Acta Scientific CANCER BIOLOGY (ISSN: 2582-4473)

Volume 8 Issue 6 June 2024

Review Article

Integration of Fuzzy Logic and Soft Computing Approaches for the Detection and Classification of Liver Cancer

Mohammad Alamgeer*

Assistant Professor, Department of Information Systems, College of Science and Arts, King Khalid University, Kingdom of Saudi Arabia (KSA) and Associate Professor, School of Computer Science and IT, Singhania University, Pacheri Bari, Distt. Jhunjhunu, Rajasthan, India

***Corresponding Author:** Mohammad Alamgeer, Assistant Professor, Department of Information Systems, College of Science and Arts, King Khalid University, Kingdom of Saudi Arabia (KSA) and Associate Professor, School of Computer Science and IT, Singhania University, Pacheri Bari, Distt. Jhunjhunu, Rajasthan, India.

Received: May 10, 2024

Published: May 20, 2024

Abstract

Liver cancer ranks among the leading global causes of death. The process of detecting liver tumours from computerized tomography (CT) images is crucial for the detection and management of liver cancer. It takes a significant amount of time and effort to physically identify cancer tissue. So, in order to accurately identify the right therapy, a computer-aided diagnostic is utilised in the decision-making process. As a result, the primary goal of this work is to properly identify and categorise liver cancer using deep learning technique. The volumetric data of 1800 Computerized Tomography images were taken for processing. The proposed method involves pre-processing, segmentation, classification, and feature extraction. The segmentation is processed by the Spatial Fuzzy C-means clustering algorithm to detect the affected liver region. Then the feature extraction is carried out by the Bat Optimization (BO) algorithm. The classifiers of the CNN are employed to categorize the affected and unaffected regions in the liver CT images. The findings demonstrate that the Convolutional Neural Network method performs better than competing approaches and provides possibilities for liver tumour detection and classification. The proposed methods performance criteria, including accuracy, recall, precision, and F1-Score, are assessed, and then its superiority to various existing systems is clearly shown. According to simulation results, the overall rates for accuracy, recall, precision, and F1-Score were roughly 99.80%, 100%, 99.99%, and 99.10% compared to a number of previous studies.

Keywords: Liver Cancer; Bat Optimization; Spatial Fuzzy C-means Algorithm; CNN; CT Images

Introduction

According to the World Health Organization (WHO) estimate from 2017, there were roughly 10.5 million cancer-related fatalities and 16.1 million instances of the morbidity and mortality worldwide. The liver's most common cancer is hepatocellular carcinoma (HCC). Individuals with cirrhosis or chronic liver diseases are more likely to experience it [1]. The most recent research indicates that HCC is one of the most deadly diseases globally, accounting for more than 800,000 fatalities per year. The fifth most prevalent and frequently diagnosed cancer globally, according to the WHO, is liver cancer. This information demonstrates that hepatocellular carcinoma has a significant influence on human life and that it is imperative to decrease the number of yearly fatalities attributable to HCC [2]. As a result, automated systems in the healthcare and medical fields such as precise and reliable clinical decision support systems can assist physicians make precise and timely diagnoses of a wide range of illnesses affecting their patients. These systems must be developed based on patients' prior medical history [3].

Liver tumour is a tumour that develops in the cells of the liver. The liver is a football-sized gland that is located above the abdomen in the upper right quadrant of the stomach, below the esophagus. Blood veins in the liver carry nutrients from the digestive system and drugs into the body continuously, converting them into molecules that are ready to be used [4]. The liver's additional important functions include cleaning the blood of toxins and other organic and chemical wastes and preparing it for disposal. Because the liver should serve as the major vessel that carries blood throughout the body, it is particularly prone to cancer cells moving via the circulation. There are several malignancies that potentially spread to the liver [5]. The most prevalent kind of liver tumour, hepatocellular carcinoma, begins in the primary type of liver cells called hepatocyte. Particular types of liver cancer, such as hepatoblastoma and intrahepatic cholangiocarcinoma, were much less common. Both intrinsic liver cancer, which develops in the liver, and tumours, which originate elsewhere in the body and spread to the liver, can harm the liver [6]. Primary liver cancer has previously been associated with a variety of carcinogens, mainly herbicides like arsenic and vinyl chloride but also other compounds like them. Particular types of liver cancer, such as hepatoblastoma and intrahepatic cholangiocarcinoma, were much less common. Both intrinsic liver cancer, which develops in the liver, and tumours, which originate elsewhere in the body and spread to the liver, can harm the liver [7]. Primary liver cancer has previously been associated with a variety of carcinogens, mainly herbicides like arsenic and vinyl chloride but also other compounds like them.

The common kind of liver cancer is secondary or metastasis, which means that it first appears elsewhere in the body. The liver can produce a wide range of tumours since it is made up of a number of cells in the body. Many of them are benign (noncancerous), some may be cancerous and have the potential to spread to certain other body areas. These cancers are treated and their potential causes are investigated. Cancer that begins in the liver cells is far less prevalent than cancer that extends to the liver [8]. When cancer spreads to the liver from another organ, such as the lungs, the colon, or the breast, it is said to be metastatic cancer rather than liver cancer. For instance, metastatic colon cancer starts in the gut and spreads to the liver [9]. When the Genome of liver cells changes, liver cancer can result mutates. DNA is the element that directs each chemical process in the system. Gene mutations may result from differences in these instructions. A tumour, which is a mass of malignant cells, can be created as a result of cells growing out of proportion. It is known that some conditions, such as chronic hepatitis illnesses, might cause liver cancer [10]. Furthermore, liver cancer may develop in people who do not have any chronic conditions, and its cause is yet unknown. Liver cancer is a leading cause of disease deaths due to its significant mortality rate and morbidity. Liver cancer rapid recognition and precise diagnosis might greatly reduce death rates and increase survival rates.

Computed tomography (CT), which is distinguished by its excellent spatial resolutions and fast scanning speeds, is presently one of the most frequently utilised imaging models for the diagnosis and identification of liver cancers [11]. By operators with adequate experience and knowledge, segmentation may be performed manually in normal clinical settings; nevertheless, the procedure is usually time-consuming, and different operators frequently yield inconsistent findings [12]. Because of the variable forms of tumours, the wide variety of tumour intensities and the hazy borders between both the tumour and the surrounding healthy liver tissues, developing an automated segmentation and detection approach is exceedingly difficult. There are also additional ways to identify the portions of the Computed tomography scans that show liver cancer. Between these, the fuzzy segmentation approach is regarded as being significantly more advantageous since, in contrast to the tough segmentation technique, it recovers a substantial amount of data from the original image. The pixels of the image are given to the fuzzy cluster in the fuzzy c-means clustering technique instead of to the labels [13]. Contrary to the tough clustering approach, which forces the pixels to solely belong to one class, FCM permits the pixels to connect to numerous clusters by modifying the membership function. Eventually, the doctor is shown a clustered image with a realistic image division and fuzzy bounds to repair the bordering region.

