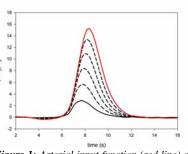
# Quantification of 3D pulmonary perfusion in pigs using a prebolus technique and singular value decomposition with a blockcirculant deconvolution matrix

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## Introduction

Quantification of contrast-enhanced pulmonary perfusion using time-resolved T1-weighted MRI has been used for the investigation of various lung diseases, e.g. pulmonary embolism or pulmonary hypertension [1,2]. A major challenge is to achieve tissue signal sufficient for diagnosis. Additionally, a linear relationship between signal and contrast agent concentration in the large pulmonary artery for the definition of the arterial input function (AIF) is required at the same time, particularly when non-prepared 3D FLASH sequences with a very limited range of linearity are used. Two publications proposed a prebolus technique for cardiac perfusion [3,4], where a low dose prebolus is used to measure the AIF and a higher dose to acquire the tissue signal. Recently, this approach was adapted for 2D perfusion (SVD) [6]. A drawback of this method is the sensitivity to delay between the AIF and the arrival of the contrast agent bolus in tissue [7]. This might especially be the case when a prebolus technique with two different bolus injections is used. Wu et al. proposed SVD with a block-circulant deconvolution matrix (cSVD) to compensate for too early or late arrival of the bolus in the tissue [7].



The aim of this work was the quantification of 3D perfusion MRI of pig lungs using a prebolus technique and cSVD.

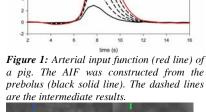
#### **Material and Methods**

Contrast-enhanced perfusion measurements (MR scanner: 1.5T Symphony, Siemens, Erlangen, Germany) were performed in 11 anesthetized pigs (mean weight 30.5 kg) with a clinical 3D FLASH sequence with the following parameters: TE/TR/flip angle: 0.7 ms/1.8 ms/40°, FOV: 450×338 mm<sup>2</sup>, acquisition matrix: 192×144, slice thickness: 4mm, 20 partitions, bandwidth: 1000Hz/px, GRAPPA: acceleration factor 2, 20 reference lines, coronal orientation. 30 consecutive measurements were performed with a temporal resolution of 0.6 s after the administration of a 0.01 mmol/kg b.w. Gd-DTPA bolus. A second bolus of 0.05 mmol/kg b.w. was administered using the same sequence but with a lower temporal resolution of 1.1 s to achieve complete coverage of the lungs (40 partitions). The CA was administered with a catheter inserted in the inferior vena cava (injection rate: 3 ml/s). Heart rate and oxygen saturation were monitored during all measurements to control the blood circulation.

Only pigs with changes in heart rate  $\leq$  15 bpm between the perfusion measurements were considered for perfusion quantification since a linear and stationary system is required for the prebolus technique [3]. Regions of interest (ROI) were defined in the pulmonary artery using the 0.01 mmol/kg (prebolus) measurements. The AIFs were constructed from these time courses by adding the known prebolus volume until the volume of the corresponding 0.05 mmol/kg bolus was reached (Fig. 1). In addition, the prebolus was shifted by its injection duration to consider not only the volume but also the kinetics of the boluses [3]. Regional pulmonary blood flow (PBF), blood volume (PBV) and mean transit time (MTT) were computed using cSVD [7] for the entire lungs. A correlation algorithm was used to suppress the influence of large vessels on the perfusion quantification when the entire lungs were segmented [8].

### Results

Pulmonary perfusion was evaluated using the prebolus technique in 4 pigs. All other pigs showed changes in heart rate > 15 bpm or the heart rate was not monitored correctly during at least one measurement. Figure 1 shows an AIF constructed from the prebolus measured in the pulmonary artery of a pig. No dependence of the quantification parameters on the bolus timing was observed when the bolus arrivals were changed manually.



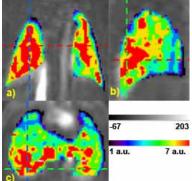


Figure 2: Maximum enhancement maps of a 3D lung volume demonstrating the gravitational gradient in the reconstructed sagittal plane (b). The dashed lines show the current plane position in the other orientations (a: coronal; c: transversal).

The deconvolution analysis revealed a mean PBF =  $602 \pm 232$  ml/min/100ml for the entire lungs (PBV =  $31 \pm 16$  orientations (a: coronal; c: transversal). ml/100ml and MTT =  $3.3 \pm 0.5$  s). Two measurements showed high perfusion parameters since the AIF was undersampled due to a high heart rate during the prebolus acquisition (Table 1). Figure 2 shows the typical gravitational gradient of the contrast agent distribution in the lung.

#### Discussion

The use of a prebolus technique for 3D perfusion measurements is feasible. It enables measurements with sufficient tissue signal and linear relationship between MR signal and contrast agent concentration. In addition, the deconvolution with a block-circulant matrix made the analysis less sensitive to differences in the tracer arrival compared to the simple SVD approach [7,9]. *Table 1: Perfusion parameters* 

One limitation of this initial study is the low number of analyzed subjects because of the changes in heart rate due to complex surgical preparation and variations in depth of anesthesia. This problem might be reduced in volunteers or patients where the heart rate is more stable but the impact of the heart rate has to be investigated further. Another drawback is the use of very low bolus volumes for the prebolus injection. The feasible time resolution is limited for 3D perfusion measurements of the lungs and might lead to an undersampling of the AIF when high heart rates occur. Thus, perfusion could be estimated too high as observed in two pies.

Table 1: Perfusion parameters				
	PBF	PBV	MTT	Heart rate
	[ml/min/100ml]	[ml/100ml]	[s]	(prebolus/bolus)
				[min <sup>-1</sup> ]
#1	$683 \pm 391$	$30 \pm 8$	$3.2 \pm 1.3$	85/88
#2	$496 \pm 169$	$22 \pm 5$	$2.8 \pm 0.5$	56/71
#3	$882 \pm 371$	$54 \pm 14$	$4.0 \pm 0.9$	100/90
#3	$345\pm139$	$18 \pm 5$	$3.3\pm0.5$	64/67

All quantified perfusion measurements revealed PBF values higher than expected. In contrast, two experiments with low heart rate and without undersampling resulted in PBV values in the expected range around 20 ml/100ml. But real reference values for pigs are missing and human perfusion parameters measured with PET [10, 11] were used for this preliminary comparison.

However, 3D pulmonary imaging improves the quantification of lung perfusion since the perfusion values depend strongly on the slice location when the usual coronal planes are used (Fig. 2). It is therefore necessary to analyze the entire lung. In conclusion, 3D pulmonary perfusion quantification is still challenging. But the use of a prebolus technique in combination with SVD and a block-circulant deconvolution might improve lung perfusion quantification when the AIF is measured adequately.

#### References

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