Perfusion quantification of the whole lung using singular value decomposition with optimized threshold

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Introduction

Contrast-enhanced 3D MRI offers the capability to assess lung perfusion non-invasively and without radiation exposure [1]. Recently, parallel imaging techniques allow the acquisition of images of the entire lung in acceptable temporal resolution [2]. As a result it is now possible to track the first pass of an injected bolus of contrast agent in the whole lung. A deconvolution method is required for a model-independent evaluation of the lung perfusion based on the indicator dilution theory.

Singular value decomposition (SVD) has shown its potential for the analysis of bolus tracking experiments in the brain [3]. Advantages of this method are the model-independence and its ability to reduce the noise contribution due to a singular value threshold. Unlike brain perfusion measurements, there is a low signal-to-noise ratio (SNR) in the lung which also varies due to the relative tissue inhomogeneity. Thus a fixed threshold can lead to inaccurate values. It is therefore necessary to optimize the threshold for every deconvolution process considering the SNR. The aim of this work was to optimize the singular value threshold for the application of SVD in lung perfusion quantification and to evaluate of the method in 3D whole lung data sets.

Materials and Methods

Simulations were performed to obtain optimized singular value thresholds for a wide range of perfusion conditions. Arterial input functions (AIF) were modeled by a gamma variate function using parameters as found in former measurements [4]. Recirculation was added by convolving the gamma variate with an exponential function. Based on the perfusion parameters given by Ohno et al. [5], pulmonary blood flow (PBF) was varied in a range of 60 - 150 ml/min/100ml and mean transit time (MTT) from 3 - 6 s for the coverage of physiological and pathological perfusion conditions. Concentration-time curves were generated by convolving the AIFs with a residue function simulated by an exponential function. Gaussian distributed noise was added to achieve SNR between 2 and 170. The SNR was defined as the peak signal corrected for the baseline signal, divided by the standard deviation of the baseline signal [6]. AIFs and concentration-time curves were then deconvolved using singular value decomposition with singular value thresholds varying between 1% and 50%. 1000 runs were performed for all combinations of parameters. The threshold delivering the PBF closest to the given PBF was chosen as the optimal value.

To verify the method in real data sets, perfusion measurements of five healthy volunteers were analyzed. The data sets were acquired on a 1.5 T MR scanner (MAGNETOM Symphony, Siemens, Erlangen, Germany) using a T1-weighted 3D FLASH sequence with integrated parallel acquisition technique (iPAT; reconstruction algorithm: GRAPPA, acceleration factor 3, TE/TR/α: 0.8 ms/1.9 ms/40°, voxel size 3.6×2.0×5.0 mm³, temporal resolution 1.5 s) after an injection of contrast agent (0.1 mmol/kg b.w., gadobenate dimeglumine, Multihance, Bracco, Milan, Italy).

To analyze the 3D perfusion data sets, the lungs were segmented manually in all partitions and large vessels were excluded automatically to minimize their contribution to the calculations. SNRs were determined after background correction for every pixel. PBF was then calculated using SVD with the optimized thresholds according to the SNR. Moreover, MTT and pulmonary blood volume were determined. The calculations were performed for the whole lung and on a pixel-by-pixel basis to generate parameter maps.

Results

The simulated curves were corresponded with the curves found in volunteer measurements [4]. The simulations have clearly shown a strong dependence of the optimal singular value threshold on the SNR (Fig. 1). While high thresholds resulted in an underestimation of PBF for higher SNRs, lower thresholds led to better PBF estimations but at the cost of statistical accuracy. There was also a minor influence of MTT and PBF which was neglected in the calculation of the optimal threshold.

The application of SVD with optimized thresholds to the data sets was feasible. Fig. 2 shows the PBF and MTT parameter maps for a central 3D partition of a healthy volunteer. Most large vessels were sucessfully removed, but some still remained in the analyzed section especially for peripherical partitions. The mean values for the five volunteers were PBF = 142.4 ± 62.2 ml/min/100ml, PBV = 8.8 ± 2.9 ml/100ml and MTT = 4.0 ± 1.4 s. Similar to former studies, the PBF values revealed a gradient in gravitional direction.

Discussion

Evaluation of whole lung perfusion by SVD deconvolution analysis is feasible. The results are affected greatly by the SNR and it is therefore necessary to optimize the threshold to a certain degree. Generally, the best results were achieved in the central partitions of the 3D volume. Nevertheless, the results have to be judged semiquantitatively due to the fact that the analyis is hampered by several factors: The dose of contrast agent was chosen to deliver images valuable for diagnosis. Therefore the required linearity between signal and concentration was not necessarily given. Otherwise, a too low dose would lead to a low SNR and therefore to higher errors. A compromise between both requirements has to be found. In addition, the impact of temporal resolution must be verified.

Nevertheless, SVD with optimized threshold is a suitable tool for perfusion analysis because of its ability to reduce the noise contribution and its model-independence, i.e. no knowledge about the lung haemodynamics is necessary.

References

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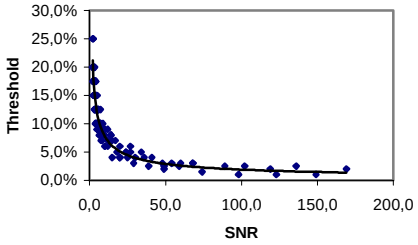

Fig.1: Optimal threshold depending on the SNR for all chosen combinations of PBF and MTT.

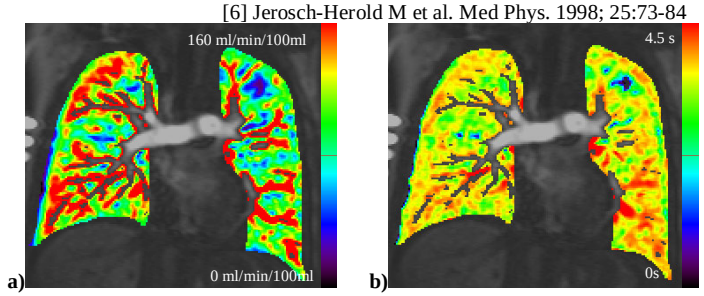

Fig. 2: Paramter maps of a) PBF and b) MTT for a healthy volunteer in the central partition of a 3D data set.