can separate and extend to additional regions of the human body. Because of the circulatory or lymphatic systems, a new tumor can spread to a location distance from the main malignant mass. Benign tumors can frequently be removed, and they do not return or extend to additional regions of the human body [2]. In accordance the forecasts of the World Health Organization (WHO), there will be around twenty millions of new cancer cases and ten million deaths due to cancer worldwide in 2023. Breast cancer (2.25 million cases) and lung cancer (2.20 million cases) were the most common types of cancer in 2020.

In accordance with the American Cancer Society, over 800,000 individuals are diagnosed through liver cancer annually. In 2020, 905,800 individuals around the globe were diagnosed with liver cancer. By 2040, the total number of cases rising and people passing away with liver cancer could nearly more than 56%. Liver cancer ranks as the sixth-highest diagnosed and second most harmful cancer worldwide, and it is also one of the most rapidly increasing tumors in the US. To enhance survival chances by delivering effective therapies, early detection and correct diagnosis of liver cancer is crucial. The liver performs many vital functions, such as eliminating toxins from the blood, breaking down medicines, creating blood proteins, and producing bile, which aids in absorption. Nonetheless, a variety of problems can arise in the liver, some of which can be life-threatening. These ailments include viral infection, drug or alcohol-induced reactions, malignancies, genetic disorders, and immune system problems [3]. One among the most significant factors in death due to cancer is a liver tumor [4].

Lung cancer seems to be one of the most commonly diagnosed cancers and the leading cause of mortality for both men and women all over the world. Each year, around 1.82 million people die from lung cancer, accounting for the 2.20 million new cases that are diagnosed worldwide [5, 6]. In 2023, the American Cancer society estimated that 2,38,340 people will be diagnosed and 1,27,070 will die from lung cancer. It often presents with hemoptysis (coughing up blood), weight loss and fatigue, among other symptoms. In addition, a number of risk variables, such as food, alcohol, smoking, and air quality, are linked to lung cancer [7]. Lung cancer, however, requires more focus from the biological, medical, and scientific domains in order to develop novel approaches to support early detection that help in healthcare decision-making and evaluate suggestions to improve medical treatment [8].

Several methods for automatic cancer tumor classification have recently been provided, and they can be classified as ML or DL techniques on the basis of feature selection and the learning process [9]. Feature selection and extraction are critical for classification in ML techniques, whereas DL techniques instantly retrieve and gain knowledge of the image′s features. The use of Deep Learning (DL) techniques has made it possible for computers to interpret high-dimensional data, including video, images, and multidimensional anatomical scans [10]. Deep learning algorithms that are popular for sequence and visual data classification include RNN and CNN [11]. DL is typically a straightforward method of levelling off all of an image′s pixels. For pre-processed photos, the extracted images might thus mirror the features of original image; nevertheless, the exactness of the task is greatly determined by the nature of the retrieved features [12]. CNN designs often consist of blocks that combine fully connected layers, a classification layer, convolutional layers, and pooling operations. For better classification performance and accuracy, a careful combination of hyperparameters is needed when building CNN architecture. Taking a manual approach to combinatorial problems is intimidating and inefficient. Nonetheless, in order to optimize the procedure and find the ideal set of hyperparameters needed for increased performance, metaheuristic methods have been put forth. Metaheuristic algorithms are high-performing, nature-inspired optimization methods that are used to identify appropriate optimization constructs. They frequently call for little processing power, which has been used to effectively resolve challenging real-world issues in the sciences, engineering, and medical fields, particularly in swarm intelligence algorithms [13].

ResNet, Dense Net, DPN, and Mix Net are most often used CNN architectures in our day and age [14]. Based on the assumption that a network will be more reliable and also easier to train if each one of the layers connects directly to subsequent layer in the feed-forward manner, Dense Nets was developed [15].

The current paper is divided into sections, where Sect. 2 describes reviews and relevant work. Section 3 describes the suggested technique in full. The experimental and simulation results are discussed in Sect. 4. Finally, the document ends with a conclusion.

2 Literature Review

In 2023, Tehnan. I. A et.al [16], Mohamed et.al proposed a classification method for detecting malignant or benign Lung tumor with digital images. The success of using EOSA model, the virus-based optimization method, to develop the approach vector using suggested CNN network is the study′s contribution, with probable uses in early identification and enhanced choices for treatment of patients. Here they used EOSACNN algorithm which contains large set of hyperparameters.

In 2022, Hameedur Rahman et.al [17], was developed a method based on tomography volumetric layers obtained from patients having liver cancers and tested on the publicly available three-dimensional dataset IRCADB01. And they didn't classify the tumor they directly taken liver tumor images.

In 2020, Jabber et al. [18], analyzed lung tumor sufferers with SVM, Naïve Bayes, ANN and Logistic Regression methodologies for early identification as well as mortality prediction. They addressed the causation of lung cancer and contrasted these approaches using UCI MLDb data, data from other hospitals, and CT scans. They emphasized that cigarette smoking and a gas called radon were the primary causes of lung cancer mortality. They only focused on Lung cancer detection only with less accuracy.

