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Automated and Large-Scale Liver Segmentation Using Deep Learning: a Promising Approach for Accurate Diagnosis

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Automated and Large-Scale Liver Segmentation using Deep Learning: A Promising Approach for Accurate Diagnosis

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Abstract: In this paper proposes an automated and large-scale segmentation of liver based on deep learning. Segmentation of the liver and liver lesions is very important in the initial diagnosis of the doctor. In the past, manual segmentation was usually used, but it took too long and there was human error. The automatically liver and lesions segmentation on a large scale can greatly reduce the diagnosis time. First of all, we will do a variety of pre-processing of the slice map, including preliminary organ differences and histogram equalization. Furthermore, due to the lack of pre-processing training data, we use data augmentation methods to increase our training data. We divide the model into two parts. The first part focuses on the prediction of the liver and the second part focuses on the segmentation of the liver. We trained more than 30,000 liver slice maps. Experiments show that our DICE Score can exceed 89% in the liver segmentation, and the lesion prediction is 65%.

Keywords: CNN, Deep learning, LITS dataset, Automatic segmentation, Liver tumors.

1 Introduction

The motivation of machine learning is solving the problems of computer vision that related with simulating the human visual. Humans was born without the ability of seen but using supervised learning for perception the different between colors and then the ability of object detection[1]. It is known as a challenging task for two reasons. First, the number of training data is small. Second, the data is collected from different clinical sites with different scanners and protocols, causing large variations of the data quality, appearance and spacing [2][3]. The lack of data is a common challenge during the process of training that depends on basic Convolutional Neural Networks (CNNs) architectures [4]. The problem becomes more complex when it uses 3D data. The human brain has a great an ability of understanding millions per second of information that takes over our eyes for learning models that around us. Contract Tomography (CT) images are an important tool in medical imaging to diagnose several diseases where doctors rely on manual or semi-automatic techniques to

study anomalies in the shape and texture of organs of CT scans[6]. We will focus on liver and its lesions segmentation tasks for afterwards segmenting several organs and other anatomical structures [7][8]. Low contrast between lesion, liver and other organs Lesions are variable in terms of shape, size and texture. Noise in CT scans Typically statistical shape and intensity distribution models Medical imaging processing have many challenges where liver cancer is the sixth most common cause of cancer-related deaths, and liver cancer is the third most common cause. Primary tumors such as breast cancer, colon cancer, and Pancreatic cancer often migrate to the liver part, so analyzing the liver and its lesions is its most important task. CT of liver segments and liver lesions both are an important basis for the diagnosis of primary and secondary liver tumors. In the past, in order to get the liver and its disease the variable segmentation graph is usually manual or semi-manual [5]. Recently, humans have special abilities to understand a huge different of objects in both low and high resolution images. 3D Shapes Analysis Algorithms Based on Artificial Intelligence Techniques simulates the idea of human brain that encoding for orientations of the object distinguishes many objects and also at propagating through viewpoints from CNNs. The aim behind improvement of deep learning algorithms illustration of neurons order in the brain and solving the problem of 3D object classification and segmentation. Our research objectives are to apply different 3D data algorithms and techniques to increase accuracy and decrease the error rate. We also intend to improve the computational efficiency and decrease the complexity of computations [9][25]. We explain many computer vision problems with deep learning and performance of these models compared with traditional approaches. We show how to improve performance of these models by geometric solutions [10]. The activity of 3D object recognition and segmentation is growing in last researchers propose algorithms and approaches and implementing them. The applications for which 3D object recognition technology is used in many fields where 3D object recognition technology can make tasks like maintenance more active in machinery Industries and video surveillance, the purpose of 3D technology includes segmenting moving crowds into individuals, face analysis. In health care, deep learning is used in computer aided diagnosis systems [5][8]. Various applications include analysis of 3D images, in autonomous driving for recognition and prediction of the motion of other cars, pedestrians, bikes etc[2].

