# MAGNETIC RESONANCE FINGERPRINT COMPRESSION

Martijn A Cloos[1,2], Tiejun Zhao[2,3], Florian Knoll[1,2], Leeor Alon[1,2], Riccardo Lattanzi[1,2], and Daniel K Sodickson[1,2]

*[1]Center for Biomedical Imaging, Department of Radiology, New York University School of Medicine, New York, NY, United States, [2]Center for Advanced Imaging Innovation and Research (CAI2R), New York University School of Medicine, New York, NY, United States, [3]Siemens Medical Solutions USA Inc., Malvern, PA, United States*

**INTRODUCTION:** Magnetic Resonance Fingerprinting (MRF) enables rapid multi-parametric mapping [1]. By interweaving multiple transmit-channels into the fingerprinting sequence an elegant parallel transmission (PTX) framework can be constructed [2]. Forgoing uniform excitations, this generalized MRF framework circumvents a pitched battle against the electro-dynamic interactions that cause $B_1^+$ artifacts in the traditional MR paradigm while maintaining a tractable "plug & play" workflow. In this work we introduce the concept of "fingerprint compression", which enables even greater acceleration factors while simultaneously speeding up the reconstruction process.

**THEORY & METHODS:** The proposed compression step serves two purposes. Firstly, to reduce the size of the dictionary by projecting the matching processes from a complex space (phase and amplitude) onto a real space of lower dimension. However, MRF depends on a high degree of incoherence between data samples. Therefore, a clever compression algorithm is needed that captures the valuable incoherences in the signal. Secondly, to accelerate the matching process by reducing the number of data points in each fingerprint. This is of particular interest in the context of PTX where the need to resolve the interplay between different transmit phase contributions is a computational burden. In general, each additional transmit-channel adds two more dimensions to the dictionary, which carry little or no information of relevance to everyday clinical imaging. By pairing fingerprint compression with a sequence engineered to decouple the transmit-phase interactions, all the phase dimensions (one per transmit channel) can be removed from the dictionary.

To demonstrate this principle we designed a generalized PTX fingerprinting sequence (**Fig. 1**), which consists of 4 segments each containing 120 excitations 4.8ms apart. The first and third segments contain RF spoiled gradient echoes that predominantly encode $B_1^+$ and T1, whereas the other segments also add a T2 relaxation component (no RF spoiling). Collectively, these 480 snapshots capture a distinct signal evolution (the MR fingerprint) that simultaneously identifies the RF-field distributions and tissue properties. To increase T1 accuracy and help decouple transmit phase interactions a strategically chosen delay was inserted between segments. Interleaving 6, or more, slices, each delay can be used to image a different slice, thus eliminating all dead time in the protocol. A golden angel radial sampling strategy was selected promote incoherence between undersampling artifacts [3].

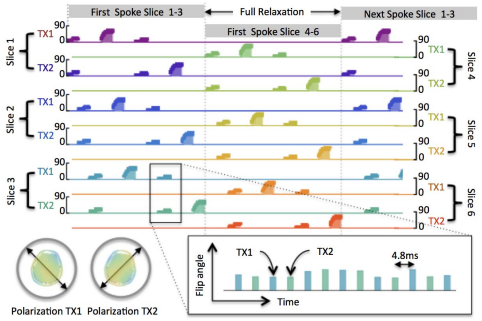


**Figure 1:** Parallel transmission enabled MR Fingerprinting sequence diagram.

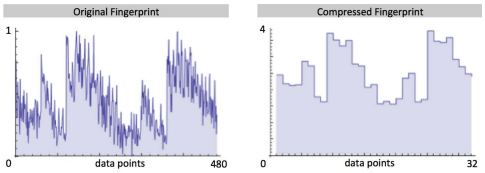


**Figure 2:** Schematic illustration of the fingerprint before and after compression.

Figure 2 shows an example fingerprint before and after compression. Effectively, the procedure integrates sets of 15 data points. Based on the sequence design, these subsets were arranged such that all data points have the same underlying transmit phase. During the scan multiple transmit-channels are interleaved (**Fig. 1**, zoomed section). Because each channel produces a different phase distribution, the compression arranges the subset based on the expected phase configuration defined in the sequence. Prior to summation, the signal contributions from each receiver is multiplied by the conjugate of the receive sensitivity estimated from the k-space center. This way, the incoherent phase contributions due to aliasing artifacts interfere destructively. Under ideal conditions, this would result in a real valued compressed fingerprint. In practice, some phase variations and residual aliasing artifacts remain. Empirically we found that these can safely be disregarded by taking the absolute value. The same compression was applied to the pre-simulated dictionary [4] and permanently stored. The underlying tissue properties were retrieved by identifying the dictionary element that best correlates with the compressed fingerprint. The matching algorithm was implemented in MatLab (The MathWorks, Inc., Natick, Massachusetts, United States) augmented with C++ code.

