Brain Tumor Image Segmentation Using *in vivo* Spectroscopy, Relaxometry and Diffusometry by Magnetic Resonance

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Introduction

Magnetic Resonance Spectroscopy (MRS) is a non-invasive tool that allows distinguishing brain malignant tumors from non-anaplastic tumors [1]. Metabolic maps can be obtained by the Chemical Shift Imaging (CSI) technique but they lack the spatial resolution necessary for therapy considerations. Relaxation studies have been used long ago for the assessment of tumors, being the T_2-map of a tissue often used as a basis for interpreting clinical images [2]. Diffusion-weighted MRI has been used successfully in the central nervous system (CNS), specially in the diagnosis of acute stroke, but also in distinguishing different components of brain tumors. In the present work, it is proposed the use of MRS, Relaxometry and Diffusometry for the segmentation of brain tumors.

Image Measurement and Analysis

CSI was performed axially to obtain spatial distributions of metabolite concentration across the lesion, TE = 30 ms and VOI of 96 cm^3 (80 x 80 x 15 mm). Relaxometry studies were performed using the standard multiecho sequence (CPMG) with 16 echoes, with a base echo time TE = 22 ms and 8 axial planes 5 mm thick centered at the tumor. Diffusion-weighted images were obtained for 16 b-parameter values ranging from 0 to 1350 s/mm^2 and 3 orthogonal magnetic field gradient directions (Phase, Read and Slice) for the same set of planes used in the relaxometry studies. The spectroscopy data analysis was performed based on relative values. The critical Cho/NAA ratio value for which a tissue was considered malignant was 1.3 or over. The spectra were considered atypical if the Cho/NAA ratio had a value between 0.9 and 1.29. For the analysis of relaxation and diffusion data, a special image processing algorithm was developed to extract the magnetization decays for different regions of interest or ROI´s. They were processed by an Inverse Laplace Transform (ILT) algorithm [3] to obtain the relaxation rates or diffusion tensor components present in the lesion. For each voxel the set of parameters obtained were assigned to a different state of the tissue (normal, pathologic, necrotic or edema) on comparison with the CSI data, using it as a sort of virtual biopsy.

Segmentation Procedure

Instead of applying the ILT algorithm pixel by pixel, which is a time consuming procedure with a low S/N ratio, the image intensity in each pixel (in a set of multiecho or multi-b images) was assumed to be a linear combination of exponential functions characterized each one by a decay parameter (relaxation rate or diffusion tensor component) associated to tissue type: $I(t)=b_I+A_R X_R(t)+A_G X_G(t)+A_B X_B(t)$ where $X_i(t)=\exp(-\lambda_i t)$ with i = R, G or B, λ_i is the decay parameter associated to the tissue, previously determined by application of the ILT algorithm over selected ROIs and b_I takes into account corrections in the baseline of the image intensity. The coefficients A_i, which are positive, give the proportion for each decay in the image and are determined by linear regression. The indexes were selected according to a RGB color code: R (red) corresponds to tumor, G (green) to normal or unaffected tissue and B (blue) to edema or necrosis [3], giving a color map in which each color component appears depending upon the proportion of the tissue type associated to that color. The selection of the color code is completely arbitrary and somewhat troublesome for clinical purpose, as it will be disscused below. Particular attention was paid to the correlation coefficient in the linear regression analysis so only coefficients A_i were accepted for those fittings with a correlation coefficient squared higher than 0.99. To further asses the segmentation procedure and in order to eliminate spurious and isolated "tumor positive" pixels due to the fact that exponential functions are correlated, each pixel affected by the presence of tumor, i.e., A_R is different from zero, is averaged over its neighborhood and accepted as a true "tumor positive" if and only if its average p is greater than 1/3. This kind of filter allows for a more compact segmentation of the tumor and discards scattered "tumor positive" points in the image.

