

Enhancing Segmentation Approaches from Fuzzy-MPSO Based Liver Tumor Segmentation to Gaussian Mixture Model and Expected Maximization

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ABSTRACT

Liver tumor division in restorative pictures has been generally considered as of late, of which the Level set models show an uncommon potential with the advantage of overall optima and functional effectiveness. The Gaussian mixture model (GMM) and Expected Maximization for liver tumor division are introduced. In the early liver division process Level set models are utilized. This proposed strategy uses Gaussian blend models to demonstrate the portioned liver image, and it transforms the division issue into the most significant probability parameter estimation through the use of Expected Maximisation (EM) calculations. The proposed methodology outperformed existing techniques by a significant margin, according to the results of our comparison.

Keywords: GMM, Level set segmentation, EM algorithm, Gaussian Mixture.

1. Introduction

Magnetic Resonance (MR) images can only be used to segment the liver, unlike in the central nervous system and the musculoskeletal system. When working on the liver, the largest organ in the body, it is essential to have a wide field of vision to see everything. Because of this, the spatial resolution of imaging the liver is lower than the spatial resolution of imaging the brain or joints, which both use the same field of view [1]. This is done to make up that the liver needs a larger field of view for imaging. Because MR images have motion artifacts, they cannot be used to divide the liver into parts. Because of this, MR images cannot be used to divide up the liver. Imaging with CT is also less expensive than imaging with magnetic resonance imaging [2]. Abdominal CT scans are becoming more controversial as people worry about how much radiation they expose people to and how many contrast agents they use. Magnetic resonance imaging (MR imaging), which does not use ionizing radiation and has recently benefited from improvements in image acquisition methods, digital image processing, and computer technology, is now the most commonly used clinical imaging modality. After the images have been divided, image processing can be used to determine where an anatomical structure is in relation to the tissues surrounding it. Accurate and reliable segmentation of liver tissue and tumors is necessary for CT-based hepatic diagnosis [3]. This is necessary for helping with the planning and evaluation of treatment and computer-assisted surgery. This is necessary in order to arrive at an accurate diagnosis. Even though it is labor-intensive, boring, and takes a lot of time, it is still common in clinical practice to outline the liver and tumor in each slice manually. It leads to differences between observers, which makes it hard to get the most accurate results from segmentation.

Also, liver segmentation is thought to be hard because computed tomography (CT) images of the liver usually have blurry edges and a low level of contrast, which are both features of the liver [4]. It is hard to divide up liver tumors because the images have low contrast, unclear edges, and different levels of intensity. Because of this, it is hard to tell the difference

between different kinds of liver tumors. Developing more advanced segmentation algorithms for medical image computing has become one of the most important research goals [5]. If these algorithms work, they could one day give doctors accurate, effective, and strong methods. In the last ten years, a lot of new ways of dividing up the liver and tumors have been made, and all of them have worked, though to different degrees. These methods can be divided into two categories based on whether or not the user's input is required: automatic methods and semiautomatic methods. Automatic methods require no input from the user.

2. Related Works

Model-based methods have been found to be the best kind of automatic liver segmentation algorithm. One way to speed up the segmentation process is to use model-based methods that take into account what is already known about the anatomy of the target organ. Many studies have shown that these are the most reliable ways to do things. At the MICCAI 2007 liver segmentation challenge, the first, second, and third place algorithms were fully automatic and based on statistical shape models. These models could be used to figure out how the liver is shaped. During the process of dividing up the liver, these models were used (SSMs).

Nevertheless, SSMs have a big problem in that because the training data is small, they tend to overfit the shape deformations and over-constrain the shape deformations to the training data. This is a problem because SSMs tend to make the shape deformations too tight. This is a problem because SSMs only have limited space to store training data. This is a problem because SSMs tend to restrict the shape deformations overly. Because of this, they work less efficiently than they would if they didn't have to.

