Estimation of Fractional Contributions of White and Gray Matter by Cross-Regularized Inverse Laplace Transform

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The fractional contributions of white matter (WM), gray matter (GM) and cerebro-spinal fluid (CSF) are increasingly used to describe the tissue composition of a pixel. This information may be used in the context of segmentation of the human brain, studies of demyelination and white matter lesions, tractography, and in single voxel spectroscopy. Multi-exponential fits of the water relaxation have been proposed to assess these fractions [1, 2]. In this paper, we attempt to estimate them from the distribution of T1 (relaxogram) computed by inverse Laplace transform (ILT).

Methods and Results: ***CONTIN Analysis*** – A Look-Locker train of 64 IR-images acquired at 4 Tesla, non linearly sampled from 36.5 ms to 17.1 sec, 10 mm slice thickness and 3.4 mm^2 in-plane resolution was kindly provided by Dr. Brown and Dr. Springer [3]. The quality of the inversion pulse was checked with a monoexponential fit of CSF signals (ca. 98%). A second-order regularized CONTIN [4] analysis with 64 T1 grid points logarithmically spaced between 158.5 ms and 7.943 sec was performed to explore the overall relaxogram (Figure 1). The short peak at 224 +- 15.7 ms appears to arise from white matter, but may be an artifact caused by the early rapidly repeated 5° read pulses after the adiabatic inversion pulse. While the CSF peak is well resolved at 3.93 +- 0.53 sec, white matter and gray matter are combined into a single broad peak at 1.53 +- 0.38 sec. None of the pixels displayed two resolved peaks in this WM-GM region.

Cross-Regularized ILT – In order to increase the relaxogram resolution, a cross-regularizor imposing smoothness between grid point values of 8 directly connected pixels to a target pixel was used [5]. For memory limitations pixel connectedness was imposed with a sliding neighborhood of 5-by-5 pixels. To limit processing time, the WM-GM region between 960.6 ms and 2.29 sec was described with 8 logarithmically spaced grid points, the short and CSF peaks were accounted for with 2 further grid points at 222.1 ms and 3.956 sec. The cross-regularized ILT permits to observe bi-modal peaks in the WM-GM region (pixels highlighted in red in Figure 2). The corresponding average relaxogram displays two maxima at 1.474 sec and 1.997 sec.

Fractional Contributions – T1 in white matter has been reported as scaling linearly with myelin content [6]. Correspondingly, we assumed that the fractional contribution of white matter can be estimated from the relaxogram amplitude s(T1), $T1_{wm}$ and $T1_{gm}$, the T1 for tissues respectively with the highest myelin and lowest myelin contents, such that $p_{wm}(T1)=(T1_{gm}-T1)/(T1_{gm}-T1_{wm})$ between $T1_{wm}$ and $T1_{gm}$ and the fractional contribution $f_{wm}=\Sigma\, p_{wm}(T1)\, s(T1) / \Sigma\, s(T1)$. The fractional contribution f_{gm} was similarly computed by assuming $p_{gm}(T1)=1-p_{wm}(T1)$. The CSF fraction f_{csf} was obtained by dividing the CSF grid point at 3.956 sec by $\Sigma\, s(T1)$. The T1 values of tissues with mostly white matter and mostly gray matter respectively were searched as follows. In a first step, pixels sharing the same maximum were grouped to define an ROI (inlets in Figure 3) and to compute a corresponding average T1 (plotted in Figure 3). In a second step, the minimum value at 1.188 sec was assigned to $T1_{wm}$ and the maximum value at 1.774 sec to $T1_{gm}$. The resulting fractional contributions of the three tissue types are shown in Figure 4. The short component at 222.1 ms was ignored. However when including this short component, a significantly shorter T1 was found for WM (0.983 +- 0.436 sec) which is in good agreement with the value reported by Brown et al. (0.98 +- 0.02 sec [3]). The effect of the Look-Locker train at early TIs may require some further investigation.

