Review on Recent Methods for Segmentation of Liver Using Computed Tomography and Magnetic Resonance Imaging Modalities

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Abstract The span of modern medical imaging provides new and efficient techniques for segmentation of liver that are used by the clinicians to view in order to diagnose, monitor and treat liver diseases. Liver cancer is one of the most prominent diseases which cause death. Extraction of liver in different modalities is a difficult task because of its varying shape, similarity between organ intensities and variability in liver region intensities. In this review paper, a study has been carried out on liver segmentation in CT and MRI images with different methodologies and datasets. The observation has been made to highlight the merits, demerits and performance metrics of different works published.

Keywords Liver segmentation · Computed Tomography (CT) · Magnetic Resonance Imagining (MRI)

1 Introduction

Liver is the only body's largest vascular glandular solid organ found in all vertebrates. Some of its functions are regulation of glycogen storage, decomposition of red blood cells, plasma protein synthesis, hormone production and detoxification. In human beings, it is located in the right upper quadrant of the abdomen, below the diaphragm. Normally, liver is divided into eight lobes, but from outside it is divided into a larger right lobe and smaller left lobe [1]. Liver is the only organ capable of regenerating the lost tissues. Resection of liver lobes will not regrow the lobes; instead, growth will be with respect to the function restoration not original form.

Tracing of liver is important in medical imaging for obtaining qualitative measurements such as the location finding the region of interest and quantitative mea-

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surements like area, volume or the behavioral analysis of structure anatomy over time. This provides a good computer-aided diagnosis for feature extraction and characterization of lesions. Accuracy in liver segmentation plays an important role in diagnosing the liver diseases, liver transplantation and liver resection which help the patients to survive. Hence, fully automated approaches to segment liver are being designed which help radiologists to diagnose different types of lesions accurately with less amount of time. Liver segmentation is still a challenge in diseased liver due to distortion in liver shape, complexities in liver pathologies, blurred edges and the presence of hypodense or hyperdense lesions [2].

Diagnosis of liver diseases can be made using various noninvasive imaging modalities like computed tomography (CT), magnetic resonance imaging (MRI), ultrasound (US), positron emission tomography (PET) and positron emission tomography-computed tomography (PET-CT). CT is a noninvasive imaging modality which combines X-rays and computer technology to produce horizontal images of the body parts [3]. CT scanners result with thousands of image slices which will be tedious and time-consuming for radiologists to perform accurate diagnosis [4]. Computed tomography is much preferred by the diagnosticians because of its accurate anatomical information about the structures which are visualized. Supporting arguments of CT are highly sensitive to distinguish tissue density differences and get accurate anatomical data. Opposing arguments of CT are less sensitive to pathological information. MRI modality uses strong magnetic field, radio waves and field gradient to form anatomical pictures and physiological processes of the body in both health wise and disease wise. Reason to support MRI is that it is highly effective in showing the difference between healthy and diseased soft tissues in the body, and reasons to oppose MRI include high cost, long procedure time and patient need to hold breathe for a longer time.

Various methodologies observed in the study include SLIC super-pixel with AdaBoost algorithm, graph cut method, fully convolution network with deeper bottleneck architecture, hybrid densely connected U-Net, statistical shape model, Bayesian probability atlas model with adaptive thresholding, level set method, active contour, Laplacian mesh optimization method, 3D active surface model used in computed tomography and magnetic resonance imaging modalities.

2 Literature Review

Many of the computer-aided diagnosis systems developed are semiautomatic and fully automatic systems using CT and MRI modalities which are observed through the study discussed in the following section.

