Deep Federated Machine Learning-Based Optimization Methods for Liver Tumor Diagnosis: A Review

Article *in* Archives of Computational Methods in Engineering · March 2023

DOI: 10.1007/s11831-023-09901-4

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Deep Federated Machine Learning-based Optimization Techniques for Liver Tumor Diagnosis: A Review

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Abstract

Computer-aided liver diagnosis helps doctors accurately identify liver abnormalities and reduce the risk of liver surgery. Early diagnosis and detection of liver lesions depend mainly on medical imaging techniques such as magnetic resonance imaging (MRI) and computed tomography (CT). Segmentation and identification of hepatic lesions in these images are very challenging because these images often come with low resolution and severe noise. Many new machine learning and image analysis techniques have been gradually used on this topic, and their performance is still limited. An automatic and accurate model that incorporates tracking, detection, and diagnosis of hepatic lesions in the 3D volumes of CT and MRI is still lacking. This paper aims to review different models for automatic detection, diagnosis of the hepatic lesion with CT and MRI and discusses the medical background of liver tumors and the standard elements of the CAD liver diagnosis system. In addition, the concept of federated learning has been introduced, and the fused information from multi-modality (CT and MRI) and the robust and complex features that represent liver lesions accurately have been discussed. More specifically, this paper presents a comprehensive study of the latest work on liver tumor detection and diagnosis, which identifies the contributions of these different approaches and the recommendation model suggested for practical use. Furthermore, this paper was intended to encourage researchers from the medical community, image processing, and machine learning community to pay much attention to the use of deep and federated learning, spiking neuron model, bio-inspired optimization algorithms, fuzzy logic, and neutrosophic logic to address the problems of segmentation and prediction/classification for real-time diagnosis.

Keywords: Deep learning, Optimization, Segmentation, Feature selection, Federated learning, and Spiking neuron model.

1. Introduction

Liver disease is a leading cause of sickness and death around the world. Around 300 million individuals are affected by liver disorders, notably viral hepatitis (HBV, HCV), non-alcoholic fatty liver disease (NAFLD), and alcoholic liver disease (ALD). Moreover, the number of individuals suffering from alcoholic and non-alcoholic fatty liver disease increases at an alarming rate. Liver cancer is the second most prevalent malignancy and one of the worst. Each year, over 383,000 individuals die from liver cancer in China, accounting for 51% of all liver cancer deaths worldwide [1-3].

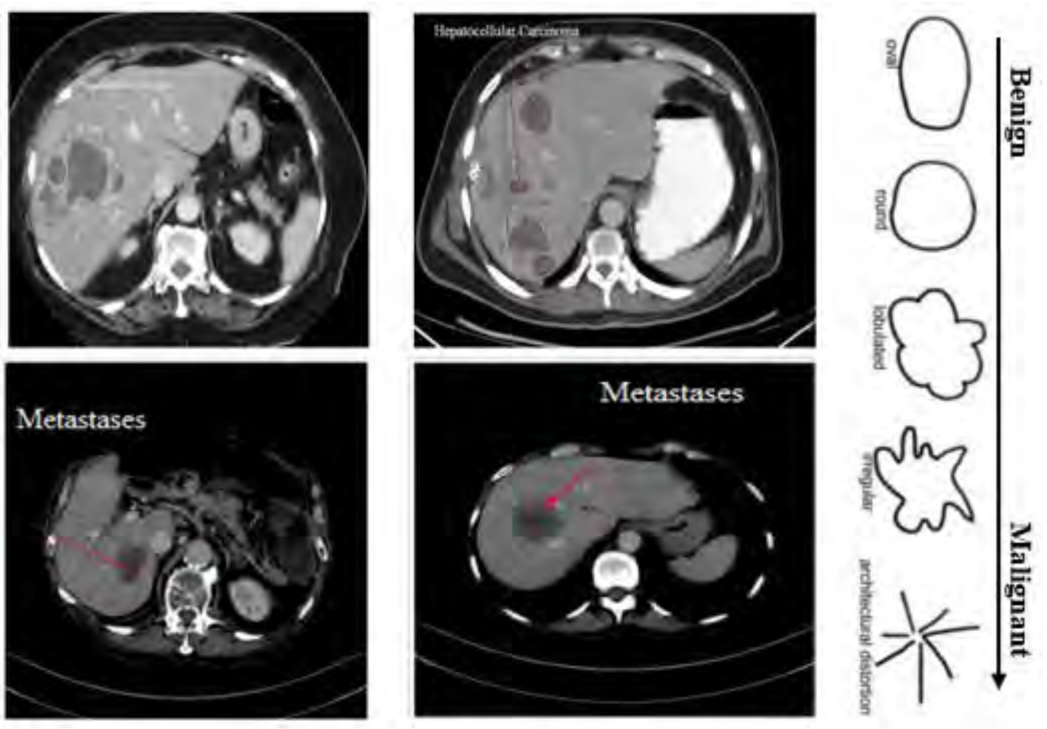
Medical imaging, such as CT and MRI, continues to be the gold standard for detecting, examining, and diagnosing liver cancers. A doctor's typical duty is to establish a measurement that defines the liver lesions in these images. A measurement of this type might define the object's size, mean density, or relative location. The most frequently used software in hospitals has capabilities for making such measures. However, these tools are typically not user-friendly or require a significant amount of user input. Despite its inefficiency, the method is very subjective, and even the same doctor frequently marks the same thing differently, yielding various findings. As a result, developing an automated computer-assisted diagnosis (CAD) model for analyzing medical images and aiding clinicians with diagnosis and treatment is essential. On the other hand, CAD systems can’t wholly replace radiologists; instead, they have aided tools for them [4].

1.1 Clinical Background

The liver is the largest organ in the human body and serves several functions. This results in a large blood volume flowing into the liver, rendering it susceptible to secondary tumor occurrence. According to [5], the vast majority of liver cancers originate in other organs. Tumors must be localized and diagnosed in order for treatment to be effective.

Cancer is the general name in which cells develop out of control in one part of the body. Cancer cells grow and proliferate in order to produce more cells than the needs of the human body. These additional cells are called tumors. Tumors may be benign or malignant [5]. Types of malignant tumors are (Hepatocellular-carcinoma (HCC), Cholangio-carcinoma (CC), and Metastases), and types of benign tumors are (Hemangioma, Focal-nodular-hyperplasia (FNH), Adenoma, and Cyst). Figure 1(a) shows a sample of hepatic focal lesions with different sizes and shape for different patients.

Tumors occur in a variety range of shapes, sizes, and contrasts. They can be highly diffused and regularly obscured by normal tissue. Depending on the morphological features of the tumor, clinicians attempt to estimate the probability of malignancy. Their shape categorizes tumors into round, oval, lobular, and irregular shapes [6]. Figure 1(b) shows a sample of such tumor shapes.



(a) **(b)**

Figure 1. Liver tumors and their shapes. (a) The first row is two patients with metastases, and the second row is two patients with hepatocellular liver carcinoma (HCC). (b) The shape of the tumor is a vital sign of their malignancy/ benignancy degree.

1.2 Liver tumor diagnosis and its challenges

The hepatic diagnosis via CAD model usually follows two stages; computer-assisted detection and computer-assisted diagnosis, as shown in Figure 2.

The stage of detection consists of pre-processing, segmentation of the liver, and detection of lesions. During the detection stage, lesion boundary delineation is very challenging due to various factors such as low contrast of soft tissue, noise level, irregularity of liver shape and size, the similar intensity with other organs, fuzzy boundary, and variation of lesion shape. Furthermore, the voxel spacing along the z-axis spans from 0.45mm to 6.0mm [7-9]. Because of these issues, automated and precise liver and lesions segmentation are exceedingly complicated.

Traditional imaging segmentation methods, such as edge detection, regional transformation, watershed transformation, fuzzy logic, and others, are widely used. However, these methods have certain disadvantages, which means that they cannot be used for the exact results. Deep learning (DL)-based segmentation has recently become a popular method with many types of architecture, such as (SurvivalNet, ResNet, GAN, CNN, etc.). DL can accurately segment organs and predict crucial regional characteristics. However, DL is time-consuming, has many hidden layers ranging from 30 to 150 layers, and the parameters must be adjusted [10-13].

On the other hand, the diagnostic stage consists of extraction of features, selection of significant features, and classification/prediction. The extraction of texture/shape features plays a significant role in different medical imaging tasks. Features are extracted from each region of interest (ROI) which is segmented from the previous stage. Features of each ROI passed to the classifier differentiate between liver lesions (benign and malignant). A critical issue of big medical data is the feature selection for the best and hidden knowledge instead of using all real data. Many different search methods are used for feature selection (forward selection search, selection random search, relief, fisher, mutual information, etc.). However, all these techniques still suffer from the stucking and recession in local minima and being computationally expensive [14]. In addition, the prediction/classification machine learning algorithms have limitations on stochastic training, time consumption, stuck in local minima, lack of strength and tuning parameters (such as; radius, learning rate, decay rates, size of the network, etc). Further, they cannot be incrementally learned, making it unable to correct recognition errors dynamically.

