TẠP CHÍ KHOA HỌC
TRƯỜNG ĐẠI HỌC QUY NHƠN

Một kỹ thuật phát hiện u gan dựa trên mô hình chất liệu

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TÓM TẮT

Việc phát hiện bất thường trên ảnh y tế nói chung và ảnh chụp cắt lớp vùng gan nói riêng là một vấn đề quan trọng được quan tâm nghiên cứu nhiều trong những năm gần đây tại Việt Nam. Bài báo trình bày một kỹ thuật phát hiện u gan trên ảnh vùng gan dựa trên mô hình chất liệu vùng gan, kết hợp với phân tích dữ liệu trên ảnh chụp cắt lớp vùng gan. Kỹ thuật đã được cài đặt thử nghiệm với bộ dữ liệu mẫu 3D-IRCADb-01 và dữ liệu thu thập thực tế tại Bệnh viện Đa khoa Bình Định.

Từ khóa: *U gan, chất liệu, bất thường.*

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A technique to detect liver tumor based on texture model

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ABSTRACT

The detection of abnormalities in medical images in general and tomography of liver areas in particular is an important issue of great research interest in recent years in Vietnam. The paper presents a technique for detecting liver tumors in the image of the liver based on the texture model of the liver region, combined with data analysis on the CT scan. The technique has been experimentally installed with 3D-IRCADb-01 sample dataset and actual collected data at Binh Dinh General Hospital.

Keywords: *Liver tumor, texture, abnormal.*

1. INTRODUCTION

The socio-economic development leads to the increasing demand for health care. The research and application of high technologies and modern information technology in the field of health in order to improve the quality of human health care always attracts the attention of the community of professionals. In recent years, the development of image recognition technology and artificial intelligence based on deep learning, deep neural networks with large training datasets has led to a lot of research and development in the field of image processing. medical, especially in detecting abnormalities, liver tumors on the image of the liver areas. Research results in this direction open up the prospect, allowing for important advances in the diagnosis of liver diseases. According to statistics, about 750,000 people were diagnosed with liver cancer and nearly 696,000 people died from the disease[1] worldwide in 2008.

In diagnosing based on medical imaging, the study of processing, analyzing and identifying liver images is difficult because this is a complex object and it is difficult to observe details even with the human eye. CT images of the liver area have low contrast compared to the surrounding tissue. This contrast is altered by the influence of fat concentration in the liver. Another important point is that the shape of the liver has many variants. In addition, medical imaging data is private and is taken on specialized hospital equipment, so in fact, it is not simple to collect a large enough data to train deep learning model which meets diagnostic requirements.

To overcome the difficulties of liver image data, Lu et al[2] proposed an approach to segment the image of liver region through two steps: detecting and estimating the probability map for segmentation using 3D convolutional neural network; and next step is adjusting with graph cut. Authors built a completely automated

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process, without user control. The Hoogi et al[2] used the adaptive estimation method with active contour model in the liver segmentation and the test achieved good results on the dataset of 164 MRI images and 112 CT images of liver images with low contrast and noise.

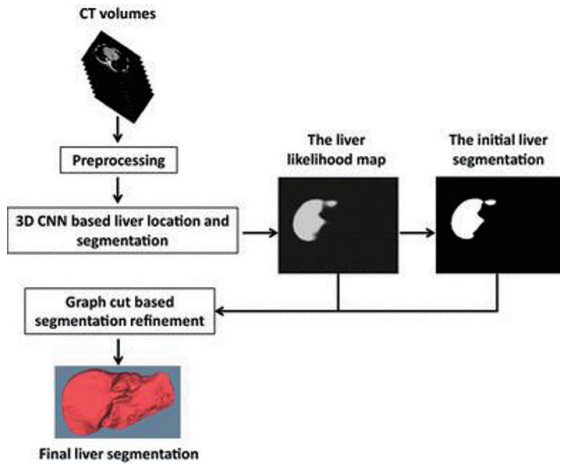

Figure 1. Processing steps of Lu et al[3]

The paper proposes a texture model approach in combination with data analysis on liver CT image. The texture model assumes the homogeneity in the image regions, meaning that all sub-regions within the liver image area will have the same liver texture. Thus, the idea is: randomly sample sub-regions of the liver image area and analyze them to find outlier, abnormal areas based on the assumption that in terms of image, abnormal areas, such as liver tumors appear in the liver image area, there will be certain differences in structure and contrast with the surrounding liver region. Part 2 of the paper will present technical details, including the following: limiting the area of the liver on the image, the sampling method and the classification. Part 3 will then describe the test results and evaluation comments.

