

# Multi-Channel Line-Sharing for Rapid T1 Mapping: Application to TAPIR

N. J. Shah<sup>1</sup>, I. A. Gilani<sup>1</sup>, H. Neeb<sup>1</sup>, and A. M. Oros-Peusquens<sup>1</sup>

<sup>1</sup>Institute of Neurosciences and Biophysics (Medicine), Research Centre Jülich, Jülich, Germany

**INTRODUCTION:**  $T_1$  mapping with partial inversion recovery (TAPIR) is a novel sequence which enables high-resolution, multislice  $T_1$  relaxation-time mapping [1-3]. TAPIR is a Look-Locker-based  $T_1$  mapping approach based on a partial inversion recovery scheme which is typically faster than traditional inversion recovery based methods. The accuracy and precision of TAPIR to measure  $T_1$  are high, but a reduction in the acquisition time is required to allow for  $T_1$  mapping in clinically acceptable measurement times. Therefore, a scheme termed multi-channel, line-sharing is introduced here as modification of the traditional full  $k$ -space sampling scheme in TAPIR. In the new approach, the central  $k$ -space region (the keyhole) is fully sampled whereas the high-frequency  $k$ -space region in the phase-encode direction is undersampled. In order to avoid fold-over artefacts, missing  $k$ -space lines are reconstructed using linear interpolation of the corresponding lines acquired for the neighbouring time-points on the  $T_1$  relaxation curve. The method is generally applicable to any mapping scheme acquiring the full  $k$ -space and is fully compatible with parallel imaging.

**METHODS:** *In vivo* data of a single healthy volunteer were acquired on a 4T system using TAPIR. The sequence parameters were: TR=15 ms, TE=2.5 ms, BW=700 Hz/Px,  $\tau$ =2000 ms,  $\alpha$ =40°, TI=10 ms, 14 slices, slice thickness=2 mm, FOV=256 mm x 256 mm, EPI factor=1 and time-points=20. The matrix size was 256x256. An 8-channel phased-array receive coil was used and the *in vivo* data were acquired from each of the 8 channels. The multi-channel, line-sharing method was performed in using Matlab for each of the single-channel  $k$ -spaces as follows: the high frequency part of  $k$ -space was undersampled by omitting every second line while fully sampling the keyhole which comprises one-eighth of the full  $k$ -space. As multiple time-points on the  $T_1$  relaxation curve are sampled in TAPIR, omission of lines is performed in an interleaved way. For odd time-points ( 1, 3, ... ), even lines ( 2, 4, ... ) of  $k$ -space were omitted whereas that scheme was reversed for even time-points (see Fig. 1) i.e., lines 1,3,5, .. were sampled for the first acquired time-point on the relaxation curve while lines 2, 4, 6, .. were acquired for the second time-point. For each time-point, except the first and the last, the complex valued  $k$ -space data for the omitted lines were linearly interpolated using the complex-valued data of the corresponding lines from the preceding time-point and the succeeding time-point as shown in Figure 1. The omitted lines of the last time-point were substituted from the corresponding lines of the second last time-point. Correspondingly, omitted lines at the first time-point were substituted from the corresponding lines of the second time-point. The resulting data from each of the 8 channels were Fourier transformed resulting in the reconstruction of so called line-shared images. For each time-point, the line-shared images from each of the 8 channels were combined by using the sum-of-squares algorithm. Those were used to calculate the line-shared  $T_1$  map. There were no visible fold-over artefacts in the combined line-shared images and line-shared  $T_1$  map. In addition, the original  $T_1$  map was reconstructed using the original data without line-sharing. All  $T_1$  maps were obtained using an in-house tool based on the Levenberg-Marquardt algorithm. The relative difference between the original  $T_1$  map and the line-shared  $T_1$  map was calculated. Based on the relative difference image, average difference values for different ranges of  $T_1$  were determined.

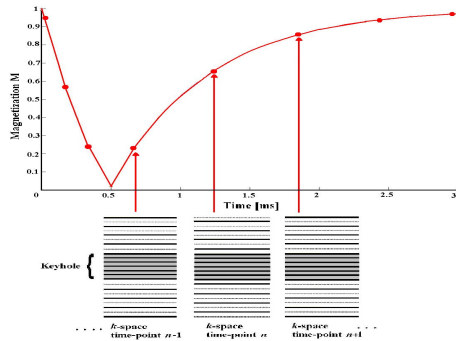


Fig.1.

