How many compartments are needed to analyze pulmonary perfusion data?

L. Vidarsson[1], S-P. Wu[1], J. F. van Amerom[1], T. Rayner[2], and C. K. Macgowan[1]

[1]Departments of Medical Imaging and Medical Biophysics, Hospital for Sick Children and University of Toronto, Toronto, ON, Canada, [2]Department of Medical Imaging, Hospital for Sick Children, Toronto, ON, Canada

Introduction:

Accurate blood perfusion measurements are of great importance for assessment of lung function. Measuring pulmonary perfusion is challenging due to the low SNR of lung tissue on MRI images. The singular value decomposition (SVD) de-convolution method is commonly used to estimate perfusion parameters, but it is very noise sensitive (1-3). Alternatively one could use the multiple-compartment method, which is well rooted in physiology (4-5). In this work we wanted to compare the multiple-compartment method to the SVD as a function of SNR as well as explore how many compartments are needed to adequately describe the observed data.

Theory:

In the SVD based deconvolution method tissue contrast kinetics are modeled by the tissue residue function, r(t). The recieved signal from the tissue, s(t), is described by the convolution relationship $s(t)=(AIF \otimes r)(t)$, where AIF is the arterial input function. Using this relationship the tissue residue function can be estimated from dynamic contrast enhanced (DCE) MRI data. Unfortunatelly this is a very noise sensitive model. The SVD de-convolution method addresses this by using only the largest singular values, as determined by a cuttoff value (in our case 90%, 97% and 100% of the maximum singular value). The multiple-compartment (MC) model can be described as well with a convolution relationship, by restricting the tissue residue function to be a positive linear combination of exponentials (5). The number of exponentials used corresponds to the number of components in the model. We minimized the L1 norm of the exponential coefficients as it tends to minimize the number of exponentials in the residue function (6). To ensure data consistency, we constrained the resulting error increase to be no more than 5% over a least squares fit.

Methods:

Three juvenile pigs (10-15 kg) were studied. All scanning was performed on a Signa Excite 1.5T MRI scanner (GE Healthcare, Milwaukee, WI). We used a 3DFT gradient echo sequence with these imaging parameters: TR/TE = 2.9/1 ms, 64 kHz bandwidth, 128 by 96 by 20 matrix, 20 cm by 15 cm by 10 cm FOV and a 45 degree flip angle. To improve temporal resolution TRICKS aceleration was used to obtain a temporal resolution of 1.4 s, 57 frames were acquired giving a total scan time of 1min 26 seconds. Two regions of interest (ROI) were drawn in each lung (upper and lower) along with an arterial input function region over the main pulmonary artery. Both the methods above were used to calculate the pulmonary blood flow in each ROI. In addition, noise was added to deteriorate the SNR of the perfusion data, the pulmonary blood flow was recalculated and the mean squared deviation (MSD) from noiseless data was calculated at each SNR level. A perfusion map was calculated and the number of coeficients used by the algorithm at each voxel location was recorded.

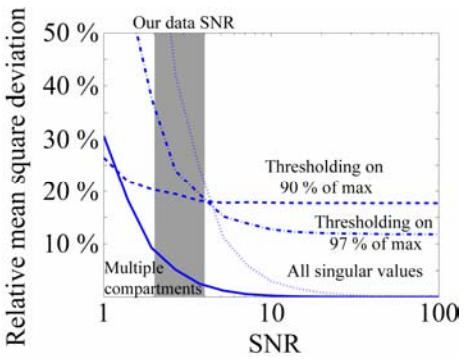

Figure 1. Relative MSD as a function of SNR for the SVD based de-convolution method as well as the MC method. Our DCE-MRI data rarely has a higher SNR than 4 in the lung parenchyma, where MC performs dramatically better.

Results:

The performance of the MC method was dramatically better to that of the SVD de-convolution method (See Fig. 1), especially when SNR was low. This was not surprising, as the SVD method does not assume a specific residue function. A trend was seen towards higher pulmonary blood flow values for the SVD method (P-value = 0.06). A color-coded perfusion map is shown in Fig 2. When calculating the perfusion map our algorithm used a single exponential in 88 % of the voxels.

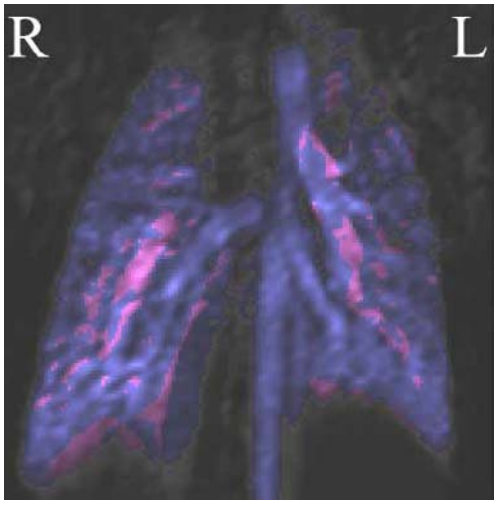

Figure 2. Colorized perfusion map. Shown in light red are regions where a three-compartment model was needed, and in dark blue are regions where a two-compartment model was sufficient.

Discussion:

The results indicate that 88 % of the time the two-compartment model can accurately describe pulmonary perfusion. The other 12 % of the time, a three-compartment model is used. Partial volume effects could explain why a three-compartment model was needed, because some of the three-compartment model voxels on Fig 2. are at the edge of the lung or the main blood vessels. It should be stated that the SNR analysis is based on real data; the true pulmonary blood flow is unknown, and we cannot determine if the SVD method is overestimating or our method is underestimating. In conclusion, our data indicates that the two-compartment model can accurately describe pulmonary perfusion. Further study is planned to verify our findings in a larger animal population.

References:

(1) Hatabu et al. MRM 36:503-508 (1996),
(2) Ostergaard L. et al. MRM 36:715-725 (1996)
(3) Ohno et al. AJR 182:73-78 (2004),
(4) Tofts et al. JMRI 10(3):223-232 (1999)
(5) Murase Ann. Nucl. Med. 17(6):427-434(2003)
(6) Boyd et al. Convex optimization (2004)