2. ALGORITHM

2.1. Limit object area

Usually, in practical problems, the objects of interest do not always appear in a fixed position in the image. For example, when recognizing face in an image, the face image (the object of interest) can appear at any location in the image, with different sizes and rotation. However, CT images have a fixed pose, the organs are usually located in certain areas with relatively stable arrangements between body parts. This also means that for each slice position, visceral objects on CT images usually appear in relatively stable positions on the image. Therefore, in the position of a specific slice image when you want to identify an internal object, such as the liver, kidneys, etc., it is possible to locate the corresponding area of the image object of interest on the image. Limiting the area of interest allows a significant reduction in search space, identifying objects, increasing processing speed and eliminating false detection.

To identify the target area of liver tumors, techniques to limit the area of interest can be used as follows:

Limit coordinates: To limit the position of the liver tumor, we will use the interval corresponding to the minimum and maximum limits in the x and y dimensions. More specifically, when there are pixels (x, y) in the liver object area, that is (x, y) $\in$ *[Xmin, Xmax]* x [*Ymin, Ymax*]. In there, these ranges are estimated based on the statistics of locations of liver objects in the CT images. This technique is quite simple, allowing quick implementation. However, the boundary is still quite large.

Limit by mask image: This technique uses binary images, on which white areas are able to appear liver tumors, black areas are not. In other words, if the pixel (x, y) on the slice image is a liver tumor, then the (x, y) point on the mask image must be a white pixel. This technique is quite simple and fast, allowing the boundary to be narrower than technique using coordinate.

Limit by liver segmentation: After segmentation, we are able to determine the specific boundary and circumference of the liver region on the image. The accuracy as well as the speed of limiting the image area of interest

depend directly on the accuracy and speed of the segmentation technique. In general, this technique closer to reality than the above two, but takes more time.

2.2. Sampling method

After localizing the liver boundary, the next step is sampling liver image areas, in other hand, is determining the list of sub-image areas within the liver object area. According to the texture approach, if the region is normal, there are no abnormalities, then all sub-image areas in the liver image area will have the same output value when performing classification. In the case of an abnormal liver area, there are sub-regions in the liver image that give values unlike most of the remaining sub-regions.

Sampling is performed by following these steps: Select a square in the liver image area, rotate at any angle and conduct random image flip transform.

The sampling is described as follows:

Input : I, M

Output : S

Process:

1. S : = Ø

2. brect : = bounding_rectangle(M)

3. for each wsize ∈ [MIN_WND_SIZE, MAX_WND_SIZE]

4. for each x ∈ [brect.left, brect.right]

5. for each wsize ∈ [brect.top, brect.bottom]

6. R : = rectangle(x, y, wsize, wsize)

7. if (is_inside(R, M))

8. s : = calculate_sample(R, I)

9. S : = S ∪ {s}

In the description above, I is the slice image, M is the limited liver area. In programming, M is a binary image, with a white area corresponding to region may contain liver, the black area is not the liver area. The brect parameter is the limited area in the iteration step to select the sampling window, and [MIN_WND_SIZE, MAX_WND_SIZE] is a limited size of the sampling window. The sample received is the input of the machine learning process. Before classifying, the system needs to be trained, using a machine learning model on the set U of training data.

Each training data sample s in the U set must be specifically labeled: normal or abnormal. $U = \{< s, l > : s \in S, l \in \{0,1\}\}$, where l is the label of training data sample s, 1 corresponds to normal, 0 is abnormal. The training dataset is constructed by experienced experts on liver images. For each sub-image region marked in the liver region M, depending on whether expert's opinion is abnormal or normal, $< s, 0 >$ or $< s, 1 >$ will be added accordingly to U.

2.3. Process sample

Taking the output of the sampling process as an input, the classifier will give conclusion corresponding to the state of liver is tumor or not. This is a binary classifier with input is sample, the output is a corresponding state. The classifier is based on the Resnet network architecture.[4] In the application made here, use Resnet because this network architecture is resistant to gradient signal loss during back propagation. Therefore, application designers can build deep networks with thousands of layers. Continuing with the array of Residual Block, the network is designed to add an output of fully connected layer, and using sigmoid function to determine two status values. To reduce the rate of false positives, after being classified, samples will be aggregated into a result mask image and proceeded to remove too small areas. This processing allows the elimination of noise results. On a sequence of CT images, this will not affect you as much. Tumor regions in slices at the beginning or end of the tumor may be mistakenly removed because they are too small, but later slices at a deeper position into tumor will not be removed. Therefore, results throughout the image sequence are not affected. If the sequence of images is sparse, this should be corrected accordingly.

3. EXPERIMENT

The technique is implemented with the support of open source libraries such as OpenCV, VTK and Tensorflow. The dataset is selected for testing is 3D-IRCADb-01.[5] The dataset consists of several sets of anonymous medical imaging of patients, in which organs are manually marked by experts. The dataset includes CT scans of 10 women and 10 men, each patient's data was stored in one folder. The medical image data and the annotated data are stored in DICOM format.

