Liver Tumor Segmentation and Subsequent Risk Prediction Based on Deeplabv3+

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Abstract. As the largest glandular organ in the human body, liver has a large number of blood vessels and is connected with many important organs, such as spleen, pancreas and gallbladder, etc. The segmentation of liver and its lesions on medical images can help doctors accurately diagnose liver tumor and assess the probability of subsequent deterioration of the patient. Generally speaking, it is not only subjective but also wastes time if doctors rely on experience to manually analyze liver CT images. Therefore, it has been extensively studied in recent years. The segmentation of liver lesions is a kind of challenging task due to the low contrast ratio between the liver, lesions and nearby organs. To this end, we proposed to use the Deeplabv3+ semantic segmentation model based on the tensorflow architecture to segment the CT image of liver and locate the lesion positions. It combined deep convolutional neural networks (DCNNs) and probabilistic graphical model (DenseCRFs) and has been proven to have very good performance in a variety of computer vision tasks.

1. Introduction
The spatial pyramid module applies multi-sampling rate expansion convolution, multi-reception wild convolution or pooling on the input feature to explore multi-scale context information. The Encoder-Decoder structure captures the clear target boundary through gradually restoring spatial information.

DeepLabv3+ combined the advantages of both. Specifically, DeepLabv3+ is regarded as the encoder architecture and the simple but effective decoder module is added to refine the segmentation results based on this. The Xception model is used in the semantic segmentation task and the depthwise separable convolution is used in the ASPP and decoding modules to improve the running speed and robustness of the encoder-decoder network. It has verified the validity of the model on PASCAL VOC 2012 and reached 89% mIoU without adding any back-end processing, as shown in Figure 1.
2. Liver tumor CT image segmentation

2.1. Experimental part
The Cancer Imaging Archive (TCIA) is a large-scale public database of medical images for cancer research. TCIA contains medical images of common tumors (such as lung cancer and liver cancer, etc.) and the corresponding clinical information (such as treatment plan details, genes and pathology, etc.), the image modality of which includes MRI and CT, etc., and all of the image formats are DICOM. CH-001-LT is an enhanced CT data set collected by the affiliated hospital of Qingdao University.

We selected 6000 CT images in TCGA-LIHC data set of TCIA, of which 5,500 were training sets and 500 were test sets. At the same time, we selected 300 images in the CH-001-LT data set as the test set of the trained Deeplab V3+ segmentation model.

Through parsing the DICOM and other related files in the TCIA data set, we extracted the position coordinate information of the liver tumor region manually segmented by the doctor and marked it, as shown in Figure 2.

2.2. Verification and results
In order to evaluate the effect of Deeplab V3+ model in improving the accuracy of liver lesion segmentation, we propose the following five error measurement methods: Volumetric Overlap Error,
Relative Volume Difference, Average Symmetric Surface Distance, Root Mean Square Symmetric Surface Distance and Maximum Surface Distance.

We tested Deeplab V3+ model by using the public data set CH-001-LT in order to test the effect of Deeplab V3+ on liver lesion segmentation. The green outline represents our model segmentation, while the red outline represents the segmentation manually performed by experts. Partial segmentation results are shown in Figure 3, then we can see that the segmentation is very accurate.

![Segmented results](image)

Figure 3. Segmented results.

At the same time, in order to verify the specific performance of the algorithm, we compared the results of this experiment with the segmentation results of FCN model, GACD model and LLC model that used the same data set. The results are shown in Table 1.

| Model     | VOE (%) | RVD (%) | ASD (%) | RMSD (%) | MSD (%) |
|-----------|---------|---------|---------|----------|---------|
| FCN       | 13.2    | 5.6     | 2.0     | 2.9      | 7.6     |
| LLC       | 14      | 8.3     | 2.6     | 2.9      | 7.8     |
| GACD      | 40      | 13.2    | 10.7    | 11.6     | 14.5    |
| DeeplabV3+| 9       | 4.4     | 1.6     | 2.5      | 6.8     |

Table 1. Four model comparing.