Depending on the severity of the malignancy, there are various therapeutic methods available, including for specific situations. Understanding the cancerization degree is crucial due to this reason. Some of the techniques used to detect liver cancer include nuclear magnetic resonance imaging, ultrasonography, and pathological biopsy evaluation [14]. Numerous machine learning techniques have already been created for the automatic or semi-automatic segmentation and classification of liver tumours; however the effectiveness of these techniques is significantly impacted by the size of the feature dimensions. Deep learning methods utilising CNN have been effectively employed in recent researches to address a variety

of issues, and it is a frequently researched topic in the area of image processing. Convolutional neural networks (CNN) are efficiently employed in an automated technique to classify afflicted tumours in Computed tomography images. Numerous researches have demonstrated that CNNs may achieve outstanding achievement on extremely difficult applications, such as visual object identification and images categorization [15]. The CNNs approach was also employed to separate the cartilage in the knees. A supervised learning model made up of multi-layer neural networks is called Deep CNNs. Each intermediate layer represents an increasingly more complex level. It may be able to record very complicated input–output transformations. Due to their complete reliance on data, CNNs are capable of retrieving hierarchical characteristics by creating high-level characteristics from low-level ones.

The research's main contributions are as follows:

- A significant number of patients' CT images are first gathered, and the CT datasets are processed in the system.
- Furthermore, the recovered real CT lung images contain unwanted noises, which are filtered using a combined wavelet and Gaussian filter model.
- The spatial Fuzzy C-mean clustering algorithm has been utilized for the segmentation process.
- The Bat Optimization algorithm is employed for the feature extraction.
- The Convolutional Neural Network classifies the affected and unaffected liver regions.
- The performance of the applied technique is validated and related to the present-day approaches to show its effectiveness.

The proposed paper's manuscript is structured as follows: Numerous similar works are covered in section 2. The proposed methodology architectures are detailed in full in section 3. In section 4, experiment findings are shown, evaluated, and a thorough assessment of the suggested strategy in comparison to existing best practises is made. The paper's conclusion is offered in section 5.

Related works

The Early Recognition of HCC Employing ML techniques was proposed by Zi Mei Zhang., *et al*. A deadly malignancy, hepatocellular carcinoma is responsible for the fourth-greatest number of cancer-related deaths globally. In order to help in the early identification of HCC in clinical circumstances and subsequently enhance HCC therapy and survivability, more precise diagnostic techniques are considered necessary. For individuals without HCC, a number of standard techniques have indeed been utilised to distinguish cirrhosis tissues from HCC tissues. The chances of success for identification continue to be far from ideal. In the work, a collection of microarray data produced from HCC instances and CwoHCCs instances was subjected to a computational technique that utilized machine learning. Numerical descriptors were extracted from genomic profile datasets use the method of within-sample expression levels orderings. With the help of sequential selecting features and maximum redundancy minimal relevance, researchers were able to develop a "11-gene-pair" that may yield exceptional outcomes. On a number of different datasets, researchers subsequently examined the "11-gene- pair's" capacity to discriminate for the detection of HCC. The fantastic outcomes showed that the chosen gene pairs might be a hallmark for HCC. Even with small biopsy samples and improperly collected specimens, the suggested computer model can distinguish between HCC and nearby non-cancerous tissues and CwoHCC, making it useful and efficient for assisting with initial HCC diagnosis at the individual basis. However, this paradigm is not one that is user-friendly [16].

A Novel Machine Learning Technique was employed by Wojciech Ksiek., *et al*. to identify patients with hepatocellular carcinoma initially [17]. The most prevalent kind of cancer around the world is liver tumour. The most harmful kind of liver tumour is called HCC. It has a significant influence on people's lives, and timely screening can reduce the number of fatalities each year. The study suggests a novel machine learning method to identify HCC. Researchers use ten well-known machine learning methods. The normalisation strategy is utilised in the preliminary processing stage. The evolutionary algorithm has been used repeatedly, once for parameter optimization and once for feature selection, along with the stratified 5-fold cross validation approach. The most accurate method employed in the research was the support vector machine with a novel two-level genetic optimizer. The performance of the suggested approach may be evaluated using a sizable database, helping clinicians. Nevertheless it only utilises a small number of databases will lower its performance.

An automated liver and tumour segmentation method using a joint deep learning approach was proposed by Nadja Gruber and

Stephan Antholzer [18]. The main liver tumour that occurs most often in adults is hepatocellular carcinoma, which also kills cirrhotic patients most frequently. The segmentation of liver abnormalities in CT scans enables evaluation of tumour density, selection of the appropriate course of action, prediction, and surveillance of the therapeutic outcome. Automatic technologies for tumour identification and segmentation are preferred since manual segmentation takes a lot of time and is frequently inaccurate. In the study, researchers contrast two network frameworks: one that handles the segmentation job in a single movement and is made up of a single neural network, and another that is made up of two sequential fully connected CNN network. While the second networks divide the actual tumour within the liver, the first network divides the liver itself. The networks are tested using information given by the radiological facility in Innsbruck and developed on a portion of the Liver Tumour Segmentation Challenge. However, the approach did not adequately describe the categorization process.

Hepatocellular carcinoma initial recurrence predictions following removal utilizing digital pathological images evaluated by ML was a proposal made by Akira Saito., *et al*. Hepatocellular carcinoma, a main liver cancer type, is brought on by continual and recurring liver injury. Typically, surgical resection is the preferred radical curative method. Identifying first HCC reappearance after resection is crucial in medical treatment since it is connected to poor overall fatality. The early pathologic indicators of HCC recurrence are yet unknown, though. Researchers aimed to detect the fast recurrence of HCC following resection by utilising machine learning utilizing a SVM and digitised pathologic images of eosin-stained and hematoxylin tissues. HCC patients who satisfied the Milan requirements and underwent surgical removal were included in the research. Three groups of patients were separated. 89.9% of the time, the SVM-based prediction method successfully distinguished between the three categories. Group 1 was properly guessed in every case, Group 2 in one case, and Group 3 in eight cases. Group 1 was correctly estimated in every case. Machine learning and digitized histology could be employed to more accurately predict HCC recurrence after surgical resection and to have a greater understanding of recurrence. The majority of patients today utilize standard diagnostic testing and blood test for follow-up screening after HCC resection, however any application of diagnostic imaging in conjunction with computer vision has potential as a method for precise postoperative follow-up monitoring [19].