2 Related Works

Recently, latest related models have been proposed for liver segmentation. These models can be categorized as semi-automatic, automatic and interactive approaches. Automatic approaches are more desirable as they require no user-interaction but semi-automatic and interactive approaches remain significant due to the ambiguity of liver segmentation. This section discusses the method used to conduct the literature review and the related works done in liver region of interest detection and liver segmentation [11]. Sihong Chen et al. in [12] proposed the deep learning model for training data volume such as The ImageNet model, the large dataset enhances the accuracy and accelerates the convergence speed. And also in the 3D medical images, the models which rely on huge datasets improve the development of the deep learning. However, it is a big challenge to construct a huge dataset because it is hard to combine and explain data in 3D medical imaging [13][14][15]. The dataset is collected from many medical challenges with several patterns, aimed organs, and pathologies to construct 3DSeg-8 dataset. A heterogeneous 3D network called Med3D is designed to abstract the features of the 3D medical dataset to train multi-scope 3DSeg-8 to provide a chain of pre-trained models. These pre-trained models will then transfer to LIDC dataset, pulmonary nodule classification in LIDC dataset and liver segmentation on LiTS challenge [16][17][18]. The experimental results prove that the Med3D can speed up the training convergence 2 times comparing to the Kinetics dataset, and 10 times comparing to the training from scratch. The Med3D also enhances the accuracy from 3% to 20%. The Med3D model achieved 94.6% Dice coefficient which is near to the result of the perfectible algorithms on the LiTS challenge. Xiaomeng et al. in [13] proposed a DenseUNet for liver and tumor segmentation, where the densely connected path and UNet connections are integrated depends on pre-defined design models for improving the liver tumor segmentation performance. They proposed a H-DenseUNet for exploring hybrid features for liver and tumor segmentation. The hybrid feature learning well avoid the problems that 2D networks ignore the volumetric contexts and 3D networks and can be produce as a new model for effectively employing 3D shapes by using LiTS dataset[29]. Raunak Dey et al. in [14] proposed a model for solving an automatic liver lesion segmentation task and helping to assist medical in the proposal of efficient curing. Dey designed a cascaded model that combines both 2D and 3D CNNs to effectively segment. 2D network work on a slice by slice for segment the liver and huge tumors. 3D network for detect small lesions that are often missed in a 2D segmentation. The algorithm implemented on the LiTS dataset by a Dice score of 68.1% per case [19][20]. The authors proceed two-fold cross-validation for reveal the under and over segmentation problems in the LiTS challenge.

3 Proposed works

Deep Learning achieved unique success in computer vision challenges such as image classification and segmentation. This paper modified the U-net architecture to make it suitable for liver segmentation and its prediction of lesions[15]. We depends on the 3D CT scans images for training dataset[16]. The ultimate goal is to obtain a segmentation map of the lesions on the liver, so segment of liver is implemented in two parts. The first part focuses only on the segmentation of the liver, not the whole the image is trained because there are too many irrelevant organs in the scan[15][16]. The second part is the liver map is used to make predictions on the lesions[17]. Our pre-processing is useful for preliminary removal and screening of irrelevant voxels, training set, data augmentation, etc., and finally uses cross-validation to test our final results. The proposed model consists of three main steps as shown in figure() which are:

(i) Raw 3D CT train volume (ii) Data preprocessing (iii) Histogram Equalization (iv) Data enhancement (v) Mixed UNet for liver segmentation (vi) Mixed Unet for lesion segmentation (vii)3D conditional Random field(prediction)

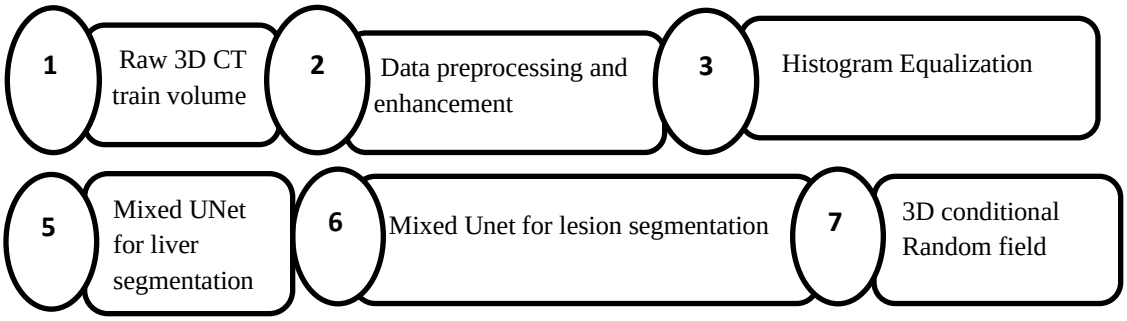

Figure (): The main steps for liver segmentation and predictions on the lesions.

