Matlab Extension for 3DSlicer: A Robust MR Image Processing Tool

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Abstract— Using magnetic resonance tomography to scan biological tissues is currently a very dynamic approach. Based on various image parameters, the method enables us to analyze tissue properties, recognize healthy and pathological tissues, and diagnose the disease or indicate its progression. However, the acquired data must be correctly interpreted and visualized by means of a suitable software tool, such as 3DSlicer (http://www.slicer.org). This well-designed platform provides an interface between the user and the data available in the popular DICOM format, and it facilitates very simple 3D visualization of the MR-based data. One of the main advantages of the open-source software package is undoubtedly its ability to be extended with supplementary modules, for example the Matlab script. The paper describes the open-source environment with a focus on Slicer3D and introduces possible extension of this platform with a module for MR data processing via the three-dimensional, mutiparametric, SVM trainable segmentation method. The module is freely downloadable. The paper also presents a comparison of the processing results with respect to the cycle time and the necessary interactivity. Moreover, the author proposes multiparametric segmentation of a brain tumor edema from T1 and T2-weighted images, and the advantages of the SVM technique are compared with corresponding features of both other fast segmentation methods and the one-parameter approach.

1. INTRODUCTION

In the past, the processing of medical images obtained via magnetic resonance (MR) tomography was reduced to a mere analysis of parameters in a slice [1]. However, the determination of real properties in the examined tissues invariably requires us to produce and process an image via the three-dimensional method, securing the smallest and (if possible) equidistant resolution.

This paper presents a procedure for simple, three-dimensional processing of an MR image of the human brain; the aim of the proposed technique is to facilitate segmentation of the edema in the vicinity of a tumor [2, 3]. Segmentation quality constitutes a very important factor. The boundary accuracy further influences the precision of the time examination of the contrast agent perfusion into the investigated tissue [4, 5]. Moreover, as the perfusion analysis is obviously assumed in the entire volume of the tissue to be analyzed, there follows the necessity of three-dimensional segmentation.

Generally, all segmentation methods can be modified to enable three-dimensional data segmentation. Yet the set of available techniques is very wide, and we therefore need to select the procedure most suitable for the given application. In medical image processing, trainable segmentation methods are frequently used because, as a rule, more images showing the same type of pathological tissue are accessible. Based on such images, it is then possible to set up a model of the investigated tissue, which can be subsequently utilized in the automatic processing of other images [6, 7]. This type of image processing was applied in the described segmentation procedure; here, the conversion of image segmentation to the data classification problem is used. The input data consist in the intensities of the selected pixels/voxels in the regions of the examined tissue and adjacent areas. Each intensity value of the individual pixels is assigned one of the two classifier classes, and the data are further used to train the classifier until suitable coefficients are found. The three-dimensional image processing is carried out in the 3DSlicer environment; this is open-source software for the visualisation and processing of multidimensional tomographic data. The package contains many available plugins, and it can be extended with other tools, such as Matlab scripts. This option is used precisely for the extension with a tool learning multiparametric segmentation. The DICOM format is obviously supported.

2. METHODS

The segmentation method is based on the binary classification of multidimensional data; the processing chain is shown in Fig. 1. First, randomly selected pixels inside and outside the area of

interest are marked with the mouse. The values of intensities at indicated points across all images (T1W, T2W, DWI) constitute the input data for the training of the segmentation model/classifier. In addition to the coordinates of the points, the input to the model comprises also original images and their blurred versions obtained via the application of a Gaussian blurring filter. The output of the model is a grayscale image that has to be thresholded; the threshold level was chosen to be in the middle of the range of intensities. As pointed out above, the actual segmentation is carried out using an SVM classification model. The SVM approach, which finds wide application in the binary classification of data, is based on the search for the optimum hyperplane dividing the data into two groups with minimum error; moreover, there is maximum distance between the hyperplane and the data within both these groups. The training of the model is performed over a set of manually selected points, while the testing is carried out over the set of all image points. Good segmentation results can be achieved if the SVM model parameters are suitably selected; in this context, an important step is the selection of the SVM model kernel. For the purposes of multidimensional data segmentation, the Gaussian radial basis function was chosen to constitute the kernel of the model:

$$K(x,y) = e^{\left(-\frac{\|x-y\|^2}{2\sigma^2}\right)}, \tag{1}$$

where K is the kernel of the function, x is the vector of the classified data, y is the auxiliary vector, and the selection of the parameter σ influences the decision power of the auxiliary vector.

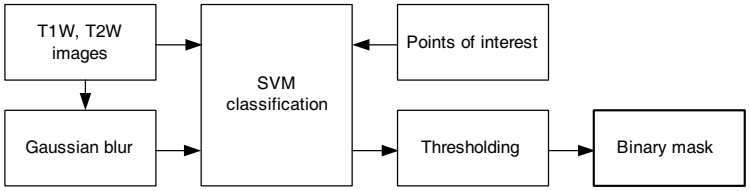

Figure 1: Image processing via the SVM classification model.

3. IMPLEMENTATION

The 3DSlicer application window is shown in Fig. 2. This window comprises several sections: The left part contains a panel enabling the application or the plugins to communicate with the user, and the right portion presents views of the 3D image from several planes. The view planes can be changed arbitrarily; furthermore, it is also possible to display a 3D model, for example after segmentation.