For automated HCC segmentation in H&E-stained whole slide images, Xiyue Wang., *et al*. presented a hybrid network. Hepatocellular carcinoma (HCC), a considerably more prevalent type of commonly affected liver tumour, has become historically the biggest factor in mortality from cancer. The automated segmentation of HCC tumours and postoperative assessment were essential components of surgical planning for tumour loading measurement. HCC tumours have a very variable form from case to case, making identification and segmentation a time-consuming and error-prone operation. Researchers use multi-task training and ensemble learning models to create a special hybrid neural network for effective HCC identification of full slide images stained with eosin and hematoxylin. The feature matrix is first expanded by combining three task-specific branching, which enables the system to pick up more fundamental traits and lessens the risk of over fitting. In order to collect features from multiple areas and dimensions, spatially and channel-wise squeeze-and-excitation and components selected kernel modules are employed during a supervised learning process. The proposed method demonstrates cutting-edge on three openly accessible datasets, performance, with higher segmentation accuracy and reliability, demonstrating how well it handles the HCC segmentation issue. However, the study did not investigate if an optimized plan that utilised strategies like domain flexibility and learning stages couldn't attain an accuracy level comparable to the ensemble technique [20].

Amita Das., *et al*. proposed employing Gaussian mixture and watershed transform model approaches to identify liver tumour utilizing DL [21]. One of the main reasons for mortality worldwide is liver cancer. It takes a significant amount of time and effort to physically find cancer tissue. So, in order to accurately identify the right therapy, a computer-aided diagnostic is utilised in the decision-making procedure. Hence, the primary goal of the research is to properly identify liver cancer utilizing an automated technique. Using CT images of the liver, researchers have suggested a brand-new method termed the WGDL framework for effectively delineating the tumour lesion. Marker-controlled watershed segmentation was first employed to partition the liver, and then the Gaussian mixtures technique was applied to separate the tumour-affected region. Different textural characteristics were retrieved from the segmented area after tumour segmentation. For the automatic categorization of the three kinds of liver tumour hepatocellular carci-

noma, hemangioma, and metastatic carcinoma, these segmented characteristics were supplied to a deep neural network classifier. The proposed technology is ready to be evaluated with a large database and can help radiologists identify liver cancer utilizing CT scans. It obtained the best classification accuracy. The greatest limitation of the study is the determination of the volume of the tumour, which may be generated by creating a 3-D mesh structured from various slices of the image.

With Regard to the Differentiations of MRI Liver Tumors, Eleftherios Trivizakis., *et al*. utilized Extending 2-D CNN to 3-D for Improving DL tumour Categorization [22]. Deep learning (DL) frameworks have expanded the field of medical image analysis by achieving previously unheard-of levels of effectiveness in applications like tissue segmentation and classification as well as medical outcome prediction. In the study, researchers develop and assess a unique 3-D CNN utilized to differentiate between metastatic and primary liver tumours utilizing diffusion-weighted MRI data and tailored for tissue categorization in medical imaging. The suggested network is made up of four stretched 3-Dimensional CNN layers that are applied in succession, and then comes a layer of neurons that is completely linked, and a Softmax layer for binary categorization. As far to our knowledge aware, it is the first Deep learning solution for the particular clinical situation and the first 3-D CNN for categorization methods that operates directly on the entire 3-D tomographic data without the requirement for any pre-processing steps like annotating, detecting regions of interest or region cropping. The categorization performance measures showed a considerable enhancement in tissue categorization accuracy when contrasted to two 2-D CNNs of various designs that were also formed for the particular medical challenge utilizing the original dataset. The findings imply that, particularly in size-restricted, disease-specific clinical datasets, the suggested 3-D CNN architecture can significantly improve DW-MRI liver differentiation as well as possibly a wide range of other tissue categorization issues based on tomographic data. However, the approach requires a lot of time and can only analyse a few datasets.

An automatic slices sorting method for multi-slice CT liver tumour images was proposed by Amandeep Kaur utilising convolutional networks. The radiation oncologist can choose the target region and the dose rate to be administered to the individuals with the aid of a rapid recognition and identification of liver cancer. The radiologists often spend a significant amount of time narrowing down the thousands of image, which are typically collected from multi-slices CT scanner, down to the most pertinent slices. In order to categorise various organs in 3D CT images of people accused of carrying liver cancer, the paper uses a convolutional network. The suggested technique has been backed up by a dataset made up of CT scans of individuals with liver cancer. For classifying CT liver cancer images, a CNN has been used. The classification results have been calculated in terms of F1 score, false negative rates, true positive rates, sensitivity, specificity, and accuracy. The outcomes show a high level of accuracy rate. The study's important component is that it will make it easier for the radiation therapists to concentrate on a select group of CT imaging data. The suggested model may be expanded to take the patient's breathing motion into account in order to use respiratory gated radiotherapy to reduce the radiation given during radiotherapy [23].

With Multi-phase CT Image and Medical Data, Welbin wang., *et al*. suggested a DL-Based Radiomics Frameworks for Timely Recurrence Prediction of HCC [24]. The second most prevalent source of tumour-related mortality is hepatocellular carcinoma, the fifth most widespread tumour worldwide. Patients who have hepatocellular carcinoma surgically removed risk an early return within a year. Latest researches have shown that CT radiomics characteristics may effectively forecast the initial recurrence of HCC. The radiomics characteristics, on the other hand, are dependent on manually created low-level properties like volume and surface. In the study, researchers present a radiomics strategy based on deep learning for forecasting hepatocellular carcinoma initial recurrence employing multi-phase computed tomography (CT) images. In order to increase prediction accuracy, researchers also suggest a number of models that integrate high-level radiomics properties with clinical data but still the approach has poor accuracy rates.

Utilizing Modified SegNet, Sultan Almotairi suggested Liver Tumor Segmentation in CT Scans. Hepatic cancer is the primary cancer-related cause of mortality in the globe. Computed tomography (CT)-assisted early identification of liver cancer might spare the lives of millions of people each year. Radiologists must study thousands or even hundreds of these CT images, which is a tremendous load. Consequently, there is a pressing need for automated, rapid, and accurate CT scan reading, detection, and evaluation. Consequently, liver extraction and segmentation from CT images remains a difficult task and a barrier for any system. In the study, a deep

learning-based method for semantic pixel-by-pixel categorization of road sceneries is implemented and adjusted to match liver CT segmentation and categorization. SegNet is the name of the deep convolutional encoder-architecture, decoder's which comprises of layers of encoders and decoders arranged in a hierarchy. A typical dataset for liver CT images was utilized to evaluate the suggested architecture, which showed improved tumour accuracy after training. However the method has an increased false negative rate [25].

