Sequence optimization for T_1-based tissue separation

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Introduction

Relaxation times T_1 and T_2 have served as a principal source of contrast in magnetic resonance images, helping to distinguish between different kinds of healthy tissue or between healthy and or unhealthy tissues. In the current study, we tried to develop a sensitivity-optimized pulse sequence to selectively highlight a narrow range of T_1 values. Our main field of interest was 3D MRI of the human brain, and the differentiation between grey matter, white matter and cerebrospinal fluid (CSF).

Methods

The MRI signal from a single voxel may be regarded as the linear superposition of N signals, each originating from a different type of substance, and each weighted by the substance's concentration in the voxel. Thus, the signal for every given time t can be written as $S(t) = \Sigma_i \rho_i b_i(t)$, where ρ_i denotes the individual tissue type's density and relative weighting for the specific voxel, while $b_i(t)$ corresponds to the evolution of the tissue's signal over time, as defined by its relaxation times and the sequence characteristics.

Contributions from individual tissue types can be distinguished by taking M images, $M \geq N$, at time points t_j and calculating coefficients a_{ij} so that $\Sigma_j a_{ij} b_k(t_j) = \delta(i-k)$, δ being the Kronecker delta function. In this case, $\Sigma_j a_{ij} S(t_j) = \rho_i$, which corresponds to the contribution of a specific type of tissue.

It can be shown that the noise in the combined image is proportional to $\Sigma_j a_{ij}^2$. Thus, we tried to minimize this quantity using simulated annealing [1] in a sequence producing two images, one of white matter with suppressed grey matter and CSF, and one of grey matter with suppressed white matter and CSF signal. No assumptions were made as to the number, timings (other than minimum intra-pulse spacing) or flip angles of the pulses involved.

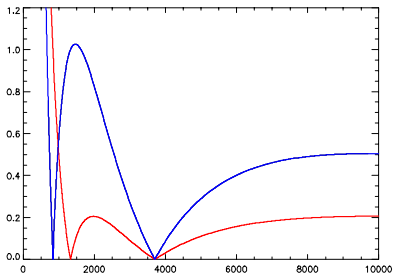

Figure 1: Signal intensity in the combined image as a function of T_1 in ms (red – white matter reconstruction, blue – grey matter reconstruction)

Results

The resulting sequence, with target duration of 6 seconds, consisted of 5 pulses, three imaging pulses interleaved with two inversion pulses. Thus, it can be regarded as a modification of the double inversion recovery sequence [2]. Each imaging pulse was followed by a standard gradient echo EPI acquisition scheme, with TE=43ms, acquisition time 72ms, slice thickness 4mm, 128x96 resolution and FOV 220x165mm. Adiabatic pulses were used for the inversion pulses. Actual flip angles and timings varied according to the assumed T_1 values. Signal sensitivity in the combined images, as a function of T_1 is shown in figure 1. The design was tested on healthy volunteers, scanned after giving informed consent under IRB protocol on a GE 3T scanner with a 16 channel Nova head coil and home built digitizer [3]. Since the expected sign of $b(t_j)$ for all tissue types was constant for each original image, magnitude data was used in order to avoid phase errors. Resulting grey and white matter images are shown in figures 2 and 3 respectively. Some lipid contamination is apparent in the images, despite the use of fat suppression. This is subject of further optimization.

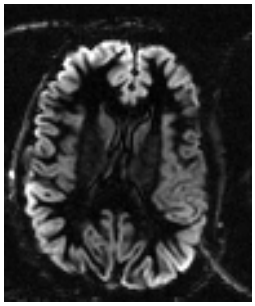

Figure 2: Grey matter image

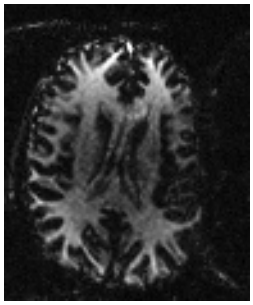

Figure 3: White matter image

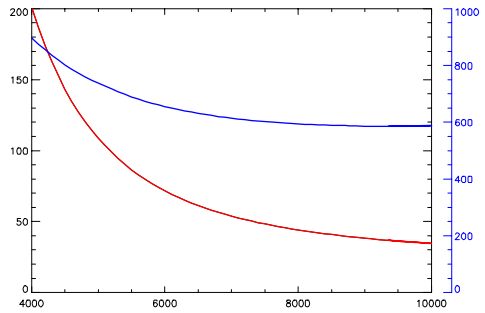

Figure 4: Noise power as a function of sequence duration in ms for grey matter reconstruction. (Red – noise power relative to reference image, blue – square root of noise power amplification multiplied by the square root of sequence duration)

Discussion

Our optimized pulse sequence allowed for the generation of single-slice grey and white matter images with high sensitivity. For 3D application, a remaining design issue is sequence duration. Figure 4 shows noise amplification as a function of sequence duration. The optimal duration for this design and the elected T_1 values occurs at about 9 seconds. However, in the case of three dimensional (3D) scanning, where scan time equals sequence time * number of slices, this might not be practical due to time constraints. Under these conditions, sequence duration is a compromise between SNR, resolution and examination time.

The dependence of signal sensitivity on T_1, as shown in figure 1, allows for slight variation in the actual T_1 values, which is to be expected even within a single tissue between different parts of the brain [4]. For larger variations, the coefficients a_{ij} can be recalculated using the $b_i(t)$ corresponding to the actual T_1 values.

Conclusion

We have presented a sequence that allows distinction between different tissue types based on T_1. The scheme is optimized to simultaneously produce images of different tissue types. It also permits post-acquisition correction of the initial T_1 estimation.

References

[1] Vanderbilt D, Louie SG, *J. Comp. Phys.* **56**: 259 (1984), [2] Redpath TW, Smith FW, *Br. J. Radiol.* **67**: 1258 (1994), [3] de Zwart JA *et al.*, *Magn. Res. Med.*, in press, [4] Wansapura JP *et al.*, *J. Magn. Reson. Imaging*, **9**: 531 (1999)