Zhang et al. came up with a method called Sparse Shape Composition (SSC) shape prior modeling within a unified framework [7] to get around the problems that come with SSMs. The goal of this method is to avoid the problems that SSMs cause. This method is called "Sparse Shape Composition," which is also what it is called. As a result, the SSMs would be able to change even more. This method was extensively tested on 2D lung localization and 3D liver segmentation, and it did better in both studies than methods that are considered the best in their fields. Also, this method made it possible to divide the liver more accurately in 3D. Also, this method was able to divide the liver into its parts in a precise way in three dimensions. Shi et al. were inspired by the work of earlier researchers when they set out to create a new framework based on active shape models for accurate and reliable liver segmentation in the portal phase of abdominal CT images. This was done when Shi et al. tried to make a new framework for accurate and reliable liver segmentation in the portal phase of abdominal CT images. [6] Shi et al. showed a framework that they had made on their own [ASMs]. The most important changes were made to a new shape simulation model called MLR-SSC, which stands for "multilevel local region-based shape simulation." The name was given to this model. This particular model has been given the name MLR-SSC. Its goal was to make earlier shape models more flexible while also getting more accurate information about the shape of the local area [8-9].

Additionally, there is a growing interest in the possibility of achieving automatic segmentation by making use of deep learning strategies. This interest has been on the rise recently. Recently, Dou et al. presented a novel and efficient 3D fully convolutional network for 3D image segmentation [10]. This network was developed in recent times. A mechanism for deep three-dimensional supervision is built into this network. Lu et al. devised a method that uses graph cuts in conjunction with a convolutional neural network (CNN) to locate and divide the liver in three dimensions [11]. After finding and probabilistically dividing the liver with a three-dimensional convolutional neural network (3D CNN), the first division was improved with the assistance of graph cuts and a learned probability map [12]. In the research paper that Yang and his colleagues wrote, they demonstrated how they improved the performance of their deep image-to-image network by employing adversarial training. Their approach was trained using information from more than a thousand distinct 3D datasets that had been annotated [13]. The validation showed that their method can achieve encouraging results in segmentation and a more rapid processing speed. This was demonstrated by the fact that the method was faster. Lu et al. came up with an idea for a method that could be used to perform 3D localization and segmentation of the liver by using a convolutional neural network (CNN) and graph cuts [11]. First, a three-dimensional convolutional neural network (3D CNN) was used for probabilistic

liver segmentation and detection. Following that, the initial segmentation was refined with the assistance of graph cuts and a learned probability map. Yang et al. presented in their paper a deep image-to-image network that had been improved through the use of adversarial training. In this presentation, the network was discussed. Their approach was trained using information from more than a thousand distinct 3D datasets that had been annotated. The validation showed that their method could achieve encouraging results in segmentation and a more rapid processing speed. This was demonstrated by the fact that the method was faster.

There are currently a growing number of automatic methods available, and more are being developed all the time that can segment liver tumors. According to Goetz et al. [13], for example, an automatic algorithm in which all voxels were classified into healthy or tumorous tissue through the use of Extremely Randomized Trees with an auto-context learning scheme allowed the liver to be segmented first. The liver had to be segmented before the tumor could be segmented in this algorithm. This was done in order to achieve the segmentation of the tumor. This was done to segment the tumor into its constituent parts successfully. The application of a method known as domain-adapted learning from sparse annotations, also known as DALSA for its acronym in full, was the most significant thing that they did. They did this so that they could learn from the few annotations that were provided and get a quick setup for the new image settings. Moghbel et al. came up with a hybrid method of the random walker's method with priors and the fuzzy c-means algorithm with cuckoo optimization [14]. The researchers proposed this method. Deep learning schemes are becoming increasingly popular for many reasons, including their large model capacity and their capability to learn highly discriminative characteristics associated with liver tumors. Deep learning is a powerful alternative to traditional machine learning, and it is becoming increasingly popular for several reasons. Li et al. came up with a fully automated method and made use of deep CNNs in their research [15]. Their methodology was evaluated compared to three well-known machine learning algorithms: AdaBoost, Random Forests, and support vector machine. The goal of this comparison was to demonstrate the superiority of their approach. The proposal comprised two distinct stages that needed to be completed to identify tumors successfully [16]. The liver is needed to be removed from the CT scans. When using deep convolutional neural networks, the probability of each pixel in a segmented liver belonging to tumors could be calculated (CNN). Sun et al. developed a fully convolutional multichannel, abbreviated as MC-FCN [17], to segment liver tumors from multiphase contrast-enhanced CT images. This network's purpose was to segment the liver tumors. According to the findings, this method provided a higher level of accuracy and robustness than the methods that came before it. In addition to this, it can fully utilize the properties associated with the various stages of CT image enhancement, which is a significant advantage. In other words, it can improve the quality of the image in a way that is not limited by these properties. When it comes to segmenting the liver and liver tumors, fully automatic methods, such as the ones described above, may, on occasion, call for the utilization of large training datasets. This leads to a drawn-out process of training and the construction of statistical models that requires much manual labor. This can be a challenge for fully automatic methods. In addition to this, they typically have a lower level of accuracy and robustness and a significantly higher level of computational cost. In other words, this is not a good option [18]. On the other hand, a competitive and essential method for clinical practice is a semiautomatic method that enables a quick and accurate segmentation while still allowing the user to maintain full control over the process. Following this, we will provide a summary of several different semiautomatic approaches, respectively, to segmenting the liver and liver tumors. After that, we will proceed to the following segment of the discussion.

