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Direct Reconstruction of Tracer Kinetic Parameter Maps in Abbreviated Breast MRI

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Synopsis

Keywords: Data Processing, Breast, Dynamic Contrast Enhanced MRI

Motivation: Quantitative assessment of DCE-MRI data as abbreviated breast MRI data is non-trivial as robust image reconstruction of highly undersampled DCE-MRI data with a short scan time remains challenging, especially to determine an optimal regularization method.

Goal(s): This study aims to develop a direct reconstruction of tracer kinetic parameter maps such that the temporal regularization is embedded in the reconstruction process.

Approach: The reconstruction method was assessed using numerically generated phantom data and realistic digital reference objects of breast MRI.

Results: The results suggest that the tracer kinetic parameter maps from the proposed direct reconstruction could differentiate malignant lesions from benign ones.

Impact: This proposed direct reconstruction method aims to streamline the complex image reconstruction and data analysis processes of DCE-MRI and has the potential to make DCE MRI a more efficient, faster, and accessible tool for breast cancer exams.

INTRODUCTION

Abbreviated breast MRI has been proposed to make MRI cheaper, faster, and potentially more accessible. An essential part of breast MRI is Dynamic Contrast-Enhanced Magnetic Resonance Imaging (DCE MRI), a noninvasive approach that provides insights into tissue perfusion and vascular dynamics, key in breast cancer diagnostics. DCE-MRI of a short scan time of ~2-3 min can be a plausible option for quantitative abbreviated breast MRI. However, a primary challenge in DCE-MRI is modeling the contrast dynamics efficiently, especially to enable faster image interpretation while preserving diagnostic integrity[1-3].Traditional methods rely on dynamic image reconstruction, followed by estimation of tracer kinetic (TK) parameters from reconstructed anatomical images. Recent studies[4,5] suggest that direct reconstruction from undersampled k-space data may yield higher diagnostic accuracy. However, its application in breast DCE-MRI has not been reported. Hence, the goal of our study is to assess the feasibility of using a direct reconstruction pipeline for breast DCE-MRI using the Patlak model (PM) for simplification in the case of a short scan time of 2.5 min. We conducted a validation study using numerical phantoms with fully sampled and under-sampled data and realistic digital reference objects (DRO) of breast DCE-MRI data for benign and malignant cases[6].

Direct reconstruction of TK parameter maps:

The direct reconstruction of TK parameters (K_{trans}, V_p) is formulated as solving the following optimization problem:
$(K^{\text{trans}}, V_p) = \min \frac{1}{2} \| P \cdot F \cdot C \cdot S \cdot f(K^{\text{trans}}, V_p) - Y_{\text{meas}} \|^2$
where PFCS represents the series of transformations needed to model the data acquisition process, including sampling of K-space data, Fourier transformation to k-space, application of coil sensitivity maps, and conversion of tracer concentrations to MR signal. *f*(Ktrans, Vp) denotes the forward function that maps the tracer kinetic parameters to a time-concentration curve. Y_{meas} is the measured k-space data and serves as the target structure, guiding the optimization process to find K_{trans} and V_p values that minimize the MSE. The DCE pipeline (Fig. 1) estimates TK parameters using a forward model and optimization loop via backward calculation. The forward model calculates concentration maps from parameter maps via the PM equation, then converts concentration to signal with the SPGR equation. In the optimization loop, parameters are iteratively refined by minimizing the MSE between observed and model-generated k-space data, using the Adam optimizer for convergence.

Simulation and validation:

The pipeline's accuracy was validated through a numerical phantom to generate k-space data with known ground truth K_{trans} and V_p values between 0 and 0.5. Testing included fully sampled and 30x undersampled k-space data, both noise-free and with added 10% Gaussian noise. Bland-Altman analysis was performed to compare simulated and estimated maps, assessing the pipeline's performance under realistic conditions.

Test with DRO of Breast MRI:

The proposed pipeline was used to process breast DRO data. Initially, the temporal resolution was fixed at 5 s/frame while the undersampling rate was varied. This data was used to evaluate the effect of undersampling. We also used the DRO to assess the effect of temporal resolution. The simulated data with a radial trajectory golden angle sampling method were converted to Cartesian data using GROG. Lesion analysis involved overlaying DRO masks on estimated parameter maps for 15 malignant and 18 benign cases, extracting mean values for each region, and comparing data distributions using box-and-whisker plots.