The CAD system is still facing challenges in the automatic segmentation and diagnosis of liver tumors such as:

- Liver and tumor irregularity and similarity to other organs.
- Two common characteristics in CT/MRI images are severe noise and low resolution.
- The algorithms used for liver diagnosis may consume time and error regions.
- The detection and diagnosis process should not take more than a few minutes.
- CT images are gray instead of color. Even an intensity change may not clearly display lesions.
- The diagnostic process in hospitals should not require unrealistic resources, such as supercomputers or grid computing. The entire process should be run on individual computers.

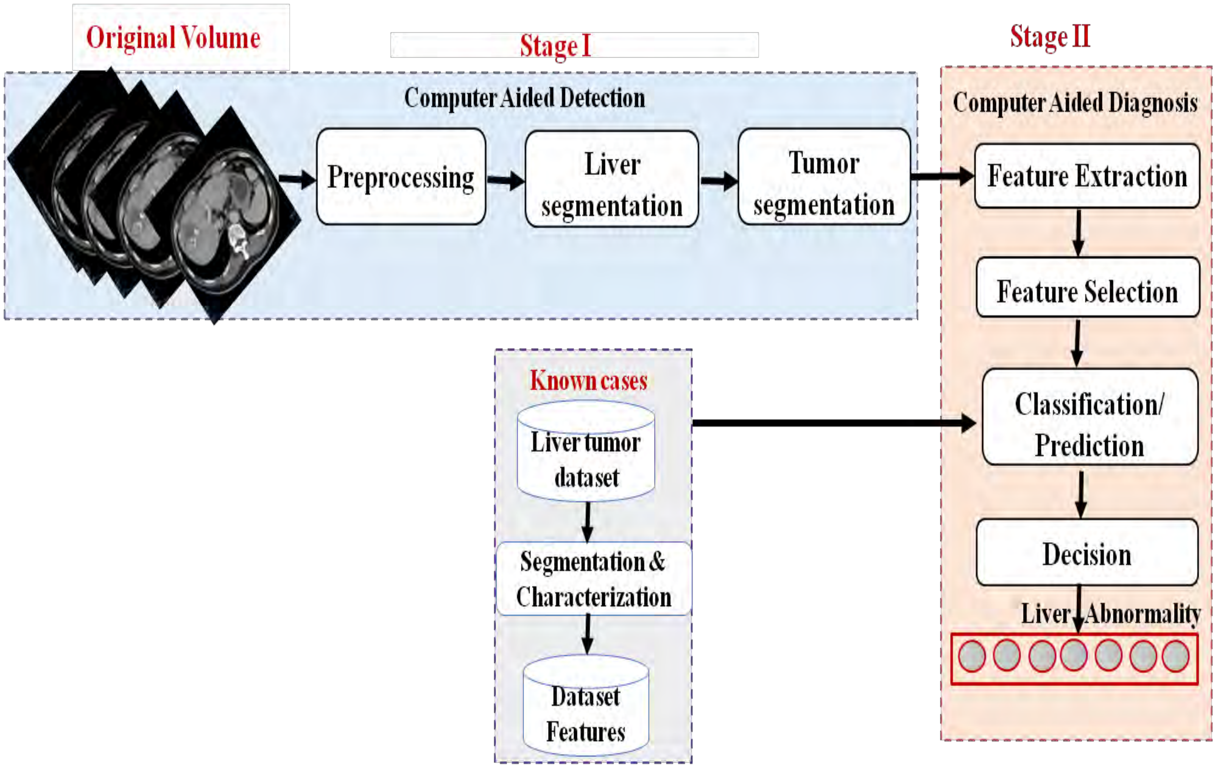


Figure 2. Schematic diagram of CAD model phases.

1.3 Key scientific problems

The segmentation process is used to segment the liver, localize and delineate lesions. However, the classical segmentation methods have no exact solutions for all cases, high time computation, and stuck in local minima. The feature extraction process analyzes ROIs that depict lesions at only a single scale, thereby losing many dominant characteristics. Feature selection methods have high time computation in the feature selection process, are stuck in local minima, and do not agree to get the optimal solution. The classifiers used have limitations on stochastic training, time consumption, lack of strength, and tuning parameters.

The following vital problems can be concluded from the above issues as follow:

- Difficult to segment liver and localize lesions in abdominal CT/MRI imaging techniques. The liver has irregularity and variation in both shape and scale for each patient and has similar intensity with neighbor organs. In addition, liver lesion segmentation is considered a more challenging task due to appearances, have no clear boundary, and visible edges.

- The diagnosis approach needs to keep the model continues learning, adapt parameters automatically by federated learning, needs spikes neuron signals to carry more information than classical coding features, needs optimized and in-depth features for real-time diagnosis model.

This review aims to provide a comprehensive survey of the current state of the art and discuss open problems and challenges for future work for live tumor diagnosis via the CAD system. Moreover, this paper suggested a recommendation model for liver tumor diagnosis based on federated deep neural network, spiking neuron model, bio-inspired optimization algorithms, and fuzzy and neutrosophic sets. We expect that this survey will attract researchers working on different diagnostic fields of CT/MRI further to investigate effective and efficient approaches to new challenges. This paper is also intended to encourage researchers from the medical community, image processing, and machine learning community to pay much attention to deep federated learning, spiking neuron models, bio-inspired evolutionary algorithms, fuzzy and neutrosophic logic the problems of segmentation and classification.

The rest of this paper is as follows. Section 2 reviews different related work for liver tumor detection and diagnosis; various cases of deep learning, swarm optimization, and neutrosophic logic are introduced for analyzing liver tumors from CT/MRI scans. Section 3 suggests a recommendation model for liver tumor diagnosis. Finally, the conclusion is given in Section 4.

2. Current Status and Trends

The segmentation of liver lesions is regarded as a more complex process due to the wide range of lesion tissue appearances. In addition, because of the low contrast of liver lesions, this segmentation is often performed on a noisy background. CT/MRI abdominal imaging presents an additional problem from the diagnostic point of view: the uneven enhancement caused by anatomical variations between lesions Further, certain lesions lack clearly visible boundaries, making the use of edge-based segmentation approaches as the sole segmentation method ineffective. Unfortunately, hepatic lesion segmentation has received low interest from researchers compared to many proposed methods of liver segmentation. This can be related to the challenges involved with the segmentation of liver lesions and an exciting lack of public datasets, limiting the development of lesion segmentation and diagnostic techniques.

Many studies have developed numerous methods for image segmentation, and they can be categorized into full, semi, or interactive by the degree of automation. Currently, computerized liver and lesion segmentation approaches can be classified into histogram-based [15-17], region growing [18,19,4], active contour models or level sets [20,21], graph cuts [22], watershed [23-25], fuzzy logic [26,27], and recently deep learning algorithms were used [23]. Each of these techniques offers advantages and drawbacks in terms of applicability, appropriateness, performance, and computational cost. However, extracting liver lesions from CT/MRI images, particularly those with low contrast, remains difficult. In histogram-based segmentation methods, Soler suggested the first method of liver lesion segmentation [24]. Several authors then used a threshold technique to detect liver lesions. A thresholding technique is simple but powerful. The main limitation is that the threshold does not account for the spatial properties and is highly noisy [25].

The advantages and disadvantages of various segmentation methods are shown in Table 1. However, extracting liver tumors from CT/MRI images, particularly those with low contrast, remains challenging.

Table 1: Summarize advantages and disadvantages for different segmentation methods.

Methods	Advantages	Disadvantages
Histogram-based	High-performance speed and simplicity.	Hard to identify valleys and peaks. Also, it does not take the spatial characteristics into account and highly sensitive to noise.
Edge-based	Computationally fast and straightforward. Not sensitive to noise	ROIs edges sometimes are disconnected
Regional-based	Simple and can separate the regions correctly. Multiple stop conditions can be chosen.	Seed points are critical. Reduce stability of segmentation. Sensitive to noise. Time-consuming.
Model-based	Finds certain-shaped regions.	Regions need to fit a particular model.
Watershed	Boundaries ROIs are continuous. The regions extracted are connected based on the topographic interpretation.	Over-segmentation, sensitive to noise, and time-consuming.

Clustering-based	Fully automatic without user intervention. It takes into account the uncertainty of data.	Results may contain many false positive. It needs post-processing. It cannot handle Indeterminacy and is affected by initial clusters.
Neutrosophic-based	Able to handle Indeterminacy. Better than fuzzy logic and may use in many real-time applications.	Hard to extract the *NL* components *(T, I, F).*
Machine learning	Have stability, and different lesions can be classified using pixel-based or region-based.	It does not converge well, have much time for training. Training over or under-fitting; test images should come from the same environment.
Swarm-based	It can integrate with classical methods, decreases computational time, has high convergence speed, and avoids local minima.	Work in random behavior. Gives unstable results.

The objective of the detection stage is to delineate and segment certain ROIs that may contain abnormalities from the original abdominal CT/MRI scans and increase the efficiency of diagnostic procedures.

In the ***histogram-based segmentation approach***, Soler suggested the first method of liver lesion segmentation [24]. Several authors then used a threshold technique to detect liver lesions. A thresholding technique is simple but powerful. The main limitation is that the threshold does not account for the spatial properties and is highly noisy [25].