Proposed methodology

A framework is employed to detect and categorise liver cancer using the techniques presented. Image gathering, image segmentation, pre-processing, feature extraction, and categorization are the five stages of the suggested methodology. Initially, 1800 photos containing a mix of both healthy and unhealthy liver images are gathered. The recommended research has pre-processed the real-time images because of their poor quality. The proposed approach makes utilisation pre-processing techniques to enhance the image's overall quality. During pre-processing, a wavelet-and-Gaussian filter combination is being utilized. Following that, the feature extraction is completed utilising bat optimization approach, and the segmentation is completed by employing the spatial fuzzy c-means clustering. The categorization of affected and unaffected areas is done utilizing CNN. The proposed methods framework is shown in Figure 1 and Figure 2 represents the Flow chart of the proposed methodology.

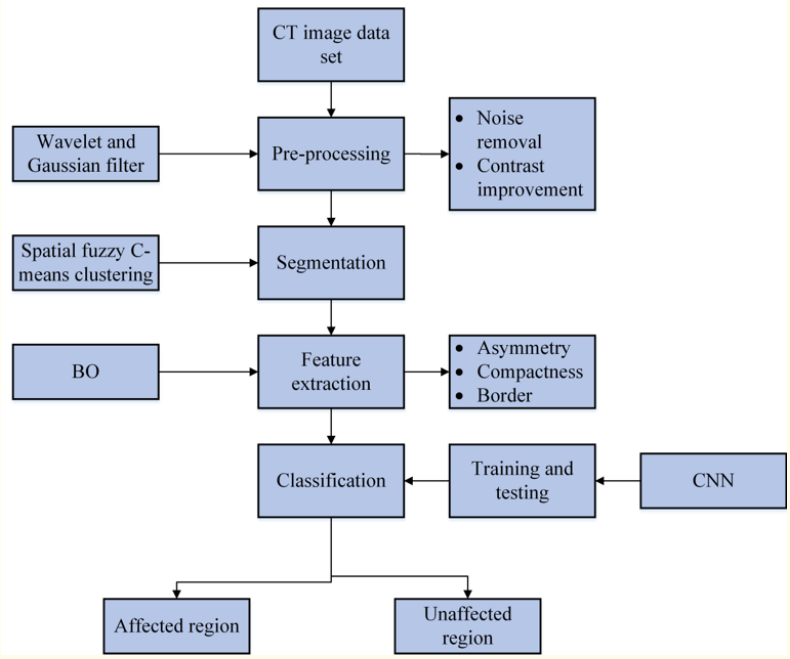


Figure 1: Proposed Method's Framework.

Dataset collection

A minimum of 1800 CT liver cancer images were gathered from the imaging department of the SUM and IMS Hospital in India. These are drawn from 500 patients with metastatic carcinoma (MET) and 550 patients with hepatocellular carcinoma (HCC) and hemangioma (HEM), and 200 normal individuals respectively. There are 280 male and 270 female patients with hemangioma, 260 males and 290 female patients with hepatocellular carcinoma and 230 males and 270 female patients from metastatic carcinoma. The images were captured utilizing a CT scanner from the GE medical system with 512 x 512 resolution slices that ranged in thickness from 0.5 to 1.5 mm.

Table 1: Dataset Collection.

Types of cancer	No. of patients
Metastatic Carcinoma	500 (230 male, 270 female)
Hemangioma	550 (280 male, 270 female)
Hepatocellular Carcinoma	550 (260 male, 290 female)

Pre-processing

The initial step in enhancing an image and preparing it for additional processing is pre-processing. Pre-processing increases computational accuracy and shortens processing time before the features are extracted. Cropping is necessary if a complicated backdrop is present. In order to reduce image damage and minimize image data, a hybrid filter that combines wavelet and Gaussian filters is employed in this work. The low-level and high-level data of the image are separated utilizing wavelet filters. Utilizing a discrete wavelet transform, the image with standard deviation is split into 1 lowest-frequency and 3 highest-frequency sub-images. In eqn (1), the Wavelet filter is provided.

$$B'(p,T) = \int_{-\infty}^{\infty} b(t') \frac{1}{\sqrt{p}} \varphi * \left(\frac{t'-T}{p}\right) dt \quad \text{----(1)}$$

Here, the wavelet transforms, and T demonstrates the function over. The asterisk (*) represents the complicated conjugation while ‘represents the dilation factor. The data that has already been denoised is removed through the use of a Gaussian filter. By applying a simple Gaussian filter to the data, the image is normalized and any distortions are removed. Thus, it is discovered to be quite successful to combine the wavelet and Gaussian filters, and it is employed in this work. The Gaussian filter is shown in eqn. (2)

$$R(y) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{y^2}{2\pi\sigma^2}} \quad \text{------(2)}$$

Where, represents the standard deviations of the distribution and y is the input image. A combined novel filter proposed is illustrated in eqn. (3)

$$B'(p,T) = \int_{-\infty}^{\infty} R(y) \frac{1}{\sqrt{p}} \varphi * \left(\frac{t'-T}{p}\right) dt \quad \text{------ (3)}$$

Segmentation

The segmentation process is largely utilised in CT scan images to separate the injured region. The efficiency of image processing depends on how well the segmentation process works. The position of the impacted nodules and the limitations associated with lines and curves in the images are often known by image segmentation. The process of image segmentation separates images into groups of labels and pixels each group in accordance with the desired presentation. In medical image analysis, image segmentation’s primary goal is to locate cancer spots and generate sufficient information for subsequent identification. The spatial fuzzy C-Means Clustering method is utilized in this instance to complete the image segmentation.

Spatial Fuzzy C-Means Clustering

There are two types of clustering approaches: partitional and hierarchical. Unlike hierarchical clustering, which produces a clustering tree, partitional clustering produces a single division of the data. Typically, it entails improving an objective function. The Euclidean distance, which measures the separation between centroids and data points, is a common objective function. When employing a hard or crisp approach, each point is assigned to a single cluster. However, in a fuzzy method, membership degrees are utilized to assign data points. The FCM method is capable of modelling uncertainty and has a stable characteristic. However, because FCM lacks spatial information, it is noise-sensitive. The supplied formula for the FCM objective function is

$$S_{FCM} = \sum_{y=1}^{F} \sum_{x=1}^{D} \mu_{xy}^{l} \left\| i_y - v_x \right\|^2 \quad \text{------- (4)}$$

Where F is the quantity of image pixels l (>1) is a parameter regulating the fuzziness of the resulting segmentation. The subsequent restrictions apply to the membership functions.

$$\sum_{x=1}^{D} \mu_{xy} = 1; 0 \le \mu_{xy} \le 1; \sum_{y=1}^{F} \mu_{xy} > 0 \quad \text{------ (5)}$$