It was discovered that the method proposed by Yang et al. hybrid for the semiautomatic segmentation of liver tissue was successful [19]. In the beginning, the CT volume was segmented by using a specialized fast-marching LSM. In order to use this method, multiple seed points had to be chosen by hand. After that, a threshold-based LSM was applied so that the initial segmentation could be refined even further. This was done so that the results could be more accurate. These two different activities were carried out in the specified order, with the one that was required to be done first being the activity that got started off the list. It was explained how Yamaguchi et al. [20] developed a methodology that was founded on probabilistic atlas and a correlation map of locoregional histograms. This methodology was used to develop a map of correlations between locoregional histograms. Yamaguchi is the one who proposed that we consider this strategy. The first

step in determining the definitive liver region using this strategy was to harvest a candidate liver region using the region-growing method. This was the first step in determining the definitive liver region. After that, determining the definitive liver region continued in its next stage. This was the first thing that needed to be done in the process. After it was established that a candidate region of the liver did exist, the process continued to the next stage, which consisted of carrying out the appropriate procedures. After that, a correlation map and probabilistic atlas were utilized to zero in on the particular liver region that required analysis. Chartrand et al. presented their findings and developed an algorithm that makes use of Laplacian mesh optimization [21]. To get started, a three-dimensional model of the liver was created in an approximation by starting with a few user-generated contours that were used to outline the overall shape of the liver. This was done to get a general idea of how the liver is structured. After that, a three-dimensional space was occupied by the construction of this model. Following that, a Laplacian mesh optimization scheme was applied to the model in order to carry out an automatic deformation in order to differentiate the liver. This was done in order to distinguish the liver from the other organs. An innovative active contour model (ACM) based method was proposed by Zareei et al. [22]. In this method, preprocessing was used first to extract the initial contour, then a genetic algorithm was used to obtain optimal parameters for the ACM, and finally, the ACM was used to refine the initial contour. The idea behind this method is that the ACM can more accurately represent the shape of an object than any other representation can. The order in which these procedures were carried out was followed very precisely at all times. Within the context of a Bayesian level set framework, Eapen et al. [23] proposed a method for the semisupervised segmentation of the liver. In this scenario, the level set was initialized with the assistance of a Bayesian probability model that included a spatial prior. The spatial prior was taken into consideration. It was also used to derive an enhanced variable force and an edge indication function, both of which assisted the level set evolution in getting closer and closer to the actual boundaries of the liver. Another use for it was that it was utilised to develop the level set. It was also put to use in the process of developing the level set, which is another one of its many applications.

When it comes to the semiautomatic segmentation of liver tumors, Smeets et al. proposed a method that makes use of a hidden Markov measure field model and nonparametric distribution estimation [24]. Before beginning the segmentation process, the user was prompted to select two points for the construction of the region of interest located on opposite edges of the tumor. These points would be used in the segmentation of the tumor. The segmentation would make use of these points at various points (ROI). In addition, after the segmentation was finished, a postprocessing operation was carried out in order to remove any unnecessary data that was produced as a result of the segmentation. This was done in order to keep the data as clean as possible. A method for segmenting three-dimensional data using graph cuts and an improved fuzzy c-means was described.

The confidence-connected region-growing algorithm was initially used to extract a tumour ROI. In order to complete the segmentation process, a kernelized FCM that included spatial information was subsequently incorporated into graph cuts segmentation. Because of this, the authors were able to accomplish their segmentation goal successfully. Utilization of this method resulted in the completion of the segmentation project in its entirety. Hoogi et al. [25] came up with the concept of utilising an adaptive local window to improve the level set to improve liver tumors' segmentation. This was accomplished by improving the level set. During the process of segmentation, the window was estimated in a manner that was unique and specific for each point, as well as for each object. This was done so in order to ensure accurate results. It was necessary to do this in order to obtain reliable results. This method demonstrated significantly better segmentation when dealing with complex lesions, and in terms of performance, it outperformed the other three energy models. A novel method was presented by Rousseau et al. [26]. This method involved the application of random forest on super voxels and involved robust multiphase cluster-wise features extracted from registered multiphase contrast-enhanced CT scans. It was determined, based on the findings of the evaluation, that this technique had the capacity to segment parenchyma, active accurately successfully, and necrotic tissues.

