Standalone functional CAD system for multi-object case analysis in hepatic disorders

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ABSTRACT

A new algorithm able to automatically diagnose the presence of the hemangioma areas in the hepatic ultrasonographic image is proposed. The algorithm uses a new multi-object approach which decomposes the image into three biological regions: a normal hepatic area, a hemangioma area and other areas. The de-noising process is efficiently accomplished for both Gaussian and Rayleigh noise distributions. Furthermore, a segmentation technique, based on gray level intensity analysis and the Moore-Neighbor contour tracing algorithm for a robust differentiation of the hemangioma area are employed. This new proposed technique is almost fully automatic, fast, and simple and its results are satisfactory.

1. Introduction

Hepatic hemangioma is a common benign tumor that affects the liver tissue. It affects up to 20% of the population and tends to have higher incidents in women. The hepatic hemangioma is a slow-growing mass of blood vessels in the liver; it can vary in size from few millimeters to giant dimensions of more than 20 cm [1]. Mayerhoefer et al. [2] used textural features to diagnose liver cysts and hemangiomas. The diagnosis efficiency was investigated based on both the nearest neighbor and on the k-mean statistical algorithms. Bahrami et al. [3] focused on the segmentation method of the hemangioma areas based on the active contour model. They reached their goal using an adaptive threshold method. A similarity of 73% for the boundary delineation methods was found when the de-noising operation was avoided and 90% similarity exists when the de-noising and contrast enhancement operations were performed. Lee et al. [4] proposed a CAD application capable of classifying the focal hepatic lesions. The classification algorithm is based on the Gabor wavelet filtering technique, the gray-level co-occurrence matrix and a support vector machine. Sugimoto et al. [5] showed that the number of reported CAD applications dedicated to the classification of focal liver lesions as liver metastasis, hemangioma or hepatocellular carcinoma is smaller as compared to the reports on CAD for diffuse liver disease. Also, they reported

an overall performance of their computerized classification scheme of 93.8% for hemangioma.

Most of the above mentioned methods are echography-wise, although CT and MRI methods are currently reported on this topic [6–9]. However, our paper takes the advantages of echography; it is cheaper, non-invasive and non-toxic and it is an accessible tool, able to provide more functional information.

The main contribution of this paper is the development of an algorithm which is able to automatically diagnose the presence of the hemangioma areas in the entire acquired image. It is implemented as a standalone CAD software application, offering independence from the framework of the MATLAB software and performing similar robust approach as the CAD packages integrated in a workstation. In our approach, the image information is confined to two mean of gray level intensity intervals and three analyzed classes. In this multi-object concept, three main liver regions are analyzed: the right or/and left lobe of the liver, the problematic hemangioma areas and other areas (such as the subcutaneous and diaphragm areas). They are labeled as follows. Class 1 comprises the normal hepatic area, class 2—the hemangioma area, and class 3—other areas. For a sound analysis, we assumed that the images are corrupted by additive and multiplicative Gaussian and by multiplicative Rayleigh noise; also the most suitable ways to remove noise were analyzed. Two mobile squared masks were put to scan the image and to effectively capture texture variations and to identify the hemangioma area. The Otsu binarization method and the Moore-Neighbor contour tracing algorithm were used. The CAD application also provides the possibility to make geometric measurements associated with the hemangioma area.

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The efficiency of this study is successfully confirmed and the relevance of the proposed method is validated. Note that our method is an original and different approach from the ones known in the literature. Also, a comparative analysis with the results reported in terms of specificity and sensitivity [4,5] is accomplished.

The rest of this paper is organized as follows. In Section 2 we review the theoretical method and the proposed algorithm is introduced. The results are given in Section 3, followed by some discussions in Section 4. The paper is summarized in Section 5.

2. Materials and methods

2.1. Data set

The experimental study used 80 images, separated by the sonographer physician in two sets. One set contained 40 healthy liver images and the second set enclosed 40 hepatic hemangioma images. The data were acquired by means of a SLE-401 echography medical device (manufactured by Medelkom Ltd.), provided with a linear probe of 3–6 MHz frequency. The image parameters are bitmap images (size of 524×512 pixels, 8 bit/pixel). A standalone CAD application [10] was developed by using the Matlab software ver. 9a and an Intel Core I3 CPU, 4-GB RAM as hardware platform. The statistical analysis was accomplished by using the SPSS ver. 17 software (SPSS Inc., Chicago, IL).