The membership function and the centroids are updated iteratively

$$\mu_{xy} = \frac{\frac{\|i_y - v_x\|^{-2}}{(l-1)}}{\frac{\sum_{j=1}^{D} \|i_y - v_j\|^{-2}}{(l-1)}} \quad \text{-------(6)}$$

$$V_i = \frac{\sum_{y=1}^{F} \mu_{xy}^{l} i_y}{\sum_{y=1}^{F} \mu_{xy}^{l}} \quad \text{------- (7)}$$

When pixels near their centroid are given high membership values and those further away are given low values, the typical FCM method is optimised. The absence of spatial information is one of the issues with traditional FCM algorithms in image segmentation. Incorporating spatial features into an FCM would be desirable since artefacts and image noise frequently degrade the effectiveness of FCM segmentation. Fuzzy membership functions can integrate spatial information by

$$\mu_{xy} = \frac{\mu_{xy}^{m}\mu_{xy}^{n}}{\sum_{j=1}^{D}\mu_{jy}^{m}\mu_{jy}^{n}} \quad \text{-----(8)}$$

x and y are two variables regulating each contribution, respectively. Spatial data is included in the variable by

G_{xy} by

$$G_{xy} = \sum_{j\in F_c}\mu_{yj} \quad \text{------ (9)}$$

Fc stands for a local window that is centred on image pixel y.

Feature extraction

The feature extraction process entails transforming unstructured data into numerical qualities that can be utilized to store all the data included in the initial set of data. Images are interpreted in different ways by each patient; these characteristics are determined from the total amount of images captured. While the length of the images is increased throughout testing, the dimensionality of the images must be reduced in order to identify lung nodules. The feature extraction procedure is applied to resolve this issue. The Bat optimization is applied in this work to extract the characteristics from CT scans of liver cancer.

Bat optimization

A metaheuristic global optimization technique is the Bat algorithm. It was modelled after the changing pulse frequencies and loudness of microbats' echolocation behaviour's. Xin-She Yang created the Bat algorithm in 2010. Frequency tuning is a feature that has never been used in an algorithm before. At iteration t, each bat is assigned a velocity v_i (h+1) and a position W_i (h+1) in a d-dimensional searching or solution space. There remains a present right solution among all the bats. The following updated equations for W_i (h+1) and velocities v_i (h+1) can be utilized to transform the three previous rules:

$$W_i(h+1) = w_i(h) + v_i(h) \quad \text{------ (10)}$$

$$v_i(h+1) = v_i(h) + \big(w_i(h) - p(t)\big).f_i \quad \text{-------(11)}$$

$$f_i = f_{min} + (f_{max} - f_{min}).\beta \quad \text{-------(12)}$$

p(t) is the present global optimal solution and $f_{min} = 0$, $f_{max} = 1$, where β is a random vector with similar distribution, the range of which is [0, 1].

The following equations control the pulse emission and loudness rates:

$$L_i(t+1) = \propto L_i(t) \quad \text{----- (13)}$$

$$e_i(t+1) = e_i^0[1 - \exp(-\gamma t)] \quad \text{-----(14)}$$

Where, 0 <α< 1 and γ > 0 are constants. In general would be comparable to the cooling phase component in evolutionary algorithms.

In BA, frequencies adjusting effectively functions as mutations, but selection pressure is maintained rather steadily by using the best solution x that has been discovered so far. Although there are no apparent crossovers, there are differences in mutation because of changes in pulse emission and loudness. Additionally, the differences in pulse emission rates and loudness offer an auto zooming capability, enabling more extensive exploration as the search gets closer to the global optimal solutions.

Classification

The majority of DL research focuses on CNN. By reducing network design complexity and reducing the number of weights, its weight-sharing network structure more closely resembles biological brain networks. A CNN, which is a multi-layer artificial network, consists primarily of input, down-sampling or pooling, convolutional, fully linked, and output layers. In comparison to a normal neural network, a CNN may extract more flexible and extended characteristics from raw data. For feature extraction, the pooling layer and the convolutional layer are being utilized. The characteristics produced from the output layer afterwards are synthesised by the fully linked layer. The architecture of the CNN is given in Figure 2.

Convolutional neural network

To identify the lung tumour nodules, convolutional neural network classifiers are employed [26]. Through its multi-layered design, it accurately assesses the CT images and obtains the necessary attributes. Four layers make up a CNN classifier: the image input layer, the fully connected layer, the Max pooling layer, the convolutional layer, and the output layer. In order to prepare for training,

the convolutional neural network modifies the image's pixel intensity. The technique with the fastest training time is CNN. The size of the CT scans used as input should be uniform. Each representation's equation in the training set is given in eqn. (15)

$$p(l, m) = \frac{o(l,m)-\mu}{\sigma} \quad \text{-------(15)}$$

Convolutional layer

The convolutional layer gathers a range of images as input and measures each layer's complexity. It is closely connected to the characteristics that the submitted image must possess. It is expressed in eqn. (16)

$$f_i^u = y(\sum_{j\in N_i} f_j^{u-1} * q_{ji}^u + t_i^u) \quad \text{-------(16)}$$

N_i–It represents an input selection. The outcome is a bias that is additive. When the sum of the maps l and m across map i the kernel is transferred to map i.

Max pooling layer

The down sampling application combines the layer to reduce fitting and reduce the amount of the neurons it requires. The Calculation rate, parameter number, training time, size of the feature map, limits over fitting are all reduced by the pooling layer. 50% of test data and 100% of the training dataset constitute over fitting and it is calculated by using eqn. (17)

$$x_{mab} = \max_{(v,w)\in} f_{nvw} \quad \text{-------(17)}$$

Map, is the element as (v, w) within the pooling region pts which represents a local neighbourhood around the place (l, m).

Fully connected layer

Fully Connected Layer has been employed in the area of categorising images. Just after Convolutional layers comes the FC layers. The mappings of the image between the output and input is aided by the FC layer. Fully linked layers make up the network's final tiers. The fully connected layer receives its inputs from the outputs of the max pooling layer.

