Simply Segmentation Technique for Computed Tomography Images

Kalina Serwata
Institute of Mathematics
Silesian University of Technology
Kaszubska 23, 44-100 Gliwice, Poland
Email: kalarcika@gmail.com

Abstract—**Computed tomography is one of the most accurate studies of every fragment of the human body. Especially compared to the X-ray, tomography allows the detection of much smaller, and sometimes even any embryos of the disease that are invisible during other tests. In the case of a doctor, the analysis of the results from the tomography may be time-consuming due to the number of photos, and for the computer, quite the opposite. The occurrence of such activity, i.e. detection and classification of diseases in photographs obtained from a CT scanner, requires segmentation before classification. In this work, I suggest a simple combination of various filters that allow segmentation of these images. Numerous tests were carried out, which allowed for discussion on the advantages and disadvantages of this solution.**

I. Introduction

Nowadays, going to the doctor is understood as setting yourself in a queue and waiting for a short visit. The next step is to do the prescribed tests, although the queue dates again. In addition, the doctor indicating the test must make a decision not only about his selection, but also the costs associated with it. An additional problem is the aforementioned queue, because often the dates are so remote that from the embryo of the disease until the examination can grow quite quickly. Additionally, making the test does not mean knowing the diagnosis. Measurements are made, which in the next stage are analyzed and given back to the patient, who again has to queue up to the doctor who will assess these measurements.

Making a test becomes a long-term process that can be very disadvantageous to the patient. To make it easier, automation of these tasks is being introduced. An important aspect is allowing machines to segment and classify found objects on the images obtained from various medical tests. In this type of solutions, different types of algorithms and techniques are used. Especially, artificial intelligence methods are a basic components of such a support decision system. An interesting approach is to use heuristics to locate embryos of various diseases on X-ray images [11]. These types of methods can be very burdensome for computers, so there are various possibilities for their parallelization [6], [7]. Another well-known solution is artificial neural networks [2], [10], or mathematical models of neuronal activity in the human brain.

Not only artificial intelligence, but also mathematical fields can be used such as statistics [5], [9], [14].

In this paper, I propose a segmentation technique that can be used as detection of suspicious elements on images obtained from a computer tomograph.

II. Segmentation technique

Image segmentation is a process of dividing a picture into parts defined as areas that are homogeneous in terms of certain selected properties, i.e. they are consistent, i.e. of the same color and brightness, with a similar texture, without a clear boundary and the criterion is sometimes difficult to determine. The areas are sets of pixels. Properties that are often chosen as criteria for homogeneity of areas are: gray level, hue, texture.

The image obtained as a result of segmentation is simplified in relation to the image subjected to segmentation – this image does not contain many detailed information appearing in the original image. A similar situation also occurs when detecting edges in an image.

There is no single segmentation method – only the goal is defined, there are many ways:

- they are competing with each other or complementing universal and specialized methods,
- two-dimensional and three-dimensional,
- automatic, semi-automatic, not all automatic methods are accepted
- often multi-stage, hybrid methods,
- self-learning methods,
- global and local methods,

It is possible to distinguish two main groups of segmentation methods. Based on the similarities inside the areas – the result is a set of pixels that do not differ from each other. Based on the boundaries between areas – the result is a set of edges across which the pixels are very different.

Segmentation is the method of the simplest division of areas. We can save the steps of this algorithm in a fairly consistent way. The image is treated as a whole should be a square, the number of pixels defining the height and width is a multiple of 2, if an image that does not meet this criterion has been loaded, an error should be returned. Next, the condition of uniformity is checked. The area that does not meet this criterion is divided into four sub-images. In the next step, 4 areas are considered. If one of them does not meet the criterion of uniformity – it

is divided again into 4 equal subareas, etc. The algorithm is interrupted at the moment of obtaining a set of areas that meet the criterion of uniformity.

Here, I propose a technique based on the hierarchical use of several filters. A whole process is presented in Fig. 1.

A. Sobel

Sobel Edge Detection Algorithm [4], [12] uses the derivate approximation to find edges. This method returns edges at those points where the gradient of the consider image is maximum. The Sobel operator performs a 2D spatial gradient measurement on an image and so emphasizes regions of high spatial frequency that correspond to edges. Each pixel from the environmental brings his own contribution – weigh while calculating.

These weights are saved in the form of a mask. Typical mask sizes are 3×3, 5×5, or 7×7. Mask sizes are usually odd because the pixel in the center represents the pixel for which the filter transformation operation is performed. Each pixel from the environmental brings his own contribution – weigh while calculating. These weights are saved in the form of a mask. Typical mask sizes are 3×3, 5×5, or 7×7. Mask sizes are usually odd because the pixel in the center represents the pixel for which the filter transformation operation is performed.

