

Accelerated R_2 mapping through undersampling and k - t reconstruction

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Introduction: A R_2 mapping experiment is based on the acquisition of several echoes produced by a train of 180° RF pulses with a given echo spacing [1]. This multi-echo experiment must be repeated with different phase-encoding gradients, until the entire k -space has been covered, which results in long acquisition times. Hence, the measurement is prone to motion artefacts, may require long breathholds, and has a reduced temporal resolution. Moreover, the associated SAR is high. This work presents a method combining k -space undersampling and reconstruction in k - t space in order to reduce the number of phase-encoding steps, while preserving measurement accuracy and spatial resolution.

Theory: The proposed k -space sampling pattern is similar to that used in k - t BLAST [2], with the difference that the temporal axis represents here the time after the initial RF pulse, during which relaxation takes place. Only every R phase-encoding step is acquired, where R is the target reduction factor. To achieve a better coverage of k -space over time, the position in k -space of the measured readout is shifted from one echo to the next. Hence, after R echoes, each k -space line has been acquired once. The shift in k -space between two consecutive echoes can be achieved through the introduction of a blip gradient. On top of that, a number of blocks consisting each of $R-1$ consecutive k -space lines without reduction need to be acquired for calibration purposes, preferably in the centre of k -space. Fig. 1 summarizes the sampling pattern for $R=2$.

Due to the sub-sampling, images obtained for each echo contain fold-over artefacts, if reconstructed with a standard Fourier transform. Hence, it is proposed to first estimate the missing k -space data. As a first approximation, the ratio of the magnetization signals of two consecutive echoes is a constant depending on R_2 and the echo spacing. Hence, k -space data of consecutive echoes are linked via a convolution product whose kernel is the same for all echoes. This intrinsic temporal redundancy is the basis of the proposed k - t reconstruction and calibration scheme. Each missing sample $S_i(k_x, k_y)$ is reconstructed on the basis of a linear combination of its neighbors in the k - t space, as illustrated in Fig. 1 for a 3×3 neighbourhood size. For example, for $R=2$, the reconstruction of the odd lines of the even echoes with a neighbourhood of size $(2n_x+1) \times (2n_x+1) \times (2n_y+1)$ can be written as:

$$\hat{S}_{2t}(k_x, 2k+1) = \sum_{\tau=-n_\tau}^{n_\tau} \sum_{i=-n_x}^{n_x} \sum_{j=-n_y}^{n_y} w_{\tau,i,j} S_{2t+\tau}(k_x+i, 2k+2j+(\tau\%2)),$$

The computation of the reconstruction coefficients w is performed on the basis of a least-squares fit that involves the calibration samples, as in GRAPPA [3].

Methods: R_2 mapping in the brain was performed to evaluate the proposed acceleration scheme. A turbo spin echo train consisting of 24 echoes with 6.5ms echo spacing (resolution $1.6 \times 1.6 \times 6$ mm, $TR=400$ ms) was acquired with a head-coil on a 1.5T scanner (Achieva, Philips Medical Systems). A reference R_2 map was computed from the fully sampled acquisition. Then, the data were decimated off-line according to the proposed sub-sampling scheme for different reduction factors R , and reconstructed with the k - t space algorithm described above. 8 blocks of calibration lines were used to compute the reconstruction coefficients. The effective reduction factors achieved were 1.8 for $R=2$, and 2.5 for $R=4$. A neighbourhood size of $5 \times 9 \times 8$ was used for reconstruction. R_2 maps were computed by means of a non-linear least squares algorithm.

Results and discussion: The R_2 maps computed after reduction and the reference map are shown in Fig. 2a-c. Some folding artefacts can be seen on the fourfold-accelerated map (Fig. 2c), otherwise differences in the R_2 values are mainly due to noise in the data, as can be seen on the difference maps (Fig. 2d-e). The root mean square error over a ROI comprising the brain was $0.8s^{-1}$ for $R=2$, and $1.3s^{-1}$ for $R=4$.

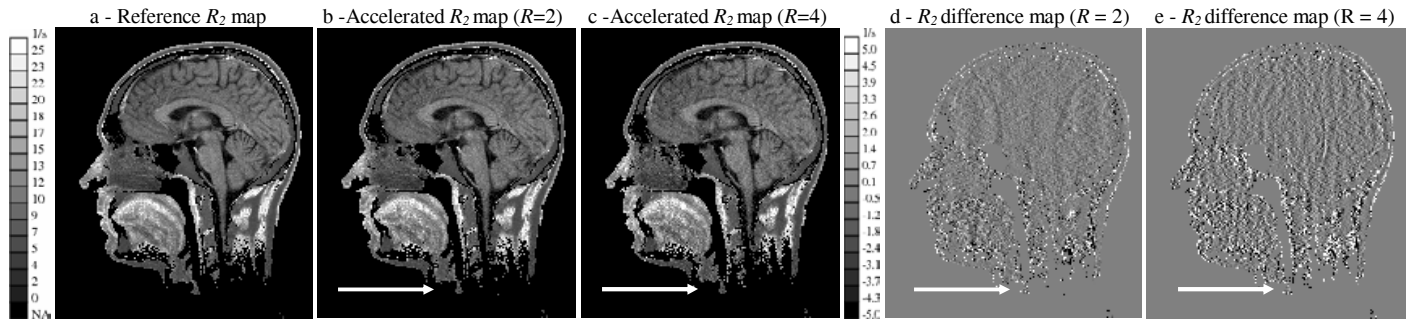


Fig. 2: R_2 maps computed with the different undersampling factors and corresponding difference maps. The white arrow indicates the sub-sampling direction.

Residual folding artefacts in the reconstructed images may be caused by the rapidly vanishing signal of species having short T_2 values, especially at the first echo times. These artefacts can be removed by means of a larger neighbourhood size during reconstruction. Also, the effects of a deviation from a strict mono-exponential decay remains to be assessed. Despite these limitations, the obtained results show that the number of phase-encoding steps can be significantly decreased with the proposed method. Further investigations are needed to determine the optimal achievable reduction factor, also in combination with other fast imaging techniques.

Conclusion: A new method has been proposed to reduce the number of phase-encoding steps in a R_2 mapping experiment and has been tested in the brain. Relaxation rates could be accurately estimated, with only a slight increase of noise. The method promises to significantly reduce scan time and SAR in R_2 mapping experiments.

References: [1] Haacke et al, Magnetic Resonance Imaging (1999). [2] Tsao et al, MRM, 50:1031-1042 (2003). [3] Griswold et al, MRM, 47:1202-1210 (2002). [4] J. S en egas et al, ISMRM, # 227 (2006).