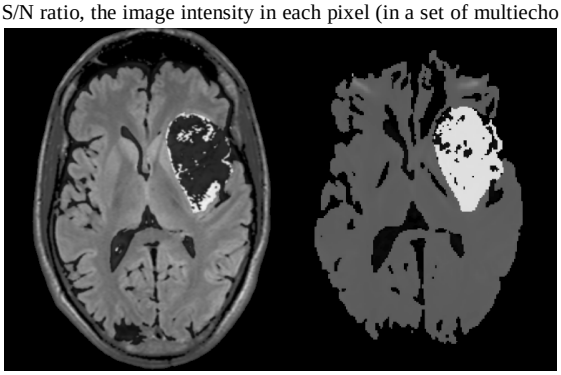

Figure 1. Left, segmented image using relaxation data. Right, segmented image using the trace of the diffusion tensor

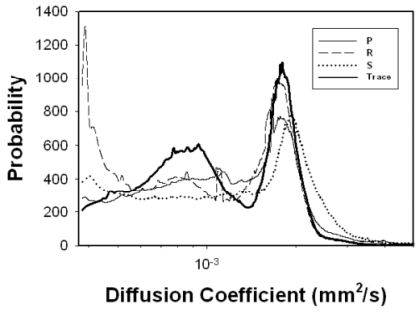

Figure 2. Distributions of diffusion coefficient

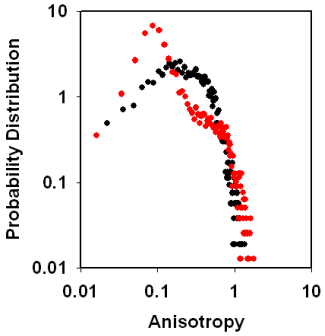

Figure 3. Comparison of anisotropy distributions between tumoral lesion (red dots) and unaffected tissue (black dots)

Results and Discussion

For a total of 10 patients the relaxation rates were within the following ranges: edema or necrotic tissue, 0.65 - 3.43 s^{-1}, tumor tissue, 5.05 - 7.47 s^{-1} and normal or non affected tissue (gray/white matter or meningeal tissue), 8.67 - 25.26 s^{-1}. Typical values for the average p covered a range 0.71 - 0.96. Control values of p were found in the range of 0.44 - 0.69. Figure 1 shows a typical result of segmentation using relaxometry and diffusometry data. Instead of using a color map in Figure 1, the RGB code is mapped on a gray scale as follows: for each pixel, the maximum of the A_i coefficients is determined; depending on the outcome (R,G or B), its value is mapped as: A_R in 206 - 255 (light gray), A_G in 51 - 205 (gray) and A_B in 0 - 50 (dark gray). This type of mapping resembles very well gadolinium contrasted images, which are familiar to radiologists. It preserves anatomical details, which are of relevance for image co-registration in therapy planning. The segmentation based on diffusion-weighted images is more troublesome since diffusion is anysotropic and so it depends on the gradient direction. In order to deal with scalar quantities, the diffusion-weighted images corresponding to the three orthogonal directions (P,R,S) are combined into a single set of diffusion-weighted images corresponding to the trace of the diffusion tensor. The distribution of apparent diffusion coefficients (P,R,S,T) over the lesion is shown in Figure 2. The same happens if other scalar quantities are considered, such as fractional anisotropy or relative anisotropy. Nevertheless, diffusion-weighted images can be used to define clearly what corresponds to unaffected tissue which exhibits high anisotropy opposed to tumoral or necrotic tissue with low anisotropy. In Figure 3 it is shown the resultant distribution of anisotropy for a tumoral lesion and unaffected tissue..

Conclusions

The methodology presented in this work clearly segments brain tumor images with appropriate spatial resolution for therapeutical needs. Other parameters, such as anisotropy can be considered to further improve the segmentation quality, but depends on the software available to the MRI facility. Finally, image registration for different data such as relaxometry or diffusometry seems to be the best way to assess a confident segmentation of the tumor image.

References

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