The operator consists of a pair of 3×3 convolution kernels smooths the input image to a greater extent and so makes the operator less sensitive to noise and also generally produces considerably higher output values for similar edges. They are significant local changes of intensity in an image and typically occur on the boundary between two different regions in an image. The Sobel algorithm uses two masks filtering horizontal S_x and vertical S_y. The S_x component determines the gradient value in the direction rows, while the S_y component in the direction of the columns. The value of the edge response and its the direction is determined in accordance with equations

$$G_{mag} = \sqrt{(S_x)^2 \cdot (S_y)^2} \tag{1}$$

$$G_{dir} = \arctan \frac{S_y}{S_x} \tag{2}$$

Normally a 3×3 Sobel mask is understood as gradient along x-axis and align y-axis by using following equations

$$Gx = \frac{\partial f(x,y)}{\partial x} = f(x+1,y) - f(x,y) \tag{3}$$

$$Gy = \frac{\partial f(x,y)}{\partial y} = f(x,y+1) - f(x,y) \tag{4}$$

Then the total magnitude or the gradient can be found by this formula

$$G = Gx + Gy \tag{5}$$

To find the edge direction is minor when the gradient in the x and y direction are known. But it can still create errors when sum GX is equal to zero. So during implementation a restrain

must be set out to handle such cases. The main formula that is used

$$\theta = \tan^{-1} \frac{Gx}{Gy} \tag{6}$$

It takes place by means of the operation of a two-dimensional discrete plexus of the image matrix with a 3×3 matrix characteristic for a given direction called the kernel (kernel) of the transformation. These matrices are anti-symmetrical in relation to the direction of the detected edge.

The set of 8 matrices allows to determine the direction from $0°$ to $315°$ with a $45°$ step. Vertical edges are detected for the $0°$ direction, and horizontal edges for $90°$. The convolution operation determines in the first case the partial derivative estimate with respect to the X axis and the second with respect to the Y axis. The obtained partial derivative values define the gradient vector for each point of the image. Another simpler way to approach gradient approximation is the so-called "compass method". In this method, the mask giving the maximum value of the derivative determines the module and gradient direction with a resolution of $45°$.

The next masks are obtained by rotating the masks given by $180°$. It is worth noting that it is enough to calculate the tangles with the first four masks, because the others differ only by the sign $S_j + 4 = -S_j$.

$$S_1 = \begin{bmatrix} -1 & 0 & +1 \\ -2 & 0 & +2 \\ -1 & 0 & +1 \end{bmatrix}$$

$$S_2 = \begin{bmatrix} 0 & +1 & +2 \\ -1 & 0 & +1 \\ -2 & -1 & 0 \end{bmatrix}$$

$$S_3 = \begin{bmatrix} +1 & +2 & +1 \\ 0 & 0 & 0 \\ -1 & -2 & -1 \end{bmatrix}$$

$$S_4 = \begin{bmatrix} +2 & +1 & 0 \\ +1 & 0 & -1 \\ 0 & -1 & -2 \end{bmatrix}$$

The Sobel operator performs a derivation averaging operation (with weights 1, 2, 1) from three lines parallel to the direction of differentiation. The modified method has 6 stages: Convert into Grayscale image, Blurring the image, Find Edges using Sobel operator, Angle Of Gradient, Quantizing the angle, Hysterious Thresholding.

B. Otsu

Otsu's Thresholding Method [8] is based on a very simple idea – find the threshold that minimizes the weight within-class variance. This turns out to be the same as maximizing the between-class variance. Operates directly on the gray level histogram [e.g. 256 numbers, $P(i)$], so it's fast (once the histogram is computes).

