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An Effective Biomedical Segmentation of Liver Tumor Identification Using DCNN

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ABSTRACT: The ResU-Net model to automatically segment the liver and its tumors into pixels from the liver CT scan images. The proposed technique is one of the best techniques that can be used in the segmentation of the liver and its tumors. It can also be used even though this technique can enhance the result for other research work related to tumors like lung and brain tumors, etc. Researchers are working on a performance-based study of various networks specifically employed for liver and tumours. A wide range of data sets can be counted and used extensively by testing and implementing this approach and enhancing the result time by time. The proposed ResU-Net network in this study outperforms state-of-the-art techniques in the liver and its tumor segmentation. The deep learning-based techniques can improve performance when using large numbers of liver datasets. Additionally, data preparation techniques such as the generative adversarial network (GAN) can be utilised to increase the size of liver images. Although the ResU-Net demonstrated promising results, the authors should try alternative deep learning-based networks in the future to see if they can increase performance further.

KEYWORDS: liver segmentation; ResU-Net; deep learning; medical imaging; tumor detection.

I. INTRODUCTION

Smart healthcare systems, in particular those that make use of IoMT technology, have benefited from recent expansions in machine learning and computer communication [1,2]. A multimedia-based medical diagnostic system is one of the major demands in the medical healthcare business. Radiologists and doctors can benefit even more from the solutions provided by these intelligently built diagnostic systems [3]. Liver cancer ranks as the sixth most common form of cancer worldwide. The liver is a massive granular organ situated inside in humans. Cirrhosis, acute and chronic liver are on the rise as a direct result of changing lifestyles. As a direct result of these underlying conditions, liver cancer has become the most prevalent form of the disease in many regions [4]. There are more therapy choices available when the cancer is detected early. Liver cancer can only be diagnosed through imaging or radiology testing, as a physical examination is not possible. Imagination tests aid to screen cancer at initial phase and assistance to assess the healthiness of post-treatments [5].

CT scan is an imaging method that is used for both visualizing liver structure and diagnosing/treating liver cancer. Clinicians can use it to assess the liver's useful volume, tumour size, shape, and location to better tailor a treatment plan. The radiologist needs precise separation of liver tumours to perform these calculations [6]. Usually, the segmentation is performed by evaluating each slice of the CT scan. This process is tedious, laborious and fraught with opportunities for error, which can be categorized into three areas. First and foremost, errors can result from the variation in the appearance, size, and location of tumours from one patient to the next. Second, the line dividing tumour tissue from healthy tissue is not sharply delineated. Third, cancerous tissues can be found in close proximity to other organs. Furthermore, due to the wide range in tumour appearances and densities, liver tumour segmentation is a difficult task [7]. Thus, there is an immediate need for investigate into hepatic tumour segmentation, which improves treatment planning, lessens manual labour, and boosts the success rate of liver cancer procedures by advising oncologists pre- and post-operation.

Over the past few decades, scientists have created numerous interactive and autonomous methods for segmenting liver tumours. The radiologists' productivity is increased thanks to the development and training of semiautomatic methods made possible by computer-aided designs (CAD). Automatic segmentation of liver tumours is challenging due to several obstacles, such as variations in tumour size, shape, and proximity to adjacent organs [8,9,10]. Incomplete volume effects and increased noise due to CT enhancement are also among the challenges encountered. The automation of liverwort liver tumour division is a challenging study topic with opportunity for development.

