ESMRMB
European Society for Magnetic Resonance in Medicine and Biology

ESMRMB 2019 Congress

October 3-5, Rotterdam/NL

Book of Abstracts

Saturday

DOI: 10.1007/s10334-019-00755-1

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S24.04

Comparison of fitting approaches in dynamic contrast-enhanced magnetic resonance imaging: direct estimation from raw k-space signals vs. conventional approach from concentration–time curves

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Purpose/Introduction: DCE-MRI provides information about tissue perfusion and capillary permeability. It is based on T1-weighted image acquisition before, during, and after an intravenous administration of a contrast agent [1].
Conventionally, image sequences are first reconstructed from the k-space data, followed by conversion to contrast-agent concentration [1]. The quantitative perfusion-parameter maps are then obtained by fitting a pharmacokinetic (PK) model to the measured data, which relates the PK parameters to concentration–time curves. Recently, a direct estimation scheme has been presented employing a full compound model including the preprocessing [2]. Alternatively, an intermediate model working with the reconstructed images can be formed. We have extended the approaches using a more realistic PK model and a state-of-the-art spatial regularization and compared them.
Subjects and Methods: Estimation of PK parameters is a least-mean-squares minimization problem: $\mathbf{p} = \arg\min_{\mathbf{p}} \|f(\mathbf{p})-\mathbf{y}\|^2 + R(\mathbf{p})$, where $\mathbf{p}$ are the PK parameter maps, $\mathbf{y}$ is the measured data, $f(\mathbf{p})$ is the model and $R(\mathbf{p})$ is a spatial regularizer. We solve this non-linear non-differentiable problem using the recently proposed Gauss–Newton approach with the primal–dual algorithm [3]. Table 1 defines the data and gives an overview of the three fitting approaches we used in this work.

Approach	Conventional	T1w	Direct
Data to fit, y	Concentration images	T1-weighted images	K-space samples
Model, f(p)	PK model	PK model + SPGR model	PK model + SPGR model + Coil sensitivities + K-space sampling
Additional preprocessing steps	Image reconstruction Conversion to concentration	Image reconstruction	Estimation of coil profiles
Noise in data	Non-Gaussian with spatial-dependent variance	Rician (close to Gaussian) with constant variance	Gaussian with constant variance
Pros	Voxel-wise computation The simplest model The fastest computation Estimation in ROI	Voxel-wise computation Noise characteristic Estimation in ROI	Complete information Noise characteristic No image reconstruction
Cons	Image reconstruction needed Conversion needed Noise characteristic Strongly nonlinear Potentially accumulated errors	Image reconstruction needed	Computationally demanding No arterial voxel available for AIF Coil profiles needed

Table 1: Overview of the fitting approaches

The comparison was performed on a numerical rat phantom (41 tissue regions with experiment- and literature-based PK parameters) simulating DCE-MRI using the PK tissue homogeneity model [4] combined with an SPGR sequence under realistic noise conditions. The T1-weighted images were reconstructed from the 4 channels using the sum-of-squared reconstruction. Coil profile, SNR and sequence parameters are given in Fig. 1.

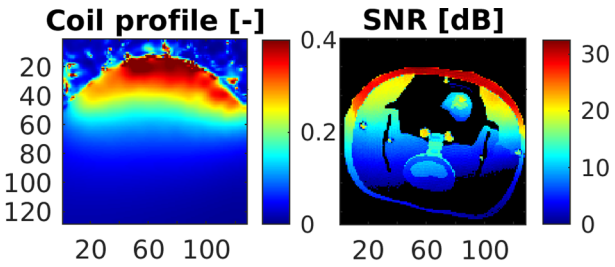

Figure 1: Coil profile of 4-channel rat head surface coil used with simulated SPGR sequence and SNR of the phantom. Simulation parameters: 1mm slice, TR/TE 8/2.1 ms, FA 17°, acquisition matrix 128×128, temporal resolution 0.8 s, scan time ~13 min.

Results: The approaches are compared in Fig. 2 together with their spatial-regularized variants. The regularization always improved the readability of the estimated maps. The conventional approach led to the worst result. The T1w and direct approaches appeared to be equal, however the non-regularized direct approach had values closer to the ground truth.

