Model-Based Iterative Reconstruction

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Currently, MR images are mostly evaluated qualitatively, i.e. by using the relative intensity differences between pathological and healthy tissue. In spite of the huge success of MRI in the last decades, this approach is not optimal in terms of image comparability and traceability. Instead, one could measure the underlying physical properties which generate the contrast differences, having the advantage of directly measuring «hard» physical parameters which are better comparable.

Background

However, corresponding parameter mapping acquisition techniques are typically very long, impeding their clinical application. The goal of this project was to overcome this limitation by using an iterative reconstruction approach which allows high data undersampling and thus drastically reduces the acquisition time. The a-priori information used for the image reconstruction is a model of the signal behaviour, in the present case of the longitudinal relaxation. Using this knowledge and an iterative reconstruction approach allows for high under-sampling of the data and thus to speed up the acquisition.

Realization

An existing iterative reconstruction framework for T2 mapping was extended to allow for T1 quantification (see Fig. 1). A mono-exponential signal model, which serves as a-priori information, was developed and evaluated by phantom and in-vivo measurements. A numerical phantom was used to optimize the employed MR sequence parameters, i.e. the number of samples on the T1 relaxation curve required and the different sampling patterns. Furthermore, by using in-vivo measurements, the performance of the algorithm for different sampling schemes was tested and practical limits were investigated. All implementation was performed in Matlab (The Mathworks Inc., MA, USA).

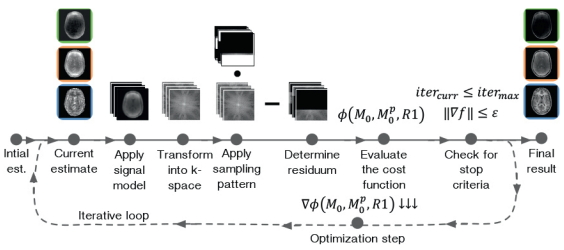

Fig. 1 Illustration of the model-based iterative reconstruction algorithm.

Results

A T1 relaxation model was developed, optimized and implemented in the reconstruction framework. Using acquired phantom and in-vivo data, it was found that randomly distributed sampling patterns yield the best reconstruction results. Furthermore, optimal acquisition parameters were deduced. Obtained in-vivo T1 maps were compared to a reference mapping technique (MP2RAGE). It has been shown that, by applying iterative reconstruction techniques and exploiting recent progress in mathematical methods, it is possible to sample the MR signal below the Nyquist limit while retaining good image quality. In conclusion, it was found that clinically usable T1 maps can be obtained with up to 4-fold acceleration (see Fig. 2). This reduces the typical, non-accelerated acquisition time of 12 minutes to only 3 minutes.

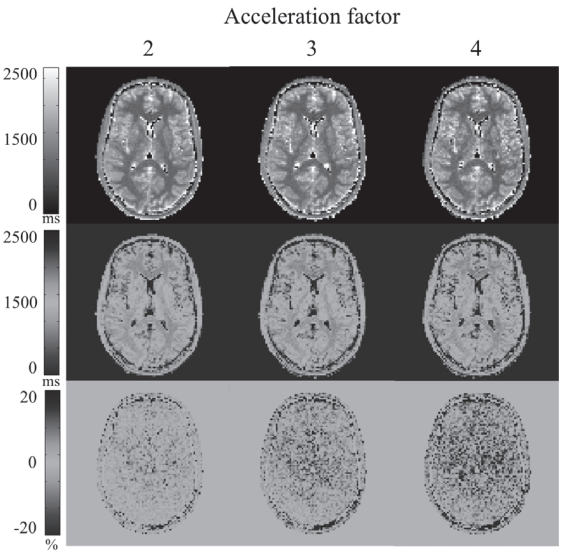

Fig. 2 T1 maps reconstructed from in-vivo measurements are shown for different acceleration factors.

Michael Rieger