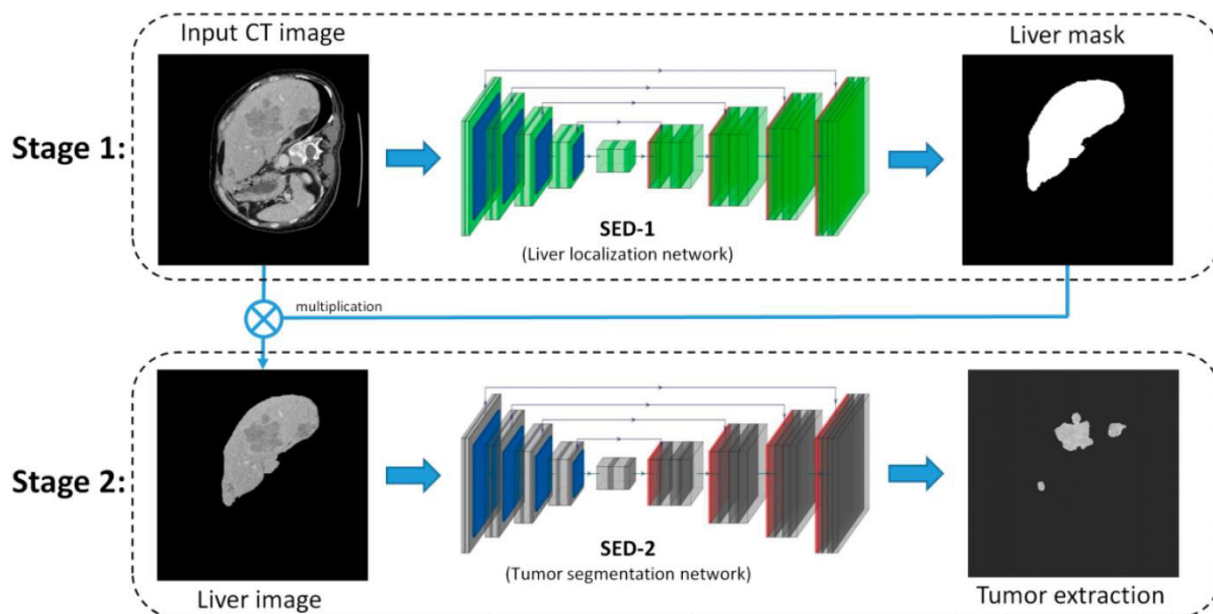


Fig 1: Liver cancer ranks analysis

In addition, differing encoding procedures have a significant effect on the interactive segmentation performance, making it a practical challenge for CNN-based algorithms to properly encode user interactions. The majority of the literature encodes user relations by translating them, the Gaussian heatmap, or the iso-contours obtained from the user's clicks [11,12,13]. However, the context of the image is ignored by these encoding techniques. The geodesic distance transform, on the other hand, is sensitive to spatial contrast and spatial smoothness, allowing it to encode user interactions. To handle user-provided interactions, DeepIGeoS employs a transform with a custom-tailored verge. To truncate the resulting geodesic distance map at a suitable threshold value, however, might be a time-consuming process when dealing with objects of varying shapes and sizes [14,15]. In order to enhance the precision and scalability of the segmentation, we hypothesise encoding approach is useful.

We present a new medical picture to address the aforementioned problems, with the ultimate goal of not only achieving high presentation and competence for segmentation of liver tumour. The usage of CNNs is central to our strategy, and the user interface is minimal. For better segmentation from the CNN, we provide a new method based on the Exponential zed Geodesic Distance (EGD) transform for encoding user interactions, which is both context-aware and parameter-free. In addition, we offer an information fusion technique that can fuse new intensity levels with the original segmentation in an effective way. The results demonstrated that our method is significantly better than other interactive segmentation procedures.

II. RELATED WORK

Over the past decade, researchers have used different machine learning strategies to separate liver and tumors. proposed an autonomous 3D liver segmentation approach that uses a total variation with the L1 norm (TV-L1) to detect an initial liver border, followed by a level set method that uses both local and global energy functions. A texture analysis method based on the grey level co-occurrence matrix (GLCM) is used for refined segmentation. proposed a multi-atlas segmentation (MAS) based performance level estimation (SIMPLE) method for automatic segmentation of abdominal