In 2021, Kaur, Chauhan, and Aggarwal et.al [19], proposed the CNN method based on multi organ categorizing method. It is an effective instrument for identifying cancer. It aids in early identification of malignancy in the liver and the avoidance of unneeded biopsy. Using a method as the basis, this work provided an automated approach for multi organ categorization of three-dimensional CT liver tumor images. They define only the tumor is present or not.

In 2022, Ramakrishnan M et al. [20], proposed a method to identify Lung Tumor Nodule with CT images, A novel model for establishing CNN in lung tumor diagnosis that employs the VGG algorithm for extraction of features and the RNN structure for classification of features. This study combined image processing and methods for classification to create a complete method for spotting lung tumor nodules with accuracy of 70%. Processing an image takes a long time due to the huge quantity of data found in every patient′s CT image.

In 2022, R. Pandian et.al [21], was developed a model that uses VGG-16 Convolutional Neural Network for tumor detection and its classification. Despite the fact that images in the identical class appear differently, the suggested method for CNN. And discusses about an automatic tumor detection and classification of Computed Tomography images using DL algorithm. The proposed method efficiently identifies the Lung tumor. The method detects with low accuracy and they fully focused on Lung tumor detection only.

In 2021, Mrs. A. selvarani et.al [22], was presents the Machine learning classifiers model for detection and segmentation of Liver cancer. Various phases of the neural network are used to acquire features from medical images in order to increase the accuracy in medical image recognition and classification. They use Machine Learning algorithm and only focused on liver tumor detection only.

In 2021, Rim Messeoudi et.al [23], was proposed a method through DL with CNN architecture for HCC detection. It developed an approach using DL which provided a preprocessing text that offers the required data for DL algorithm′s entry. For develop their approach they used Python programming language.

2.1 Contribution

- A novel deep learning method, named DenseNet, is proposed for effectively lung and liver cancer classification.
- Two types of cancers i.e., lung and liver cancers detected by Otsu Multilevel thresholding.
- Otsu thresholding is used for segmentation.
- Grey Level Co-occurrence Matrix (GLCM) along with deep learning was proposed for feature extraction.

As previous studies have shown, multiple machine learning algorithms have been used to detect the cancer. Most of these algorithms predict only single cancer with less accuracy and some algorithms shows up to segmentation but not classification of the tumor.

3 Methodology

The research demonstrates CNN-based lung and liver cancer diagnoses using chest CT images. The first step involves extracting the lung and liver regions from the CT scan, then segmenting each slice to identify any malignancies. The CNN architecture is trained using the segmented tumor regions. The patient photos are then tested using

CNN. Finding out if a patient has a benign or malignant tumor in their liver and lung is the major goal of this investigation. The suggested system's block diagram is displayed in Fig. 1. The trained algorithm can identify the presence of cancer in lung and liver CT images, as depicted in Fig. 1.

There are two sections in the work: the training and testing sections. The essential component of every ML or DL strategy is the dataset. The supplied data quality facilitates the development, training, and optimization of the algorithms. For healthcare imaging applications to be considered for growth and development, the data must be demonstrated and indicated by experts.

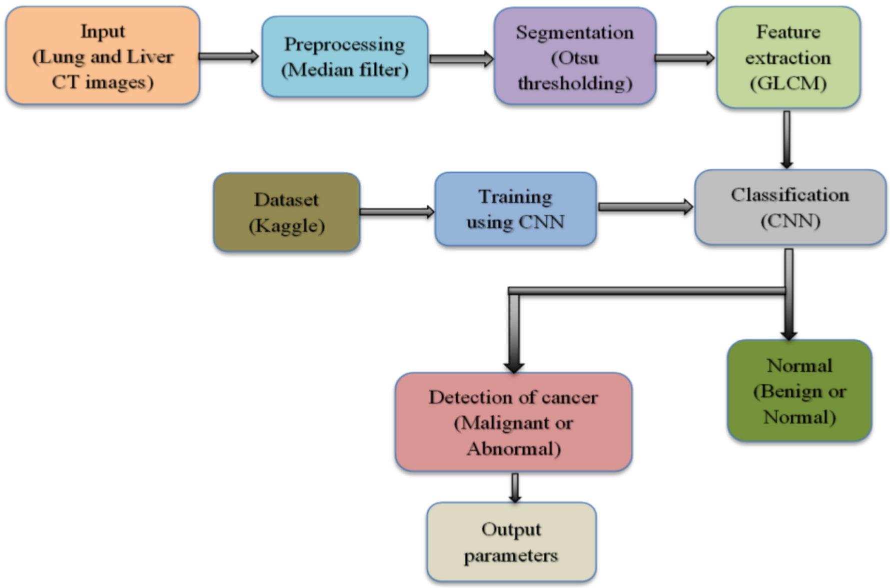

Fig. 1. Proposed block diagram.

3.1 Input Images

A computerized tomography (CT) machine is typically used to acquire precise images or scans of areas inside the body. A CT is a type of imaging procedure. Furthermore, an MRI scan is quite expensive and produces blurry images of the tissues. However, a CT scan is not very expensive, and it also makes the tissues quite visible [24]. These images were acquired from some public and private resources, such as Kaggle.