Based on the above table, we can see that the comprehensive performance of Deeplab V3+ algorithm based on tensorflow is better than that of other three algorithms.
3. The subsequent risk prediction of liver tumor

Inputted the CT image into the Deeplab V3+ network segmentation model to determine whether the region was the lesion position according to the output value of the model and the visual image. If it was determined to be the lesion, the entire lesion area was carried out with image color processing to form a map of lesion area; Extracted one-dimensional numerical characteristics of them respectively, such as the proportion of lesion area, etc. After that, exported the characteristics and labels, and constructed a binary classification model to evaluate and feedback the effect of the model, so as to meet the prediction accuracy requirements of the follow-up risk of lung tumor.

3.1. Image pre-processing

1. Inputted the test image into the Deeplab V3+ network model and saved the lesion coordinate values of the predicted result as a file with txt text format.
2. Used the f.readline function in python to read the coordinate information in the txt file, and highlighted the lesion area in red based on the circle function in the opencv library.

3.2. Image segmentation and feature extraction based on k-means clustering algorithm

After completing the map of lesion area, it is necessary to perform dimension reduction process for the image in order to extract the deep information of the data. The most effective dimension reduction method is to extract the eigenvalues of each map of lesion area and transform the two-dimensional image feature into one-dimensional numerical feature, thereby reflecting the essential structure of the data and constructing the subspace of feature with higher recognition rate.

Because the morphological features of the lesion area map obtained are obvious, but considering that the prediction of a small number of features will lead to contingency and error, then multi-feature extraction based on morphology is adopted. Firstly, the K-means clustering method (K-MEANS) in the clustering algorithms was used to segment the image and extracted the part of lesion area that shall be predicted, so as to avoid the interference of other tissue areas and facilitate the subsequent feature extraction. Figure 4 is the effect picture of image segmentation in the predicted lesion area after magnifying 20 times.

3.3. Construct a data set

3.3.1. Introduction to data set. There are 400 test samples in this experimental data training set. The lesion area map of each sample was performed with image segmentation. Afterwards, the regionprops() function of the measure submodule in the skimage library was used to conduct the morphological feature extraction for each image, then 10 one-dimensional numerical eigenvalues were obtained.

3.3.2. Normalization processing. Normalization processing for the features is beneficial to improve the convergence speed when the gradient is degraded to find the optimal solution. Since the obtained
eigenvalues are more concentrated, linear normalization (also known as the min-max normalization) is adopted to process the features here.

After normalization processing, the data was labeled according to the labeling criteria. There are two categories in this experiment, namely, predicting the lesion area and predicting the non-lesion area. Therefore, all sample data diagnosed as liver tumor were marked as 1, and the remaining sample data not diagnosed as liver tumor were marked as 0. In consequence, among the data set of 400 cases, the number of samples labeled 1 and the samples labeled 0 was 151 and 239, respectively, then the proportion of positive and negative samples was relatively even, and all of them were saved as csv format files.

3.4. Establishment and training of liver tumor risk prediction model

3.4.1. Model building. Logistic Regression model actually belongs to a kind of disaggregated model, which converts the output value into 0 to 1 interval by using the sigmoid logarithmic probability function, as well as obtains the category to which each sample belongs by selecting the appropriate threshold.

In this experiment, the network structure includes vectors composed of 10 eigenvalues as the model input, followed by a summator and sigmoid logarithmic probability function, so as to output the probability value to achieve the final classification.

3.4.2. Model training. After the model is trained well, input the data into the model for training. The specific steps are as follows:

1) Import data
   Firstly, import the CSV file of the input data, and stipulate that the first 270 data are used for model training and the last 130 data are used for testing.

2) The corresponding parameter settings of algorithm
   In this experiment, the logistic algorithm is used to train the model. Here, select LogisticRegression in the machine learning library scikit-learn. The parameters are set as follows:
   Penalty: Regularization selection parameters. L2 regularization is selected to reduce the risk of overfitting due to the fewer features.
   Solver: Loss function optimization algorithm parameters. Since this experiment is a small data set, liblinear is selected to iteratively optimize the loss function.
   Class-weight: Various types of weight parameters in the disaggregated model. The application scenario of this experiment is the auxiliary medical diagnosis, so it is necessary to classify the persons with and without liver cancer. At this point, the cost of misclassification is relatively high, that is, the cost that the persons with liver cancer are diagnosed as the persons without liver cancer is high. However, if the persons without liver cancer are diagnosed as the persons with liver cancer by mistake, a professional doctor can perform artificial screening to avoid misdiagnosis later. Therefore, define the class weight= {0:0.6, 1:0.4}, that is, the weight of type 0 (with liver cancer) is 0.6, while that of type 1 is 0.4.
   The model is trained by calling the fit function and the threshold of classification is set to 0.5. The output value of the logistic regression model is between 0 and 1. It is stipulated that the predicted value is classified as 1 if it is more than the threshold of 0.5, while it is classified as 0 if it is less than the threshold of 0.5.