In the experiment setting, data of 10 patients were selected as training data, data of 10 patients were selected as evaluation data. The information of the limited area was established based on annotated data of 10 cases. In particular, the coordinate boundary area is set to a rectangular area with {x: 36, y: 64, width: 447, height: 349}.

Figure 2. Image of limited region in case using coordinates and mask image

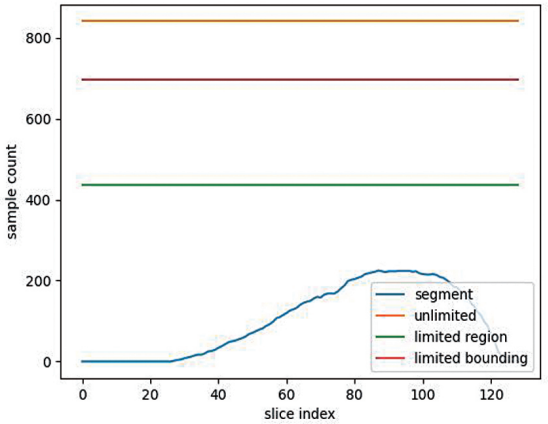

Figure 3. Diagram about sample amount in each slice of one patient: unlimited (Orange), limit coordinates (Red), Limit by mask image (Green), Limiting by liver segmentation (Blue)

It is easy to see that in the case of different limits, there will be different number of selected samples. This will affect the processing speed, because it is necessary to classify all input samples. From the results of assigning a status classification label to the samples, it is possible to evaluate whether the input image has liver tumor appearance. The testing of the input image will give conclusions, in one of 4 cases: True Positive, True Negative, False Positive, False Negative.

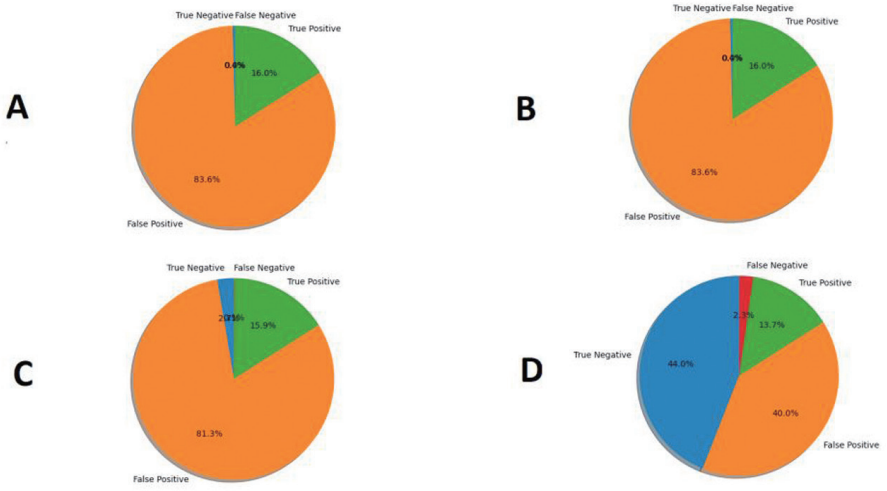

Figure 4. Conclusion rate in 4 limited cases: A. unlimited, B. limit coordinates, C. Limit by mask image, D. Limiting by liver segmentation

It is easy to see that, in the first case, the False Positive rate is quite high. This is quite understandable, since the classifier is trained on liver texture areas. When the limited region contains more area than the actual liver, the conclusions of the classifier in those outward areas are more likely to be wrong, thus increasing the rate of false positives. However, in practice the results for these areas are acceptable, considering the circumstances in which a doctor can easily assess that the results are not of concern.