Softmax layer

The scores are transformed into a normalised ratio distribution using the Softmax layer. The classifiers receive the outputs as an input. The Softmax classifier is a standard contribution classifier that applies the softmax layer's architecture to liver cancer cells. It is shown in eqn. (18)

$$\sigma(\vec{X})_b = \frac{e^{x_b}}{\sum_{i=1}^{n} e^{x_i}} \quad \text{-------- (18)}$$

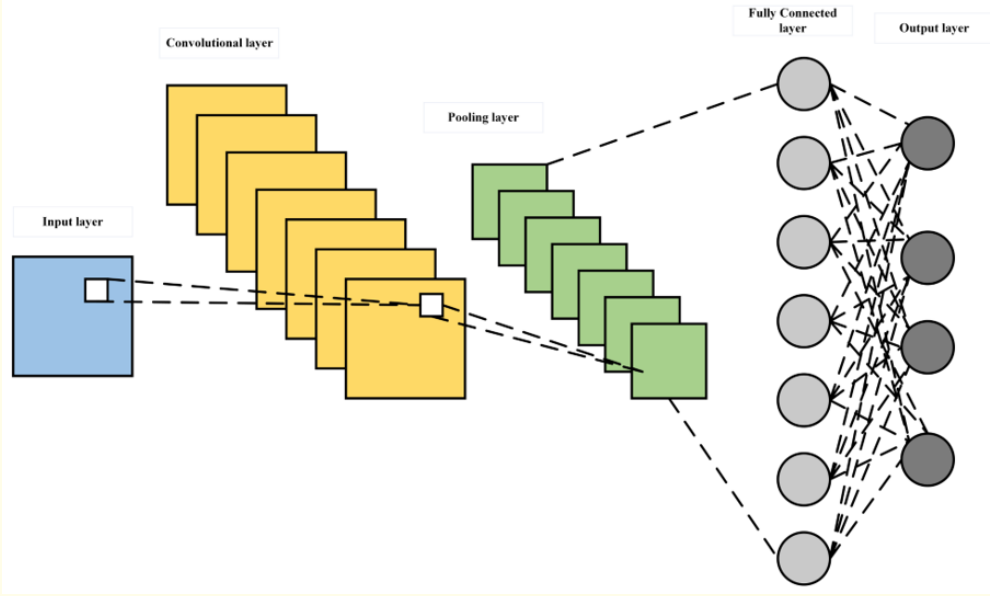
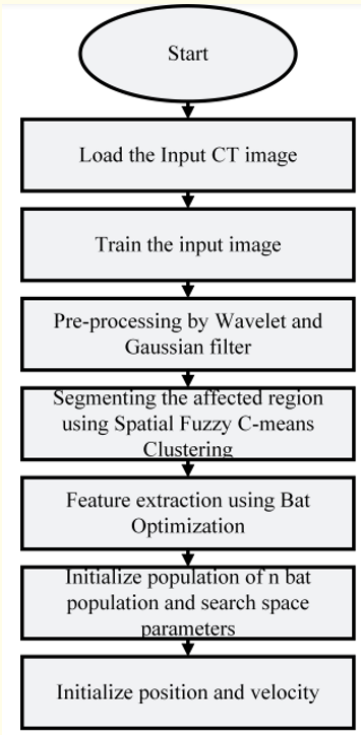


Figure 2: CNN Architecture.

Algorithm: BO-CNN method

Input: CT images of liver cancer
Output: Identification of affected and unaffected liver images
Load input image data
Train the input images
Pre-processing of images // Wavelet and Gaussian filte
Segmenting the affected region //Spatial Fuzzy C-means clust
Extracting the features of the segmented image // Bat Optimization
Initialize the bat population $W_i(h + 1)(i=1,2,.....n)$ and $v_i(h + 1)$
Characterize the pulse rate f_i at $W_i(h + 1)$
Initialize loudness $e_i(t + 1)$ and the pulse rates $L_i(t + 1)$
While (t< Maximum number of iterations)
Create a new solution by changing velocities and solutions and altering frequency
If(rand > $L_i(t + 1)$)
Choose at random one of the top solutions
Create a neighbourhood solution utilising a local random stroll all around the right choice
end if
if (rand <$e_i(t + 1)$)
Accept the creative solution
Enhance $L_i(t + 1)$ and decrease $e_i(t + 1)$
end if
Ranking the bats at each iteration and find their present best p(t)
end while
Return //CNN classifier
Classification of affected and unaffected regions



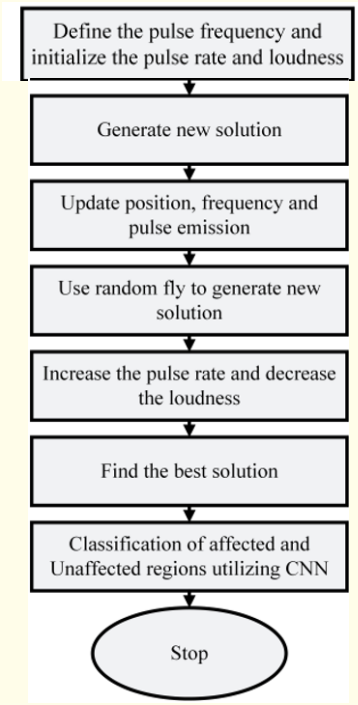


Figure 3: Flow chart of the suggested methodology.

Results and Discussion

The developed method is examined using a dataset from computerised tomography. A mixed wavelet and Gaussian filter was employed to pre-process 1800 images of various liver diseases. The average person cannot immediately realize the cancers in the images. Computed tomography images must be pre-processed in order to improve the visual impact of the images before processing. Since the collection frequently includes low-quality photos, deformation must be eliminated, and the image should be improved. Consequently, several characteristics are first obtained. Fuzzy C means clustering is utilized to identify and categorise the condition. The Bat optimization algorithm is then utilized as part of the feature extraction process. The categorization of liver disorders is then done employing CNN. The proposed technique satisfies the metric characteristics of recall, accuracy, and specificity. 200 images of healthy liver tissue and 1600 images of various liver cancers are found by extracting and segmenting image attributes. The proposed technique's utility is demonstrated, and it achieves the greatest levels of recall, accuracy, and precision value for the detection of liver cancer.

Evaluation metrics

Measurements for evaluations are essential for assessing classification performance. A measure of accuracy is the technique that is most usually utilized for this purpose. The percentage of a testing dataset that classifiers correctly categorise reveals the classifier's effectiveness for that datasets. As the accuracy measure as a whole is not adequate for optimal decision-makings, researchers additionally employed a few other metrics to evaluate performance of the classifier. Three important measures that are widely utilized are F-measure, recall, and precision.

- (True Positive) refers to the volume of data that has been successfully classified.
- The term (False Positive) describes the quantity of reliable data that was misclassified.
- False negatives () are circumstances in which incorrect data has been classified as legitimate.
- The categorization of incorrect data values is referred to as (True Negative).

Performance evaluation

In addition to achieving a greater accuracy of 99.80%, the suggested technique also obtained 100%, 99.99%, and 99.10% in other areas including precision, recall, and F-measure. In comparison to the current methods, the system performance is greater. As a result, the proposed strategy performs better in terms of precision, recall, F-measure, and accuracy.

Table 2: Performance Evaluation of the proposed model.