organs, including the liver. developed an adaptive FMM-based fully automatic liver segmentation algorithm. Self-adaptive parameter adjustment is used in the proposed adaptive FMM. In FMM, the arrival time is adjusted based on the intensity statistics of the potential liver region, which can be used to estimate the size of the liver region on the corresponding computed tomography (CT) slices. developed a semi-automated method for fragmenting the hepatic low-intensity tumor using CT images that utilized abdominal arterial channels in the entrance stage. Peng et al. [9] proposed a finite difference energy technique that incorporates brightness, region attractiveness, or surface smoothing. Automatic and robust liver segmentation from CT volumes is challenging due to the low-intensity contrast between the liver and neighbouring organs. Deep neural networks are used extensively in present healthcare image segmentation frameworks. introduced quality-aware memory network for interactive segmentation of 3D medical images. The memory-augmented network can quickly encode and retrieve segments from the past for segmentation of new slices. Elshaer et al. [13] used two trained deep CNN models to reduce the computational time of a large number of slices. After obtaining the liver segmentation with the first model, the second model was used to avoid the impact of image resampling by removing small missing lesions.

Employed a convolutional neural network (CNN) that used image patches. Each pixel is considered as a patch of the image, with the pixel of interest at its center. It divides the patches into normal or tumor liver tissues. The patch is considered positive if it contains at least 50 percent or more tumor tissue. Merged a 2D DenseNet network that combined the extracted intra-slice features and the 3D counterpart for hierarchically aggregating volumetric contexts for liver and lesion segmentation. The liver tumour was segmented by using a cascading architecture in which soft and harsh focus techniques and long or short skip linkages were integrated. False positives were reduced by using a joint dice loss function. Jiang et al. developed an edge system by incorporating spatial stream convolution into the U-Net network's modules. Furthermore, current liver segment techniques are designed for segmenting diagnostic CT pictures and may not even be suitable for segmenting interventional CT images. In addition, CT scans frequently show low gentle brightness, roughness, and other abnormalities. Current tumor segmentation approaches have had mixed results in resolving these challenging problems. As a result, U-Net was used in conjunction with a recurrent neural block [19] to resolve the limitation of the state-of-the-art models and schemes. The U-Net will use the recurrent neural network to gain relevant data about the hepatic area, aiding in improved liver and hepatic segmentation methods.

III. METHODS

The proposed DNN method has the input of $1 \times N \times N$ 2D patch of CT scan images. The most important and necessary layer for building the CNN model is a convolutional layer. Numerous convolutional layers are placed on top of one another to create a feature hierarchy. Each layer receives its input from the layer that was previously connected. The convolutional layer executes the stack of input CT image patches and outputs the number of feature maps. Each region of interest corresponds to a topological arrangement inside the responsive map of a specific nonlinear spatial feature abstraction. These learning parameters could very certainly be applied to any spatial neighborhood layout using the sliding window architecture. The convolutional layer activation process is dependent on the single plan of an input CT image. The feature map from previous layers is often included in the information plan for subsequent layers. In the proposed model, we are using three convolutional and two fully connected layers.

