

## Effective data sharing method for extreme cartesian undersampling in MRF

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### Introduction

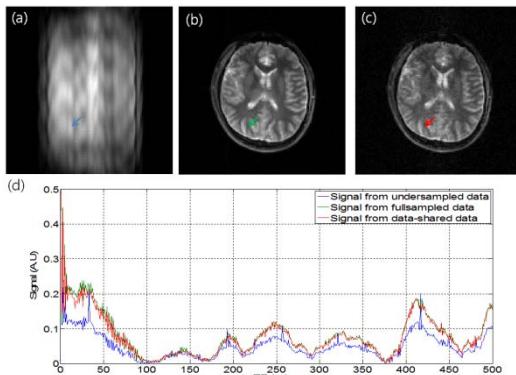
Magnetic resonance fingerprinting (MRF) is a new powerful method for fast MR parameter ( $M_0$ ,  $T_1$ ,  $T_2$ ,  $\Delta B$ ) mapping. The parameter maps are obtained by matching the signal evolutions from specific tissues with the calculated signal evolutions based on the MR forward modelling (dictionaries) [1]. This method uses variable density spiral (VDS) trajectory for fast data acquisition through undersampling scheme. However, VDS trajectory is not widely used for clinical settings because its implementation is not robust depending on the stability of MR systems. Therefore, the well-established Cartesian trajectory needs to be considered for the applications of MRF in the clinical settings. In order to use Cartesian trajectory in MRF, extreme undersampling has to be performed to k-space data for fast data acquisition. This undersampling causes severe aliasing or blurring artifacts on images, so the parameter mapping becomes almost impossible. To resolve this problem, various methods such as compressed sensing (CS) and iterative method have been developed. However, the current CS methods are limited to the reduction factor of up to 5, which is not enough for the extreme undersampling need required in MRF. In this paper, we propose an efficient data sharing method to overcome this problem for extremely undersampled Cartesian trajectory data with reduction factor of up to 21. The results demonstrate that the accurate parameter mapping can be possible even with extreme undersampling in Cartesian trajectory acquisition, which can bring robustness to the implementation of MRF in the current clinical settings.

### Methods

For simulation studies, realistic distribution of *MR* parameter maps ( $M_0$ ,  $T_1$ ,  $T_2$ ,  $\Delta B$ ) were used (Fig1 and 2). Series of multiple images were generated from these parameter maps through the Bloch simulation with random flip angle (FA) and repetition time (TR) patterns similar to [1]. Number of time points were 1000, and the ranges of FAs and TRs were  $0\sim 80^\circ$  and 4~8ms, respectively. All image reconstruction and processing were performed using MATLAB (The MathWorks, Inc., Natick, MA).

In the proposed data sharing method, an empty k-space line due to undersampling at the specific time point is filled with a weighted combination of several k-space lines in the same k-space position at other time points. The data sharing process was performed by following 4 steps: (1) Center k-space lines are acquired for all time points during data acquisition; (2) In order to fill the  $i$ -th empty k-space line at the  $j$ -th time point, select time points that contain the  $i$ -th k-space line; (3) Find weighting coefficients that can best represent the center k-space line at the  $j$ -th time point as a weighted combination of center k-space lines at the selected time points in (2) using orthogonal matching pursuit (OMP) [2] algorithm; (4) Fill the  $i$ -th empty k-space line at the  $j$ -th time point by:  $\vec{k}(l_i, t_j) = \sum_{k \in P_i} w(l_i, t_k) \vec{k}(l_i, t_k)$ , where  $\vec{k}(l_i, t_j)$  is the  $i$ -th empty k-space line at the  $j$ -th time point,  $P_i$  is the set of time points which sampled the  $i$ -th k-space line, and  $w(l_i, t_k)$  is the calculated weighting coefficient in (3) for the  $i$ -th k-space line at the  $k$ -th time point.

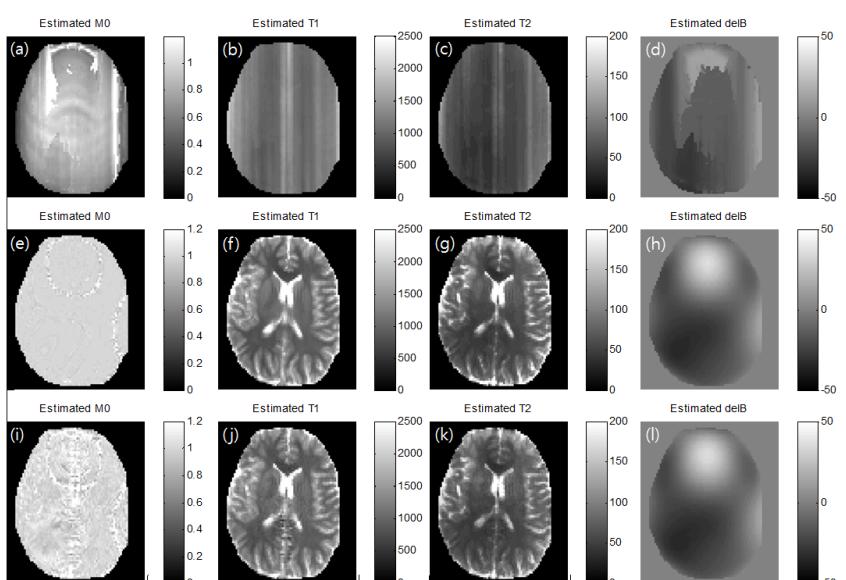
### Results



**Fig 1.** Images at the 30th TR from highly undersampled data (Reduction factor = 21) (a), full sampled data (b) and data-shared undersampled-data (c). (d) is a plot of signal evolutions from voxels indicated by arrows.

Fig 1-(a) is a reconstructed image from extremely undersampled data (Reduction factor = 21) at the 30th TR. The shape of the brain is not recognizable because of severe artifacts compared to fig 1-(b) which is obtained from full sampled data at the 30th TR. On the other hand, fig 1-(c) which is a reconstructed image from the same undersampled data with the proposed data sharing method shows similar result compared to fig 1-(b). Fig 1-(d) shows signal evolutions at the same voxels indicated by arrows in Fig 1-(a-c). The signal evolutions from data-shared undersampled data and full sampled data are quite similar while the signal evolution from undersampled data without data sharing produced completely different pattern.

Fig 2 shows the estimated parameter maps ( $M_0$ ,  $T_1$ ,  $T_2$ , and  $\Delta B$  map, from left to right). While maps obtained from undersampled data (reduction factor = 21, a-d) show completely wrong parameter estimations due to extreme undersampling, the maps obtained from data-shared undersampled data (i-l) show similar results with maps from full sampled data (e-h).



**Fig 2.** Estimated maps ( $M_0$ ,  $T_1$ ,  $T_2$  and  $\Delta B$  map, from left to right) from highly undersampled data (Reduction factor = 21) (a-d), full sampled data (e-h), and data shared data (i-l)

### Conclusion

This study demonstrates that the accurate parameter maps can be obtained from extremely undersampled Cartesian trajectory data in MRF by applying the proposed data sharing method. While conventional CS methods are known to work with the reduction factor up to 5, our proposed data sharing method can increase the reduction factor up to 21 in Cartesian trajectory. Therefore, ultrafast MR parameter mapping by MRF can be feasible in the current clinical settings with Cartesian trajectory acquisition.

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### Reference

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- [2] Y.C. PATI et. al., "Orthogonal Matching Pursuit : Recursive Function Approximation with Applications to Wavelet Decomposition", IEEE, 1993