Kaggle. The data scientist and machine learning medical professionals' online community, it is a subsidiary of Google LLC. Users can use Kaggle to communicate along with data scientists and ML experts, find and circulate data sets, investigate and create methods in an internet-based data analysis environment, and solve data scientific problems. [25].

3.2 Preprocessing

Prior to testing, the images are pre-processed, shrinking and removing blur from the photographs using redistributing pixel values [26]. Pre-processing′s primary goal is to enhance image quality by reducing or eliminating unnecessary elements from images. The stage of pre-processing is critical for improving image quality. Filters remove noise along with other frequently occurring segments, preparing the datasets for further processing [27]. By reducing the impact of acquisition-related degradation, the median filter is employed in the preprocessing stage to restore the image being tested [28]. Unwanted signals in an image are called noise.

Median filter. The image which contains various types of noise: Gaussian, Impulse and Salt and Pepper noise. The Median filter chooses the middle intensity for the window. Its robust average that is, an insufficiently representative pixel in neighborhood doesn't influence the median value and its ability to maintain crisp edges are two benefits of employing a median filter [29]. This median filter runs pixel by pixel through the image, replacing each pixel by the median value of its neighbors, the window that results is a collection of neighbors that shifts pixel by pixel across the image as a whole. The median value computed using Eq. (1)

$$(x, y) = \underset{(r_o, c_o)\varepsilon S_{xy}}{median} \{g(r_o, c_o)\} \tag{1}$$

- (x, y): Dimensions of the grid or array S_{xy}. x represent the no. of rows, and y represent the no. of columns.
- S_{xy}: Two-dimensional grid or array denoted as $g(r_o, c_o)$, where r_o and c_o are indices for rows and columns, respectively.
- $(r_o, c_o) \in S_{xy}$: (r_o, c_o) represents a specific element within the grid S_{xy}.
- $g(r_o, c_o)$: The set of values of the elements $g(r_o, c_o)$ within the grid.
- *median*: ″*median* ″ indicates that median value from the set of values $g(r_o, c_o)$.

As a result, the median filter effectively reduces salt and pepper noises [30]. The noise can be of various types, and this Median filter enhances efficiency for any kind of noise.

3.3 Segmentation

A classic topic in computer vision research, image segmentation has emerged as major area of study for image interpretation. The whole process of splitting or dividing an image into multiple disconnected regions based on features including color, grayscale, spatial texture, and geometric shapes is known as "image segmentation". Medical image segmentation is considered a semantic segmentation task. In the modern era, there are an increasing number of image segmentation research subfields, including autonomous driving, medical image segmentation, satellite image segmentation, and more [31]. The suggested network structure has grown significantly, and as a result, the ima segmentation technique has been gradually enhanced to produce segmentation result that are increasingly accurate. Unfortunately, there is no specific segmentation technique that is applicable to all photos, nevertheless, according to several segmentation examples. Image thresholding is a fundamental technique in image processing with various applications.

Thresholding. In digital image processing, thresholding is the simplest basic method for image segmentation. Since it enables the separation and extraction of important information from images, it is essential to image processing. Using pixel intensity or pixel value to divide an image into distinct areas, thresholding makes it easier to separate interesting objects or features from their backgrounds. This technique makes it possible to analyze and comprehend digital images more effectively. It is commonly applied to many different tasks, including as character recognition, image segmentation, and object identification. By lowering noise and boosting overall visual clarity, image thresholding also enhances image quality. The accuracy and efficacy of image analysis are significantly influenced by the thresholding technique selected. Each thresholding method has advantages and disadvantages of its own. The desired result, noise levels in the image, and image complexity all play a role in choosing the right technique. To achieve the best outcome in image processing activities, it is crucial to carefully evaluate the choice and to carry out experiments.

Multi-level and bilevel thresholding are two different categories of image thresholding techniques. While multilevel thresholding (MTH) divides an image into many levels using more than one threshold, bi-level thresholding segmentation divides an image into two groups using a single threshold value [32]. Two approaches parametric and non-parametric can be used to group thresholding strategies in order to get optimal threshold values for MTH segmentation. Each grayscale range group in parametric approaches should be compatible with a Gaussian distribution. Mathematical processes are used to evaluate the histogram in parametric techniques. The most effective thresholds are subsequently chosen using the widely utilized Gaussian mixture, which describes the group of activities used to integrate the histogram. Non-parametric techniques use several techniques to divide the pixels into homogeneous region; the optimal threshold is then determined by utilizing statistical data, such as variance or entropy. The Kapur and Otsu methods are the two techniques which are used to determine the variance or entropy. In which the Otsu technique maximizes the variance between groups to get the optimal thresholds.

