

GUI FOR SPLEEN SEGMENTATION FROM ABDOMINAL MRI SEQUENCES

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Abstract

Nowadays the medical images processing is an important step to the modern computer aided medical diagnostic. Specialists such as radiologists, surgeons and other are able to use several of medical image diagnostics in their work. But not always the medical equipment has the image processing tools that the doctors need. For that reason a Genuine User Interface (GUI) for Spleen Segmentation of abdominal MRI sequences is proposed in this paper. It works in the MATLAB environment and uses its Image processing toolbox. The interface is giving a choice between different techniques of segmentation based on active contours without edges and other image processing tools. The main advantage of the GUI is the possibility of automatic segmentation of a whole abdominal MRI sequence that is loaded from the user. Other important operations are image pre-processing (Optional), 3D visualisation of the results and validation of the segmentation, if their ground true images are available.

1. INTRODUCTION

The shape and volume of the human organs are very important for studying their functionality, making statistical representation of the normal and disordered organs by the human populations. By epidemiological studies and in the daily work radiologists are sometimes forced to do hundreds of manual segmentations per hand. That is way a tool for automatic or semi-automatic spleen segmentation could be very useful in such cases.

The form of the human spleen is very variable by the different individuals. So the visualization of this organ is very interesting and helpful by studying its shape, functionality and disorders. The spleen has the same relationship to the circulatory system that the lymph nodes have to the lymphatic system [1]. A wide range of diseases can affect the spleen. MR imaging is an excellent tool for diagnosis and evaluation of focal lesions and pathologic conditions of the spleen. Also for studies of health, because of the harmless magnetic field that is used by MRI.

There are a lot of segmentation techniques, but not all of them are giving good results in the different cases. Because of the partial volume effect, the gray level of the spleen and grayscale similarity of the adjacent abdominal fat, spleen segmentation has always been a problem [2]. In this case an active contour method for segmentation has been chosen. The "Active Contours Without Edges" by Chan and Vese, that ignores edges completely [3].

The performance of the image and video segmentation algorithms is judged mainly on how well the

region is segmented. Generally there exists no segmentation algorithm which can be commonly applied on all the domains [20].

The outline of the research paper is organized as follows: Section 2 discusses about image segmentation based on "Active Contours Without Edges" by Chan and Vese, also presents combination of the active contour model with other segmentation methods, such as K-mean clustering as primary segmentation, atlas template method with automatic match of the used template and demonstrates the results. Section 3 describes the proposed GUI for image segmentation and its functionalities. The results of the relative evaluation methods are illustrated in section 4 and section 5 finally draws the concluding remarks of the paper.

2. SPLEEN SEGMENTATION METHODS

2.1. The active contour model by Chan and Vese

All of the methods in the GUI are based on the segmentation via active contours without edges. The active contour model of Chan and Vese is used for the next two stages of segmentation. It is a gray level based method and is a special case of the Mumford-Shah function.

We consider f to be the given grayscale image on a domain Ω to be segmented. Mumford and Shah approximate the image f by a piecewise-smooth function u as the solution of the minimization problem. The Chan - Vese model has an additional term penalizing the enclosed area and a further simplification that u is allowed to have only two values,

c_1 where x is inside C and c_1 where x is inside C , where C is the boundary of a closed set and c_1 , c_2 are the values of u respectively inside and outside of C [8]. By the method of Chan – Vese the purpose is to find among all u of this from the one that best approximates f .

2.2. Hybrid approach for spleen segmentation

For the fully automated mode of the GUI is used a hybrid method for spleen segmentation from MRI sequences that is presented in a previous work [21]. The approach is combining K-mean clustering for primary segmentation of the image sequence and an atlas template method is used for the primary segmentation of the primary image of the sequence, where the segmentation begins.

K-means clustering can be used because it is simple and has relatively low computational complexity [15]. So we can obtain two clusters. The first cluster image presents the background and some small structures extracted from the image. The second one presents the MR image with extracted organs and tissues. This cluster image shows a better differentiation between the spleen and the surrounding area. The goal of a clustering method is to find cluster centers $CC = \{c_1, \dots, c_k\}$ in feature space such that the distance of all samples to their center is minimal [11]:

$$CC_{min} = \arg \min_{CC} d_{CC}(f) = \arg \min_{CC} \sum_{i=1}^M ||f_i - c(f_i)||$$

where $c(f_i)$ delivers the cluster center c_k , which is closest to f_i .