Choudhary et al. proposed the semi-automatic segmentation approach. The watershed algorithm for liver segmentation and adaptive multi-thresholding based on minimum cross-entropy was used for tumor segmentation with high accuracy and less computation [28]. Patil et al. proposed a tumor segment approach using adaptive threshold, global threshold, and morphological operators for liver segmentation. The second phase tumor is segmented using an adaptive hybrid threshold with morphological operators, fuzzy c-mean, and region-growing techniques. This approach improves the accuracy of segmentation for various CT image quality [17]. Campadelli et al. proposed significant edges to segment liver volume from coronal, sagittal, and axial phases. A prominent histogram peak identifies the region of the liver [29]. Campadelli et al. presented another study of abdominal organ segmentation based on morphology operators, threshold, neural network, level set, model fitting, and data-driven methods [30].

Dixit and Pruthi proposed a simple method for the global threshold and morphological operator segmentation process. However, the global threshold cannot take advantage of the image characteristics [16]. Kumar and Moni proposed adaptive threshold operations and morphology. Each ROIs depict tumor region was automatically extracted using a fuzzy c-mean method [31]. Mahjoub proposed an approach based on the histogram threshold, the algorithm for connected labeling components, morphological operators, and detection of contours. This approach depends on prior knowledge, such as liver position and shape [15]. Akram et al. the adaptive threshold was used, and morphological operations were applied. This approach has achieved a precision of 96% for 100 patients [32].

Region growing (RG)-based segmentation approach is presumptively based on the assumption that neighboring pixels in one region have the same intensity value. The RG algorithm is one of the most fundamental algorithms for regional segmentation. It performs image segmentation by analyzing neighboring pixels of a set of pixels known as seed points and determining whether the pixels can be categorized in the seed point cluster. The advantages of this method are that it is the simplest and can accurately separate areas with similar features. The main drawbacks of the RG are that it is sensitive to seed point location and threshold, fails in the presence of weak boundaries, resulting in leakage, and takes much time to scan each pixel prosperity. As a result, several pre/post-processing stages are required to refine the segmentation. These problems reduce the fragmentation stability of the image segmentation. RG problems can be solved by integrating RG with different algorithms such as watershed, fuzzy c-means, connected component algorithm [17, 33]. Finally, liver segmentation cannot be handled only using a regional global approach; it is generally coupled with other approaches.

Massieh et al. proposed an automatic RG method with the FCM method to find the seed point automatically [34]. Mostafa et al. proposed RG to isolate the liver region from scans with morphological operators to achieve the highest contrast stretching filter performance with the precision of 84% [35]. Rusko et al. proposed a hybrid approach to segment liver using RG algorithm with post-processing operations (pre-defined intensity range to image threshold and smooth histogram to reach the full significance). Then, image erosion was used to remove the small regions. The intensity of the liver was not wholly different from other organs. However, this approach could not work well for the lesions segmentation [36]. Deokar and Hambarde proposed approach depends on using the median filter to improve the image quality; RG and morphological operators are used to achieve a good liver segmentation region [18].

The watershed-based segmentation approach (WS) is utilized to separate tumors from liver images, one of the most challenging processing tasks. This type of issue is frequently handled through watershed transformation. The WS method's primary goal is to find the "watershed lines" in an image to separate the distinct regions. WS expresses topography using three image segmentation dimensions: "minimum," "catchment basin," and "watershed line". The WS method has the benefit of continuous ROI borders and may combine with other algorithms to improve segmentation accuracy; nevertheless, the drawbacks and criticisms of this algorithm are the results of over-segmentation and time consumption.

Lim et al. [37] used prior knowledge in the morphological filter algorithm to automatically segment the liver and detect initial liver contour utilizing a morphological label and clustering operator. The main problem of this approach requires an amount of manual parameter setting at each step. Yim and Foran proposed WS and active contour methods for liver segmentation to obtain hepatic liver. Comparison with different methods showed that active contour was able to detect lesions compared to the WS algorithm [38]. WS algorithm causes segmentation. Over segmentation, the problem was solved by reducing the number of false regions resulting by [39]. Abdalla et al. applied a hybrid approach by combining the level set with the WS for liver segmentation from abdominal CT scans. They achieved accuracy reached 92.1% [40]. Sudhamani and Raju extracted the liver using the WS method and the RG algorithm. However, their technique relies on the initial seed point for human expert assistance in identifying the suspected region [25]. For tumor segmentation, Jean et al. introduced the WS method with random Markov fields. This algorithm is fast and gives decent segmentation results [41].

A contour-based segmentation approach is used to segment liver parenchyma and lesions from CT/MRI images. An active contour, also referred to as "snacks or deformable models," is based on contour. Active contour and level sets models are popular liver lesion segmentation methods. However, they have drawbacks due to complicated initialization and usually utilize a speed function that assumes good contrast images.

Pan and Dawant were the first to employ level sets for liver segmentation [42]. This method is highly regarded and extensively used for segmentation and a final optimization step. The main disadvantage is the high computational time for the segmentation process [43]. Massoptier and Casciaro integrated a gradient vector flow active contour to get the liver from the CT scan. This method proves that high textures and low contrast content in images are insufficient [44]. Zidan et al. proposed a level set method to segment abdominal CT into a set of interesting ROIs. The challenge with this algorithm is to define a suitable speed function and its parameters [40]. Li et al. proposed a level set incorporated with minimized likelihood energy with the edge energy. The minimization of the energy approximates the target density distribution, and the proposed edge detector preserves the ramp for weak borders. The dataset contains 18 scans, and the results showed that the Jaccard distance error was 14.4 ± 5.3% [20]. Li et al. proposed approach consist of three steps, and the first step is to enhance the image using a statistical model based on the primary component analysis (PCA) and filter the anisotropic diffusion of the curvature. In the second step, the mean shape model was moved using the threshold and Euclidean distance to reach a coarse position in a test image. The liver was finally detected using a deformable graph cut. The proposed approach uses 50 images from the two standard databases Sliver07 and 3Dircadb. The experiments have shown that this approach effectively detects hepatic parenchyma in abdominal CT scans [45].

The cluster-based Segmentation approach is a fully automatic segmentation that does not require human intervention and considers data uncertainty and ambiguity. Because of the diversity of the liver and tumors from patient to patient, several clustering approaches, such as k-means clustering, fuzzy c-means, self-organizing map (SOM), and others, were used to segment CT/MRI images extract ROIs that represent tumors. The drawbacks of these methods are that the results contain many false positive regions that need post-processing steps to focus on liver tumors and cannot handle the Indeterminacy and effects by initial clusters. Anter et al. improved liver segmentation using hybrid fuzzy c-means and neutrosophic sets (NS). The CT image is converted to NS domain represented by True (T), Indeterminacy (I), and False (F). Then the threshold adapted using the FCM algorithm [46]. Massoptier used k-means to classify the lesions against the parenchyma inside a liver envelope [47].

Li and Luo proposed a fully automatic approach for liver segmentation using hybrid FCM and level set. First, the images were pre-processed. Then, FCM and the level set were used to extract and refine the region of the liver [21]. Kumar and Moni proposed an automatic CT scanning approach for liver and tumor segmentation. The approach uses a modified FCM version called Alternative Fuzzy c-means (AFCM) for tumor segmentation [31]. Ben-Cohen et al. used an essential segmentation mask to identify the lesion location in the CT scan using non-rigid image registration and matching template to reduce the search area for segmentation. The adaptive RG and the mean shift algorithm have been used to segment lesions. The database includes 127 Sheba Medical Center CT scans. The result was 83%, and the error rate 0.08 [48]. Alahmer and Ahmed proposed two phase processes for the segmentation of liver and its tumor. First, the liver is segmented by the binary mask of the liver. Then the image was split into three classes using fast FCM. Morphological operators were used to refine the clustering process for removing small objects outside the region of the liver. Then region growing was used to segment tumors from the segmented liver [49].

Probabilistic atlas-based segmentation approach. A common technique for incorporating prior experience into the segmentation process. The authors [50,51] utilized a probabilistic atlas (PA) and a statistical shape model (SSM) to segment liver tumors. Both PA and SSM rely on prior liver information. PA can only deal with non-contrast images, and when working with improved CT/MRI images, SSM outperforms PA. In addition, the initialization of an SSM is complicated while critical, and the possible liver deformations represented by an SSM are limited. Platero and Tobar used low-level operations, affine probabilistic atlas, and a multi-atlas-based liver segmentation. This approach provides highly accurate segmentation due to registrations and atlas selections based on the ROIs and coarse segmentation [52]. Linguraru et al. utilized probabilistic atlases for liver segmentation, which was progressively enhanced by an active geodesic contour, patient-specific contrast-enhancement features fed to an adaptive convolution, and correction for shape and location problems. The accuracy achieved from this approach variant from 92.7%-96.2% [53].