3.5. The results and performance evaluation of the model
   Input the test set into the trained model to obtain the predicted value of each test sample. The experimental results obtained by comparing with the actual label of the sample are shown in Table 2.
Table 2. The result of experiment.

|                | Positive prediction | Negative prediction |
|----------------|---------------------|---------------------|
| True positive  | 35                  | 14                  |
| True negative  | 16                  | 65                  |

The performance parameters are shown in Table 3.

Table 3. Performance of logistic model.

| Algorithm name | Accuracy rate | Specificity | Sensitivity | Accuracy rate of training set |
|----------------|---------------|-------------|-------------|-------------------------------|
| Logistic model | 0.7846        | 0.7407      | 0.8571      | 0.8561                        |

The logistic regression model has high sensitivity, indicating that the proportion that the patient samples with cancer can be recognized is high, while the proportion that the patient samples with liver cancer cannot be recognized is small, that is, the missed diagnosis rate of the diseased samples is low. In medical diagnostic scenarios, sensitivity is more important and urgent compared with specificity. Therefore, the model is required to show the potential cancer risk of each sample as much as possible, and then the professional physicians perform the disease risk diagnosis subsequently.

4. Conclusion

According to the above, in terms of the accuracy rate, specificity, sensitivity and performance of the training set, the logistic regression model can be used to better classify whether the person suffers from liver cancer or not. Ordinary physicians often have an accuracy rate of 70%~80%, so the accuracy rate of this model can meet the basic requirements of classification.

References

[1] Chen, Liang-Chieh, Papandreou, George, Kokkinos, Iasonas, et al. DeepLab: Semantic Image Segmentation with Deep Convolutional Nets, Atrous Convolution, and Fully Connected CRFs[J]., 2016.()

[2] Chen Ying, Wang Jing and Duan Xilong, Liver CT Image Segmentation Method Based on Improved Level Set [J]. Sensor and microsystem, 2018, 37(10): 44-46. DOI: 10.13873/J.1000-9787(2018)10-0044-03.

[3] Huang Yanqi, Ma Zelan and He lan, etc., Texture Analysis and Identification of Liver Focal Lesions Based on CT Images [J]. Chinese Journal of Medical Imaging, 2016, 24(4): 289-292, 297. DOI: 10.3969/j.issn.1005-5185.2016.04.013.

[4] Lee. J, Kim. K. W, and Kim. S. Y, et al, “Automatic detection method of hepatocellular carcinomas using the non-rigid registration method of multi-phase liver CT images,” Journal of X-Ray Science and Technology, vol.23, Issue.3, 2015, pp. 275-288.

[5] L. Cao, J. K. Udupa, and D. Odhnera, et al, “A General Approach to Liver Lesion Segmentation in CT Images,” Proceedings of SPIE, vol.9786, Issue.978623, 2016, pp.1-7.

[6] F. Lu, F. Wu, and P. Hu, et al, “Automatic 3D liver location and segmentation via convolutional neural networks and graph cut,” International Journal of Computer Assisted Radiology & Surgery, vol. 2016, 2016, pp. 275-288.

[7] W. Li, F. Jia, and Q. Hu, “Automatic Segmentation of Liver Tumor in CT Images with Deep Convolutional Neural Networks,” Journal of Computer & Communications, vol.03, Issue.11, 2015, pp. 146-151.

[8] Häme. Y, “Liver Tumor Segmentation Using Implicit Surface Evolution,” Proceedings of the MICCAI Workshop on 3D Segmentation in the Clinic: A Grand Challenge II 2008.

[9] Massoptier. L, and Casciaro. S, “A New Fully Automatic and Robust Algorithm for Fast Segmentation of Liver Tissue,’’ European Radiology, vol.18, Issue.8, 2008, pp.1658-1665