Two atlas models of the spleen have been made and one of them is used for initial contour in the segmentation of the initial image. They are created up of 10 abdominal MRI images, which are our training data and are different from the test data. First, the spleen was manually segmented from these 10 images. After that we get 10 binary images. In the next step the spleen is surrounded in a rectangle and cut off. These cuts are rescaled to 50x50 pixels. Then we find the intersection and union of the scaled images, which presented two atlas models given in Fig. 1.



Figure 1. Spleen atlas models: a) obtained after intersection of the scaled images; b) obtained by union of the scaled images

2.3. Automatic segmentation of the whole sequence

The sequence is processed in two directions (forwards and backwards from the initial image). That means we can build two loops: one incrementing and other decrementing to crawl the array of images with spleen in the sequence. This approach is appropriate, because in the most cases the spleen is getting smaller in these two directions in the sequence. Each image could be primarily pre-processed and pre-segmented using the methods described in the previous subsection 2.2, if the user chooses this kind of segmentation. If not an initial contour could be chosen in the initial image as a rectangle without a template or as a polygonal figure closer to the spleen. Each subsequent image uses as mask for its segmentation with active contours without edges the result of the segmentation of the previous image [14]. For termination condition we use the difference between the segmentation result in the initial image and the segmentation in each processed image in the sequence. This is made on the base of the correlation function. This function gives the statistical correlation between random variables, contingent on the spatial or temporal distance between those variables. By value of 1 there is 100% matching between the images. In our case we select the value of the threshold equal to 0.65.

The segmented spleen is visualized with yellow contour on the original images from the entire sequence. The result is a new sequence of binary images of the segmented spleen, saved in a new file folder in the folder of the original file with the sequence.

3. FUNCTIONALITY OF THE GUI FOR SPLEEN SEGMENTATION

A view of the GUI is given in Fig. 2. The main algorithm of the GUI is presented in Fig. 3 [01]. It describes the flowchart of the main interactions without observation of the different segmentation abilities and other optional options of the GUI.