2.1 Liver Segmentation Using Computed Tomography (CT) Images

Barstugan et al. [5] have put forward an automatic technique for splitting up of liver on CT images using SLIC super-pixel and AdaBoost algorithm, which uses two AdaBoost algorithms to train spinal cord and liver with image clustering performed using SLIC super-pixel algorithm. A fully automatic method (except initial slice selection) is proposed by Liao et al. [6] using graph cut and border marching to split up the liver. A fully automatic approach to segment liver from 3D CT scans based on fully convolution network with deeper bottleneck architecture (DBA) which decreases the number of parameters in the network and increases network depth is proposed by Jin et al. [7]. Zhang et al. [8] recommended a cascaded structure to section the liver by utilizing a fully convolution neural network with postprocessing which refines the liver. Liver segmentation in CT images is developed by Li et al. in [9] using hybrid densely connected U-Net which produces a coarse segmentation of liver quickly by training simple ResNet architecture [10] which reduces computation time. Zheng et al. in [11] projected a methodology to fragment liver in 2D CT images using statistical shape model (SSM) with enforced local statistical features. Farzaneh et al. [12] put forward a Bayesian probability atlas model with adaptive thresholding and super-pixel algorithm to segment liver by creating two Bayesian probability atlases for intensity and location of liver using adaptive thresholding and incorporate anatomical information with super-pixel algorithm to find final ROI. A noninvasive approach to segment liver is projected by Saito et al. by [13] using level set method for multiphase CT images.

2.2 Liver Segmentation Using Magnetic Resonance Imaging (MRI) Images

Christ et al. [14] submitted algorithm to segment liver with hepatic lesions in MR images using the cascaded fully convolutional neural network, where preprocessing is done using N4 Bias Correction algorithm [15], and several data augmentation steps are included to increase the training set like elastic deformation, translation, rotation, addition of Gaussian noise with standard deviation. Fully automated approach for breaking up the liver is preferred by Mohamed et al. [16] which uses active contours by considering image enhancement phase, liver localization phase, liver segmentation phase and segmented result enhancement phase. Liver fragmentation using Laplacian mesh optimization which is a semiautomatic model is suggested by Chartrand et al. [17]. Bereciartua et al. [18] proposed a novel approach to segment liver using compact descriptor integrated into 3D active surfaces in multiple sequence MRI images which use multi-sequential spatial descriptor, namely axial gap, axial arterial, axial venous, late axial (VIBE sequences) and blade which comprises of spatial variation.

3 Methodologies

Observations made in the study for segmentation of liver based on techniques are discussed in the following section using computed tomography and magnetic resonance imaging modalities.

3.1 *Liver Segmentation Methods Using Computed Tomography Images*

Ecabert et al. [4] use AdaBoost classifier constructed using decision trees and trained on patches of 3 × 3, 5 × 5, 7 × 7, 9 × 9. It is used to train liver and spinal cord which consist of base learners which were taken as 100, and classification result was based on weight voting given in Eq. (1)

$$H(x) = sign\sum_{t=1}^{T}(a_t h_t(x)) \tag{1}$$

where a_t, h_t are referred as weight and base learner, respectively. SLIC super-pixel algorithm used in [19] is faster and efficient compared to existing super-pixel algorithm which adapts k-means method for super-pixel algorithm which is used to cluster the image.

Liao et al. of [6] come up with an unsupervised method for selecting a initial slice and segmented using density peak clustering technique [20] which divides it into three clusters. Author uses minimization energy function in Eq. (2) using graph cut method [21] which integrates intensity model, PCA-based appearance model and location constrained used to iteratively recognize liver in the remaining slices.

$$E(f) = \sum_{p\in P}\left(\alpha \cdot F_{intensity}\left(f_p\right) + \beta \cdot F_{PCA}\left(f_p\right)\right) \cdot f_{location}\left(f_p\right) + \sum_{p\in P, q\in Np} B(f_p, f_q) \tag{2}$$

where P is the set of pixels of image f, N_p is the set of neighborhood pixels, α and β are the weights of the intensity and appearance penalties, and α + β = 1. Lastly, under-segmented vessels are compensated using marching of liver border.

Jin et al. [7] build a new FCN-based liver segmentation U-Net referring to the classical deep convolutional U-Net model proposed by Ronneberger et al. [22]. FCN-based liver segmentation U-Net is build along with three DBAs (deeper bottleneck architectures) to decrease the number of network parameters and increase the hidden layer, which varies with height, width and number of channels with 53 convolution layers called as U-Net-53. The data augmentation (move, rotation, mirror, noise, cut) is also done in this method to increase the performance compared to Ben-Cohen et al. [23] and Christ et al. [24] who use fully convolution neural network.