Otsu Thresholding method for segmentation The Otsu segmentation technique is non-parametric, automatic method for determining out an image's ideal thresholds. The most significant variance of the different classes serves as the basic for this method's images segmentation criteria. Using the intensity level L from a grayscale image, the probability distribution for the intensity value is computed using Eq. (2).

$$ph_i = \frac{n_i}{nk}, ph_i \geq 0, \sum_{i=1}^{L} ph_i = 1 \quad (2)$$

where i = intensity level ($0 \leq i \leq L - 1$)

n_i = no. of grey levels i appearing

nk = no. of pixels

ph_i = probability distribution for intensity levels

Following that, the optimization issue is simplified by figuring out the intensity level which maximizes in Eq. (3):

$$F_{Otsu}(th) = Max\left(\sigma_B^2(th)\right); 0 \le th \le L - 1 \tag{3}$$

where $\sigma_B^2(th)$ defines the variance of th value for Otsu method. According to Eq. (4), EBO approaches are employed to figure out the intensity level that will maximize the purpose of fitness. For MTH, the level of fitness or goal function $FOtsu(TH)$ could be modified as follows:

$$F_{Otsu}(TH) = Max\left(\sigma_B^2(th_i)\right); 0 \le th \le L - 1 \tag{4}$$

$TH = [th_1, th_2, \ldots\ldots\ldots.th_n - 1]$, it is a vector which includes MTH, and variance computations are shown in Eq. (5):

$$\sigma_B^2 = \sum\nolimits_{i=1}^{n} \sigma_i = \sum\nolimits_{i=1}^{n} w_i(\mu_1 - \mu_T)^2 \tag{5}$$

where i is a class, w_i represents occurrence probability, and μ_T represents mean [33].

The values are derived for MTH by using Eq. (6–7) as:

$$w_{n-1}(th) = \sum\nolimits_{i=th_n}^{L} iph_i \tag{6}$$

$$\mu_{n-1} = \sum\nolimits_{i=th_n+1}^{L} \frac{iph_i}{w_1(th_{n)}} \tag{7}$$

3.4 Feature Extraction

It is a process in data analysis and machine or deep learning where relevant information or characteristics are derived from raw data, which may be high-dimensional or complex, to create a more compact and informative representation the objective of feature extraction is to diminish data dimensionality while conserving as many pertinent details as possible, facilitating collaboration and enabling better performance in various data analysis tasks, such as classification, clustering, and regression.

Grey Level Co-occurrence Matrix (GLCM). Our suggested approach relies heavily on feature extraction from images. The GLCM textures are according to the phenomenon of neighbouring grey level co-occurrence and Its values in an image. The texture feature of GLCM in Xray images are determined that uses a matrix of squares based on the region of interest (ROI) measurements of N number of grey levels. This approach allows us to capture and analyse the spatial relationships of grey levels, particularly relevant in the context of medical imaging, where identifying textures within specific regions is critical for tasks such as disease detection and classification [34].

The Eq. (8) is used to calculate the GLCM is as follows:

$$P(i, j, d, \theta) = \frac{n(i, j)}{tn(i, j)} \tag{8}$$

- " i " and " j are the grey levels of the two pixels being considered in the co- occurrence.
- " d" is the distance between the two pixels.
- "θ" is the orientation or angle at which the pixels are considered
- The numerator counts the number of times pixel pairs with intensity values (u, v) are found at the specified distance and angle in the image.
- The denominator is the total count of all possible pixel pairs at that distance and angle in the image.

3.5 Classification

The mask or patch gets applied to cover the whole image for recognition of images. Because these models undergo training on tiny portions of the image, we require an approach for splitting the initial validation image into regions of image. The more patches or filters we extract from an image, the better the result; however, extracting more features or patches takes longer and increases the time required for computation. The suggested CNN algorithm extract features from images in the Kaggle dataset and classifies them as benign or malignant tumors. We used GLCM for feature extraction and CNN for classification in our model. In the last layer (SoftMax), the image is classified into 2 categories: Benign or Malignant.

Convolutional Neural Network (CNN). In our study, we employed CNN architecture with several parameter adjustments to get the best outcome, which contains the following layers as shown in Fig. 2:

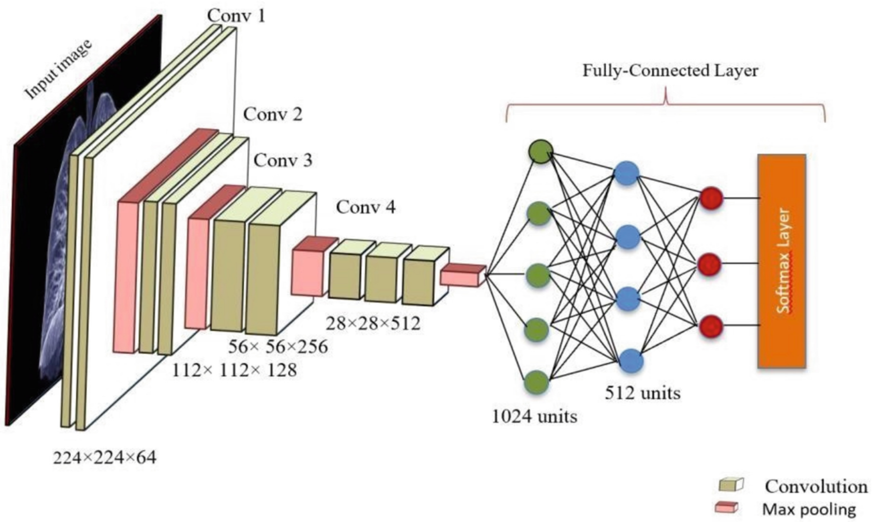

Fig. 2. Architecture of CNN

Input layer: The input layer of a CNN is responsible for handling the initial input data, which is typically an image or a set of images. It processes the data through convolutional operations, applies normalization or preprocessing as needed, and prepares the input for subsequent layers in the network. The design of the input layer is critical in capturing meaningful features from the input data.