3.1 Raw 3D CT train volume

The LiTS dataset consists of 3D scan images from codalab site [29] as shown in Figure() for hepatic tumor segmentation challenge of patient liver. LiTS challenge is organized by universities, research institutes. It is dedicated to solving the automatic segmentation of 3D CT images of liver tumor lesions with innovative algorithms to diagnose diseases and guide the image and the visualization of medical data. It provides a reliable basis for clinical diagnosis and pathology research. The dataset contains unlabeled data for patients, which we divide into training 90%, and test 10%.

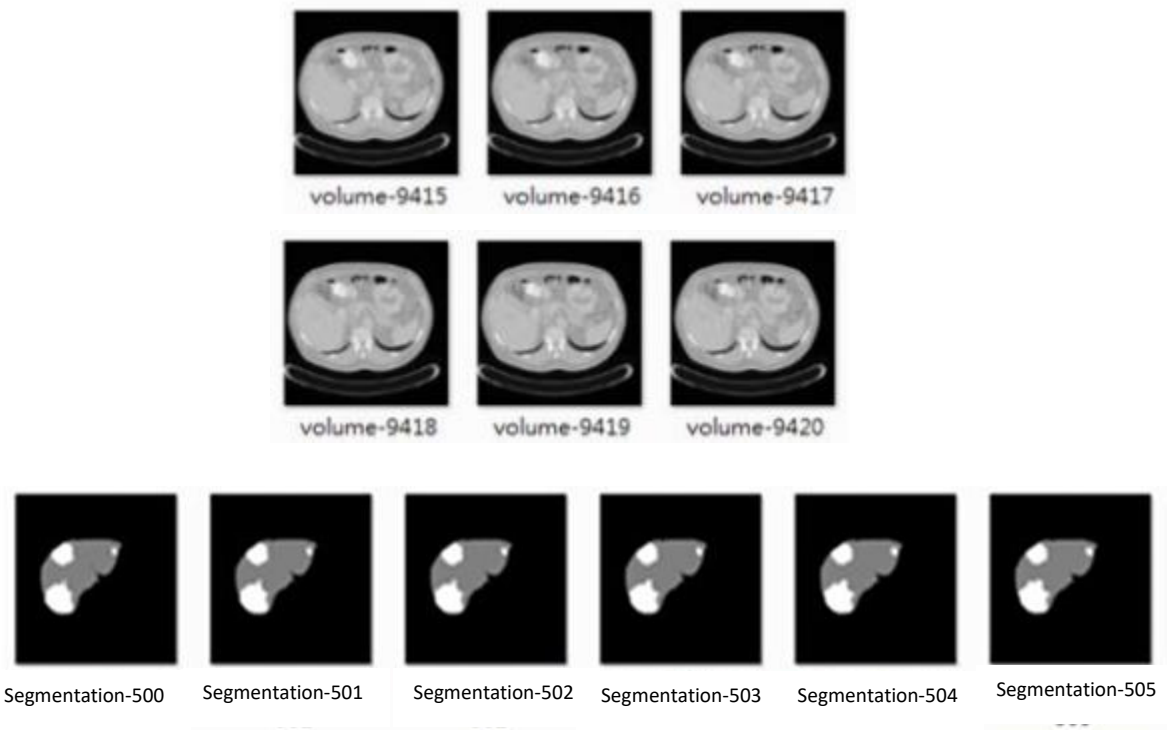

Figure (1): Samples from LiTS dataset for CT scan images and liver lesion part.