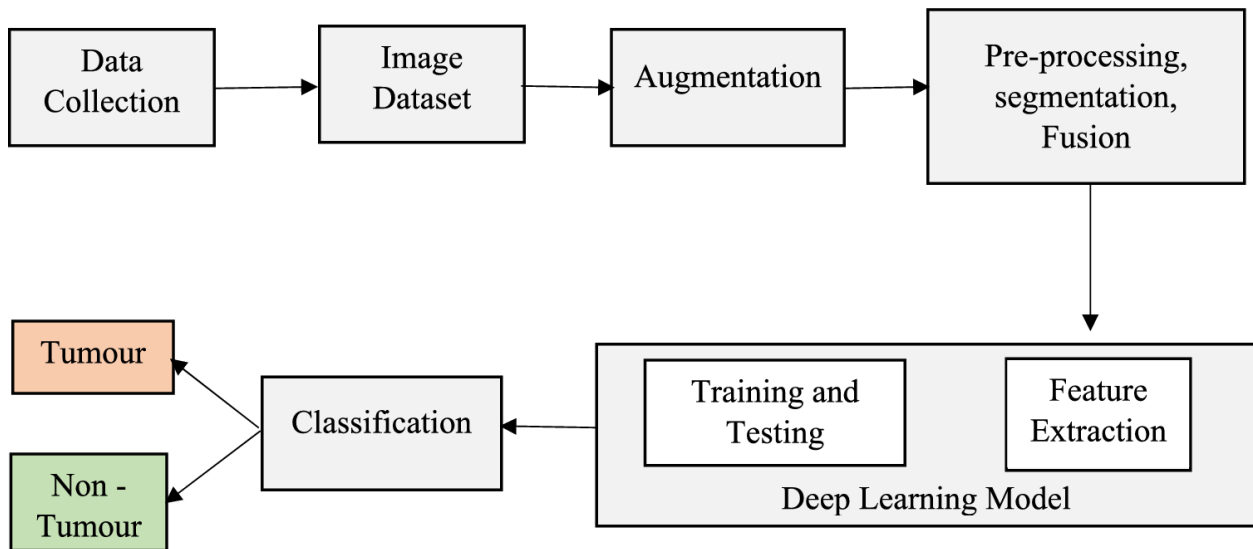


Fig 2: Work Flow

We used the same LRN hyperparameters as in [51]. The convolutional layer produces the output of the feature mapping procedure as an input from the preceding convolutional layer. From the perspective of the neural network, feature maps are associated with the hidden layers of neurons. Each coordinate subset of features is associated with a single neuron, and the size of the receptive field is proportional to the kernel size. Finally, at the network’s end, two fully connected layers are added. The fully connected layer executes the scalar product, where the input is a vector and it returns a scalar. The first fully connected layer with a neuron size of 4096 and the dropout factor of 0.3 is used. Dropout is employed during the training phase to keep the network from overfitting. The second fully connected layer which is final layer of our system, and then softmax classifier is used to perform classification for our model (Background and Liver). We reconstructed the image on the bases of classification results to perform a segmentation. Meanwhile, after segmenting each 2D liver image, we used a 5×5 median filter to smother the resultant liver.

IV. RESULT ANALYSIS

After the training, the trained CNN algorithm is learned iteratively from the initial liver probability map. One of the test volumes in Figure 6 shows the iterative results of the liver probability map. In the 8th iteration, the liver and spleen had the same intensity and texture level but in the 15th iteration, the liver becomes brighter which means liver pixels are stronger and easily differentiable. In a 25th iteration, the spleen becomes smaller as in previous iterations. In the 35th iteration, the spleen disappeared and the liver becomes brighter. In the 60th to 70th iterations, the validation results converge and the shape of the liver becomes accurate.