Convolutional layer: In this layer, the image that was provided is condensed with a collection of applicable filters, and it generates a map of features for every image in the resulting image. Our model which has five layers. The first three layers' kernel size is 5 × 5, padding is 0, and stride is 2, and the other layers' kernel size is 3 × 3.

ReLU layer: Another name for this type of layer is the Rectified Linear Unit. Neurons are activated by this activation function when their activity beyond a threshold. The ReLU layers take a given input value of v and calculate the neurons' output as v if f(v) > 0 and 0 if f(v) < = 0.

Pooling layer: It is generally used to decrease the overall dimension of an image yet retaining its high-level characteristics. Pooling layer is answerable for decreasing the spatial dimensions of the given image. After every layer of convolution, we can add one layer for pooling. Each pooling layer has a 3 × 3 receptive field spatial size and a stride of 2. The max pixel value for each window is calculated by applying the max pooling mechanism on the image from the initial three pooling layers. For the last two layers of pooling is used for average pooling.

Fully connected layer: The outcome is produced by fully linked neurons in this layer. In this instance, both the input and the outputs are simply handled as vectors. Two internal merchandise layers were employed. The final layer is a fully connected layer that uses a SoftMax layer for input image classification. Two classes one for benign and one for malignant were used in our instance [35].

3.6 Parameter Analysis:

Using a variety of performance metrics, including sensitivity, specificity, and accuracy, the classification capacity of the numerous characteristics proposed in this work has been statistically assessed.

To gauge system performance, statistical metrics are expressed as mathematical equations. Here *TPo*, *TNe*, *FNe* and *FPo* represents true positive, true negative, false negative, false positive respectively. True Positive (*TPo*) refers to a categorization result that is positive in an indication of a clinical anomaly. True Negative (*TNe*) refers to a negative categorization result that does not indicate a clinical problem. False Positive (*FPo*) is a positive categorization result without a clinical anomaly. False Negative (*FNe*) refers to a negative categorization result due to a clinical anomaly. Sensitivity measures the *TPo* rate while avoiding *FNe*. Specificity measures the *TNe* rate.

Sensitivity: It gauges how well a system can differentiate between positive and negative samples. Equation (9) can be utilized for its calculation.

$$\text{Sensitivity} = \frac{TP_o}{TP_o + TP_e} \quad (9)$$

Specificity: It is an evaluation of a system's ability to correctly identify negative samples. It can be calculated using Eq. (10).

$$\text{Specificity} = \frac{TP_e}{TP_e + TP_o} \tag{10}$$

Accuracy: The accuracy of classification of a strategy is a measure of its usefulness [36]. It is calculated using Eq. (11) based on the number of effectively characterized samples.

$$\text{Accuracy} = \frac{TP_o + TN_e}{TP_o + TP_e + FP_o + FP_e} \tag{11}$$

Suppose that we have a M co-occurrence matrix of size N, with the coefficient and element coordinates being represented by a,b.

Correlation: The measure of a pixel′s association with its neighbor over the entire image is called an image correlation feature. For an image that is positively correlated but not negatively, the correlation value falls between -1 and 1, and for a constant image, it is infinite. Equation (12) defines the correlation aspect of an image as follows:

$$Correlation = \sum\nolimits_a \sum\nolimits_b \frac{(a - \mu_a)(b - \mu_b)p(a, b)}{\sqrt{\sum_{a,b} p_{a,b}a^2 \sum_{a,b} p_{a,b}b^2}} \tag{12}$$

Entropy: A image′s degree of uniformity between pixels is measured by the entropy feature, while the texture of the image is described by randomness. Energy and entropy have a strong but negative relationship; images with more gray levels also have higher entropies. The definition of the entropy operates of an image, or "Entropy," can be found in Eq. (13):

$$\text{Entropy} = \sum\nolimits_{a=0}^{N_g-1} \sum\nolimits_{b=0}^{N_g-1} p(a, b)\log(p(a, b)) \tag{13}$$

Structure Similarity Index (SSI): It′s a method for forecasting the perceived quality of images. It is evaluated using Eq. (14):

$$SSI = \frac{(2M_X M_Y + C1)(2N_{XY} + C2)}{(M_x^2 + N_y^2 + C1)\left(N_X^2 N_Y^2 + C2\right)} \tag{14}$$

where X, Y are segmented image and recovered image, MX & My are average values of X and y, NX & NY are variance of X & Y and NXY is the covariance of image X and Y

4 Simulation Results

The suggested method focuses on the identification and classification of lung and liver cancer. The convolutional neural network and thresholding segmentation were built in MATLAB, and the system is now being trained on input data. The lung (or) liver dataset was fed into the trained model as input, and the model detected tumors and cancer sites in the input images, as shown in Fig. 3.