2.2. Image denoising

Usually, the echographic images are corrupted by noise [11]. Medical imaging equipments use coherent waves during the acquisition processes and multiplicative noise is prevalent in the image processing. The speckle noise disturbs the visual interpretation of the image and hampers the automatic diagnosis tasks. Our study aimed to compare the data in the frame of Gaussian and Rayleigh noise distributions. The Gaussian and Rayleigh noise distributions are described as follows [12, 13]:

$$\Gamma_G(i) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-(i-\mu)^2/2\sigma^2}$$

$$\Gamma_R(i) = \frac{i}{\sigma^2} e^{-i^2/2\sigma^2}$$

where i is the gray level and μ and σ^2 are the mean and the variance, respectively. The additive and multiplicative noise consists of additive and multiplicative overlap, respectively, of the noise to the pixels in the image [14].

Fourier transforms (FT) and Gaussian low pass filter (GLPF) were used for images de-noising [15]. The FT with a GLPF filter is an efficient method, successfully used in medical denoising tasks [16]. Let $f[x,y]$ be the gray level matrix associated with the image, while M and N denote its resolutions. The direct Fourier transform $F[u,v]$ and the inverse Fourier transform $h[x,y]$ are

$$F[u,v] = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f[x,y] e^{-i2\pi(ux/M+vy/N)}$$

$$h[x,y] = \frac{1}{MN} \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} F[u,v] e^{i2\pi(ux/M+vy/N)}$$

The filter transfer function of the GLPF is

$$H(u,v) = e^{-D^2(u,v)/2D_0^2}$$

where $D(u, v)$ is the distance from the point (u, v) to the center of the filter and D_0 is a non-negative parameter.

We have aimed to optimize the value of the D_0 parameter. The optimization problem was dealt with by adding various amounts of noise (having various values of the mean and of the variance parameters) into the images, followed by a restoration operation.

The optimal D_0 value was that which suitably reconstructs the images corrupted by noise. The efficiency of the de-noising process was analyzed by using the well-known noise quality parameters as: the signal-to-noise ratio (SNR), the peak signal-to-noise ratio (PSNR), the mean squared error (MSE) and mean absolute error (MAE) [17,18]. The performance of the proposed approach was characterized by higher values of SNR and PSNR parameters and by lower values of the MSE and MAE parameters.

2.3. Statistical analysis and image binarization

The mean value of intensities in the image is [19,20]

$$\mu = \sum_{i=0}^{L-1} ip(i) = \frac{1}{M} \sum_{i=0}^{L-1} i \cdot h(i)$$

where $L=256$ denotes the number of the gray levels, $p(i)$ is the probability of occurrence of the gray level i, and $h(i)$ is the number of pixels having the gray-level i. Based on our previous work [20], the aim was to find a relevant first-order statistical feature which could identify the biological classes. In the decision step, the proposed algorithm requires images binarization by means of the Otsu method [21]. The Otsu method consists of dividing the pixels in two classes, followed by the variance maximization of both classes. The main issue was to select a reasonable threshold. In order to discriminate between pairs of investigated biological classes and to provide a correct class assignment, the statistical t test and k-means algorithms were used [22,23]. Two clusters containing pixels which belong to the selected area were found. These clusters were associated with the pairs of biological classes which aimed to evaluate the correctness of the classification. Cluster 1 is assigned to the first component in the pair and Cluster 2 to the second component in the pair. Each cluster had a centroid and, subsequently, every studied biological class was assigned to the cluster whose centroid was the closest to the center value. The centroid's value was iteratively calculated every time when a new component was added to the cluster.

2.4. Image segmentation

The Moore-Neighbor contour tracing algorithm was used to trace the object boundaries in binary images [24]. We assumed that the image contained the black background and the white objects. The underlying rationale was that, in order to highlight the inner border of the objects, the image had to be scanned until the first white pixel was detected. By initializing the algorithm at this point, it recursively searched into a 3×3 neighborhood and in an anti-clockwise manner until the next white pixel was found. The algorithm restarted as soon as a new white pixel was found. This recursive process was stopped when the start pixel of the algorithm was reached. The method used an 8-connectivity neighborhood.

2.5. Computer-aided diagnosis application

The architecture of the proposed standalone CAD system is shown in Fig. 1. The framework consists of four modules: (i) image pre-processing; (ii) scanning process followed by biological objects detection; (iii) binarization of the images and contour extraction, followed by object identification and classification, and (iv) geometric measurements of the identified hemangioma areas and saving the results into the database.

For better emphasizing our contribution, we shortly present the implementation steps. The algorithm starts with the acquisition of the image data in the CAD application. To robustly segment the image, we accomplished the noise removal, by assuming the image being corrupted by Gaussian and Rayleigh noise.

A preliminary identification of the potential hemangioma areas was realized by scanning the image by using two concentric squared