3. Proposed System

The GMM is an unsupervised classification method and uses a probabilistic approach to data analysis. It is getting trained during the phase of the classifier. The probability density functions of the images being used are analyzed and estimated. This pixel-labeling classifier works based on the assumption that the grey level value of each pixel in the observed image is a sample taken from a mixture distribution. This distribution has a limited number of possible permutations, and there is a limit to the number of possible labels that can be assigned to each pixel. In the form of a block diagram, the illustration of the proposed method that can be found in Figure 1 is presented.

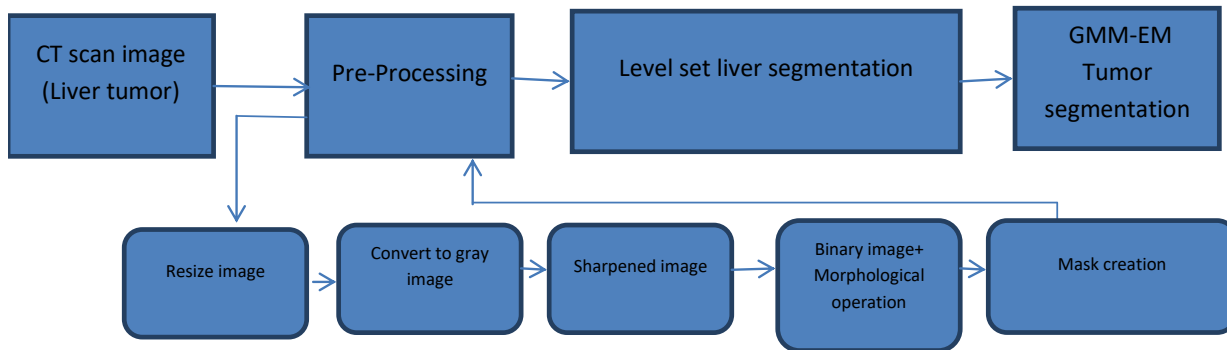


Fig.1. Block Diagram of Proposed method

3.1. Pre-processing

The proposed data segmentation method begins with a preprocessing stage that organizes and cleans the data in preparation for the segmentation process. In order to simplify the calculation and reduce the amount of complexity involved, the input image is scaled down to ranges of 250 by 250 pixels. If the image is represented using RGB color space, then it will need to be converted into a grayscale image. The enhancement of an image's edges and the finer details come from the sharpening process. After the image has been transformed into its binary equivalent, the imperfection in the structure of the image can be smoothed out through the use of a morphological operation. The majority of the procedures that are carried out in this location are a combination of two processes: erosion and dilation. In order to operate, a small matrix structure known as a structuring element is used. The form and dimensions of the structuring element have a considerable bearing on the outcome of the overall process. After that, the smaller organs are removed, and the larger organs, which are the source of the tumour cells, are extracted. After that, we perform the Level set segmentation, which helps to improve the quality of the liver image.

3.2. Level sets

The initial level set is modeled as an implicit function denoted by (x,t) , which is then subjected to the transformational effects of a speed image. For computation efficiency, a local level set method is utilized due to its definition.

$$\frac{d}{dt} \varphi = -\alpha A(x) \cdot \nabla \varphi - \beta P(x) |\nabla \varphi| + \gamma Z(x) K |\nabla \varphi| \tag{1}$$

Where A is a term that describes advection, P is a term that describes propagation, and Z is a term that describes a spatial modifier for the mean curvature k . The level set moves closer to the margins of the tumor as a result of the advection term $A(x) = -\nabla I_v(x)$. The level set will broaden whenever the gradient of the speed function is seen to be negative. When there is a positive gradient, the level set will get smaller. Both the propagation term $P(x) = I_v(x)$ and the curvature term $Z(x) = I_v(x)$ are responsible for the speed-dependent expansion of the level set. Additionally, the curvature term $Z(x) = I_v(x)$ softens the level set's sharp edges. When determining whether or not the solution has converged, a maximum RMS error of 1 percent is used to compare the results of the various iterations. In addition, there is a cap placed on the number of repetitions in order to prevent infinite loops.