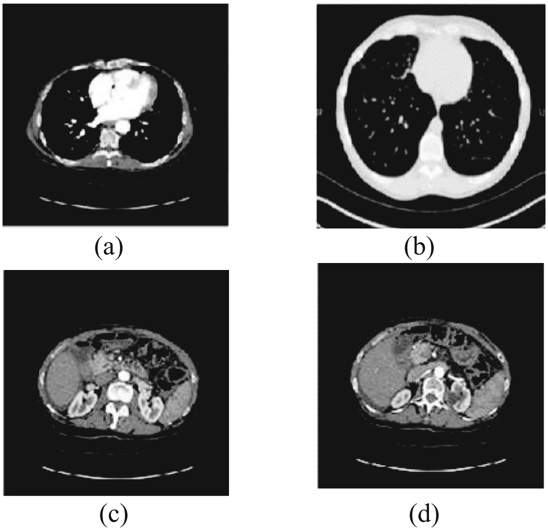

Fig. 3. Input Images (a) Lung Img-1 (b) Lung Img-2 (c) Liver Img-1 (d) Liver Img-2

The acquired input images from the database are not uniform in size. To process such images for further steps, the image must be of uniform size. In this work, The images have been resized to 256 × 256. Generally, the acquired input image from the CT scanner has salt and pepper noise, which is very less and it is difficult to remove. To remove such noise, the noise must be added externally. The noisy images related to input images after adding noise are shown in Fig. 4:

Once the noise is added to the original images, it is easy to remove the entire noise along with the internal noise. The entire noise is removed by passing through a median filter, which eliminates salt and pepper noise. The obtained De-noised images for input images are shown in Fig. 5.

After obtaining the high-quality image from the pre-processed stage, such an image is fed to a multilevel segmentation technique to identify lung and liver tumors. In this work, Otsu-multilevel thresholding is employed for segmentation, where it divides the dataset into two or more groups (or) clusters based on thresholding levels. In this work, the thresholding level is considered as '3'. The segmented images with threshold level '3' for input images are shown in Fig. 6:

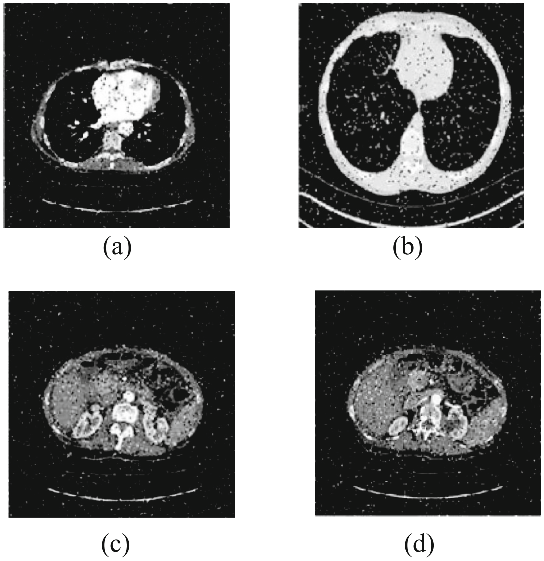

Fig. 4. Noisy Images (a) Lung Img-1 (b) Lung Img-2 (c) Liver Img-1 (d) Liver Img-2

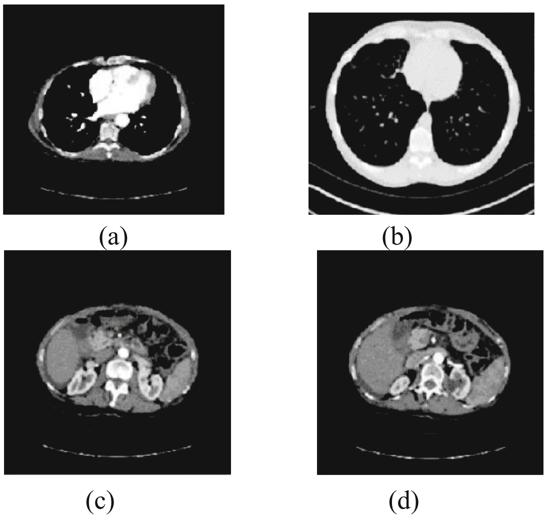

Fig. 5. De-noised Images (a) Lung Img-1 (b) Lung Img-2 (c) Liver Img-1 (d) Liver Img-2

Finally, after obtaining the segmented images according to the pixel intensity, like low contrast, high contrast, the Otsu multilevel thresholding selects the best segmentation output image for tumor detection. The detected tumor images are shown in Fig. 7:

Based on the properties of the discovered tumor, the classification network must be trained to determine whether the tumor is benign or malignant. To extract the features in this work, GLCM, which is a textural-based method, is used. GLCM extracts the features