Zhang et al. [8] build 21 layers of fully convolutional neural network, i.e., 15 convolution layers, 3 pooling layers and 3 deconvolutional layers followed by ReLU [25], inspired by the U-Net of [22] to segment liver and generate probability map. Batch is normalized after convolution using mean and standard deviation [26]. To balance class, weighting factor ω is introduced in the cross-entropy loss function F_ℓ of the FCN, which is given in Eq. (3)

$$F_\ell = -\frac{1}{n}\sum_{i=1}^{N} \omega i\left[\hat{p}_i \log p_i + \left(1-\hat{p}_i\right)\log(1-p_i)\right] \tag{3}$$

where p_i is the probability of foreground pixel and $\hat{p}_i$ is ground truth. Three post-processing models level set based, graph cut based and conditional random field are used for comparison with the probability map to increase the accuracy.

Li et al. [9] proposed a hybrid densely connected U-Net which includes both 2D Dense U-Net f_{2d} extracts intra-slice features and 3D Dense U-Net f_{3d} extracts volumetric inter-slice features, and optimized using hybrid feature fusion (HFF) layer for segmentation of both liver and its lesions; 2D Dense U-Net follows the structure of Dense-Net-161 [27], which is extended to 167 layers called 2D Dense U-Net-167. The feature maps and score maps of 2D Dense U-Net are given in Eq. (4) as follows:

$$\begin{aligned} X_{2d} &= f_{2d}(I_{2d};\theta d); X_{2d} \in R^{12nX\,224X\,224X\,64} \\ \hat{Y}_{2d} &= f_{2dcls}(X_{2d};\theta_{2dcls}); \hat{Y}_{2d} \in R^{12nX\,224X\,224X\,3} \end{aligned} \tag{4}$$

where X_{2d} is feature map, $\hat{Y}_{2d}$ is predicted pixel-wise probabilities corresponding to the input three adjacent slices and I_{2d} input samples of 2D Dense U-Net. The feature maps and score maps of 2D Dense U-Net transformed to volumetric are given in Eq. (5) as follows:

$$\begin{aligned} X'_{2d} &= f^{-1}(X_{2d})\,; X'_{2d} \in R^{nx224X\,224X\,12X\,64} \\ \hat{Y}'_{2d} &= f^{-1}\left(\hat{Y}_{2d}\right); \hat{Y}'_{2d} \in R^{nX\,224X\,224X\,12X\,3} \end{aligned} \tag{5}$$

The learning process of 3D Dense U-Net is described in Eq. (6)

$$\begin{aligned} X_{3d} &= f_{3d}(I, \hat{Y}'_{2d}\,; \theta_{3d}), \\ Z &= X_{3d} + X'_{2d} \end{aligned} \tag{6}$$

where X_{3d} denotes the feature volume from layer in 3D Dense U-Net-65 and Z denotes the hybrid feature. Features are learned and optimized using HFF layer as shown in Eq. (7)

$$\begin{aligned} H &= f_{HFF}(Z;\theta_{HFF}) \\ \hat{y}h &= f_{HFFcls}(H;\theta_{HFFcls}) \end{aligned} \tag{7}$$

where H denotes the optimized hybrid features and ŷh denotes pixel-wise probabilities generated from HFF layer.

Zheng et al. in [11] project a segmentation model (F) based on statistical shape prior model by applying PCA on signed distance function (SDF), global Gaussian fitting energy (F_G) in Eq. (9) and local statistical consistency energy (F_L) in Eq. (10) to move the contour toward the liver boundary which is given in Eq. (8)

$$F(\alpha; X_T; f_1; f_2) = w_1 F_G + w_2 F_L \tag{8}$$

$$F_G = \sum_{i=1}^{2} \frac{\lambda_i A_i}{2} \log(\int_{\Omega 1} \frac{(A_i I(x) - \int_{\Omega 1} I(x)dx)^2}{A_i^3} dx) \tag{9}$$