Neutrosophic Sets (NS)-based Segmentation Approach. NS used to deal with Indeterminacy and uncertainty, but a fuzzy set was used only to deal with uncertainty. The fuzzy set uses a real number $\mu A(X) \in [0, 1]$ to represent the membership of set A defined on universe X. In real-time applications that depending on Indeterminacy, neutrosophic sets should be used. Fuzzy logic cannot be considered for these applications because it is limited to the truth and false percentage. So, it is hard for the fuzzy set to solve problems like this [54].

Neutrosophic logic (NL) introduces a percentage of "indeterminacy" due to unexpected parameters hidden in some propositions. NL is an extension of fuzzy logic, includes a new component termed "indeterminacy" and carries more information than fuzzy logic. Applications that use neutrosophic sets outperform those that use fuzzy logic. NL is so new that it is worth exploring in many fields [54].

Anter et al. proposed a hybrid NS and adaptive FCM approach for CT liver segmentation. This approach achieved accuracy reached 94% [55]. Cheng et al. proposed neutrosophic logic and a modified fuzzy clustering approach for CT segmentation [54]. Zhang proposed WS based on NS to Image Segmentation. The CT images were interpreted into different components, objects referred to T and background referred to F. This approach is suitable for handling blurred edges objects [56].

Anter et al. applied a new hybrid approach based on NS and particle swarm optimization (PSO) to the liver tumor segmentation. The CT image was enhanced, and the noise was removed using neutrosophic sets components (*T*,*I*, and *F*).

PSOFCM technique used to segment liver parenchyma and lesions from abdominal CT scan. The results showed that this approach was robust and precise with quick convergence and time-consuming [4]. Siri and Latte proposed NS and Fast Marching Method (FMM) for liver segmentation. First, noise has been reduced by a median filter, and CT images were expressed in a neutrosophic domain in order to extract the liver. Morphological operations were then performed on the subset of Indeterminacy (*I*). The fast-marching method automatically identifies the starting points in the liver section to detect the exact liver boundary. This method achieved a high accuracy reached to 91.61% [57]. In addition, Siri and Latte improved their work by combining NS efforts to extract liver tumors. Without user intervention, the Chan-Vese model was used to detect the initial contour in the liver. This approach achieved high results of 95.59%. Experiments have shown that this approach is robust and effective [58].

Swarm Optimization-based Segmentation Approach**.** Many problems have been solved by considering bio-inspired meta-heuristic optimization algorithms such as Particle-swarms-optimization (PSO), Genetic-algorithm (GA), Firefly algorithm (FFA), Grey-wolf-optimization (GWO), Crow-search algorithm (CSA), Social-spider-optimization algorithm (SSO), etc. Meta-heuristic and optimization techniques have been used in situations where conventional optimization methods cannot find a satisfactory solution or take too much time. Mostafa et al. [19] have demonstrated that the bio-inspired optimization methods are high convergence speed and avoid stuck in local minima. The disadvantages of these methods are; they work in a random behavior and give inconsistent results.

Bio-inspired and meta-heuristic algorithms can be integrated with classical methods such as fuzzy c-means, watershed, region growing, etc., to solve its main drawbacks. For example, in FCM, clusters need to be specified before the clustering process, very slow convergence, and the initial selection of the centroids effect on the results performance. The main problem is the seed point in the region growing, and time-consuming to check each pixel intensity. All these problems can be solved by integrating with computational intelligence optimization algorithms. The integration results show that the hybridized approach can improve image segmentation efficiency [59].

Venkatesan and Parthiban proposed two main methods FCM and maximum entropy, to segment and detect anomalies in the image using PSO (FCM-PSO). The analysis is performed by comparing the segmentation results and the distances between clusters and intra and inters cluster distances. The FCM-PSO delivers precise results and reduces the calculation time [60]. Anter et al. proposed a new segmentation approach based on NS, FCM, and PSO to classify liver parenchyma pixels, tumors, and other organs in the abdominal CT images in different homogeneous regions. When converted to the NS domain, the CT image has been enhanced, and noise has been deleted. In order to segment the liver tumor from the abdominal CT scan, the enhanced image was then transferred to PSOFCM. The results show that NS- PSOFFCM was robust and accurate with fast convergence to the optimal solution and reduced computational time [4].

In addition, bio-inspired and meta-heuristic algorithms can be integrated with conventional and classical methods to solve its problems, affecting the results performance such as threshold method, k-means, watershed, region growing, etc. Mostafa et al. proposed an algorithm for clustering problems using artificial bee colony (ABC) to segment liver from CT images. ABC calculates the cluster centroids in the image. The extracted regions are integrated to give an initial estimate of the liver area. RG was used to refine the liver segmented. The results employed on 38 images achieved excellent segmentation accuracy, reached 93.73% [61]. Mostafa et al. enhanced their work using the grey wolf optimization algorithm (GWO). This approach combines GWO, liver statistic, RG, and medium shift clustering. GWO has been used to calculate the pre-defined number of clusters centroids. RG has been used to boost the segmented liver. In order to segment lesions, the mean shift clustering technique was finally used. The results showed that the total precision achieved was 94.08% [19].

Singh and Gupta proposed a segmentation approach for the liver using k-means and Ant Colony Optimization (ACO). ACO was used for the optimization of poorly selected k- clusters. Quantitative analyzes were carried out based on precision and specificity. The experimental result showed that high accuracy and specificity, 98.74, 99.20, respectively. This method is fully automatic compared to the standard k- means and achieves better segmentation even if the boundary is not clear [62]. El-Masry et al. proposed an automated CT liver image clustering approach based on the invasive weed optimization (IWO) evolutionary algorithm. Without prior information on the number of naturally occurring groups in the images, IWO was used [63]. Zhang et al. proposed possibility c-means algorithm (PCM) integrated with PSO and significantly improved segmentation efficiency. Experiments showed that the effect and efficiency of segmentation significantly improved compared to the FCM algorithm [64]. Ali et al. proposed integrating PSO and FCM algorithm to find optimal cluster centers in the liver tumor segmentation problem. The advantages of this approach are the convergence to an optimal solution fast, more efficient, and gave higher segmentation accuracy [46].

The approach to liver segmentation suggested by Eapen et al. includes multi-discriminative markers (prior domain information, intensity model, and regional characteristics of the liver in the graph-cut image segment). The traditional graph-cut model's energy reduction is controlled by an edge-adaptive weight function inspired by swarm intelligence. The model is validated qualitatively and quantitatively by public data sets (MICCAI 2007, 3D-IRCAD). Quantitative evaluation of segmentation results was performed with an accuracy of 80.8%, 82.5% on MICCAI, IRCAD, respectively [65]. Sayed and Hassanien proposed the segmentation of the CT liver based on PSO and an adaptive algorithm. The accuracy obtained reached 94 % [66].

***Machine Learning (ML)-based Segmentation Approach*.** ML was proposed to achieve accurate tumor segmentation. ML methods are stable and can account for the diversity of liver tumor topologies and characteristics, but they typically need many training samples or a lengthy training period [23]. Many ML techniques are used for determining the ROIs of the liver and tumor. Danciu et al. proposed a support vector machine (SVM) method to liver segmentation with wavelet characteristics [67]. SVM is an interesting classifier that does not require much training. Kumar et al. proposed a neural network to classify FCM results, identifying which regions belong to the tissue of the liver [68]. Aldeek et al. used the Bayesian model to extract the liver from the CT image for a robust and reproducible semi-automatic technique. The proposed approach generates 87% accuracy for 44 cases [69]. Susomboon et al. applied approach used four steps: In the first step, the intensity-based threshold was applied to obtain the regions. The second step, region-based, was used for texture-based classification to classify all regions based on textures. Third step, an initial liver region was determined for each patient. In the fourth step, a confidence interval of 95% determined from the region’s intensities to detect the liver ROI, the proposed approach achieved 86% accuracy [70].

Deep Learning (DL)-based Segmentation Approach. DL is a popular algorithm used to carry out many essential tasks in medical imaging in particular. DL can accurately segment organs and predict important regional properties. DL is easy to train but requires more data and much more care in the analysis of results. DL is in its early stages and gets its name because it has many layers; most systems now have 30 to 150 layers than traditional ML, which would fail if they had more than three layers. DL has improved the performance of computer algorithms outside medicine dramatically, and medical applications' performance can be expected to improve dramatically in the near future [10]. To identify and segment tumors in medical images, DL algorithms may be used.

