Multiparametric Biological Tissue Analysis: A Survey of Image Processing Tools

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Abstract— The use of 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. These activities are then necessarily accompanied by the processing of the acquired images. The paper introduces a comparison of statistical tools for the trainable segmentation of multiparametric data obtained through magnetic resonance tomography. In this context, the author briefly compares various available tools (Weka, Slicer3D, and RapidMiner) in view of the input data training and testing, applicability of the classification models, and ability of the input/output data to be extended with other systems for further processing. The paper also describes as a multiparametric task the segmentation of a brain tumor performed with real MR data. The source of the data consists in T1 and T2-weighted images. The proposed segmentation method is carried out within the following phases: data resampling; spatial data coregistration; definition of the training points; training of the SVM classification model; testing of the model and interpretation of the classification results.

1. INTRODUCTION

Magnetic resonance imaging (MRI) is currently one of the most advanced diagnostic techniques, in which the image is generated via the excitation of hydrogen nuclei in the examined tissue and the subsequent sensitive detection of the response. A multitude of imaging sequences is available, and each of them represents different tissue properties. The set of the most common tomograpically acquired parameters includes the relaxation times T1 (spin-lattice) and T2 (spin-spin). In pure water, both the relaxation times are identical. However, they can be suitably applied to recognize biological tissues, respecting that the T2 relaxation time is smaller than T1. The more tissue parameters are known, the higher their recognition rate and the better the possibility of correct pathology diagnosis [1].

2. BRAIN IMAGE PROCESSING

The presented segmentation method is based on the binary classification of multidimensional data [2–4]; the processing chain is shown in Figure 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 to train 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.

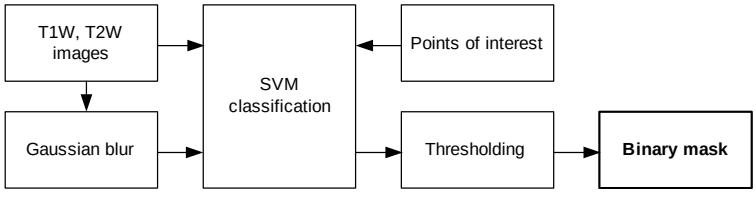

Figure 1: Image processing via the SVM classification model.

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 2 shows the result of brain tumor segmentation described by the multiparametric classification method. This technique has provided very good results in the segmentation of tumor, edema and necrotic tissues; moreover, the robustness of this approach enables us to set up models for the segmentation of concrete types of tumor. The necessity to apply the multiparametric method in the segmentation of MR tomographic data is indicated in Figure 3, which proves that the employed single-parameter classification technique fails to recognize the brain tumor parts. In the described case, the recognition is carried out based on the distribution of the T1 or T2 relaxation time [5–7].

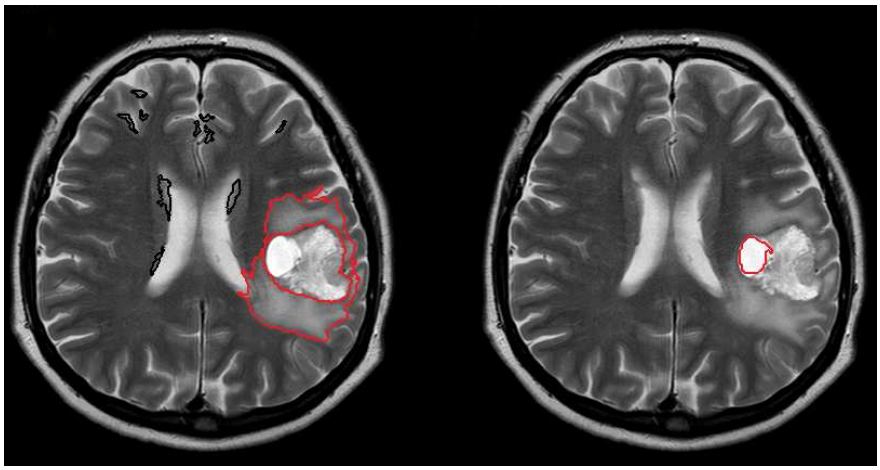

Figure 2: The multiparametric segmentation result for: (a) brain tumor and edema; (b) a necrotic tissue. The examined region is bounded by the red curve.