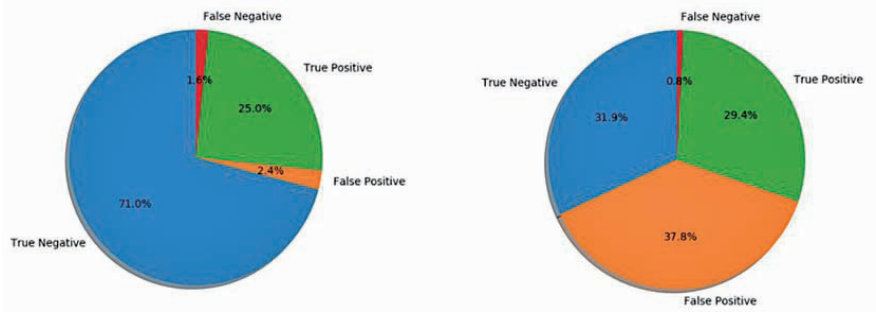

Figure 5. The rate of conclusions on data of two patients

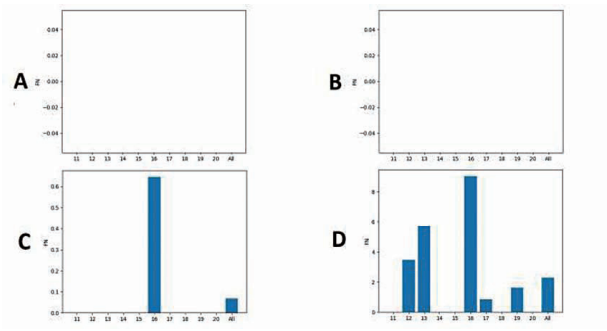

Figure 6. Statistics of False Negative per patient (%) A. unlimited, B. limit coordinates, C. Limit by mask image, D. Limiting by liver segmentation

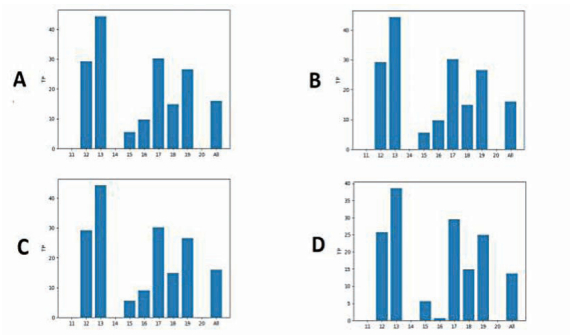

Figure 7. Statistics of True Positive per patient (%) A. unlimited, B. limit coordinates, C. Limit by mask image, D. Limiting by liver segmentation

When looking at the False Negative ratios in different cases, we find that the rates increase gradually on each case. The majority of the results were quite low and the highest case was in patient 16 data with about 9%. This result is partly due to post-processing of small sized areas. If we do not remove the small sized areas, the result is only 6.5%. Overall, however, this patient was not missed due to the positive True Positive ratio. The first two cases give false Negative ratios of zero. However, this does not reflect a good classification result, because it needs to be considered for many cases of non-liver data.

In the results of the True Positive ratio, we find that the data is relatively stable among the region restriction cases. This is quite understandable. The discrepancy between the cases is mainly also affected in the post-processing step for small size areas. Overall, no patients were missed.

The algorithm was also tested with actual data at Binh Dinh General Hospital. Test data are abdominal CT images provided by the Department of Internal Medicine. Program uses the function of reading data, conducting a value conversion based on Hounsfield indicators and conducting the detection of abnormal areas, liver tumors. In order to limit the processing area, the program also integrated one technique to locate

liver area.[6] The data is taken on the basis of linking with data of QNPACS system.[7]

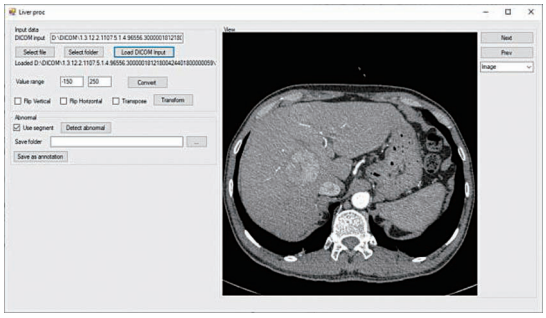

Figure 8. Program at Binh Dinh General Hospital

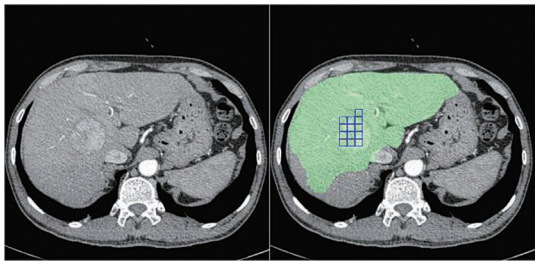

Figure 9. Result on a slice image of 52-year-old male patient has liver tumor

Green image area is liver object area, blue squares mark liver tumor. Result showed that the probability of detecting true position liver tumor within liver area is very high.

4. CONCLUSION

Processing and detecting abnormalities in medical images in general and in liver images in particular is an important issue, based on the application of research results on machine vision and machine learning in practical problems. The paper presents the technique of analyzing, processing and detecting liver abnormalities on liver CT images using the model texture approach, combined with classification task. The technique was tested on 3D-IRCADb-01 database and liver CT images were collected at Binh Dinh General Hospital. The results demonstrate the effectiveness of the proposed technique. This is an important basis for further improvement studies and more extensive testing.

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