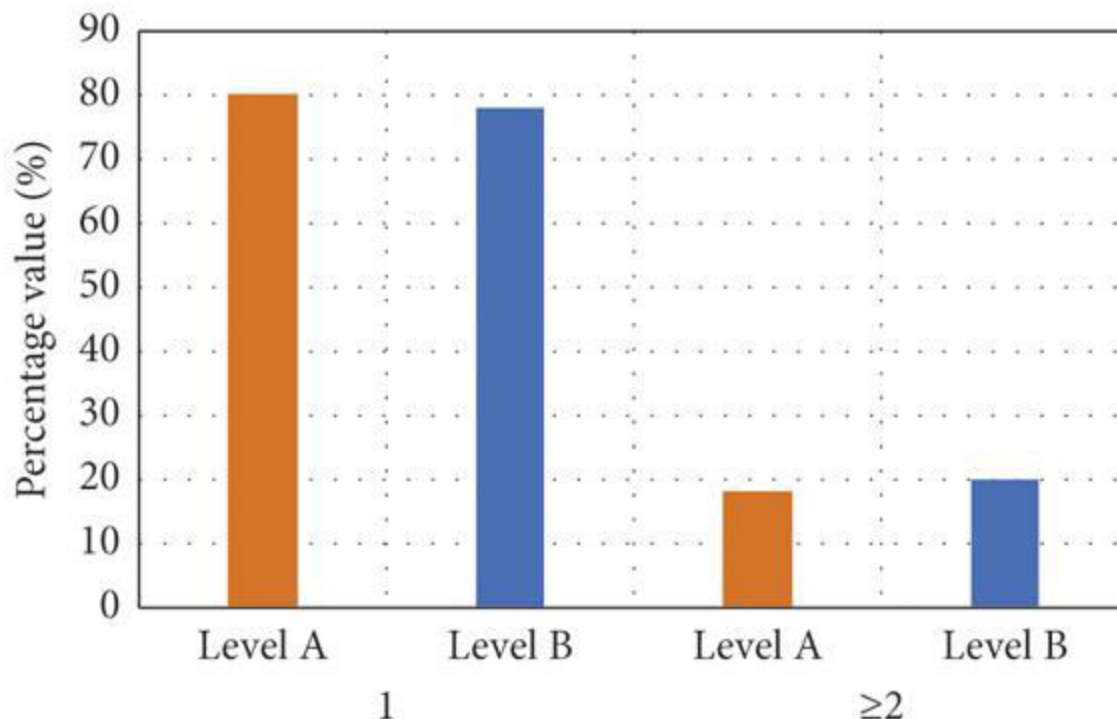


Fig 3: Result analysis

All the three benchmark datasets (having normal and abnormal CT scan images) are evaluated on eight performance metrics such as SE, SP, ACC, Precision, FPR, FNR, JSI, and DSC. In equations 4 to 11, true positive (TP) denotes all the pixels related to the liver, true negative (TN) shows all the pixels related to the background. False negative (FN) denotes the liver pixels that do not classify accurately, and false positive (FP) denotes the pixels which belong to the background but are not identified as a background. The dice similarity coefficient (DSC) is being used for the calculation of automatic and manual segmentation, and JSI is used to measure the similarity between the two images.

We presented the results of 10 CT images that were randomly selected out of 20 CT images for testing purpose in SLiver'07 dataset. The overall DSC of 95.0%, Jaccard similarity index of 90.47%, the accuracy of the proposed model of 95.1%, precision of 97.2%, sensitivity of 95%, specificity of 95.2%, FNR of 0.048, and FPR of 0.05 are noted on the SLiver'07 dataset. We observed from the above results that our method performed well in classification as well as in segmentation. Figure 7 depicts the segmentation results on 2D axial slices of the SLiver'07 dataset on the proposed model. The axial slices are randomly chosen from different CT images of the SLiver'07 dataset. Segmentation results show that the proposed model efficiently recognized the boundaries of the liver, where (a) is the original CT image, (b) is the original label, (c) is the segmentation results of Ga-CNN model, and (d) is the overlapping results of the original label (green) and segmented results of Ga-CNN (red).

V. CONCLUSIONS

We present a deep learning-based communicating system with high accuracy for segmenting tumours from liver pictures. To encode user communications to direct CNN for a decent initial subdivision, a new context-aware approach was presented. In addition to the encoding technique, we also suggested a powerful refining strategy to boost the precision of the segmentation outcomes. Segmentation is an important goal for models built using deep learning, and this framework is intended to help achieve that goal. The results of our experiments on a broad variety of input photos demonstrate that (1) our inner margin points and EGD architecture provides superior accuracy and efficiency learning-based interactive segmentation tools. In addition, the suggested framework is very generalizable with regards to liver tumour identification. As an annotation tool, it might be used to produce segmentation masks quickly and precisely for

various objects. As a future work, the classification accuracy could be improved by introducing the deep learning model in the research work for classification instead of a machine learning model.

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