$$F_L = v_1 \int_{\Omega 1} |F(x) - f1|^2 dx + v_2 \int_{\Omega 2} |F(x) - f2|^2 dx \tag{10}$$

where A_i represents number of pixels in background and foreground, f1 and f2 denote representative features, w_1, w_2, λ_1, λ_2, v_1, v_2 are parameters to balance inside and outside local and global energy, $\Omega 1 = \left\{x : \hat{\Phi} T(x) > 0\right\}$, $\Omega 2 = \left\{x : \hat{\Phi} T(x) < 0\right\}$ and X_T is parameter vector of geometric transformation.

Farzaneh et al. [12] use the Bayesian-based method [28] for liver segmentation creating two atlases, where one atlas based on location and the other atlas based on intensity. The overall probability of the liver pixel is defined in Eq. (11)

$$P(L|(i, j), I) = \frac{P(I, (i, j)|L)P(L)}{P(I, (i, j)|L)P(L) + P(I, (i, j)|L')P(L')} \tag{11}$$

where P(L|(i, j)) is location probability and P(L|I) is the intensity probability. New intensity probability atlas $P(I|L)_{new}$ is created, where probability of the pixel is calculated as Eq. (12)

$$Pnew(L|I, (i, j)) \propto P(L|I)newP(L|i, j) \tag{12}$$

Authors propose adaptive thresholding for each slice with cut-off value t which is calculated using Eq. (13) and optimum threshold value th with step wise Δ.

$$\begin{aligned} f(t) &= \frac{||Pnew \geq t - \Delta||0 - ||Pnew \geq t||0}{||Pnew \geq t||0} \\ th &= argmin(f(t)) \end{aligned} \tag{13}$$

where $Pnew \geq t$ is a binary image with the pixel value of 1 and ||.|| 0 denotes the norm zero.

Saito et al. [13] proposed a level set based method to segment liver in multiple phases (non-contrast, early arterial phase, portal phase, equilibrium phase of CT images). In non-contrast phase bone is detected and used as a predefined template in contrast phases for bone detection. For segmenting the liver, Chan–Vese-based [29] level set method is applied with the following Eq. (14)

$$\mathrm{F}(c^{+}, c^{-}, \mathrm{C}) = \mu\mathrm{length(C)} + \mathrm{vArea(Inside(c))} + \lambda^{+} \int\limits_{inside(c)} \left|u_0(x, y) - c^{+}\right|^2 dx\,dy + \lambda^{-} \int\limits_{outside(c)} \left|u_0(x, y) - c^{-}\right|^2 dx\,dy \tag{14}$$

where μ_0 is a pixel value of image, C is the boundary of a closed set and c^{+}, c^{-} are the values of u respectively inside and outside of C.

3.2 Liver Segmentation Methods Using Magnetic Resonance Imaging Images

Christ et al. [14] proposed a cascaded fully convolutional neural network to segment liver and its lesion for both CT and MRI volumes which is the extension of [30]. U-Net architecture [22] is used to find soft label probability maps by combining spatial and contextual information which consists of 19 convolution layers. With reference to [31], class balancing is important in training the network to segment small structures like lesions, so additional weighting factor ω^{class} is introduced in cross-entropy loss function L Eq. (15) of FCN

$$L = -\frac{1}{n}\sum_{i=1}^{N} \omega_i^{class}[\hat{P}_i \log P_i + (1 - \hat{P}_i)\log(1 - P_i) \tag{15}$$

where P_i is the probability of voxel i belonging to the foreground, $\hat{P}_i$ is the ground truth. It also uses pretrained U-Net models provided by Ronneberger et al. [22], who were trained on cell image segmentation data; 3D dense conditional random field (CRFs) is used as a postprocessing technique proposed by [32] to get final segmented volume.