**Fig.1.** Schematic representation of the line-sharing concept. The skipped phase-encode lines are shown as thin lines whereas the acquired phase-encode lines are shown as thick lines at the time-points  $n-1$ ,  $n$  and  $n+1$ .

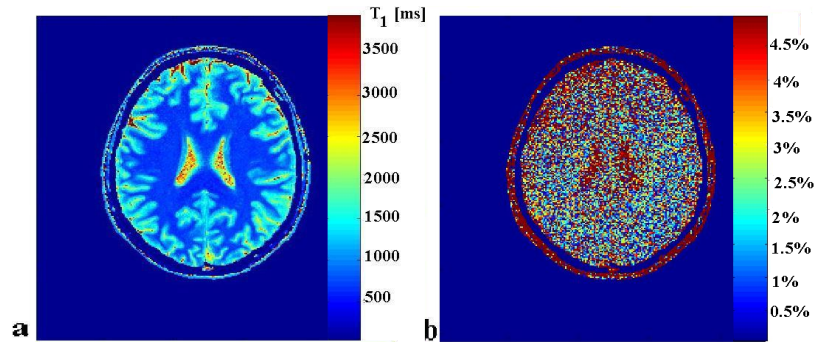


Fig.2.

**Fig.2.** a: A representative line-shared *in vivo*  $T_1$  map. b: Relative difference map between the line-shared  $T_1$  map and the original  $T_1$  map of the same slice as shown in (a) Average differences values higher than 5% were clamped to 5%.

**RESULTS:** A representative line-shared  $T_1$  map of a slice is shown in Figure 2a. The relative difference between line-shared  $T_1$  map and original  $T_1$  map is shown in Figure 2b. For most voxels, the relative difference remains below 3%, with the exception of the ventricles. This is also confirmed by the results shown in Table 1 which demonstrates that the relative systematic error of  $T_1$  due to the line-sharing approach is well below 1% for grey and white matter even at 4T.

**DISCUSSION and CONCLUSIONS:** The proposed trajectory inherently samples the centre of  $k$ -space densely at each time-point such that the central  $k$ -space, the keyhole, satisfies the Nyquist sampling rate. The rest of the  $k$ -space is sparsely sampled. The skipped  $k$ -space lines are linearly interpolated by using the preceding and succeeding time-points. This method has the potential to reduce the total acquisition time by 40%. The reconstructed line-shared  $T_1$  maps exhibit high quality without visible artefacts. As the additional systematic error for most brain tissue (i.e. grey and white matter) remains significantly below 1%, the proposed line-sharing approach offers the possibility to significantly accelerate the measurement without introducing additionally significant error components. The method is generally applicable to relaxation time mapping techniques be they  $T_1$ ,  $T_2$ , or  $T_2^*$ . Further, given the acquisition of a keyhole, the line-sharing method is fully compatible with parallel imaging whereby a further reduction in the number of peripheral lines could be achieved. The precision of the method for  $T_1$  mapping is expected to increase with increasing field (longer  $T_1$ ), where the interval of highest variation – and thus highest error for interpolation - on the relaxation curves is sampled with a larger number of points.

**REFERENCES:** [1] Shah NJ, Zaitsev M, Steinhoff S, Zilles K. A New Method for Fast Multislice  $T_1$  Mapping. *NeuroImage* 2001;14:1175–1185. [2] Steinhoff S, Zaitsev M, Zilles K and Shah NJ. Fast  $T_1$  Mapping With Volume Coverage. *Magn Reson Med* 2001;46:131–140. [3] Shah NJ, Steinhoff S, Zaitsev M. Pulse train, nuclear magnetic resonance tomograph and imaging method. US-Patent: 6,803,762 B2, Oct. 12, 2004.

Range of $T_1$ Values (ms)	Percentage Difference (%)
$500 \leq T_1 < 1000$	0.26
$1000 \leq T_1 < 1500$	0.32
$1500 \leq T_1 < 2000$	0.36
$2000 \leq T_1 < 2500$	2.81
$2500 \leq T_1 < 3000$	1.22

**Table.1.** Average difference between line-shared and original  $T_1$  map for different  $T_1$  ranges.