

Comparison of pixel-by-pixel compartment modeling and deconvolution analysis for pulmonary perfusion measurements

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Introduction

It has been previously shown [1] that a one-compartment model is sufficient to quantify pulmonary perfusion using a ROI-based analysis of dynamic contrast-enhanced (DCE) MRI data. In this study, we investigate the feasibility of a pixel-by-pixel one-compartment modeling approach and compare it to the more commonly used deconvolution approach for pulmonary perfusion analysis.

Materials and Methods

Six healthy volunteers underwent DCE-MRI of the lung at 1.5-T (Magnetom Avanto, Siemens Medical Solutions, Erlangen, Germany) using a time-resolved T1-weighted 3D-FLASH sequence (GRAPPA with external reference scan, TR=1.45ms, TE=0.5ms, temporal resolution=1.3 s, voxel size= 3.5x3.5x 5mm³). 30 datasets were acquired in a single inspiratory breathhold after administration of 5ml contrast agent bolus (Gadovist) using an injection rate of 2ml/s. Pulmonary blood flow (PBF) was analyzed in 4 central partitions of the 3D data set. For each pixel in these four partitions, two values for the pulmonary blood flow were obtained by fitting a one-compartment model to the signal enhancement (S-S0) time curves of the DCE-MRI and by Tikhonov-regularized deconvolution [2]; the arterial input function (AIF) was measured in the central pulmonary artery. To compare the deconvolution analysis with the compartment analysis, only voxels in the lung tissue were considered by excluding voxels with a high blood flow by using a threshold value (details are described in Figure 3). Histograms of the PBF of the remaining pixels were computed; the median and inter-quartile range were calculated.

Results

Despite the low SNR, both approaches describe the data consistently (Figure 1). Figure 2 shows one slice of a blood flow map obtained by pixel-by-pixel fitting of a one-compartment model. The median PBF derived from the deconvolution analysis and the compartment analysis ranged from 21 to 184 ml/100ml/min and 22 to 252 ml/100ml/min (Figure 4), respectively.

Conclusion

The results indicate that pixelwise compartment modeling is feasible for lung perfusion measurements. Although the inter-volunteer variability is large, the results are in good agreement with reference values from the literature [4]. The PBF values obtained from the compartment model are consistently higher than those obtained by deconvolution, which supports previous reports that deconvolution underestimates the blood flow [2,3].

References:

[1]Vidarsson, ISMRM 15(2007), 2761, [2] Sourbron *et al*, PMB 52 (2007) 429–447, [3] Murase *et al*, PMB 46 (2001) 3147–3159, [4] Nikolaou *et al*, Investigative Radiology 39 (2004), 537-545

Acknowledgement:

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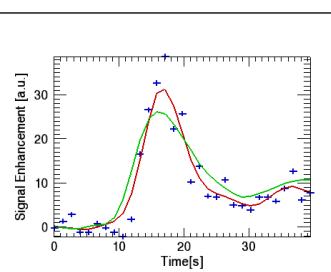


Figure 1: Pixel curve (blue), deconvolution (red) and one-compartment model (green). Note that despite the noisy data, both approaches describe the data consistently

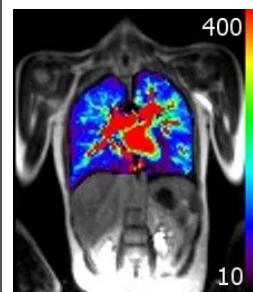


Figure 2: Blood flow map [ml/100ml/min] from the one-compartment model, overlaid over a baseline image

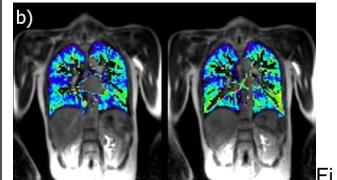
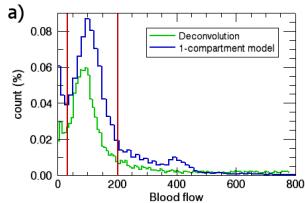


Figure 3:a) Histograms of the blood flow as obtained from deconvolution(green) and a one-compartment-model (blue). In this volunteer, only pixels with a blood flow between 30 and 200ml/100ml/min (in both applied approaches) were considered for further analysis b) Two slices of the resulting ROI (in color) overlaid over a baseline image. Note the exclusion of major vessels and the heart

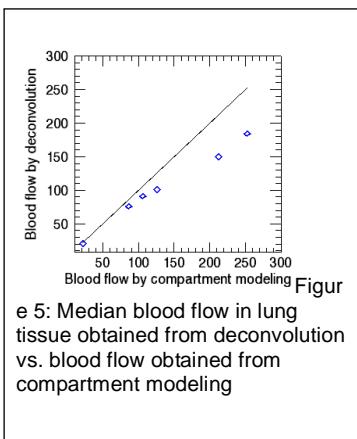


Figure 5: Median blood flow in lung tissue obtained from deconvolution vs. blood flow obtained from compartment modeling

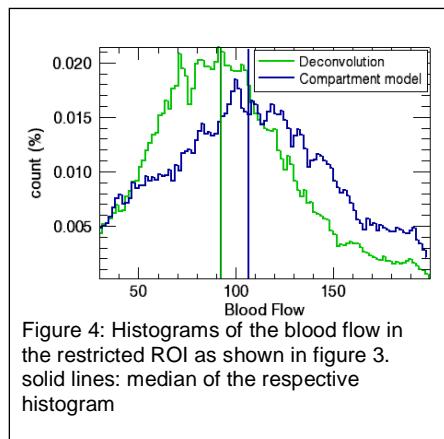


Figure 4: Histograms of the blood flow in the restricted ROI as shown in figure 3. solid lines: median of the respective histogram