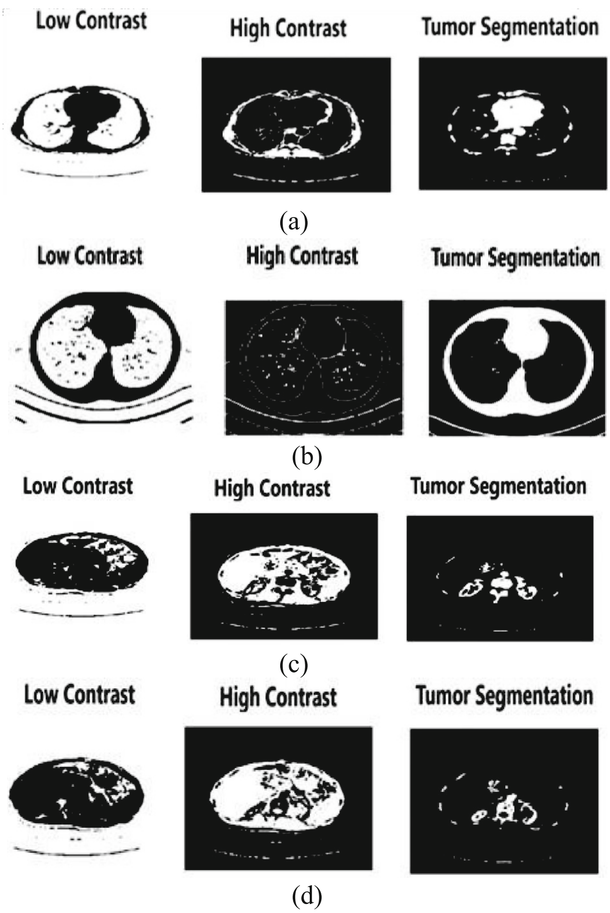

Fig. 6. Segmentation output images through Otsu multi-level thresholding (a) Lung Img-1 (b) Lung Img-2 (c) Liver Img-1 (d) Liver Img-2

like entropy, correlation, SSI, etc. It can convert the raw data into a numerical feature that works effectively on neural networks for classification. In this work, a deep learning modal, which is a CNN with a dense Net modal, is utilized for classification. Based on the features from the GLCM, the CNN with dense Net modal classifies whether the detected lung or liver tumor is effected (Abnormal) or not effected (Normal) and indicates, like a dialogue box, as shown in Fig. 8:

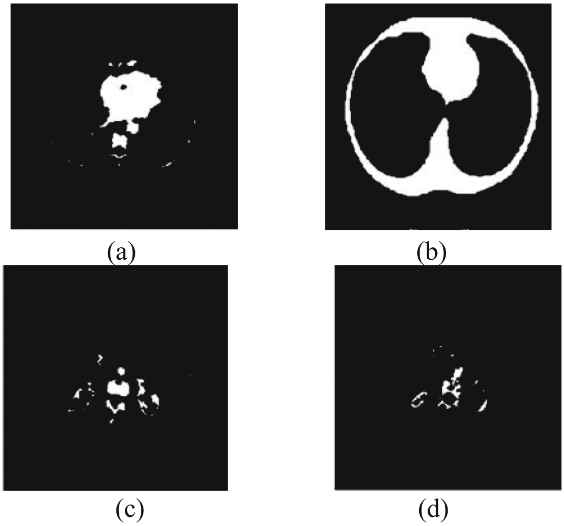

Fig. 7. Tumor detected images (a) Lung Img-1 (b) Lung Img-2 (c) Liver Img-1 (d) Liver Img-2

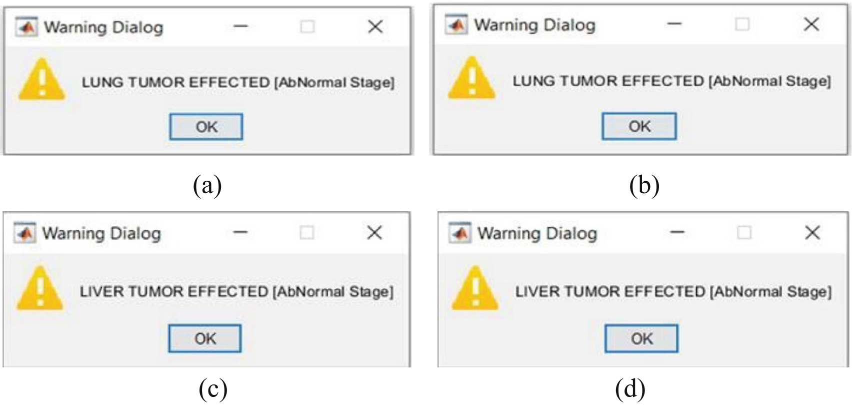

Fig. 8. Classification outputs (a) Lung Img-1 (b) Lung Img-2 (c) Liver Img-1 (d) Liver Img-2

Once the tumor has been classified by the CNN classifier with Dense Net modal the statistical parameters i.e., performance attributes and grey level attributes like Accuracy, Specificity, Sensitivity, MSE, PSNR, Entropy, Correlation and SSI were measured. These variables will assess how well the suggested approach performs. The desired parameters are shown in Tables 1 and 2.