Chlebus et al. developed a fully automated technique for segmenting liver tumors using a 2D convolutional deep neural network with shape-based post-processing. The detection and segmentation assessment was carried out on the LiTS data set. The proposed method can detect 77% of lesions accurately [71]. Bellver et al. proposed the liver segmentation method and its CT lesions using Convolutional Neural Networks (CNNs). The network used a cascaded architecture to focus on the liver region to segment the lesions [72]. Christ et al. proposed a two-step HCC malignancy prediction model, and the first step is automatically segmenting HCC tumor lesions using a fully convolutional neural cascade network (CFCN). A 3D neural network (SurvivalNet) was then used to predict the malignancy of the HCC lesions. This model assessed 31 patients with HCC and achieved a 65% accuracy [73]. Han has developed a deep convolutional neural network (DCNN) to produce the center slice segmentation map. The model has 32 layers and uses both the U-Net and the residual net (ResNet). The model was trained using the 130 slices and reached a 67% Dice score [74]. Amitai and Greenspan proposed fully convolutional (FCN) and conditional generative adversarial (GAN) networks to segment the CT liver. Dataset consists of 25 CT scans. The results showed a high detection performance of 92.3% using True Positive Rate (TPR) and 0.25 using False Positive Rate (FPR) per case [75]. Kalinovsky, Liauchuk, and Tarasau proposed a deep learning approach to detect CT cancer, training and testing of 338 3D CT scans. Deep CNN-based algorithms have been built and deployed in three ways: slice-wise lesion identification in 2D images using semantic segmentation, slice-wise lesion detection in 2D images using the sliding window approach, and detecting lesions in full 3D CT scans using semantic segmentation. This algorithm performs better than other algorithms based on conventional image analysis [76]. Todorok et al. developed a technique for identifying CT liver tumors with a deep CNN utilizing 3D multi-phase contrast-enhanced liver CT data from 75 cases. The proposed DCNN approach outperformed the Bayesian model in detection accuracy [23]. Yasaka et al. presented a deep learning technique for hepatic mass differentiation using CNN. The training was supervised using 55536 image sets, and in test set 100 liver mass image was tested. The median precision obtained was 84%. Experimental results showed that deep learning with CNN achieved high diagnostic performance in diagnosing the CT liver process [77].

Christ et al. presented a method for automatically segmenting the liver and lesions utilizing dense 3D conditional random fields (CRFs) and fully convolutional neural networks (CFCNs). According to the findings, CFCN-based segmentation of the liver and lesions obtains Dice scores of more than 94 percent for the liver with calculation times in the low 100s. Moreover, Christ et al. proposed automatic liver and lesion segmentation approach based on the Cascaded UNET approach achieved a precision of 93.1% [73]. Dou et al. proposed 3D deeply supervised CT liver segmentation network (3D-DSN). The 3D-DSN proposed benefits from an utterly revolutionary architecture. The results have been assessed using the public data set MICCAI- SLiver07. The experiments showed that this approach achieved competitive results with higher speed and performance [78]. In the same year, Hu et al. trained a 3D-CNN model to precisely segment livers with significant variations in shape or with blurred borders with adjacent organs or lesions [79]. In addition, Roth et al. proposed a two-stage method for the pancreas segmentation task. The holistic CNN generates a 3D bounding box of CT volumes with axial, sagittal, and coronal views during the detection phase. The second stage involves combining the mid-level information of CNNs trained to segment the interior and border of the pancreas inside the bounding box proposed in the first stage to obtain a more accurate final segmentation of the pancreatic [80]. Li, Jia, and Hu proposed an automated CNN- based method for segmenting CT images lesions. The CNN model was compared to the popular algorithms for machine learning: AdaBoost, Random Forests (RF), and SVM. The accuracy attained on 30 CT scans was 82.67 % and 84.34 %, respectively. The results demonstrated that CNNs outperform other techniques and are promising to segmentation liver cancers [81]. Vivanti et al. developed a fully automated approach for segmenting liver tumors using deformable baseline scan registration and tumor delineation and training CNN as a voxel classifier on all baselines. The findings revealed an average overlap error of 16.26 % in 67 tumors from 21 patients using ground-truth Segmentation and a standard deviation (*Std*=10.33) [82].

Table 2 summarizes the various proposals for liver and tumor segmentation. In addition, several other aspects of the works, such as segmentation methods and segmentation accuracy, are shown.

Table 2: Shows the different proposals for liver and tumor segmentation.

Authors	**Year**	**Data Set**		**Acc.**	**Methodology**
		No.	**Description**		
Mostafa et al.	2012	26	Clinical	84 %	Hybrid RG, CCL, and post-processing (morphological operators)
Zidan et al.	2012	27	Clinical	92.1 %	Hybrid level set and watershed
Anter et al.	2013	112	Radiopaedia	93 %	Hybrid Watershed, RG, and CCL

Aldeek et al.	2014	44	-	87 %	Gradient Vector Flow, Markov Random Field, and Naive classifier
Anter et al.	2014	30	Radiopaedia	94%	Hybrid *NS* and FCM
Siri et al.	2017	108	M/S CT Centre	91.61%	Hybrid *NS* and FMM
Siri et al.	2017a	110	M/S CT Centre	95.59%	Hybrid *NS* and Chan-Vase
Akram et al.	2010	100	Clinical	96%	Adaptive threshold and morphological operations
Ben-Cohen et al.	2015	127	Sheba Medical Center	83%	*n* liver was segmented using non-rigid image registration and template matching, and the lesions were obtained using adaptive *RG* and mean-shift.
Anter et al.	2018	30	Radiopaedia	-	NS, PSO, morphological operators, and FFCM
Mostafa et al.	2015	38	Clinical	93.73%	artificial bee colony (ABC), Morphological operators, and region growing algorithm
Mostafa et al.	2017	38	Clinical	94.08%	grey wolf optimization (GWO), morphological operators, region growing, and Mean shift clustering
Singh and Gupta	2015	-	Clinical	98.74	k-means and Ant Colony Optimization
Eapen et al.	2015	-	MICCAI 2007 (DS1), 3D-IRCAD (DS2)	DS1:80.8%, DS2:82.5%	Prior domain information, intensity model, and regional liver properties were used in graph-cut image segmentation. Based on graph-cut and edge-adaptive weight functions, swarm intelligence is constructed.
Sayed and Hassanien	2016	-	Clinical	94 %	PSO and an adaptive Watershed
Susomboon et al.	2007	-	-	86%	Threshold, region-based texture classification
Chlebus et al.	2018	-	LiTS	77%	2D deep CNN with a shape-based post-processing
Christ et al.	2017	31	Clinical HCC	65%	CFCN and 3D neural network (SurvivalNet)
Han	2017	130	MICCAI 2017	67%	Deep convolutional neural network (DCNN)
Amitai and Greenspan	2017	25	MICCAI 2017	92.3%	FCN and conditional generative adversarial networks (GAN)
Liauchuk, and Tarasau	2017	338	Clinical	-	Deep Convolutional Networks
Todoroki et al.	2017	75	-	-	Deep convolutional neural network (DCNN)

Yasaka et al.	2017	55536	Clinical	84%	CNN
Christ et al.	2016	100	Clinical	94%	CFCN and dense 3D CRFs.
Christ et al.	2016a	100	Clinical	93.1%	Cascaded UNET approach
Li, Jia, and Hu	2015	30	Clinical	82.67%	convolutional neural networks (CNNs)

3. Proposed Model for Liver Tumor Diagnosis

A dynamic CAD model is suggested for liver tumor diagnosis using multi-modality CT and MRI in this review. A unique opportunity for developing advanced new methods may be provided for a real-time diagnosis. In addition, the above limitations have been addressed to design a CAD model that can automatically diagnose liver lesions based on bio-inspired optimization algorithms, chaos theory, deep convolutional neural network, and spiking neuron model for liver tumor segmentation and diagnosis as well as neutrosophic logic can be applied to decrease and handle the Indeterminacy and uncertainty. This kind of methodology has never been proposed and applied for liver tumor localization and diagnoses presenting high characteristics to the best of the author's knowledge. This paper is potentially helpful in developing a CAD model for liver diagnosis and treatment to help physicians provide critical information for surgical planning and early tumor detection and analysis. In addition, explore the effects of treatment methods such as (radiotherapy and chemotherapy) on the hepatic tumor, which can efficiently help determine the effective doses and fractions of the therapy. In addition, this model may be possible to guide surgical doctors to directly locate live tumors and destroy tumors with minimally invasive techniques, such as ablation and embolization. Furthermore, this model could assist physicians in classifying high-risk patients and make a novel diagnosis. Moreover, this model will open up new opportunities for medical imaging applications by proposing highly accurate models with minimal human intervention, extending their use and ultimately leading to improved patient care.

The suggested model composes of mainly five phases; (1) DICOM data pre-processing, (2) Liver parenchyma segmentation and lesion detection and delineation from the multi-modality CT/MRI abdominal images, (3) Features extraction and subset feature selection from each lesion (ROIs) based on evolutionary spiking deep convolutional neural network, (4) Diagnosis and decision making based on federated deep spiking neural network, (5) Assessing the response of hepatic lesion to treatment based on deep spiking neural network, and (6) Evaluation criteria.

3.1. Pre-processing phase

Multi-modality CT and MRI series images have been collected from different modalities. Moreover, other available multi-center benchmark datasets will be used to ensure the proposed model's performance and stability [78,83,84]. First, these scans will be pre-processed; the initial step is DICOM series registration to align all CT/MRI images to a common space. Then, grayscale inhomogeneity results from the bias field of the CT/MRI scanner will correct. The subsequent combination of multiple images from multiple imaging modalities to improve features involves identifying and selecting features focusing on the relevance of features for diagnosis and evaluation purposes of a liver lesion. In addition, different filters will use to enhance contrast, smooth, remove noise and high frequencies and improve the overall visibility of features of a specific sign of malignancy.

Figure 3 (a) shows the data collection process with different modalities CT and MRI from multi-center datasets to check the stability and reliability of the proposed model. Figure 3 (b) shows the sequence of pre-processing steps for imaging data.