3.2 Data preprocessing and enhancement

The training images used LITS dataset [29] consists of 130 3D CT scans images **with** (nii) format that is divided into number of segmentation images slides. Using data preprocessing methods improve the accuracy and solving the over fitting problem as shown in Figure() the effect the preprocessing step on the dataset[18] . The liver segmentation maps at different angles have a large Different, and the shape of the lesion is not fixed, so that we need a lot of features for training during training data. It has been observed the voxel value of the liver and its lesions is in the [-100 , 300] interval. The training data size is reduced into 96X96 instead of 512X512 slice map. Deep learning requires a large amount of training data to train the model, if only a small amount of training is used data will cause serious overfitting or low accuracy. The medical images are not as good as ordinary pictures, so data augmentation is quite useful for deep learning in medical imaging. The data augmentation steps for determination and increasing dataset[19] . The training data of the liver model are randomly rotate the image by a certain angle, Transform in such a way that the center vertical axis of the image does not change, reduce the image according to the specified scale factor and horizontal and vertical movement. For increasing brightness and better distribution on the histogram of the images; using the histogram equalization can achieve good results for images where

converting into a uniform distribution in the entire gray range[20]. It enhances the data of the segmentation map, because the pre-processing deletes many irrelevant to the liver and lesions. The segmentation map results in insufficient training data for subsequent training, which is more obvious in predicting lesion models. Figure() show the evaluation of liver and lesions without data enhancement.

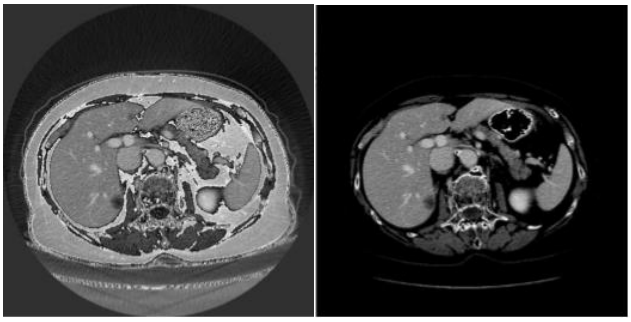

Figure (2): The effect of the preprocessing step on the CT scan image.

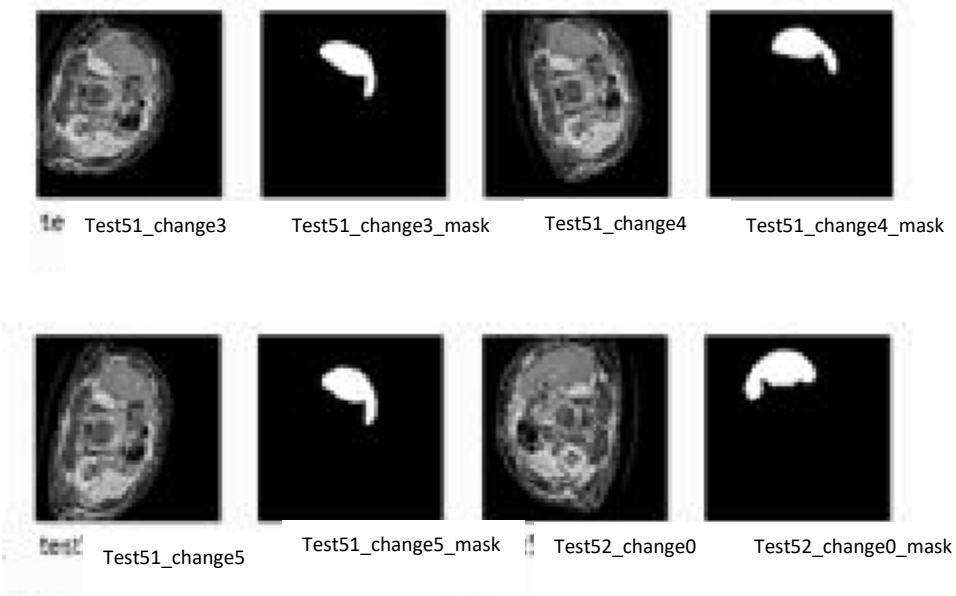

Figure (3): The effect of data augmentation on random CT images.