3.3. Gaussian mixture model

The picture is shown to the viewer in the form of a matrix, in which each individual element stands for one pixel. In the Gaussian mixture model (GMM), the image pixels are treated as a random variable and denoted with the variable x , where x represents a three-dimensional variable that contains RGB values. This model is known as a mixture model. A weighted sum of the Gaussian distribution is used to represent the probability that the image will be shown,

$$f(x) = \sum_{i=1}^k w_i N(x|\mu_i, \sigma_i^2) \tag{2}$$

Where, k represents the total number of regions and the set $\{w_1, 2, \dots, wk\}$ defines the weights which satisfy the condition $\sum_{i=1}^k w_i = 1$

The term $(x|\mu_i, \sigma_i^2)$ represents the Gaussian distribution of the i th region with the mean μ_i and standard deviation σ_i respectively

$$N(\mu_i, \sigma_i^2) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left\{-\frac{(x-\mu_i)^2}{2\sigma_i^2}\right\} \tag{3}$$

Before we can evaluate GMM, we need to estimate one of the model's parameters. The maximum-likelihood estimation method is the one that is utilised the vast majority of the time when attempting to calculate the value of the GMM parameter. The primary objective of the estimation is to achieve the highest possible likelihood with the GMM dataset. Estimation is done with an algorithm called expectation maximization, or EM for short.

4. Result and Discussion

The method proposed for detecting liver cancer was evaluated using CT scan images that already contained cancerous lesions. The procedure will be described have two stages: the first is separating the liver, and the second is looking for cancerous lesions.

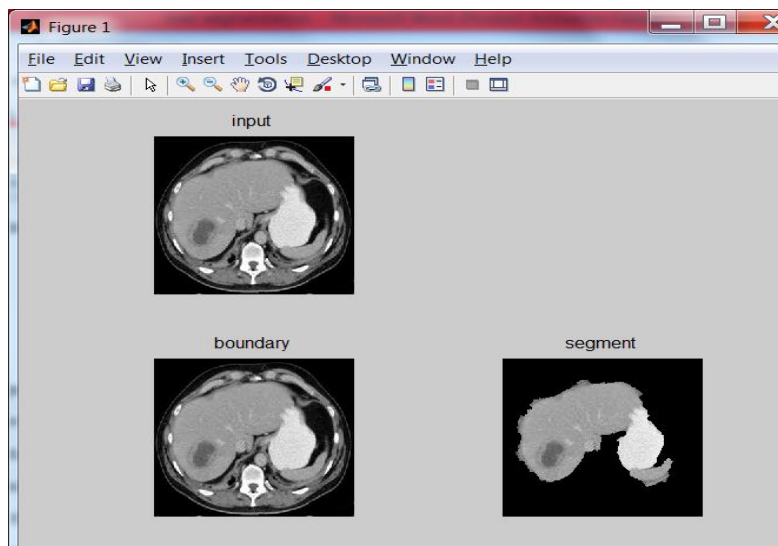
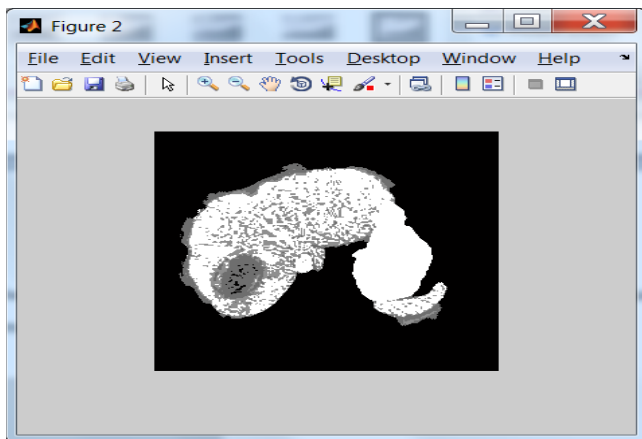
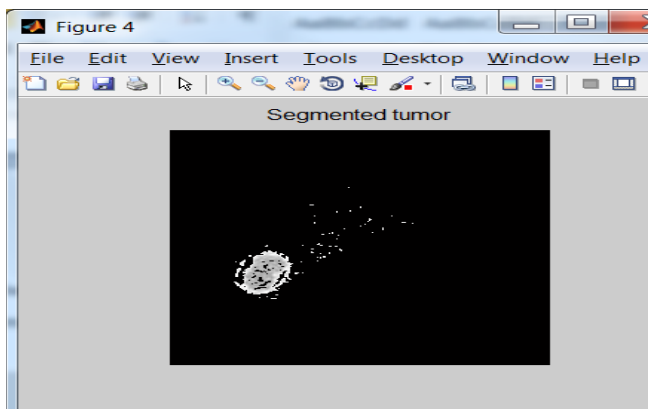