RESULTS AND DISCUSSION:

The direct reconstruction pipeline demonstrated high accuracy in TK parameter estimation, aligning closely with ground truth data and achieving strong correlations (1.0) for Ktrans and Vp on fully sampled k-space data, but showed minor deviations under undersampling and noise with slightly lower linear correlations (Fig. 2).The comparison of signal plots between the DRO and the pipeline's estimated outputs demonstrates the effective guidance of image reconstruction through TK modeling in breast DCE-MRI, yielding a high SSIM value of 0.9985. Parameter map comparisons (Fig. 3) illustrate differences between the Patlak model used in the reconstruction pipeline and the two-compartment exchange model (TCM) used by DRO toolkit. The box and whisker plots in Figure 4 show that the pipeline's PM-based parameter estimates generally yield lower K_{trans} and V_p values than the ground truth values used in DRO generation, demonstrating inherent limitations of the simplified TK model. Despite these limitations, the estimated K_{trans} and V_p values were able to show significant differences between malignant and benign cases with varying levels of undersampling (Fig. 4).

CONCLUSION:

The results in this study demonstrate that our direct reconstruction pipeline with automatic differentiation can be used to generate TK parameter maps and the estimated TK parameters can effectively distinguish tumor types in breast DCE-MRI data with a short scan time. Further evaluation of the developed method is underway with patient data (n=300)[7].

Acknowledgements

HPC resources were provided by the Erlangen National High Performance Computing Center (NHR) of Friedrich-Alexander-University Erlangen-Nuremberg (FAU) under the NHR project b143dc. NHR is funded by federal and Bavarian state authorities. NHR@FAU hardware is partially funded by DFG under project 440719683. The study was also partly supported by NIH grants (R01CA160620, R01CA219964, and UH3CA228699).

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Figures

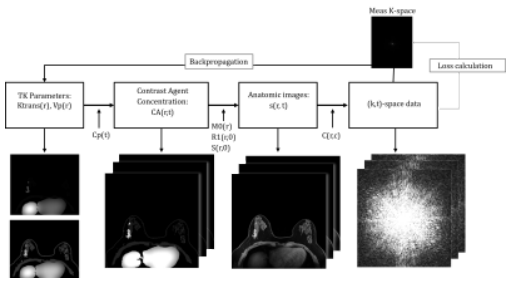

Fig.1:Pipeline Flow Chart Visual. Flowchart outlining implementation of direct reconstruction pipeline with visuals of input, intermediate, and output data.

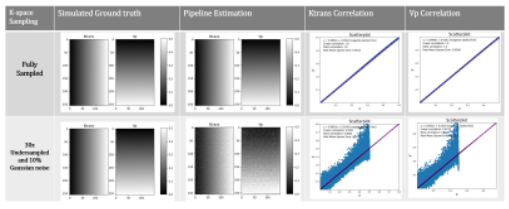

Fig.2:Comparison of simulated ground truth and pipeline results. Ground truth values range from 0 to 0.5 for both Ktrans and Vp. Pipeline estimates are based on ground truth K-space data, with both fully sampled and 30x undersampled cases, including 10% Gaussian noise. Scatter plots show linear correlations for Ktrans and Vp, with correlation values of 1.0 for fully sampled data, and 0.9685 and 0.9279 for Ktrans and Vp in the undersampled case, respectively.

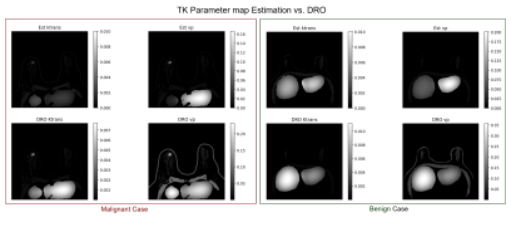

Fig.3: Pipeline Estimation and DRO results. Pipeline TK parameter map estimations (denoted as 'Est') and the known TK parameter map values (denoted as 'DRO') for both a malignant and benign lesion case.

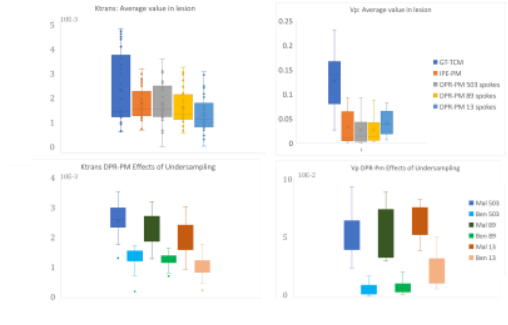

Fig.4:Comparative Analysis of Average Lesion Parameter Values Across Malignant and Benign Cases with Varying Sampling Methods. Plots showing average lesion values for K_{trans} and V_p across malignant and benign cases. Each subplot compares three methodologies: ground truth from the DRO (GT-TCM), parameter estimation from fully sampled images (IPE-PM), and undersampled direct parameter reconstruction (DPR-PM) with 503 spokes, 89 spokes, and 13 spokes per frame while keeping the temporal resolution at 5 s/frame.

Proc. Intl. Soc. Mag. Reson. Med. 33 (2025)
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