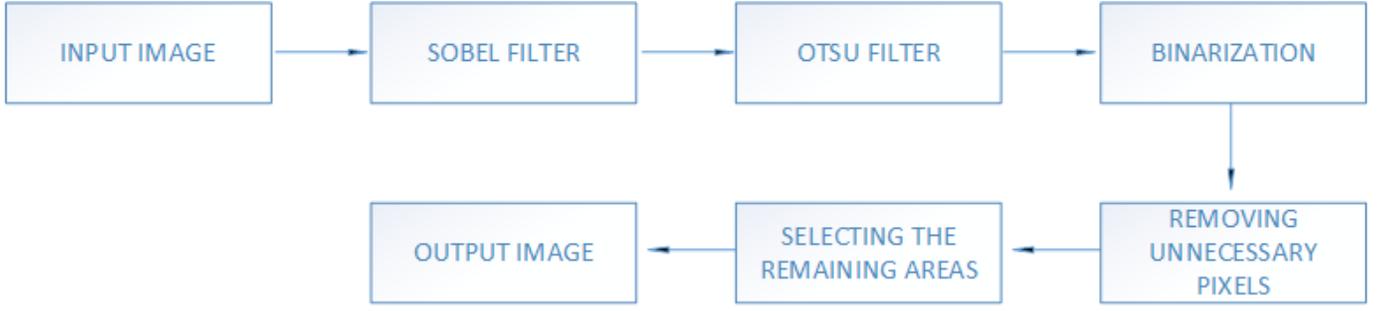Otsu: Assumptions

- Histogram (and the image) are bimodal,

Figure 1: Visualization of the hierarchical process of segmentation of computed tomography images.

- No use of spatial coherence, nor any other notion of object structure,
- Assumes stationary statistics, but can be modified to be locally adaptive. (exercises).
- Assumes uniform illumination (implicitly), so the bi-modal brightness behavior arises from object appearance differences only.

The Otsu method is an optimal prediction, in which the found threshold value is optimal in the sense of optimizing the given function. In this case, the function is the intra-class variance or inter-class variance. The selected thresholds divide the image into two classes: the object class and the background class. A feature of the Otsu method is the statistical description of both classes by two different probability functions, i.e. the distribution of the object class and the distribution of the background class. An image with separated, independent classes can be described by mean values and variances in individual classes.

The average values, respectively, of the object class and background class are equal to

$$\mu_T = \sum_{i=0}^{n-1} i \cdot p_i \tag{7}$$

$$\sigma_T^2 = \sum_{i=0}^{n-1} (i - \mu_T)^2 \cdot p_i \tag{8}$$

The global variance can be equivalently written as the sum of intra-class variation σW and inter-class variance σB. The global variance within one image is a constant, independent of the accepted threshold. The threshold influences the values intra- and inter-class variance, the sum of which gives a global variance. Minimizing intra-class variance is equivalent to maximizing inter-class variance.

As a criterion function, it is usually assumed that the interclass variance requires less computational effort

$$\sigma_B^2 = p_{ob} p_b (\mu_{ob} - \mu_b)^2 \tag{9}$$

The maximum value of the inter-class variance corresponds to the optimal separation of the two classes in the image. The threshold that makes this separation is the optimal one. The weighted within-class variance is

$$\sigma_w^2(t) = q_1(t)\sigma_1^2(t) + q_2(t)\sigma_2^2(t) \tag{10}$$

Where the class probabilities are estimated as

$$q_1(t) = \sum_{i=1}^{t} P(i) \tag{11}$$

$$q_2(t) = \sum_{i=t+1}^{I} P(i) \tag{12}$$

And the class means are given by

$$\mu_1(t) = \sum_{i=1}^{t} \frac{iP(i)}{q_1(t)} \tag{13}$$

$$\mu_2(t) = \sum_{i=t+1}^{I} \frac{iP(i)}{q_2(t)} \tag{14}$$

Finally, the individual class variances are

$$\sigma_1^2(t) = \sum_{i=1}^{t} [i - \mu_1(t)]^2 \frac{P(i)}{q_1(t)} \tag{15}$$

$$\sigma_2^2(t) = \sum_{i=t+1}^{I} [i - \mu_2(t)]^2 \frac{P(i)}{q_2(t)} \tag{16}$$

Otsu's thresholding method involves iterating through all the possible threshold values and calculating a measure of spread for the pixel levels each side of the threshold, i.e. the pixels that either fall in foreground or background. The aim is to find the threshold value where the sum of foreground and background spreads is at its minimum.