Mohamed et al. [16] use the active contour to automatically segment liver in MRI images. The first active contour model was developed by Kass et al. [33]. In active contour, initialization of curve is done by user and snake moves and deforms toward boundary. Snake is derived from the three energy functions given in Eq. (16)

$$E_{snake} = E_{int} + E_{ext} + E_{cons} \tag{16}$$

$$E_{int} = E_{elastic} + E_{bending} = \int\limits_{s} \frac{1}{2}(\alpha|v_s|^2 + \beta|v_{ss}|^2) \tag{17}$$

$$E_{ext} = \int_{s} E_{image}(\mathrm{V(s)})\mathrm{ds} \tag{18}$$

where $\mathrm{E}_{\mathrm{int}}$, E_{ext}, E_{cons} are internal energy mentioned in Eq. (17), external energy calculated using Eq. (18) and constrained energy, respectively, and α, β are the weights.

Chartrand et al. [17] developed Laplacian mesh optimization framework, a semi-automatic method to segment liver in both MRI and CT images. Initial shape was generated by a few contours carried out by users. Preserving the smoothness of the shape by using discrete Laplacian operator discussed by Nealen et al. [34] set to a target value of 0. The Laplacian energy function which is to be minimized is given in Eq. (19)

$$E_{\mathcal{L}}\left(V'\right) = \propto \sum_{i=1}^{n} w_i^2 (t_i - v_i')^2 + \left\| \mathcal{L}V' \right\|^2 \tag{19}$$

where V', $\mathrm{v_i}$, $\mathrm{t_i}$, $\mathrm{w_i}$, $\mathscr{L}$ are new vertex, target, weight and Laplacian matrix which represents delta coordinates obtained by applying discrete Laplace operator on the previously introduced mesh, respectively.

Bereciartua et al. [18] put forward 3D active surface model which takes the work of Bresson and Chan [35] to segment liver which combines active contours without edges (ACWE) introduced by Chan et al. [36] and the geodesic active contours (GAC) developed by Caselles et al. [37]. Chan and Vese [38] stated the energy functional model of ACWE to minimize is expressed in Eq. (20) as follows:

$$\begin{aligned} E_{ACWE}(\Omega_c, c_1, c_2, \lambda) = Per(\Omega_c) + \lambda \int_{\Omega_c} (c_1 - I(x, y))^2 dx\, dy \\ + \lambda \int_{\Omega \setminus \Omega_c} (c_2 - I(x, y))^2 dx\, dy \end{aligned} \tag{20}$$

where $I(x, y)$ is the image, Ω_c is a subset of the image domain bounded by closed contour, $Per\ \Omega_c$ is the perimeter of the set Ω_c, λ is a positive parameter, $c1$ and $c2$ $\in$ R. The energy functional model of GAC is expressed in Eq. (21) as follows:

$$E_{GAC}(c) = \int_{s} g\, ds \tag{21}$$

where g is an edge detecting function, and s is the arc length parameter along the contour C.

4 Discussion

Table 1 furnishes the digest of different liver slicing that confers about the literature survey along with techniques, year, datasets, outcomes, merits and demerits for each work carried on computed tomography volumes. Each of the study discussed uses different metrics used to measure the performance and varying datasets. The different approaches used by authors to segment liver CT images pose certain difficulties to analyze the performance. These difficulties are due to the use of different datasets, assumptions, different metrics to measure performance, image dimensions with different phases and ground truth marking done manually by radiologists.

The literature review in Table 2 presents with a digest consisting of diverse technologies, results with advantages and drawbacks of the whole lot on MRI Images for division of liver. Similar to CT images, performance analysis is also difficult mainly due to non-availability of public dataset, non-identical methodologies, assumptions made, varying datasets, ground truth marking done by various radiologists and different performance metrics used.

In this paper, observations have been made on different methods to segment liver and planning to develop a cascaded structure using fully convolution neural network one for liver and another for lesion segmentation using both computed tomography and magnetic resonance imaging volumes with multiple phases (both with contrast and without contrast). The factors decided to be considered while designing the structure includes reducing the computational cost, increasing the depth of the network, improving the accuracy of segmentation, decreasing number of parameters used in the network, reducing the training time by using pretrained models, considering leaky problem when the liver contour is not clear, decreasing the number of assumptions and work on huge datasets (both public and clinical datasets).