Discussion: Pixel connectedness allowed in some pixels to observe two separate peaks in the WM-GM region otherwise not distinguishable in a standard constrained relaxogram. The fractional contributions estimated by the cross-regularized ILT effectively perform a segmentation without prior neuro-anatomical knowledge. This may be helpful when studying demyelinating diseases, white matter lesions or heavily myelinated cortex. The fractions can be further used to construct an RGB composite image as proposed by Brown et al. [3]. The RGB composite image in Figure 4 combines signal intensity with T1 information encoded as a color (green for WM, red for GM and blue for CSF), thus enabling to visualize where mixtures of white matter and gray matter occur (for example yellow and orange regions).

References: [1] Vermathen P et al. (2004) Proc. 12th ISMRM, 2270. [2] Evans CJ et al. (2005), Proc. 13th ISMRM, 60. [3] Brown TR et al. (2005) Int. J. Imaging Syst. Technol. 15:2-9. [4] Provencher SW (1982) Comp. Phys. Comm. 27:229-242. [5] Labadie C & Jarchow S (2004) Proc. 12th ISMRM, 2707. [6] Stanisz GJ et al. (2000) Proc. 8th ISMRM, 1190

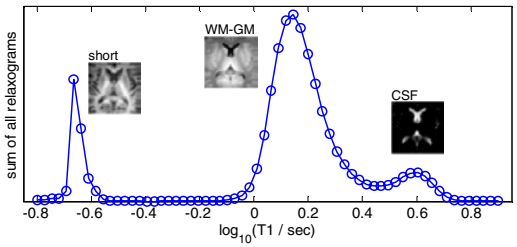

Figure 1: CONTIN analysis, sum of all relaxograms

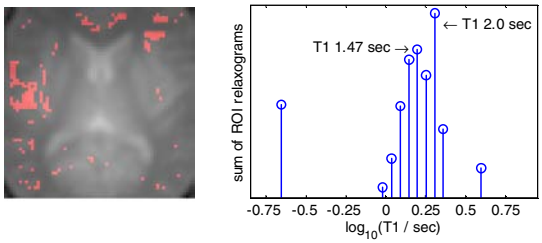

Figure 2: Cross-regularized ILT, pixels (highlighted in red) with bi-modal relaxograms in the WM-GM region

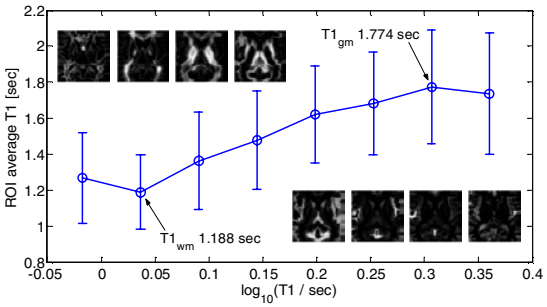

Figure 3: ROI search of $T1_{wm}$ and $T1_{gm}$

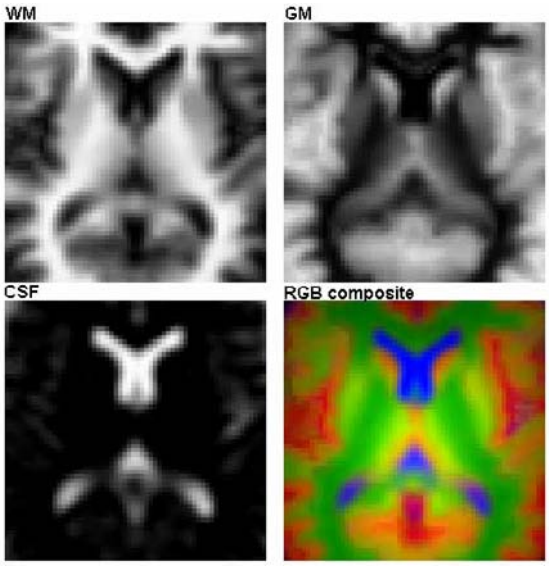

Figure 4: Fractional contributions, RGB composite image