Evaluation Metrics	Proposed model
Accuracy	99.80
Precision	100
Recall	99.99
F1-Score	99.10

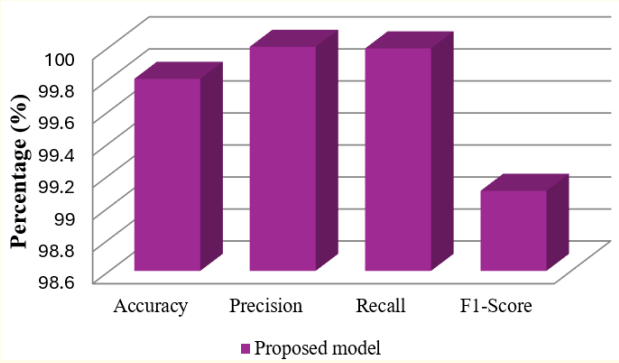


Figure 4: Performance Evaluation of the proposed model.

Accuracy

Accuracy determines how precisely the system model functions across all classes. Generally, it is the idea that all observations will be properly anticipated. Accuracy is expressed in eqn. (19),

$$\text{Accuracy} = \frac{\text{Tpos+Tneg}}{\text{Tpos+Tneg+Fpos+Fneg}} \quad \text{------(19)}$$

Table 3: Comparison of Accuracy.

Methods	Accuracy (%)
11 Gene pair method	91.93
SVM	88.49
WSDL	99.38
CNN	98.7
Proposed model	99.80

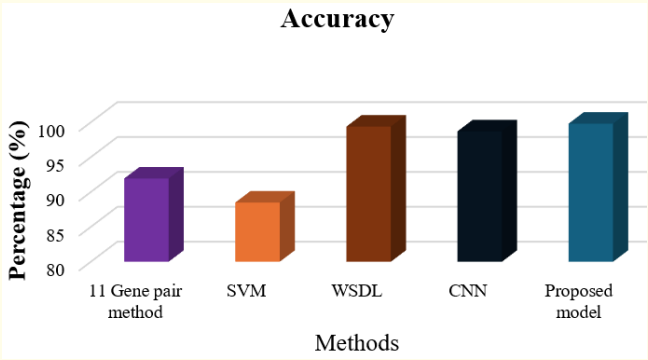


Figure 5: Comparison of Accuracy.

The suggested methodologies outperform the currently utilized techniques for identifying liver cancer, such as the 11 Gene pair methods, SVM, WSDL, and Convolutional Neural Network, which are tabulated in the Table 3. The accuracy comparison between the proposed approach and the alternatives is shown in Figure 5.

Precision

Precision is determined by counting the number of precise positive evaluations that differ from the total number of correct positive perceptions. The exact identification of the afflicted area as having cancer cells is its component that are calculated by employing eqn. (20),

$$P = \frac{Tpos}{Tpos+Fpos} \quad \text{--------- (20)}$$

Table 4: Comparison of Precision.

Methods	Precision (%)
11 Gene Pair method	100
WSDL	99.9
Proposed model	100

Table 4 contrasts the test outcomes of the proposed BO-CNN with those of different techniques, including the 11 Gene pair methods and WSDL utilizing the statistical properties of precision. The precision of the suggested method was determined to be 100%, It outperforms the currently used techniques as illustrated in Figure 6.

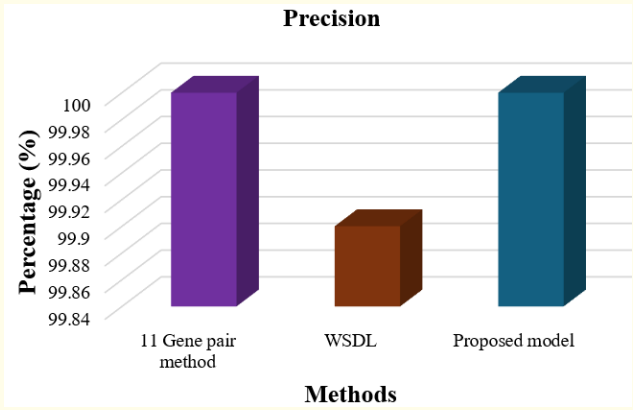


Figure 6: Comparison of Precision.

Recall

The recall is the connection between the entire amount of positive samples and the percentage of true positives that were accurately classified as positives. It displays the percentage of predictions that were accurate in identifying cancer nodules that are represented in eqn. (21),

$$R = \frac{Tpos}{Tpos+Fneg} \quad \text{------(21)}$$

Table 5: Comparison of Recall.

Methods	Recall (%)
11 Gene pair method	95.97
WSDL	99.09
Proposed model	99.99

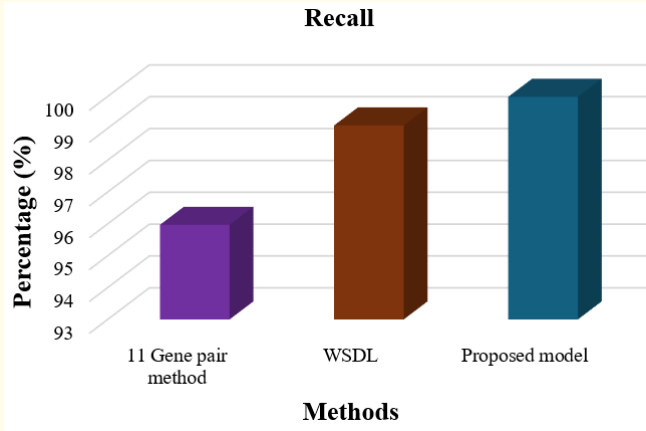


Figure 7: Comparison of Recall.

The experimental findings for the proposed BO-CNN are compared in Table 5 to those of other approaches, such as the 11 Gene pair methods and WSDL using the evaluation metrics of recall. As shown in Figure 7, the recall of the proposed approach was found to be 99.99%, which is greater than that of the current methods.

F1-Score

Recall and precision are incorporated in the F-measure computation. The F-Measure is computed utilizing recall and precision that is shown in eqn. (22),

$$F1-score = \frac{2\times precision \times recall}{precision \times recall} \quad \text{-------(22)}$$

Table 6: Comparison of F1-Score.

Methods	F1-Score (%)
WSDL	88.49
CNN	98.18
Proposed model	99.10

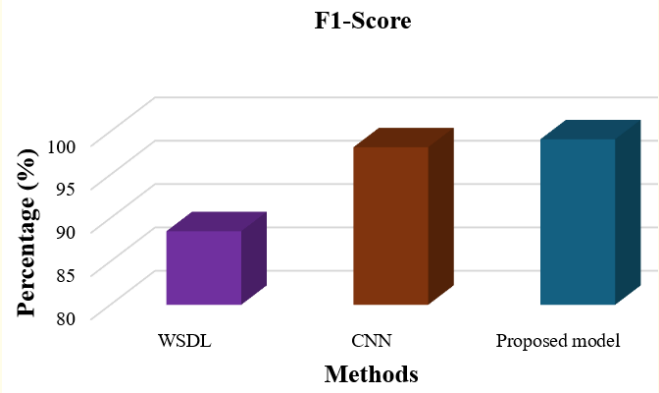


Figure 8: Comparison of F1-Score.

