Comparison of three quantification algorithms (RFM, tSVD, LCC) for absolute quantification of pulmonary perfusion in patients with COPD and Pulmonary embolism by MRI

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Introduction

In contrast-enhanced pulmonary perfusion MRI, the calculation of hemodynamic parameters requires robust deconvolution techniques [1]. Truncated singular value decomposition (tSVD) is often used in perfusion quantification. However, it is sensitive to regional contrast-to-noise (CNR) variations, which occur in lung pathologies, e.g COPD (Chronic Obstructive Pulmonary Disease). In contrast, the model-free Tikhonov regularisation with the L-curve criterion (LCC) is adapted to local SNR variations. An alternative is the residue Function Model (RFM), which is based on a priori physiological knowledge of the tissue perfusion. In this work, a recently introduced regularisation criterion, the RFM [2], which is based on a-priori physiological knowledge, is compared with tSVD and LCC based on simulated and patient data.

Methods

Simulation: As reference for the arterial input function (AIF) a representative concentration-time course measured in the pulmonary artery of a healthy volunteer and of a patient was obtained using dynamic-contrast enhanced MRI (DCE-MRI) with the same injection protocol in the patient study described below. The tissue response function (TRF) is calculated by convolving the measured AIF and an exponential residue function [1] with the given *rPBF*-values from 70 to 150 ml/min/100 ml lung tissue [3] in increments of 10 ml/min/100 ml lung tissue and a Given *MTT* of 6 s. Gaussian distributed noise was added to the TRF to achieve SNRs of 35 (volunteer) and 23 (patient). 1024 simulations were performed for each combination of *rPBF* and *MTT* using IDL (ITT Visual Solutions, Boulder, CO, USA). Perfusion parameters were calculated by deconvolving each simulated TRF with its respective AIF with the tSVD (threshold: 20% of the maximum singular values), LCC and RFM methods.

Patient study: Contrast-enhanced T_1w-3D perfusion MRI datasets were acquired using a 1.5 T MR- Scanner (Magnetom SymphonyVision, Simens Medical Solutions, Erlangen, Germany) in 5 patients with pulmonary embolism (PE) and 5 patients with COPD with a clinical 3D FLASH sequence: TE/TR/flip angle: 1.92ms/0.81ms/40°; FOV: 500 x 216mm², acquisition matrix: 256x111; slice thickness: 4mm; bandwidth: 1220Hz/px ; temporal resolution: 1.6 s. Image acquisition was started simultaneously with the administration of 0.05 mmol/kg b.w. Gd-DTPA (Magnevist, Bayer Schering Pharma, Berlin, Germany) followed by a saline flush of 30 ml with an injection rate of 5 ml/s in end-inspiratory breath-hold. A region of interest (ROI) was placed manually to cover the main pulmonary artery to obtain the AIF for each data set. ROIs were drawn to cover both lungs for quantitative analysis [4]. Perfusion parameters were calculated as for the simulations.

Results

In Fig. 1, the relationship between the given and calculated *rPBF* from the simulations is shown for the two predefined AIFs. Fig. 2 shows the calculated *rPBF*-Values for the 5 PE and 5 COPD patients. The displayed *rPBF*-value is the mean value and standard deviation averaged over 28 ± 8 slices. The results of the deconvolution analysis for the PE patients was as follows: RFM: *rPBF*= 23.5±5.9 ml/min/100 ml lung tissue; LCC: *rPBF*=21±4.7 ml/min/100 ml lung tissue; SVD:*rPBF*= 26.8±5.4 ml/min/100 ml lung tissue.For COPD patients: RFM:*rPBF*= 30.7±27.9 ml/min/100 ml lung tissue; LCC *rPBF*=28.72±22.8 ml/min/100 ml lung tissue; SVD *rPBF*= 34.3±27. 3 ml/min /100 ml lung tissue. Fig. 3. shows the color-coded maps of rPBF using pixel by pixel for all three approaches.