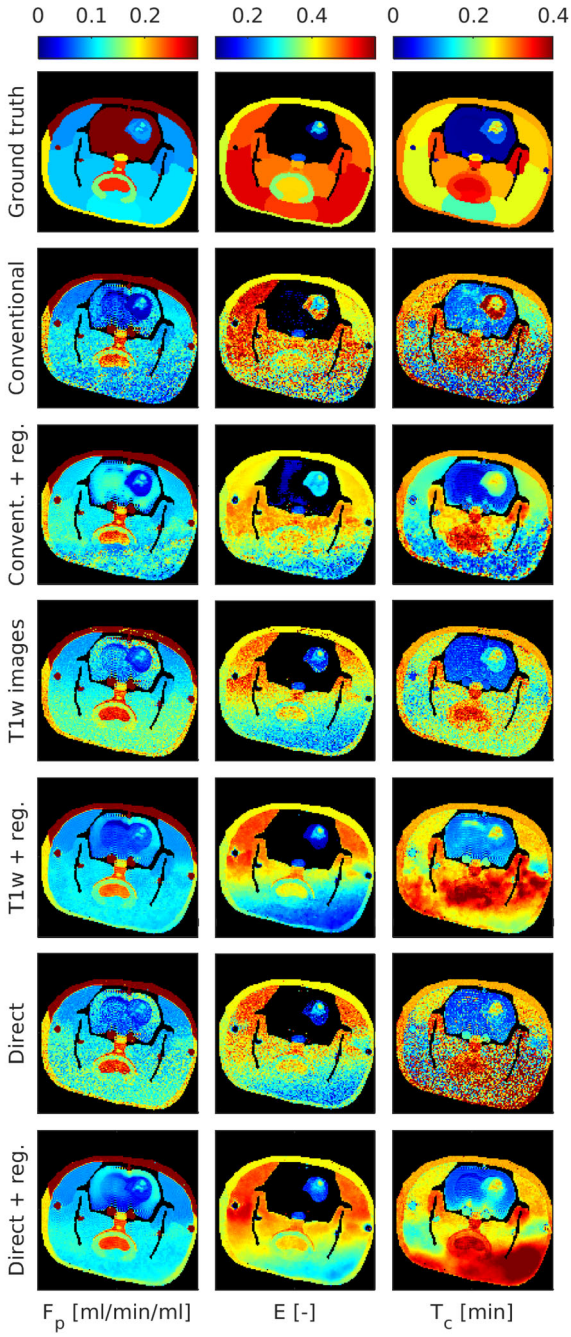

Figure 2: Comparison of the DCE-MRI fitting approaches (defined in Table 1) with and without spatial regularization. Only three out of five perfusion-parameter maps are shown.

Discussion/Conclusion: Based on the pros and cons listed in Table 1 and the comparison experiment (Fig. 2), the best approach, in our configuration, is to fit T1-weighted images. This yields results close to ground truth with tractable complexity. The conventional approach had convergence issues, even in case of regularization. The state-of-the art approach of the direct fitting is tractable, but in case of a full Cartesian sampling, it seems excessive.

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S24.05

Rapid cardiac MR myocardial perfusion quantification using machine learning trained with synthetically generated sample data

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Purpose/Introduction: While myocardial hypoperfusion is routinely diagnosed by visual assessment of dynamic contrast-enhanced (DCE) cardiac MRI, exact quantification of perfusion parameters (MBF = myocardial blood flow, PS = permeability surface area product, Vp = plasma volume, Ve = extracellular volume) is desirable. The blood tissue exchange model (BTEX)[1] applied in recent studies[2] offers detailed modelling, but its complexity increases computational costs and vulnerability to noise when applying conventional fitting. Our study sought to predict perfusion parameters fast and accurately using a convolutional neural network (CNN) trained with synthetically generated sample data.

Subjects and Methods: Perfusion standard parameters[3] (**Fig. 1a**) and an arterial input function (AIF) averaged from 6 healthy volunteers were used as input for the pharmacokinetic BTEX model (**1b**) extending the cardiac MRXCAT[4] phantom framework (**1c**). Resulting DCE images (**1d**) mimicked spoiled saturation recovery GE acquisition in breath-hold with a Gd dose of 0.05 mmol/kg bodyweight.

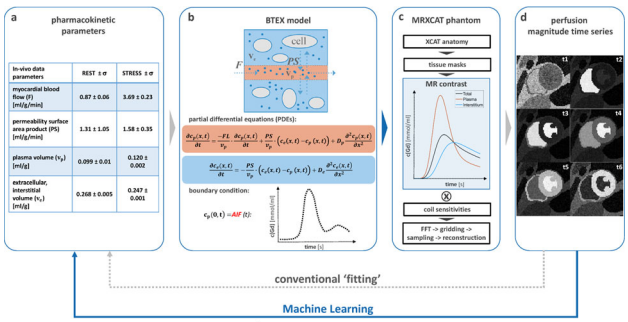

Figure 1: End-to-end perfusion mapping. a) Parameters[3] inserted into blood tissue exchange model (BTEX). b) Arterial Input Function (AIF) is required. c) Total change of concentrations defines contrast in the phantom. d) Image time series.

5000 datasets at random myocardial positions were simulated and Gaussian noise was added to model contrast-to-noise, then tested on levels (CNR = 10/15/30/100, **Fig. 2a**). Simulation data was split in test, validation, and training sets (**2b**). A 1D CNN consisting of 8 convolutional, 4 pooling, and 2 densely connected layers (**2c**) was implemented and trained using training and validation data (activation = Relu, loss function metric = MAE, optimizer = first-oder gradient based Adam, epochs = 1000, batch size = 32). For comparison, conventional least squares fitting (FIT) of the BTEX model was implemented—being dependent on simulated AIFs for finding the best-matching perfusion parameter estimates (**2d**). A pre-computed lookup-table and later refinement via L2 norm grid search were applied for computational efficiency. CNN and FIT were compared to the known ground truth as absolute difference.