From Tables 1 and2 it clearly shows that the suggested approach yields highly precise results. The accuracy for lung img-1 is 97.15%, lung img-2 is 96.32%, liver img-1 is 96.24% and liver img-2 is 94.32%. The graphical representation of all the parameters is shown in Fig. 9 and Fig. 10.

Table1: Statistical parameters for Lung Image

S.NO	Parameters	Lung Images	
		Lung Img 1	Lung Img 2
1	MSE (%)	5.905	1.404
2	PSNR (%)	10.418	6.654
3	Sensitivity (%)	1.19	0.354
4	Specificity (%)	99.965	100
5	Accuracy (%)	97.156	96.326
6	Entropy	0.405	0.801
7	Correlation	0.850	0.955
8	SSI	0.651	0.002

Table2: Statistical parameters for Liver Image

S.NO	Parameters	Liver Images	
		Liver Img 1	Liver Img 2
1	MSE (%)	5.164	5.145
2	PSNR (%)	11.00	11.016
3	Sensitivity (%)	100	100
4	Specificity (%)	96.206	94.324
5	Accuracy (%)	96.207	94.326
6	Entropy	0.241	0.209
7	Correlation	0.561	0.500
8	SSI	0.608	0.610

The average accuracy obtained for the proposed method was 97% which explicit that the suggested method was best for detection and classification of lung and liver tumor using deep learning.

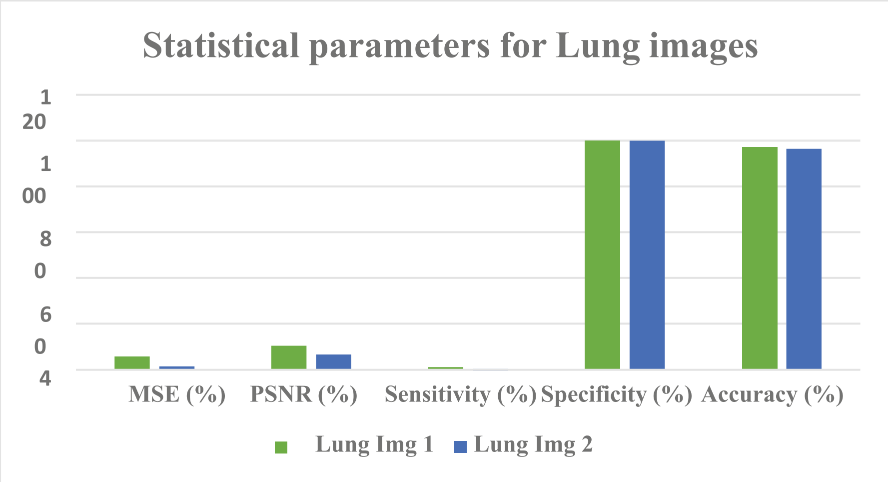

Fig. 9: Graphical representation of Statistical Parameters for Lung images

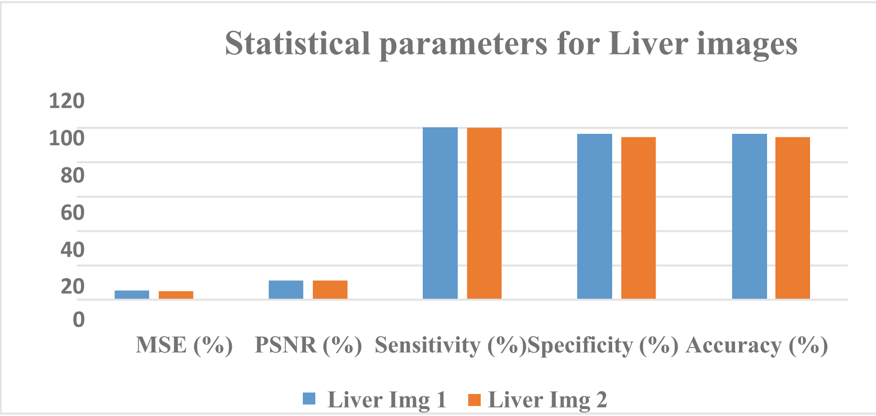

Fig. 10: Graphical representation of Statistical Parameters for Liver images

5 Conclusion

A serious health problem that affects millions of people worldwide is lung and liver cancer. A variety of classical and machine learning techniques are currently being used on computer-controlled detection systems to identify lung and liver cancer in its early stages. However, lung cancer screening is time-consuming, and computerized detection technologies do not produce precise results. Deep learning has aided advances in the analysis and prediction of a wide range of disorders in the field of medicine. Deep learning-based lung and liver cancers prediction is critical in assisting medical practitioners in diagnosing lung and liver cancers at an early stage. A novel method for identifying and categorizing liver and lung cancers was provided by this study. In the input CT images of the liver and lungs, malignant tissues were identified using a convolutional neural network with a Dense net. Images of cancerous tissues with a range of sizes and shapes taken from the liver and lung were used to train the system. Performance criteria like as specificity, sensitivity, accuracy, MSE, and PSNR were employed to assess the effectiveness of the proposed approach. The proposed technology has a 97% accuracy rate in identifying cancerous cells. In order to determine the type of cancer based on its dimensions, the system will eventually be trained on big datasets.

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