A multi-strategy method for MRI segmentation

M. Martin-Landrove[1,2], G. Padilla[3], G. Figueroa[3], M. Paluszny[3,4], and W. Torres[3,5]

[1]Center for Molecular and Medical Physics, Universidad Central de Venezuela, Caracas, Venezuela, [2]Centro de Diagnóstico Docente, Las Mercedes, Caracas, Venezuela, [3]Center of Geometry, Universidad Central de Venezuela, Caracas, Venezuela, [4]Department of Mathematics, Universidad Nacional de Colombia, Medellín, Colombia, [5]Fundación Instituto de Ingeniería, FII, Caracas, Venezuela

Abstract

An accurate method for T_2-weighted MRI segmentation according to tissue transversal magnetization decay rates is presented. By means of a sequence of geometric image filters a classification of the pixels' intensity decay curves is provided. This can be done through a double strategy: First a log-convexity filter is applied in order to regularize image intensity decay by adjusting its geometrical properties to those that are expected from noiseless data, i.e., monotonous and convex behavior. In doing so, image noise is somewhat filtered and controlled. Second a curve fitting by a suitable de Prony pseudo interpolating filter and a Montecarlo-Vandermonde robustness filter is performed. Decay rate distributions are obtained and tissue classification is performed by means of the determination of principal decay rates or decay modes using a suitable mathematical morphology operator, i.e., watershed or similar. Image segmentation is performed by linear regression analysis on a pixel by pixel basis assuming that the pixel intensity decay is composed by a linear superposition of the decay modes previously obtained from the decay rate distribution function. The main advantage of the proposed multi-strategy approach rests in the accuracy and speed of calculation with respect to other methods such as Inverse Laplace Transform algorithm or Vandermonde like equations. The method could be easily extended to any exponentially decaying set of images such as diffusion-weighted MRI.

Introduction

In T_2-weighted MRI, image intensity can be acquired at equally spaced echo times, TE, using a Carr-Purcell-Meiboom-Gill sequence. Image intensity exhibits a decay curve *f(t)* whose physical behavior can be modeled by a finite exponential sum $f(t) = \sum_{i=1}^{m} a_i e^{-b_i t}$. On each term $a_i e^{-b_i t}$, the rate of intensity decay b_i corresponds to a particular tissue type, a_i is the proportion of the *i*-th tissue and *m* is the number of different tissues that can be (theoretically) detected for this single pixel. Since only a finite number of echoes is recovered, then for each pixel a polygonal curve *g*, whose vertices should belong to the curve corresponding to *f*, is obtained. Nevertheless, due to noise there is always a difference between the theoretical model and real data. For instance, given a MRI of a homogeneous tissue (i.e. only one relaxation rate) the histogram of intensities at a single echo time has a Rician probability distribution. On the other hand, noise along the polygonal curve g for the same pixel presents a Gaussian like probability distribution function.

Methods

Usual methods are quite unsatisfactory. Inverse Laplace transform method [3,4], although it is very robust and manages image noise appropriately, it is rather slow and in consequence not applicable to image segmentation on a pixel by pixel basis. The other known method involves the resolution of overdetermined Vandermonde systems [1,2], it is faster and accurate but it takes a considerable amount of computing resources [1]. An even faster approach to find the solutions was proposed [5], based on a method developed by de Prony [6], but it appears to be very sensitive to image noise and extremely unstable if the number of exponential decays, *m* is high. To overcome this problem, a log-convex regularization of the data is proposed to determine a tolerance band as a polygonal approximant of *g*. Afterwards, the de Prony interpolation method [5] revealed to be not only fast but also accurate and quite plausible, i.e., the relaxation rate distribution function appear to be a multimodal one that fitted, in most of the cases, the usual clinical criteria. In Figure 1, some relaxation distribution functions are shown. About a 5 % of the pixels for which the de Prony method was applied did not yield a good approximation of g. For these noisy pixels a low dimensional Vandermonde-Montecarlo equation system ($m \leq 3$) was applied. We also compared the de Prony and Vandermonde-Montecarlo methods as predictors of *m* [2,7]. Once the relaxation rate distribution function is obtained, different relaxation modes can be extracted from it and used for image segmentation.

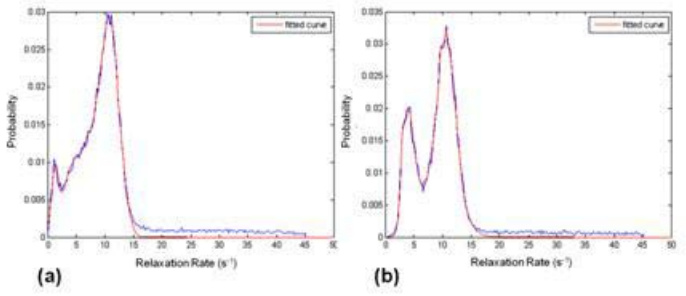

Fig. 1. Sample distribution functions for different ROI's in (a) Glioblastoma multiforme, (b) Fibrillar Astrocytoma.

Results and Conclusions

In Figure 2 some segmented images are shown. Based on these results it can be concluded that the proposed multi-strategy method: data regularization by means of a log-convex filter that adjusts the geometry of data points to the behavior of noiseless data, de Prony method to determine relaxation rates and combination with Vandermonde equations to fit to experimental data (including for some noisy pixels Vandermonde-Montecarlo) and use of the obtained decay rate distribution to select decay modes and classify tissues accordingly, provides a reliable method for image segmentation applicable not only to T_2-weighted MRI but also to diffusion-weighted MRI. Further improvement is possible by combination with other tools of mathematical morphology [8] and computational acceleration, particularly in Vandermonde method [9] and should be taken into account in the future.

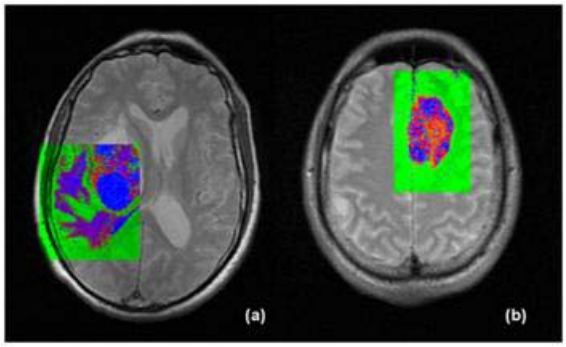

Fig. 2. Segmented images: (a) Glioblastoma multiforme, (b) Fibrillar Astrocytoma. Colors are assigned as follows: blue, cerebrospinal fluid, necrosis or edema tissue, red, tumor tissue and green, normal or unaffected tissue.

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