C. Modified binarization

Binarization is the process of converting color or monochrome images (in shades of gray) to a two-level (binary) image. Performing binarization on the image significantly reduces the amount of information in it. It is most often implemented by thresholding, consisting in establishing a threshold value below which obease's pixels are classified as object pixels, while extraneous pixels are classified as background pixels.
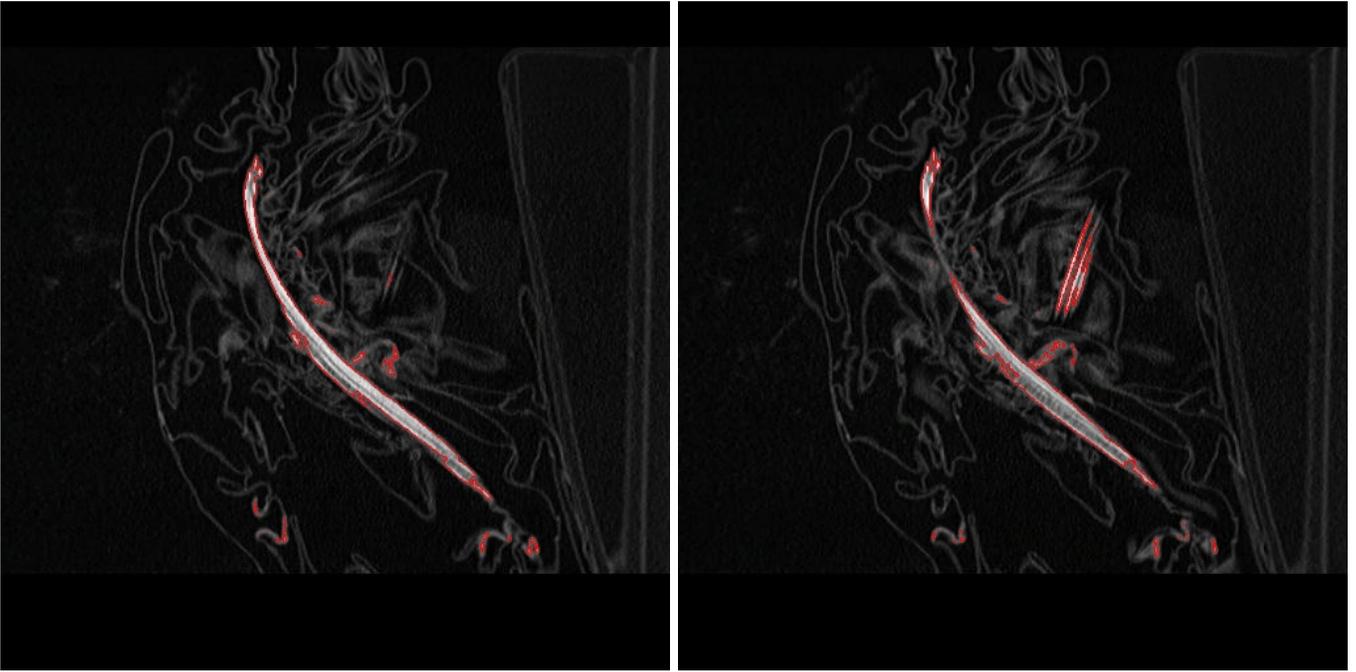
Figure 2: Segmentation on an exemplary database.

Depending on the image, the object pixel value is the minimum value, the maximum pixel value (for 8-bit images, respectively: 0 and 255). Binarization is widely used as a preliminary stage of the process of document analysis, handwriting, digitalization of maps. The effect of binarization affects the final result of the complex analysis process. The reduction of the amount of information carried out at the binarization stage reduces the complexity of the recognition algorithms and reduces the time complexity of the entire document analysis process. The purpose of binarization is to reduce unnecessary information and leave information relevant for further processing.

Binarization is the simplest method of image segmentation – the division of the image into separate regions characterized by the homogeneity of pixel values or other features taken into consideration. The purpose of binarization is to significantly reduce information in the image. The basic problem with binarization is to find the appropriate binarization threshold. In most cases, an image histogram is created to find the right threshold value, and then the binarization threshold is set.

Suppose we have an image after applying these filters and binarization process. Binarization allows to remove more than a dozen pixels, which are probably unnecessary in the analysis. This type of simplification should be modified by removing other elements which are expected properties are not very significant. Suppose that for each white color pixel, we will analyze the area given by the grid of size $k \times k$, where the selected pixel is in the center of it. Let $\Delta(\cdot)$ be a function that counts the number of white pixels in a given set of points Ξ. Then, the decision to remove or leave the pixel is made by

the following condition

$$
\begin{cases}
\Delta(\Xi) > \alpha & \text{remove} \\
\Delta(\Xi) \leq \alpha & \text{leave}
\end{cases}, \tag{17}
$$

where α is the limit value – usually half the length of the grid, so $\lfloor \frac{k}{2} \rfloor$.

III. Experiments

In order to check the operation of the proposed method, an available database of medical images was used [3] [1]. In the case of segmentation, it is difficult to analyze the obtained data. The best test is to assess the found areas, their quality and usefulness in further classification. Exemplary images subjected to segmentation are shown on Fig. 2 and 3. All areas were intuitively evaluated, and the results can be determined at 75% efficiency. To get a greater value, a classifier should be designed that would evaluate these areas.

