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Brain DCE MRI with direct estimation of pharmacokinetic parameters from highly undersampled (k,t)-space

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Introduction: In T1-weighted dynamic contrast enhanced (DCE) MRI, pharmacokinetic (PK) maps (K^{trans}, abbreviated K_t, and v_p , etc.) are derived from the dynamic image series and used for diagnostic purpose. In accelerated DCE MRI, anatomic image series are typically reconstructed from under-sampled k-space first, then fit into a PK model to derive the parameter maps [1]. As the PK parameters have much less dimension than the original multi-coil k-space, direct estimation of PK parameters will promote higher acceleration and save the resources estimating all the intermediate steps. Recently, Dikaios *et al* [2] have used a Beysian inference framework to directly estimate PK maps from under-sampled k-space and achieved 8x acceleration in phantom and prostate cancer data. In this study, we propose a novel and efficient optimization approach to directly reconstruct the PK parameters from highly under-sampled k-space, and show that whole-brain DCE, with up to 30x acceleration rate, can be achieve through this method.



Methods: Fig 1 demonstrates the forward modelling of the PK parameters, where a Patlak model was used in this study. The PK parameters (K_t, v_p) are related to the acquired under-sampled k-space data (k_u) as the steps in table1.Thus, a model-based reconstruction is to solve (K_t, v_p) from k_u by the following least-square optimization problem:

$$(K_t, v_p) = \underset{K_t, v_p}{\operatorname{arg\,min}} \| \mathbf{k}_u - F_u S\varphi(P(K_t, v_p) \cdot \Re 1 + \mathbf{R}_0) \|_2^2 + \| \psi K_t \|_1 + \| \psi v_p \|_1$$
(1)

, where sparsity is enforced by I1 norm constraints in the wavelet transform (Ψ) domain of the PK parameters as indicated Eqn 1. This nonlinear optimization problem is then solved by a quasi-newton limited-memory Broyden–Fletcher–Goldfarb–Shanno (L-BFGS) method.

A fully-sampled DCE data set from a brain tumor patient is acquired in a 3T GE scanner. The data set is retrospective under-sampled 30x by a Poisson-disc under-sampling pattern, then the proposed model-based reconstruction is used to calculate the PK maps directly from the under-sampled k-space. The PK maps are also estimated using images from fully-sampled and zero-padding k-space for reference.

Table 1 Steps to model PK parameters (K_t, v_p) to under-sampled k-space (k_u)

1. The $K^{trans}(K_t)$ and v_p are fitted to the contrast concentration(CA(t)) over time, where $C_p(t)$ is population-based AIF from Ref [3]:

$$CA(t) = P(K_t, \mathbf{v}_p) = K_t \int_{0}^{t} C_p(\tau) d\tau + v_p C_p(t)$$

2. CA(t) is related to the changes in T1 relaxation rate over time(R1(t)): where $\Re 1$ is $4.39 \text{ s}^{-1}\text{m}\text{M}^{-1}$ for gadolinium, R₀ is the precontrast R1 maps calculated from T1 mapping sequence before DCE:

 $R1(t) = CA(t) \cdot \Re 1 + \Re_0$

3. R1(t) is related to the signal intensity S(t) by the general signal equation, where TR is the repetition time, α is the flip angel, M₀ is the equilibrium longitudinal magnetization that is acquired from T1 mapping sequences:

$$S(t) = \varphi(R1(t)) = \frac{M_0 \sin \alpha (1 - e^{-TR \cdot R1(t)})}{1 - \cos \alpha e^{-TR \cdot R1(t)}}$$

4. S(t) is related to the under-sampled k-space (k_u) by coil sensitivities(S), and under-sampling Fourier transform(F_u):

 $k_u = F_u S(S(t))$

Results: Fig 2 shows the results of this model-based reconstruction for a glioblastoma patient. As it is shown, by simply enforcing the PK model in the reconstruction, the results are greatly improved compared to the PK parameters estimated from zero-padding images. By adding a wavelet sparsity constraint, the noise is further removed and the quality is comparable to the fully sampled results. **Conclusion:** In this study we have proposed a novel reconstruction method to directly estimate PK parameters from under-sampled k-space, and show that it can accurately restore PK values from highly under-sampled data, while saving the resources and time to estimate all the intermediate images. **References:** [1] R. M. Lebel, MRM 71(2): 635–644, 2014 [2] N. Dikaios, Medical Image Analysis 18:989-1001, 2014, [3] G. Parker, MRM 56:993–1000, 2006 [4] M. Lustig, MRM 58(6), 1182-1195, 2007. [5] Mark Schmidt: http://www.cs.ubc.ca/~schmidtm/Software/minFunc.html



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