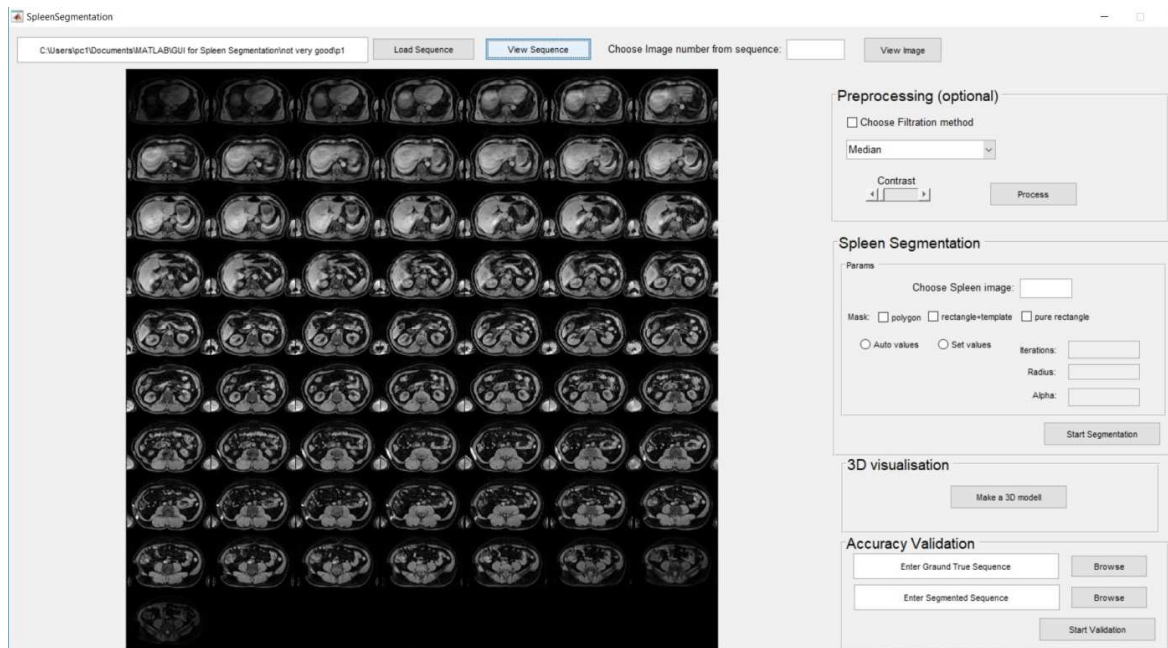


Figure 2. Main view of the GUI

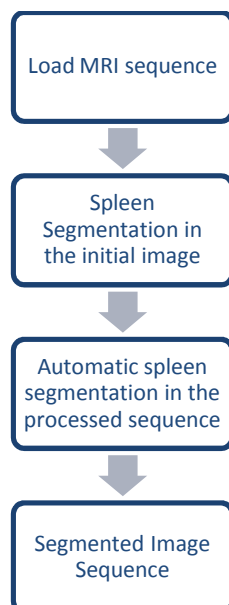


Figure 3. Flowchart of the main algorithm

The first step in the segmentation process is to load an abdominal MRI-sequence from a file that should be segmented. This happens by pushing a button “Load sequence” on the upper left corner in the GUI. After that the sequence should be visualized with the button “View sequence” next to the previous one. After this interaction the whole sequence is visualized in the visualisation sector of the GUI. In that way the radiologist can make the important and expert decision in which of the images the spleen is visible and to choose one of them as initial image for the automatic segmentation of the rest of them. The chosen image is given with its number in

the “Spleen Segmentation” field next to the visualized sequence.

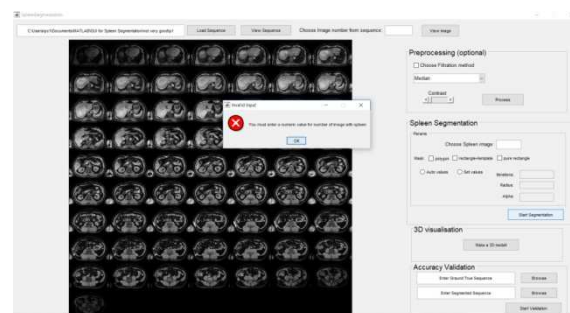


Figure 4. Error report for non existing image number

An error report acquired, when such image is not given and segmentation is tried to be done. There is also an optional field for pre-processing, where various filters could be chosen from the pop-up-menu and contrast enhancement could be provided to all of the images in the sequence before the segmentation step. Other additional fields are “3D visualisation” and “Accuracy Validation”.

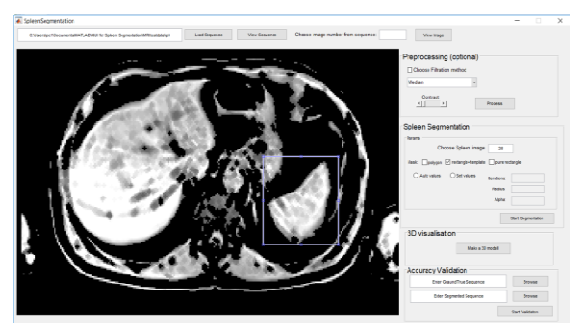


Figure 5. Start of segmentation with chosen option 'rectangle+template'

4. RESULTS AND DISCUSSION

On Table 1 are presented the results after comparing the accuracy of the segmentation results obtained by using the different segmentation methods that could be chosen with check boxes in the GUI.

Table 1. Obtained results for spleen segmentation made by different segmentation options

Segmentation options	Mean Dice for the sequence [%]	Dice for the primary image [%]	Time for processing of the sequence [sec]	Time for processing of primary image [sec]
'rectangle+template'	89.14	94.06	41.33	20.34
'polygon'	79.83	95.14	42.72	25.43
'pure rectangle'	75.62	83.45	43.45	53.75

5. CONCLUSION

In this paper is presented an effective GUI for easily automatic spleen segmentation in abdominal MRI sequence images. The proposed GUI represent different approaches for spleen segmentation all based on the active contour model. Hybrid segmentation approach on segmentation methods such as active contours without edges and k-mean clustering is compared with the other segmentation options. The proposed GUI allows extracting in short time the normal spleen, which has a variable form and unstable position at the different images in the MRI sequence. The various options of the GUI could give also the ability of making segmentation of some untypical or pathological forms of the spleen, but more experiments should be done in the future in this direction.

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