5 Conclusion

Liver segmentation used for lesion classification is difficult because of its shape and appearance which varies from person to person and similar intensities reside with liver and other organs surrounded it. From the discussion, we can observe that few algorithms are semiautomatic which have user interactions, very few methods worked for both CT and MRI images, leakage problem when liver boundary is not clear, less work on multiple sequences in MRI images, worked using limited datasets, abnormalities in tissues, training time and computationally time are high. Due to all these factors, there is still scope for developing fully automatic methods on larger datasets (both public and clinical) to segment liver and lesion accurately in both MRI and CT images.

Table 1 Overview of liver slicing in CT images

Ref. No.	Year	Methods	Datasets	Outcomes	Merits	Demerits
[5]	2018	SLIC super-pixel algorithms, AdaBoost classifier	Radiology Department in Selcuk University (16 images)	For 3 × 3 patch Sen- 95.36 ± 4.6 Spe- 98.29 ± 1.6 Acc- 97.85 ± 1.5 Pre- 89.84 ± 9.4 Dice- **92.13 ± 5.2** Jaccard- **85.8 ± 8.6** SSIM- 94.3 ± 2.1	1. Automation of locating seed point in liver region 2. Faster and efficient compared to existing super-pixel algorithm	1. Worked on limited dataset and not generalized
[6]	2017	Graph cut with border marching	Silver 07, MICCAI 2007, XHCSU14 (local database)	**Silver 07** VOE- 5.8 ± 3.2% RVD- −0.1 ± 4.1% ASD- 1.0 ± 0.5 mm RMSD- 2.0 ± 1.2 mm MSD- 21.2 ± 9.3 Time- 4.7 min	1. Works with low contrast, varying intensities and typical shapes 2. Accurate segmentation when liver and its vessels are heterogeneous	1. Poor results with serious pathological changes in liver 2. Semiautomatic due to manual selection of initial slice
[7]	2017	Fully convolution network with deeper bottleneck architecture	3D-IRCADb (20 images)	Dice- 95.7% VOE- 6.5 RVD- 1.0 ASD- 1.2 MSD- 18.3	1. Number of network parameters is decreased 2. Less dependent on appearance and more adaptive to different types of liver	1. DBA used in FCN to increase the performance in turn increases the computational cost

(continued)

Table 1 (continued)

Ref. No.	Year	Methods	Datasets	Outcomes	Merits	Demerits
[8]	2017	Fully convolution network with postprocessing	3D-IRCADb (15 training, 5 testing)	**FCN + CRF** VOE- **5.93** RVD- 1.34 ASD- 0.77 MSD- 6.97 Dice- **96.26%** **FCN + LS** VOE- 6.16 RVD- 1.05 ASD- **0.72** MSD- **5.84** Dice- 96.10% **FCN + GC** VOE- 6.72 RVD- **−0.02** ASD- 0.83 MSD- 8.69 Dice- 95.41	1. Good segmentation accuracy	1. Predefined shape priors
[9]	2017	Hybrid densely connected U-Net	MICCAI 2017 LiTS Challenge	Dice- 96.5%	1. Generalized neural network architecture can be used for other application 2. Performance increases due to use of pretrained model	1. Huge training time for H-Dense U-Net (30 hours) 2. Use of pretrained model

(continued)

Table 1 (continued)

Ref. No.	Year	Methods	Datasets	Outcomes	Merits	Demerits
[11]	2017	Statistical shape model (SSM) with enforced local statistical feature	3D-IRCADb SLIVER07 (only training part)	**SILVER07** VOE- 7.6 RVD- −0.1 ASD- 0.8 RMSD- 1.5 MSD- 20.8 **3D-IRCADb** VOE- 6.5 RVD- 4.1 ASD- 1.9 RMSD- 2.1 MSD- 18.9	1. Less user interaction 2. less training dataset 3. Liver extraction from ambiguous boundaries, large intensity and shape variation, and handle pathological liver	1. Shape prior and statistical image intensity information are defined 2. Semiautomatic approach 3. Liver should have only one connected component
[12]	2017	Bayesian probability atlas model with adaptive thresholding and super-pixels	8 patients total 332 CT images used to create two atlases. Tested on 503 slices from 10 patients 7 sets from University of Michigan Hospital and 3 sets from Virginia Common Wealth University Hospital	Dice- 93.5% Jaccard- 87.9% Sen- 90.6% Spe- 99.5%	1. Worked on liver injured by trauma 2. Fully automated	1. Atlas does not capture full variability 2. Geometrical structure and location are assumed to be same for all patients