Fig.2. (a) Input Image (b) Boundary of lesions (c) Segmentation

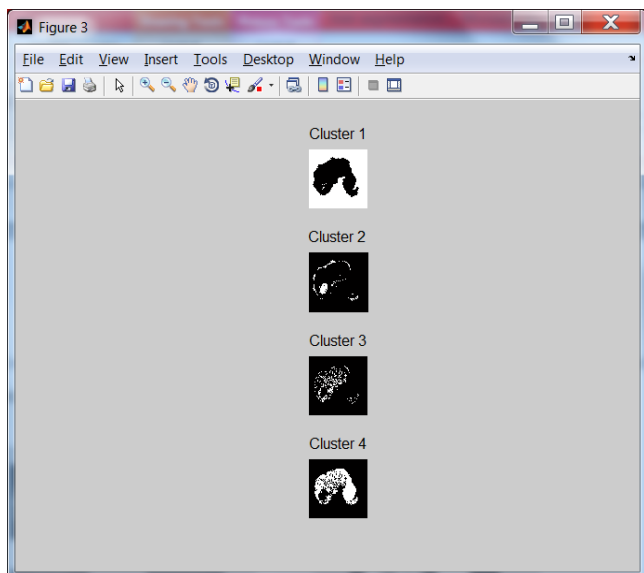
The first stage involves separating the healthy parts of the liver from the unhealthy parts of the liver. The boundary of the lesions is identified, and the segmented lesion part is shown in figure 2. The GMM procedure is repeated in the liver regions in the second stage. It has been separated in order to remove the remaining cancerous lesion



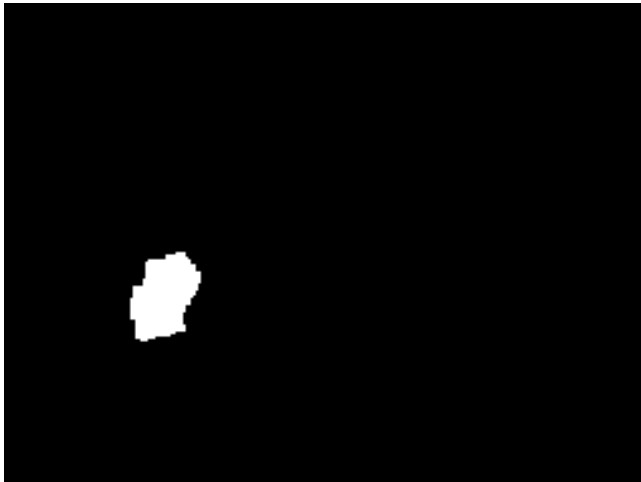
(a) Segmented lesion



(b) Clustering



(c) Segmented Tumor



(d) Ground truth

Fig.3. The Segmentation result of Gaussian mixture model

The clustering and segmentation of tumors in the liver according to the GMM model can be easily understood by referring to figure 3. Therefore, the findings of our experiments provide a precise and comprehensive description of the GMM-based liver segmentation.

5. Conclusion

We used the proposed segmentation strategy to demonstrate a fully automated method for segmenting liver CT images. Consequently, we were able to achieve our goal. A masking technique is used during the preprocessing stage of the procedure to achieve the desired goal of separating the liver from the other organs. In order to complete the liver's many distinct regions, the level set algorithm is then applied. This step is essential to the completion of the project. A Gaussian mixture model is then used to predict the tumor size. It takes into account many variables in this model (GMM). Because of this, the proposed system's accuracy will be noticeably better than the current system's accuracy, which is already significantly better. The algorithm has been tested on a wide range of images, and it has come out on top every time. It was possible to achieve effective data segmentation while drastically reducing the processing time. Tests proved to be an overwhelming success thanks to the algorithm's impressive performance in the tests themselves.

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