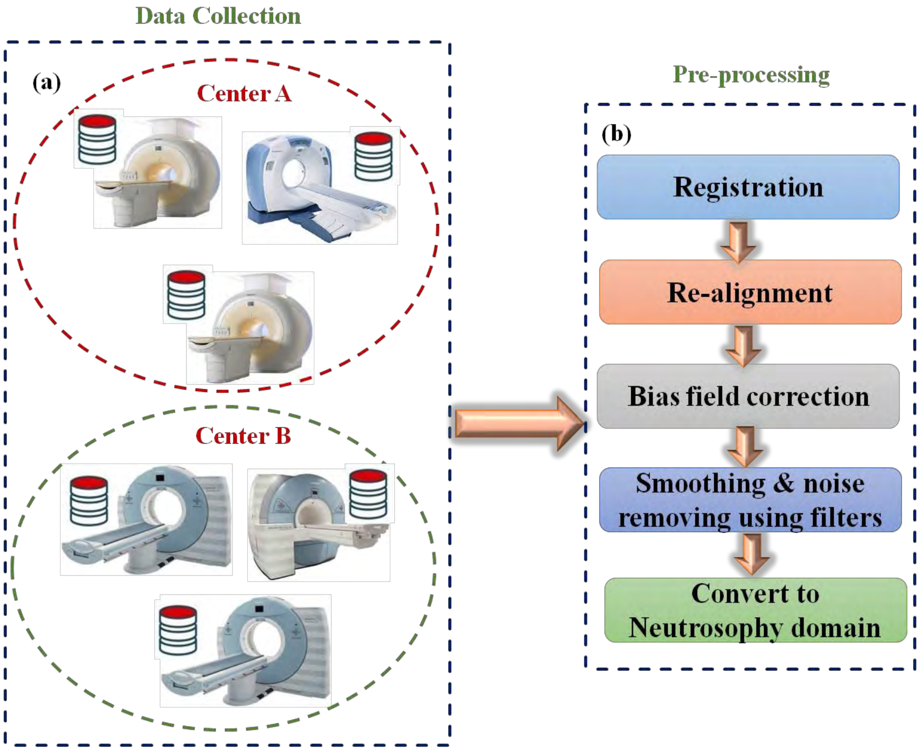


Figure 3: Data collection and pre-processing steps.

3.2. Liver segmentation, lesion detection, and localization phase

a) Pre-Segmentation

In this phase, the pre-processed images will transform to the neutrosophic domain to increase segmentation efficiency and decrease noise-level and non-uniform neutrosophy is a philosophy field that is a generalization of intuitionistic fuzzy sets para-consistent sets, and tautological sets. The neutrosophic set (NS) and its characteristics are briefly described in [26,57]. These issues that fuzzy logic cannot handle may be well solved by neutrosophic logic. NS investigates the neutrosophic logical values of propositions represented by (Percentage of true (*T*), Indeterminacy (*I*), and False (*F*)).

To use neutrosophy, an image must be moved to a neutrosophic domain P_{NS}. A pixel in the neutrosophic domain can be represented as *T*, *I*, and *F*, which means it is *t*% true, *i*% indeterminate, and *f*% false, where *t* varies in *T*, *i* varies in *I*, and *f* varies in *F*.

The neutrosophic set components are $T(i,j), I(i,j), F(i,j)$, and each pixel *P(i,j)* in the image domain is converted to the NS domain $P_{NS}(i,j)$ and computed as follows:

$$P_{NS}(i,j) = \{T(i,j), I(i,j), F(i,j)\} \tag{1}$$

$$T(i,j) = \frac{\overline{g(i,j)} - \bar{g}_{min}}{\bar{g}_{max} - \bar{g}_{min}} \tag{2}$$

$$I(i,j) = 1 - \frac{Ho(i,j) - \overline{Ho}_{min}}{\overline{Ho}_{max} - \overline{Ho}_{min}} \tag{3}$$

$$F(i,j) = 1 - T(i,j) \tag{4}$$

$$Ho(i,j) = abs(g(i,j) - \overline{g(i,j)} \tag{5}$$

where $\overline{g(i,j)}$ is the local mean value of the window size, and $Ho(i,j)$ is the homogeneity value.

b) Post-Segmentation

After the image is transformed to the NS domain, the neutrosophic truth set (*T*) is selected for the post-processing, representing the objects of the image. The indeterminacy set (*I*) that represents the edges of the image is removed, and the false set (*F*) representing the background is also removed.

In this phase, the liver will be segmented, and lesions will be localized using the improved fuzzy c-means (FCM), as shown in Figure 4. Due to its overall performance, FCM is an unsupervised learning approach and a prevalent technique for statistical data analysis utilized in many domains. In FCM, a data point can belong to any class with varying degrees of membership. FCM adopts fuzzy partitions of given data between 0 and 1. A meta-heuristic swarm intelligence algorithm will be used to guide the fast fuzzy c-means (FFCM) method for the best clusters. Bio-inspired swarm algorithms have been employed in situations where traditional approaches either fail to find a suitable solution or take a too long to find it.

The swarm intelligence algorithms will work to handle the limitations, and drawbacks of the FCM like (a) number of clusters needs to be specified beforehand, (b) results are dependent on the initial selection of the centroids, (c) FCM lacks sufficient convergence speed, particularly in emergency cases, (d) FCM gives membership ratings to each pixel. This means that each voxel is a member of each cluster, and (e) updating the cluster centers and membership grades repeatedly is a time-consuming operation.

3.3. Meta-heuristic optimization algorithms

In the context of computing, a heuristic is described as a method of addressing a problem that does not need the exhaustive execution of a technique. A meta-heuristic technique is beneficial for tackling search and optimization issues. Thus, the meta-heuristic technique (i) seeks a near-optimal solution rather than the actual ideal solution, (ii) typically lacks formal demonstration of convergence to the optimal solution, and (iii) is typically computationally quicker than exhaustive search [85].

Iterative meta-heuristic techniques frequently utilize stochastic operations in their search process to modify one or more original candidate solutions. Because many real-world optimization issues are complicated due to their inherent practicality, classical algorithms may not always be relevant or perform well in tackling such problems. The capability of meta-heuristic techniques to manage various complexity related to practical issues and arrive at a relatively acceptable solution is the primary reason for their current popularity [59].

Most meta-heuristic techniques are inspired by natural, physical, or biological principles and attempt to simulate them at a basic level using various operators. A meta-heuristic in mathematical optimization is a higher-level technique to discover an excellent solution to an optimization problem, mainly when partial or faulty information or limited computation capacity.

Meta-heuristics are frequently referred to using the following words bio-inspired and nature-inspired. They can, however, be further subdivided into evolutionary algorithms, swarm-intelligence-based algorithms, and physical phenomenon-based algorithms. Meta-heuristics follow a similar series of operations and may thus be described within standard generic stages, as seen in Algorithm 1.

The phases of the proposed model for liver and tumor segmentation utilizing the fuzzy swarm intelligence algorithm are depicted in Figure 4. The primary issue with the SI is the random behavior of agents in the search space, which produces inconsistent results and takes a long time to converge to the optimal solution. As a result, chaos theory will be used to solve this problem. The advantages of chaos theory include the capacity to avoid local minima, quick convergence, non-invertible maps, and the ability to do comprehensive search faster than stochastic search, which is based on probabilities, non-repetition, and ergodicity of chaotic behavior [86]. These benefits can significantly enhance the overall performance of meta-heuristic algorithms in terms of local minima avoidance and fast convergence.

Algorithm 1: generic steps of meta-heuristic

```
1.Initialize the possible solutions.
2. Initialize all parameters (number of agents, number of iterations).
3. Initialize fitness value to all agents in search space.
4. Evaluate the candidate solution.
5. Repeat
        a. Generate new candidate solutions via social behaviors.
        b. Evaluate the new candidate solutions.
6. Until meet the optimal criteria.
```