3.3Histogram Equalization

Histogram equalization is used for increasing the global contrast of the image by increasing brightness of it. Histogram equalization can enhance the local contrast without affecting the

overall contrast and achieving good results for images with close contrast. We use histogram equalization to increase the liver and other organs. The histogram equalization formula (3.3) is as follows:

$$h(x) = round(\frac{cdf(x) - cdf_{min}}{(LW) - cdf_{min}})(S-1)$$

where LW represent the number of pixel values of the image, S represents the gray level, and $cdf(x)$ represents the cumulative distribution

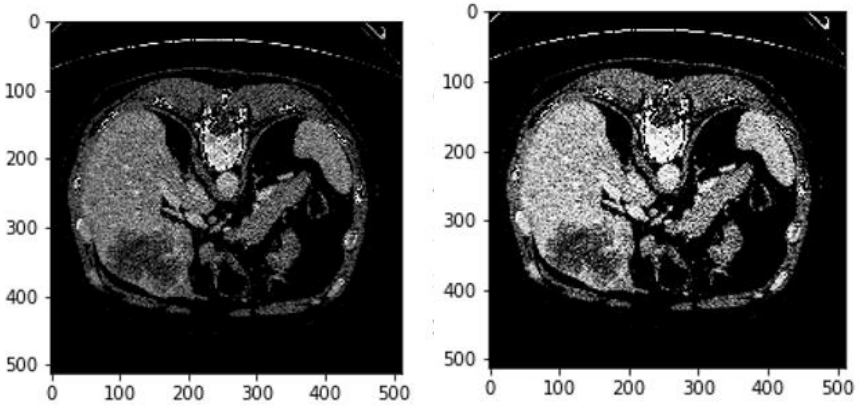

Figure (4): The right image after implement the histogram equalization of the left image.

3.4 Data training

The model architecture used in this paper is modified U-net architecture[20] that is called Mixed Unet architecture as shown in Figure() for using in liver segmentation and focuse on predicting lesions in the liver. The Mixed U-net architecture , is based on FCN That divided into two sides, and the first four layers on the left are included two identical convolution layers using 3X3 convolution kernels, each using Rectified Linear Unit (Relu) [], and each layer uses a mixed pooling layer to reduce parameters instead of max pooling. The pooling layer is used for transforming the joint feature representation into helpful one and preserve important information with discarding irrelevant details. The pooling layer summarizes the outputs of neighboring groups of neurons in the same kernel map [22][23][24]. In the pooling layer, the resolution of the feature maps is reduced by pooling over local neighborhood on the feature maps of the previous layer, thereby enhancing the invariance to distortions on the inputs[21]. In CNNs, there are two conventional pooling methods, including max pooling and average pooling[19][20]. The max pooling method selects the largest

element in each pooling region. On the other hand, both the max pooling and average pooling operators have their own drawbacks[25][26][27].

About max pooling, it only considers the maximum element and ignores the others in the pooling region. Sometimes, this will lead to an unacceptable result. For example, if most of the elements in the pooling region are of high magnitudes, the distinguishing feature vanishes after max pooling as shown in Fig. 2(a). Regarding average pooling, it calculates the mean of all the elements within the pooling region. This operator will take all the low magnitudes into consideration and the contrast of the new feature map after pooling will be reduced. Even worse, if there are many zero elements, the characteristic of the feature map will be reduced largely, as illustrated in Fig. 2(b). It is well known that images in the nature world are ever-changing, and it is of high possibility that the defective aspects of max pooling and average pooling as shown in Fig. 2 will have negative effects in applying pooling layers to CNNs[28][29][30]. Therefore, as a solution, we consider replacing the deterministic pooling operation with a stochastic procedure, which randomly employs the local max pooling and average pooling methods when training CNNs. This is the proposed mixed pooling method to be introduced next. The last 4 layers on the right, from the 6th layer to the 9th layer Use upsampling [21] the number of feature maps, followed by two layers and the previous mentioned The same layer, the last 4 layers also use the convolution layer of layer 3X3 and use Relu's excitation function. Last layer use 1X1 convolution and use the sigmoid excitation function to ensure that the pixel values of the output map are in the interval [0,1], which The final output is a 96X96 output image[22]. The first few layers are used to solve the pixel positioning problem, and the last few layers are used to solve the problem[23]. Determine the problem of pixel classification. Loss function For any pixel in the input image xij, the corresponding FCN output p(w|xij) represents an estimated posterior probability for all pixels. Since FCN essentially performs a pixel-wise segmentation , cross entropy is usually used as the loss function [24]:

$$p_k(x) = \exp\big(a_k(x)\big) / \sum_{k'=1}^{k} \exp\big(a_{k'}(x)\big)$$

Where k Feature channels, $a_k(x)$ - The activation in feature channel k at pixel position x

3.5 Optimization

Adam Optimizer [] uses first-order moment estimation and second-order moment estimation of gradients to dynamically adjust each parameter Learning rate, Adam combines the advantages of Adagrad [22] that is good at handling sparse gradients [23] is good at handling the advantages of unstable targets, and it requires relatively little memory and can be Different parameters calculate

different adaptive learning rates, which can also be used for large data sets and high-dimensional spaces. Adam After offset correction; the learning rate for each iteration has a certain range, making the parameters more stable. Its formula () []:

$$m_j = \mu\, x m_{j-1} + (1 - \mu)\mathrm{g_j}$$

$$n_j = v\, x n_{j-1} + (1 - \mathrm{v})\mathrm{g^2_j}$$

Where $\mathrm{g_j}$ is the batch gradient, μ and v are momentum factors, and m_j and n_j are the first-order moment estimates of the gradient, respectively. And the second-order moment estimation can be regarded as the estimation of the expected E | $\mathrm{g_j}$ |, E | $\mathrm{g^2_j}$|.

$$\widehat{m_j} = \frac{m_j}{1 - \mu^j}$$

$$\widehat{n_j} = \frac{n_j}{1 - v^j}$$

$\widehat{\mathrm{m_j}}$, $\widehat{\mathrm{n_j}}$ is a correction of m_j, n_j, which can be approximated as an unbiased estimate of expectations. Moment estimates of such gradients do not

But it can be dynamically adjusted according to the gradient, and there is no additional burden on memory.

$$\Delta\theta_{\mathrm{j}} = \frac{\widehat{\mathrm{m_j}}}{\sqrt{\widehat{\mathrm{n_j}} + \varepsilon}} \times \eta$$

$\frac{\widehat{\mathrm{m_j}}}{\sqrt{\widehat{\mathrm{n_j}}+\varepsilon}}$ form a dynamic constraint on the learning rate and have a clear range

3.6 Cross validation

This paper uses 10-fold cross-validation to verify our data. The original sample is divided into 10 equal parts. One of the subsamples is retained as data for the validation model, and the other 9 samples are used for training. Cross-validation Repeat 10 times, verifies each subsample once, average the results 10 times, and get the final estimate. We divided our 130 scans into a 9 to 1 ratio, and used 117 scans as a training set. The remaining 13 are test sets. Then add 13 test sets to the

training set and use another 13 scans as a test set, this process is done 10 times, and the final results are averaged to our final results.

4 Experimental Results

In this section, we introduce our system architecture and our implementation in sections 5.1. In sections 5.2 and 5.3, we will show the prediction of liver and its lesions after the model. The final section 5.4 evaluates our experimental results.

4.1 System Architecture

Table 1 show the requirement of training model and testing from hard and software.

CPU	I7-6500U
VGA	NVIDIA GTX-960 4G
Operating system	Windows 7
Environment	Tensorflow-keras
Programming language	Python3.5
RAM	8GB
Training data	26.7GB
Test data	6.84GB

We divided 130 CT scan images into training and test sets with a ratio of 9 : 1 and performed cross-validation where 117 image is selected as the training set, and the rest as the test set. Our training phase is divided into two models, the first one is a predictive liver model, focusing only on cutting the liver and background, the other is to predict the lesion model.In our segmented liver model, the training dataset is augmented with 30,600 image in size 26.7 GB, and approximately 3,400 in the test data set with size 6.84GB. In addition to predicting the lesion model, the training data set is about 35550 liver points after data enhancement. Test data is 3950 with size 6.84GB. Finally we also prepare about 3,000 test data, and use DICE Score as our evaluation performance. Table 2 shows the parameters is used where the first 4 layers contain 2 convolutional layers and are connected one by one to mixed pooling layer.