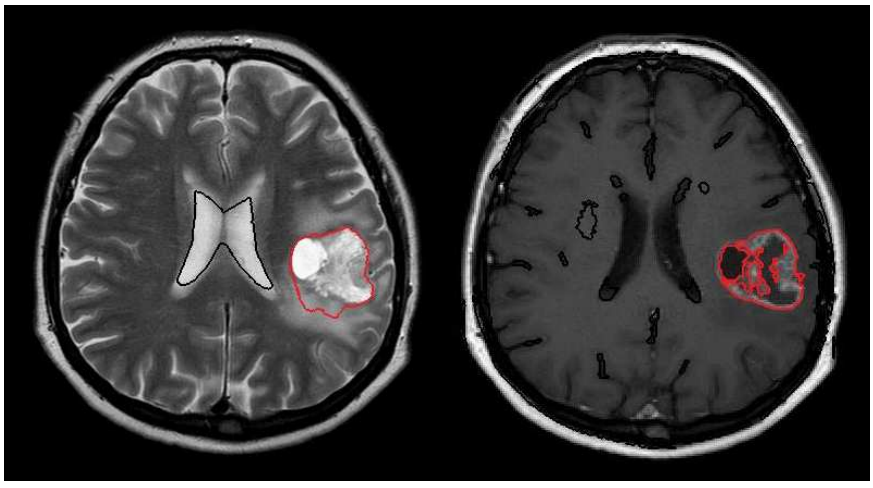

Figure 3: The result for incorrect brain tumor segmentation performed with the single-parametric approach. (a) Tumor segmentation in a T2-weighted image; (b) tumor segmentation in a T1-weighted image.

3. IMAGE PROCESSING TOOLS

Even though a large number of image processing tools are currently available, it is advisable to select software capable of solving the processing chain within the given task completely, without any exception. In practice, however, such choice constitutes the most common difficulty related to the discussed procedure; the individual tools therefore have to be suitably combined. The above-presented multiparametric segmentation of MR tomographic images may serve as a typical example. As is obvious from Figure 1, the entire processing operation involves, first of all, the reading of several three-dimensional images; after this initial stage, the images are resampled to an identical number of slices, and their directional vectors (or scanning levels) are unified. The subsequent phase consists in registering the actual image data, from which the characteristic images suitable for the tissue classification are computed. These feature images constitute the training/testing data that enter the classifier together with the coordinates of the manually selected points representing the regions inside/outside the examined tissue to be segmented. The probability image, which constitutes the output of the classification model, has to be further processed (via techniques such as simple thresholding), and the result of this step already consists in the final binary mask representing the examined tissue region. Table 1 demonstrates the use of selected free access software tools and shows their capabilities within the above-discussed operations.

Table 1: Comparison of software tools for experimental processing of tomographic images.

	3D data support	3D data visualization	advanced data segmentation	data classification	data registration	resampling	manual selection of regions/points
3DSlicer	√ √ √	√ √ √	×	×	√ √ √	√ √ √	√ √ √
ImageJ	√ √	√ √	√**	×	√**	√	√ √ √
RapidMiner	×*	×*	√ √	√ √ √	√	×	√ √
Weka	×	×	×	√ √ √	×	×	×
Matlab	√	√	×	√	√	×	√

* Support for commercial versions only. ** Only with plugins.

4. CONCLUSION

The paper presents and discusses the possibilities of multidimensional tomographic data processing by means of free access software tools. In the described case, the aim of the processing is to carry out multiparametric segmentation of three-dimensional tomographic data. The actual registration is preceded by the resampling of the data, unification of their directional vectors, registration of the image data, and computation of characteristic images. The real segmentation then consists in the selected data classification, in which the classifier model is first set up using the manually selected data; at this initial stage, the data are subdivided into groups inside/outside the examined tissue. As shown in Table 1, it is very difficult to find a tool that would enable us to materialize the entire measuring chain. Considering their individual characteristics, the software tools can be suitably combined, for example in the following manner:

- Preprocessing (resampling; rotation): 3DSlicer.
- Synthesis of the data to be classified (computation of characteristic images): Matlab.
- Data registration: 3DSlicer; Matlab.
- Manual classification and training data preparation: Matlab; ImageJ.
- Classification model setup: Matlab.
- Data visualization; DICOM import and export: 3DSlicer.

The output of the described research consists in both the implementation of the selected algorithms in Matlab and the creation of a Matlab plugin for the 3DSlicer environment. Through combining 3DSlicer and Matlab, it is possible to achieve effective implementation because all the processing chain stages can be carried out only within 3DSlicer; this procedural characteristic markedly simplifies the performance of the tasks and reduces the time necessary for the binary mask to be acquired from the multiparametric analysis of the tomographic data.

ACKNOWLEDGMENT

This work was supported in part via a grant provided by Czech Science Foundation (GAČR, No. 102/12/1104) and through the project CZ.1.07/2.3.00/30.0039 of Brno University of Technology.

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