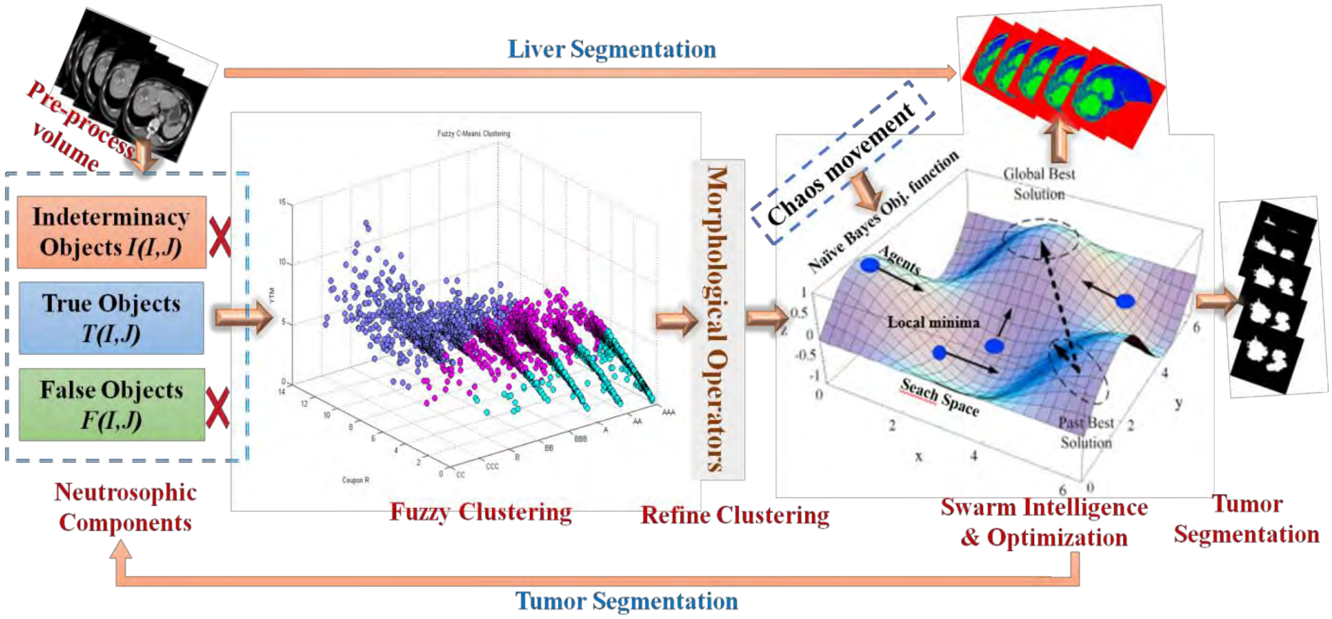


Figure 4. Liver segmentation and tumor localization.

3.4. Diagnosis-based Deep Spiking Neural Network

In this phase deep spiking neural network based on the spiking neuron model, deep convolutional neural network (DCNN), and bio-inspired SI algorithm will be used to characterize and diagnose liver lesions. The hybrid spiking neuron model and deep convolutional neural network (Spiking-DCNN) will extract features from the segmented liver tumors in multi-modality CT/MRI. Then, the features are fused to increase diagnosis performance, and the bio-inspired SI optimization algorithm will use to select the optimal and significant features from the whole extracted features. Finally, the spiking neuron model will predict liver tumors and obtain diagnosis decisions, as shown in Figure 5.

Deep learning (DL) has emerged as a primary method for completing many complex tasks, demonstrating exceptional performance in a wide range of computer vision and medical applications. This achievement, however, comes at the expense of gathering and processing vast amounts of data, which are sometimes inaccessible due to privacy concerns. As shown in Figure 6, federated learning has recently been introduced to train parameters on local hospital datasets and store them in a repository before sharing only the trained parameters with a centralized model, which is then responsible for updating other local real-time parameters models.

The Spiking-DCNN is an excellent generalization model because it can continuously learn from data and pursue the growing data pattern by recursively modifying the system structure and meta-parameters.

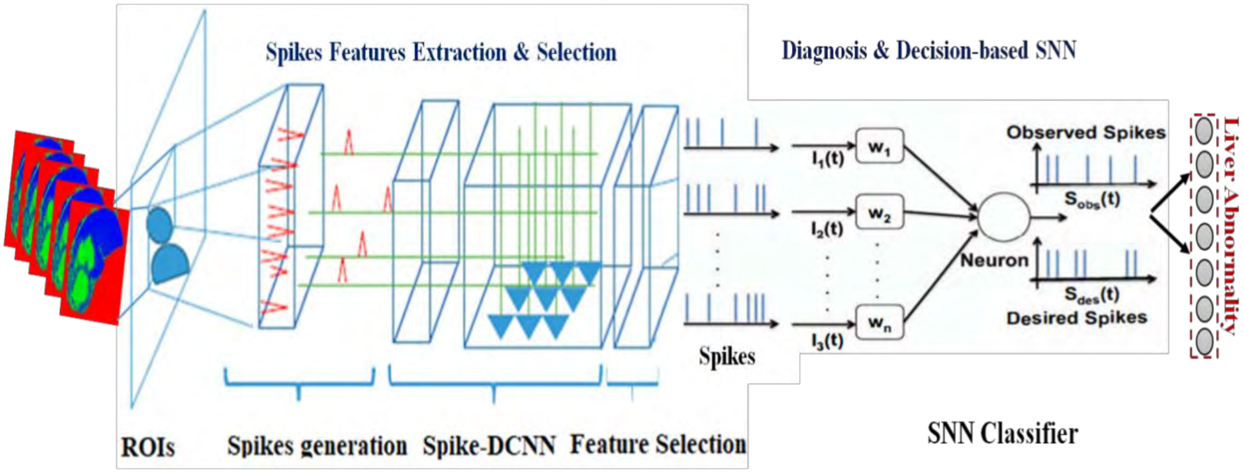


Figure 5. A general framework of the proposed Spiking-DCNN for liver lesion diagnosis.

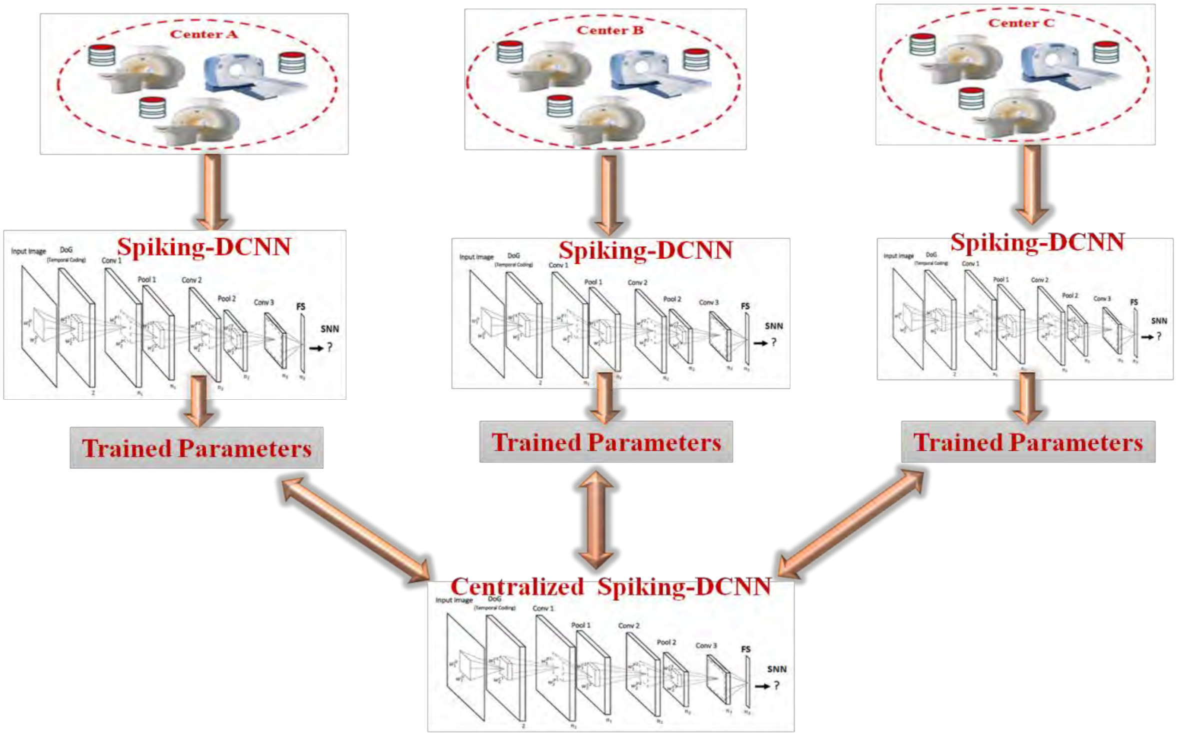


Figure 6. Sharing the trained parameters of the proposed model on other models for multi-center datasets.

(a) Spiking neuron model

Unlike conventional neural artificial networks (ANNs), the spiking neural network (SNN) aims to bridge the gap between neuroscience and machine learning by using neuronal biological realistic models to perform computation. Neurons in an ANNs are characterized by a single, static, continuous-valued activation. SNN operates using spikes, which are discrete events that take place at points in time rather than continuous values. In SNN, neurons rely on the timing of the spikes in order to communicate with each other.

SNN requires many fewer operations and is the best candidate for spatio-temporal data processing. SNN has become the focus of several recent applications as a single layer in many pattern recognition areas [87,88].

The spiking neuron model potentially used and recommended is the Leaky Integrate-and-Fire (LIF) model. The previous study found that coding with spike-timing contains meaningful information and has high computing power in biological systems [89]. Deep SNN training, on the other hand, remains challenging. Spiking neurons' transfer functions are often non-differentiable, prohibiting back-propagation. SNN also does not scale well in terms of computing complexity to actual high-dimensional pictures of size. Furthermore, spike-timing-dependent plasticity (STDP) does not enable learning hierarchical models that reflect several layers in a visual environment, such as edges or parts of objects, essential to a deep learning model.