Layer	Size
Number of layers	9 layers (each contains 2 convolutional layers and one

	Large pooling layer)
Mixed pooling layer	2X2
Convolution	3X3
Activation function	RELU
Optimizer	Adam
dropout	0.5
Learning rate	1e-5
Learning rate 1e-5	DICE Score
Batch size	32
Number of training iterations	20

4.2 Liver prediction

This section only focuses on the segmentation of the liver from the background for improving the accuracy, we use square map equalization method improves the contrast of the background and liver a result as shown in figure() . The contrast between the liver in the original image on the left and its lesion in the red circle and after histogram equalization on the right, The contrast of each organ and the most important liver and its lesions has increased significantly. Figure () shows our liver again. The predicted result, our liver prediction model can successfully segment the liver, and the DICE Score can reach 90% Above, only the edge will have redundant predictions, but it will not affect our lesion prediction[23][24].

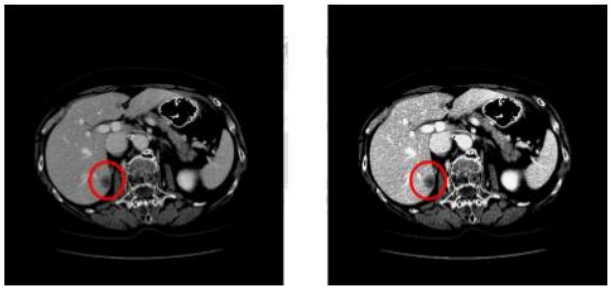

Figure (5): Histogram equalization result.

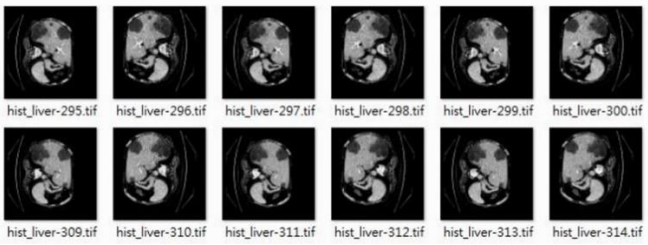

Figure (6) is a schematic model of the training data input.

4.3 Lesion prediction

This section shows the liver segmentation map containing lesions segmented from CT scans as training data. In this model, we still have the same preprocessing on the training data as the liver prediction stage, including data enhancement histogram equalization and then enter the model for training our lesions and a map of the lesion mask to be learned as shown in figure () shows the pathological changes a final lesion segmentation map after measuring the model. The first and third lines are our predicted segmentation maps, and the second and fourth lines are true actual map shows from figure (same) that we can already grasp the correct position of the lesion, and most of it can be predicted correctly, but it is still impossible to predict the smaller lesions, and it is easy for two relatively similar lesions Points easily stick together. Our lesion DICE Score can reach about 65%, Finally, evaluate the results with the real picture.

Figure (): The left two images for the liver and lesions and the two right images for the predicted lesions only.

5.4 Evaluation results

Our training time is about 3 hours, and each prediction result produced takes about Between 30 and 100 seconds. We use DICE Score as our final evaluation result. Such as formula ()

$$\mathrm{DICE}(X, Y) = \frac{2|X \cap Y|}{|X| + |Y|}$$

The DICE Score is between 0 and 1, with the best performance being 1 and the worst being 0. Figure () is a comparison between our prediction map and the real map. The first line is our prediction map, and the second line is the real segmentation map. Real picture, the last line is the cross difference diagram of the two. As shown in Figure() and there will be a small error in the surrounding parts.

The first row is the correct location of the lesion in the liver. The second line is the real segmentation map, and the last line is our final lesion prediction map. In predicting disease, There is a high recognition rate for obvious lesions, but there is still enhancement for smaller lesions.

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