(continued)

Table 1 (continued)

Ref. No.	Year	Methods	Datasets	Outcomes	Merits	Demerits
[13]	2017	Level set method for multiphase CT images	Real data	**Non-contrast** Jaccard- 86.6% APT- 1.80 s/slice **Early arterial phase** Jaccard- 84.8% APT- 1.97 s/slice **Portal phase** Jaccard- 83.8% APT- 2.02 s/slice **Equilibrium phase** Jaccard- 84.0% APT- 1.98 s/slice	1. Applied on multiple phases of CT images 2. Each phase is independent on other phases in this method 3. Method is robust because preprocessing is done based on anatomy	1. Low convergence to convex part of liver region because of constant size of morphological filters

Sensitivity (Sen), Specificity (Spe), Accuracy (Acc), Precision (Pre), Dice Co-efficient (Dice), Jaccard Index (Jaccard), Structural Similarity Index Metric (SSIM), Volumetric Overlap Error (VOE), Relative Volume Difference (RVD), Average Symmetric Surface Distance (ASD), Root Mean Square Symmetric Surface Distance (RMSD), Maximum Symmetric Surface Distance (MSD), Average Running Time (Time), Average Processing Time (ATP), Similarity Index (SI)

Table 2 Outline of liver division in MRI images

Ref. no.	Year	Methods	Datasets	Results	Merits	Demerits
[14]	2017	Cascaded fully convolution network	MRI-DW Coronal T2W and axial T1W	VOE- 23 RVD- 14 ASD- 5.2 MSD- 135.3 Dice- 87%	1. Work is carried on heterogeneous low contrast volumes 2. Data augmentation on training data to learn more invariabilities of liver 3. Network utilizes both semantic and spatial information 4. Utilizes pretrained model provided by Ronneberger et al. trained on cell segmentation 5. Training model is released which can be utilized by other researchers	1. Finding parameters of CRF in heterogeneous shape structure and appearance for lesions is time-consuming and hard 2. Lesion segmentation accuracy is low compared with liver segmentation
[16]	2017	Active contour	MRI with type T1 of 21 patients is collected from various Centers	Dice- 95%	1. Detection of liver is based on anatomical features rather than setting manual seed points 2. Fully automatic	1. Leak problem where liver contour is not clear

(continued)

Table 2 (continued)

Ref. no.	Year	Methods	Datasets	Results	Merits	Demerits
[17]	2016	Laplacian mesh optimization	20 MR dataset with Gradient recalled echo (GRE) sequence with contrast collected from Montreal university Hospital center	VOE- 7.6 RVD- 1.6 ASD- 1.5	1. Good result on MR volumes with intensity in homogeneity 2. Free from training	1. Liver contour drawing of users used in 3D model 2. Semiautomatic 3. Performance decreases due to breathing artifacts, artifacts of metal and air/tissues and thickness of slice
[18]	2016	3D active surface model	Radiology Department of Clínica Vicente San Sebastián (IMQ) Sequence are T2 Blade, VIBE: axial gap, VIBE: axial Arterial, VIBE: axial Venous, VIBE: late axial	VOE- 2.08 ± 1.83 RVD- 2.11 ± 1.93 ASD- 0.93 ± 0.77 RMSD- 2.29 ± 1.69 MSD- 10.72 ± 7.61 Acc- 99.80 ± 0.19 Dice- 98.59 ± 0.01	1. Executes over volume in statistical model 2. Multiple sequences are embedded in a compact framework where dimensionality will not increased, which improves segmentation accuracy	1. Multiple sequences used at the same time need extra scan time and need necessary image alignment

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