In Table 6, the test outcomes of the proposed BO-CNN are compared with those of existing strategies, including the CNN and WSDL, utilizing the assessment metrics of F1-Score. The F1-Score of the suggested strategy, which is higher than that of the existing approaches, was determined to be 99.10%, as shown in Figure 8.

Conclusion

One of the leading common reasons for death worldwide is liver cancer. For the early recognition and diagnosis of liver cancer, the ability to identify liver cancers from computed tomography images is essential. Physically identifying cancer tissue is a time and labour intensive process. Therefore, a computer-aided diagnostic is utilized during the decision-making process to properly identify the appropriate medication. Thus, the main objective of the research is to accurately diagnose and classify liver cancer employing deep learning technology. For processing, the computerised tomography images' volumetric data were obtained. Then the images undergo pre-processing to eliminate the unwanted sounds in the images. Here the pre-processing is processed by the combined wavelet and Gaussian filter. The Spatial Fuzzy C-means clustering technique processes the segmentation to identify the afflicted liver area. The Bat Optimization (BO) algorithm then does the feature extraction. The affected and unaffected areas in the liver CT scans are categorised using the classifiers of the CNN. The outcomes show that the CNN method outperforms rival strategies and provides opportunity for the identification and classification of liver tumours.

Acknowledgement

The author would like to express his gratitude to King Khalid University, Saudi Arabia for providing administrative, funding, and technical support.

Bibliography

1. D Anwanwan., *et al*. "Challenges in liver cancer and possible treatment approaches". *Biochimica et Biophysica Acta (BBA) - Reviews on Cancer* 1873.1 (2020): 188314.

2. J Calderaro., *et al*. "Molecular and histological correlations in liver cancer". *Journal of Hepatology* 71.3 (2019): 616-630.

3. YM Yang., *et al*. "Inflammation and liver cancer: molecular mechanisms and therapeutic targets". in *Seminars in liver disease*, Thieme Medical Publishers (2019): 026-042.

4. D Guo., *et al*. "Radiomics analysis enables recurrence prediction for hepatocellular carcinoma after liver transplantation". *European Journal of Radiology* 117 (2019): 33-40.

5. A Kiani., *et al*. "Impact of a deep learning assistant on the histopathologic classification of liver cancer". *NPJ Digital Medicine* 3.1 (2020): 1-8.

6. L Ma., *et al*. "Tumor cell biodiversity drives microenvironmental reprogramming in liver cancer". *Cancer Cell* 36.4 (2019): 418-430.

7. JN Kather and J Calderaro. "Development of AI-based pathology biomarkers in gastrointestinal and liver cancer". *Nature Reviews Gastroenterology and Hepatology* 17.10 (2020): 591-592.

8. A Das., *et al*. "Detection of liver cancer using modified fuzzy clustering and decision tree classifier in CT images". *Pattern Recognition and Image Analysis* 29.2 (2019): 201-211.

9. H Seo., *et al*. "Modified U-Net (mU-Net) with incorporation of object-dependent high level features for improved liver and liver-tumor segmentation in CT images". *IEEE Transactions on Medical Imaging* 39.5 (2019): 1316-1325.

10. X Dong., *et al*. "Liver cancer detection using hybridized fully convolutional neural network based on deep learning framework". *IEEE Access* 8 (2020): 129889-129898.

11. A Aghamohammadi., *et al*. "TPCNN: two-path convolutional neural network for tumor and liver segmentation in CT images using a novel encoding approach". *Expert Systems with Applications* 183 (2021): 115406.

12. SH Ahn., *et al*. "Comparative clinical evaluation of atlas and deep-learning-based auto-segmentation of organ structures in liver cancer". *Radiation Oncology* 14.1 (2019): 1-13.

13. V Hemalatha and C Sundar. "Automatic liver cancer detection in abdominal liver images using soft optimization techniques". *Journal of Ambient Intelligence and Humanized Computing* 12.5 (2021): 4765-4774.

14. F Özyurt., *et al*. "A novel liver image classification method using perceptual hash-based convolutional neural network". *Arabian Journal for Science and Engineering* 44.4 (2021): 3173-3182.

15. M Furuzuki., *et al*. "A Detection Method for Liver Cancer Region Based on Faster R-CNN". in *2019 19th International Conference on Control, Automation and Systems (ICCAS)*, IEEE (2021): 808-811.

16. ZM Zhang., *et al*. "Early diagnosis of hepatocellular carcinoma using machine learning method". *Frontiers in Bioengineering and Biotechnology* 8 (2020): 254.

17. W Książek., *et al*. "A Novel Machine Learning Approach for Early Detection of Hepatocellular Carcinoma Patients". *Cognitive Systems Research* 54 (2019): 116-127.

18. N Gruber., *et al*. "A Joint Deep Learning Approach for Automated Liver and Tumor Segmentation". arXiv (2020).

19. A Saito., *et al*. "Prediction of early recurrence of hepatocellular carcinoma after resection using digital pathology images assessed by machine learning". *Modern Pathology* 34.2 (2021): 417-425.

20. X Wang., *et al*. "A hybrid network for automatic hepatocellular carcinoma segmentation in H&E-stained whole slide images". *Medical Image Analysis* 68.17 (2021): 101914.

21. A Das., *et al*. "Deep learning based liver cancer detection using watershed transform and Gaussian mixture model techniques". *Cognitive Systems Research* 54 (2019): 165-175.

22. E Trivizakis., *et al*. "Extending 2-D Convolutional Neural Networks to 3-D for Advancing Deep Learning Cancer Classification With Application to MRI Liver Tumor Differentiation". *IEEE J. Biomed. Health Inform.* 23.3 (2019): 923-930.

23. A Kaur., *et al*. "An automated slice sorting technique for multislice computed tomography liver cancer images using convolutional network". *Expert Systems With Applications* 186 (2021): 115686.

24. W Wang., *et al*. "Deep Learning-Based Radiomics Models for Early Recurrence Prediction of Hepatocellular Carcinoma with Multi-phase CT Images and Clinical Data". in *2019 41st Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC)*, Berlin, Germany: IEEE (2019): 4881-4884.

25. S Almotairi., *et al*. "Liver tumor segmentation in CT scans using modified SegNet". *Sensors* 20.5 (2020): 1516.

26. R Khdhir., *et al*. "Pancreatic Cancer Segmentation and Classification in CT Imaging using Antlion Optimization and Deep Learning Mechanism". *International Journal of Advanced Science and Computer Applications* 14.3 (2023).