IV. Conclusions

The described segmentation technique allows detection of suspect areas on computed tomography images. It is the first step to model a decision support system for disease detection. The next step is to use these areas to classify and identify the found areas. The proposed solution enables fast detection using classical actions, so it is a kind of hierarchical process that leaves many areas. By *many*, it is understood as much as possible to accidentally not remove the embryo of the disease. Unfortunately, this is a naive solution, because during the segmentation could be performed a certain classification of

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[1]The results here are in whole or part based upon data generated by the TCGA Research Network: http://cancergenome.nih.gov/

the removed pixels which may indicate something worrying. However, this is an approach that has its advantages and disadvantages.

In future research, I will consider creating segmentation and classification methods that should be much more effective, efficient and accurate for support decision systems.

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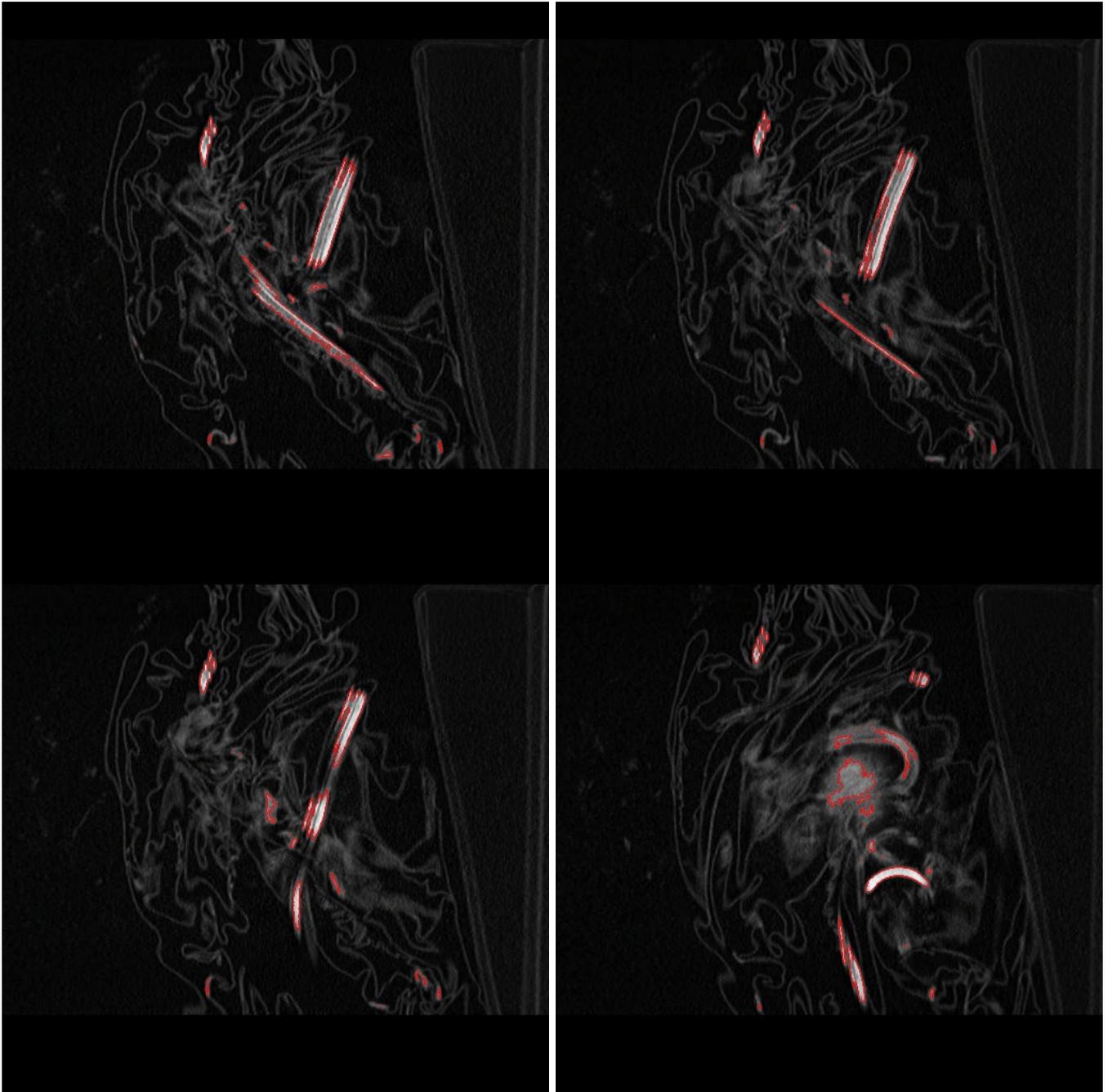
Figure 3: Segmentation on an exemplary database.