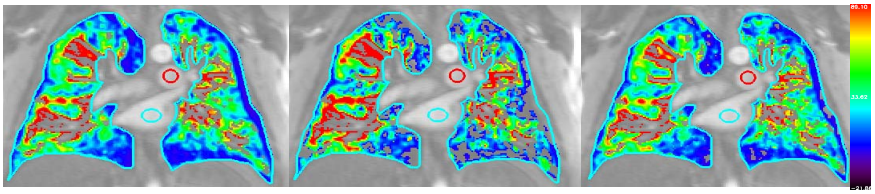

Fig.3. Color-coded rPBF-maps of a PE-patient were calculated by SVD (left), LCC (middle), and RFM (right).

Discussion

A new non-parametric deconvolution method (RFM) was validated in simulations and in patient data by comparing it with two standard methods. In the simulations, the RFM method showed reduced deviations from the given perfusion parameters compared to the two other methods over the simulated range of physiological parameters. This is due the application of a priori knowledge of the optimal shape of the residue function. It should therefore also be more suitable for the calculation of perfusion parameters maps in the presence of variable SNR. Perfusion distribution seem to be more homogenous when RFM is used. **References :**[1]Østergaard , MRM 36:715-25(1996).[2] Fieselmann ISMRM(2007).[3]Schuster ,J Nucl Med 36371-7(1995).[4]Risse ,J Magn Reson Imaging. 1284-90 (2006).

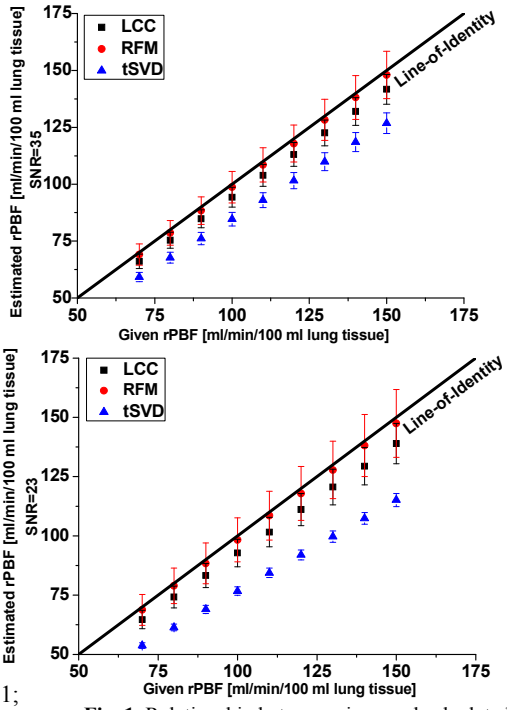

Fig. 1. Relationship between given and calculated *rPBF* for a) healthy volunteer (SNR=35) and b) patient (SNR=23). Triangular symbol represents the *rPBF* values calculated by tSVD. Square and circle symbols represent the *rPBF* values calculated with LCC and RFM. Error bars represent the standard deviation (SD) for 1024 simulations. The solid line represents the line of identity of calculated and given values.

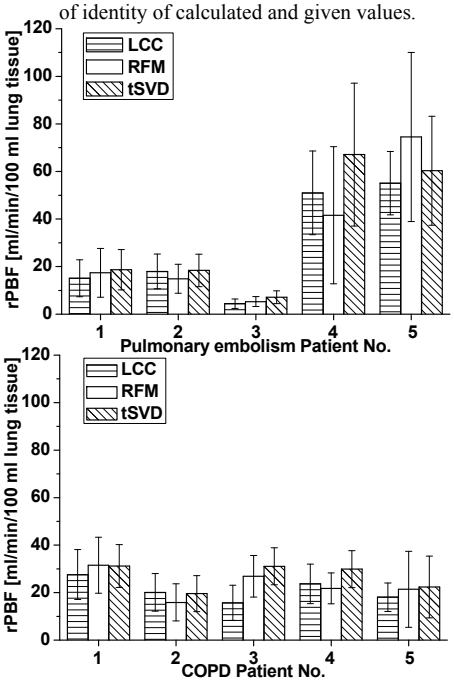

Fig. 2. Comparison of three quantification algorithms RFM, tSVD, LCC) in estimating of *rPBF* in patients with COPD and Pulmonary embolism by MRI.