(b) Deep Convolutional Neural Network (DCNN)

DCNN has proved to be a highly effective framework for image classification problems. DCNN is composed of a series of convolution and pooling layers, followed by a feed-forward classification. This network type has demonstrated exceptional performance in image recognition, bioinformatics, object detection, and segmentation. It comprises three major components: a convolutional layer, a spatial sampling/pooling layer, and a fully connected layer [90].

The representational characteristics of the DCNN's early layers are comparable to those of the neurons in the primary visual cortex, the first cortical region in the visual brain system. A CNN's weights are convolution kernels. To generate an array of output maps, a convolution layer convolves a part of the preceding layer with a set of weight kernels. The following model expresses the output maps.

$$x^k = f\left(\sum_i W^k * x^i\right) \qquad (6)$$

where f is the neurons activation function, x^k is the activation value of the neurons in the output maps, x^i is the activation of the neurons in a previous layers map, and $W^k$are the set of weight kernels. As explained in [87], the DCNN is trained using back-propagation to train the convolutional weight kernels and the fully connected weights for the final output layer.

(c) A new approach based on Deep Spiking Neural Networks (Deep-SNNs)

Deep neural networks (DNNs) inspired by cortical visual processing systems have recently experienced increased success due to the availability of increasingly powerful computing hardware (GPU accelerators) and massive data sets for training. Regardless of their effectiveness, the high computational cost of training and testing such large-scale networks have restricted their application to clouds and servers. To develop devices with cognitive capacities, specific hardware and new computational ideas are required.

Brain-like asynchronous event-based calculations power SNN. SNN focuses its computational effort on presently active network components, efficiently saving power on the remaining components and attaining lower power consumption orders than their ANN counterparts [87,88]. As a result, there is a need to design practical learning algorithms that can use the particular features of SNN (event-driven, low-ANN power, high-learning) while maintaining the qualities of the DNNs model (general-purpose, scalable to more significant issues with higher accuracy).

A new generation of neural networks has developed, combining the multilayer structure of DNN and the type of information transfer used in SNN. Deep-SNN is an excellent choice for studying neural computing and diverse coding methods in the brain. DNN is a non-spiking network that communicates through continuous-valued activations. Although DNN's energy efficiency is expected to be improved, SNN presents a unique potential in this respect because of the sparsity of spike occurrences in time. Spiking networks offer the added benefit of being naturally sensitive to the temporal patterns of information transmission in biological brain systems. Deep-SNN architectures are suitable for developing an efficient, brain-like representation [91].

In this review, a learning model based on spiking information and a deep convolutional neural network (Spike-DCNN) is suggested for liver tumor diagnosis, as shown in Figure 7. A temporal-coding layer will be followed by a cascade of subsequent convolutional (feature extraction and descriptors) and pooling layers. The first layer transforms the input image into an asynchronous spikes train, with visual information encoded in the spikes' temporal order. The second layer is regarded as extracting main visual features using the Difference-of-Gaussian (DoG) filter and shape morphology. The neurons in convolutional layers then integrate the incoming pulses and spike immediately after reaching their threshold. STDP is used in these layers to learn visual features.

Learning takes place sequentially only in the convolutional layers. When a new image of a liver lesion is shown, neurons in the convolutional layer compete with others, and those that fire first trigger STDP and learn the input pattern. A simplified STDP such as the one below may be used:

$$\Delta w_{ij} = \begin{cases} b^{+} w_{ij}\left(1 - w_{ij}\right), & if \;\; t_j - t_i \leq 0, \\ b^{-} w_{ij}\left(1 - w_{ij}\right), & if \;\; t_j - t_i > 0, \end{cases} \tag{7}$$

where i and j respectively refer to the index of post- and presynaptic neurons, t_i and t_j are the corresponding spike times, Δw_{ij} is the synaptic weight modification, and b^{+} and b^{-} are two parameters specifying the learning rate.

Pooling layers enable translation invariance as well as visual information compaction. Through the network, visual features get more extensive and more complex. In the last layer, swarm intelligence-based feature selection may be proposed to choose the best features from the entire set of complex features in order to minimize computing time and enhance the classifier's efficiency. Furthermore, the swarm intelligence will recommend integrating with a spiking neural network to enable a type of learning (weight modification) dependent on the relative timing of spikes between pairs of directly connected neurons where the information required for weight modification is locally available. Finally, an SNN classifier may be utilized to differentiate between liver lesions based on neuronal activity with global receptive fields.

This model may touch the very foundations of complex system identification. Thus its application domain will range from simple clustering-based techniques for pattern recognition, image segmentation, and so on to more general modeling, classification, and prediction problems in a variety of medical applications.

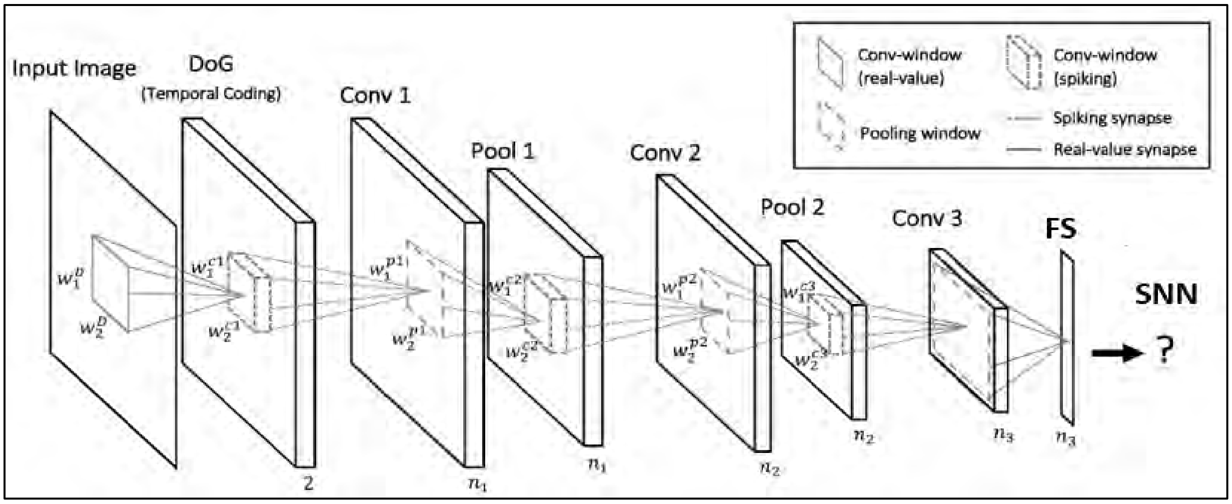


Figure 7. The first layer applies a DoG filter with size $w_1^D \times w_2^D$ on the input lesion image and encodes the image to spike trains based on pixel intensity. Three convolutional and pooling layers, a feature selection (FS) layer-

based swarm intelligence, and an SNN classifier pick the neuron with the highest activity (spike frequency) as the image's class.

3.5. Assessing the response of hepatic lesion to treatment

According to the World Health Organization (WHO), quantitative imaging plays a critical role in monitoring the response of malignant hepatic lesions to treatment, which may be measured by mass size. In clinical practice, objective tumor size measurement is widely employed to detect tumor response to therapy. In clinical studies, objective response based on tumor size change may be converted to an early clinical endpoint in place of overall survival. The CT/MRI imaging criteria are ideal for determining tumor response to treatment. This model may help explore the effectiveness of different treatment modalities, including (surgical resection, ablation, radiotherapy, and chemotherapy) in the treatment of liver tumors. This can be applied by assessing the liver mass before and after the treatment and for post-treatment follow-up using fuzzy swarm intelligence, Spiking-DCNN, and morphological characteristics of the hepatic lesion for multi-time-point images for the same subject.

4. Conclusion

This paper discussed the medical background to the liver, tumor types, and hepatic imaging techniques. A general overview has been presented of the CAD system. The paper summarizes the various approaches used to create a CAD system for the segmentation of liver tumors and diagnosis and the limitation of the abdominal CT/MRI images. Several conclusions can be drawn from these previous works. A comprehensive comparison of different approaches to a wide range of data sets with many problems to test their advantages and disadvantages can help develop new effective approaches to various problems.

The segmentation phase is used to segment and delineate liver and tumors. The classical segmentation methods do not have exact solutions for all cases, high time computation, and stuck in local minima. The feature extraction phase used to analyze ROIs that depict tumors at only a single scale loses many dominant characteristics. Feature selection methods have high time computation in the feature selection phase, are stuck in local minima, and do not agree to get the optimal solution. The classifiers used have limitations on stochastic training, time consumption, lack of strength, and tuning parameters.

The limitations of the CAD system are addressed to diagnose benign and malignant tumors of the liver automatically. In addition, this paper suggests a new model based on bio-inspired optimization algorithms, federated learning, spiking neuron model, and deep convolutional neural network for liver tumor segmentation and diagnosis and neutrosophic logic to decrease and handle the Indeterminacy and uncertainty. The interaction of individuals in the population may be used to identify optimum features of the complex search space using meta-heuristic and bio-inspired optimization methods. Furthermore, the segmentations would automatically simplify and speed up physicians who are unable to obtain the segmentation of liver tumors without a long and tedious manual process guided by bio-inspired optimization algorithms to obtain the optimal solution and accelerate the convergence rate.

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