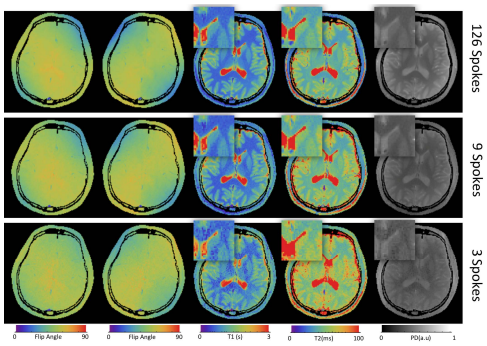


**Figure 3:** Parametric maps ($B_1^+$, $B_1^+$, T1, T2, PD) reconstructed based on the full 480 sample fingerprint.

Brain images were acquired using a standard 20-channel head-neck receive coil in a clinical dual-transmit 3 Tesla system (Siemens, Erlangen, Germany). Sequence parameters were: 160x160 matrix, 1.5x1.5mm$^2$ in-plane resolution, 4mm slice. Three different acceleration factors were used {*2, 28, 84*} corresponding to {126, 9, 3} radial spokes snapshot and to a total scan time of {*290, 21, 7*} seconds per slice (**Fig. 2**). The study was approved by our institutional review board (IRB), and written informed consent was obtained prior to the examination.

**RESULTS & DISCUSSION:** The top row of Figure 4 shows the parametric maps reconstructed using the nearly fully sampled data set (126 Spokes). Based on extensive phantom validations we know these values to be accurate (results not shown). As the acceleration factor is increased, the uncompressed reconstruction gradually starts to deviate (**Fig. 3**, center row). When pushed to the extreme (acceleration factor of 84), both T1 and T2 values are significantly deteriorated (**Fig. 3**, bottom row). Using the proposed compression approach a high accuracy is maintained, revealing almost no changes compared to a near full sampling of k-space (**Fig. 4** top row). Even at an acceleration factor of 84, the parametric maps remain comparable to the ground truth (**Fig. 4** bottom row). However, when using only 3 spokes per snapshot, noise like granularity starts to appear in the quantitative maps suggesting that the underlying SNR is starting to become a limiting factor. In addition to enabling a further 3+ fold reduction in scan time, the compression decreases dictionary size from 32GB to 1GB and reduces the reconstruction time from nearly an hour to less than one minute per slice. Although the proposed approach is also applicable to single transmit systems, its advantages are most pronounced in the context of PTX.

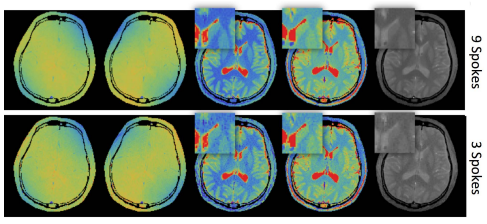


**Figure 4:** Parametric maps reconstructed with fingerprint compression (same color scale as in **Fig. 4**).

**CONCLUSIONS:** Using the concept of MR fingerprint compression, we were able to simultaneously quantify $B_1^+$ (for 2 transmit channels), T1, T2 and PD, one additional dimension compared to the original MRF publication [1], at a substantially higher resolution (1.5 vs 2.3mm) in less time (7 vs 12.3 s). Moreover, a simple "plug & play" PTX workflow is maintained, which inherently circumvents the detrimental effects of excitation non-uniformities that hamper traditional MRI and MRF experiments.

**REFERENCES:** [1] Ma, et al., Nature, 2013;479:187-192. [2] Cloos et al., ISMRM 2014 p542. [3] Winkelmann, et al. IEEE-TMI, 2007;27:68-76. [4] Weigel JMRI, 2014; DOI: 10.1002/jmri.24619