The entire image processing chain is shown in Fig. 3; the indicated processing procedure comprises several stages. First, three-dimensional images weighted by relaxation times T1 (3D-T1) and T2 (3D-T2) and the perfusion coefficient (3D-PR) are read. The images 3D-T1 and 3D-T2 enter the algorithm as structural images, whose intensity distribution provides the basis for biparametric

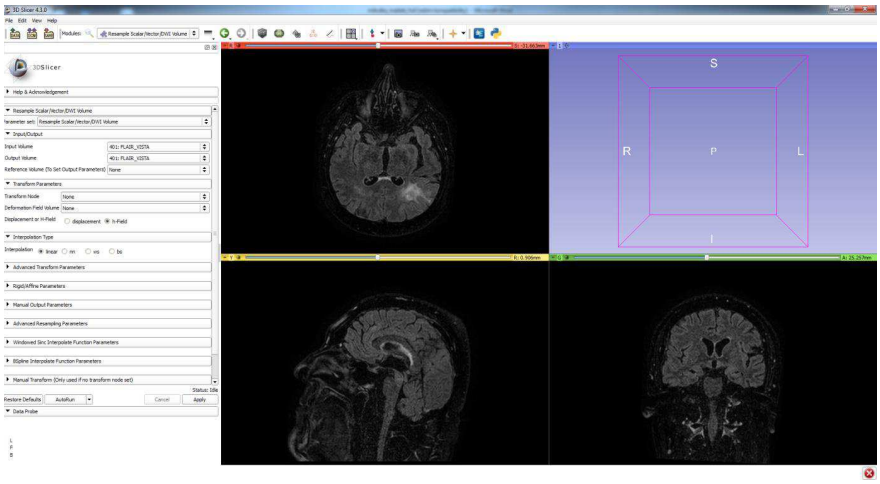

Figure 2: A representative window of the 3DSlicer application.

analysis and segmentation of the examined tissue. The segmentation practice is as follows: During the initial phase, the 3D-T2 image is resampled to the size and number of slices according to the 3D-T1 image. Subsequently, the rigid registration of both images is performed using the marked specific points in the image. Then, in the registered images, the random points are manually selected, and this operation is carried out gradually for both classified groups — inside and outside the classified tissue. The hitherto obtained data (the coordinates of the selected points and their intensities in 3D-T1 and 3D-T2) are sufficient for the classifier learning and segmentation model creation; the setup of the model enables us to segment the complete three-dimensional data and to obtain the binary mask. This 3D mask, in its number of slices and plane, corresponds to the parameters of the original 3D-T1 image and requires further processing. Our objective is to obtain the binary mask of the tissue in the perfusion image; however, due to fast scanning in time, such images exhibit significantly lower resolution than the T1 and T2-weighted images, and their directional vectors may not correspond to one another. The segmented image thus has to be resampled according to the perfusion image parameters. This constitutes the weakest point of the entire algorithm because, ideally, we should also perform registration of the perfusion-weighted images with respect to the T1-weighted images. Such operation is nevertheless almost impossible owing to tissue resolution in perfusion-weighted images; perfusion-weighted images are noise-laden and exhibit very low resolution (in our case, 20 slices with the resolution of 64×64 px). The output of the algorithm therefore consists in a binary image, where the white pixels correspond to points of the examined tissue in the analysed perfusion images; the black pixels then correspond to points in the tissue's environment.

The main advantage of the implementation in 3DSlicer consists in that the software enables the processing of multidimensional tomographic data. The described algorithm utilises the already implemented functions of three-dimensional data resampling, including the change of the image directional vector, rigid or other image registration, and visualisation involving 3D modelling.

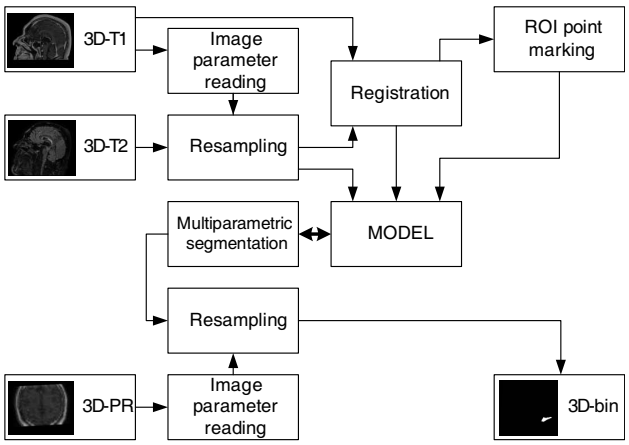

Figure 3: Diagram of the image processing chain in 3Dslicer-based tissue segmentation.

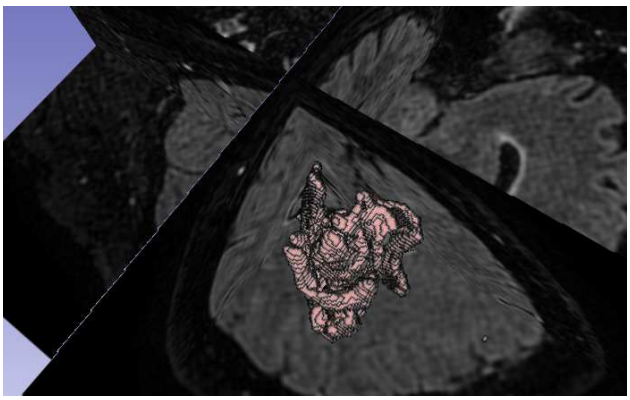

Figure 4: An example of the 3DSlicer-generated output model of the segmented tissue.

4. CONCLUSION

The paper presents and algorithm for the multiparametric segmentation of three-dimensional tomographic images and discusses the 3DSlicer-based implementation of the algorithm carried out using a Matlab plugin. The input data consist in three-dimensional tomographic images representing multiple parameters to increase segmentation efficiency; typically, these data are T1 and T2-weighted images and manually marked points located within the examined tissue. The output of the algorithm is a three-dimensional binary mask resampled to fit perfusion images in the research of perfusion tissue analysis. An example of the output model of the segmented tissue is shown in Fig. 4.

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