Fast mapping of myocardial blood flow: A new Algorithm with intravascular MR first-pass imaging

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INTRODUCTION

This study examined the accuracy of a new model-independent deconvolution method for fast first-pass perfusion myocardial blood flow (MBF) mapping. The algorithms were first evaluated with simulation and then validated in normal dogs in vivo.

MATERIALS AND METHODS

Algorithm A previously validated model-Independent method (B-splines) has shown the accuracy of calculation of MBF with intravascular contrast agent and first-pass perfusion imaging in MRI, but the speed of MBF mapping is limited. A new unregularized model-independent algorithm was recently developed, aiming at the fast mapping of MBF for better application in a clinical setting. The algorithm is linear, uses only 3 parameters, and represents the results of deconvolution using basis functions that combine the properties of both polynomial and exponential functions.

Simulation Simulated perfusion curves were generated using the MMID4 model. Curves were then noise contaminated, and analyzed using both deconvolution algorithms. Simulations were performed at multiple noise levels, with CNR ranging from 10-22.

In vivo MR Study MBF measurements were performed in five normal dogs. The multi-slice perfusion images were acquired by using a saturation-recovery-prepared TurboFLASH sequence along the short-axis view of the left ventricle (LV). An intravascular contrast agent Gadomer (Schering AG, Berlin, Germany) was injected as a bolus with a dose of 0.025 mmol/kg. Radiolabeled microsphere measurements for MBF were performed twice, simultaneously with the perfusion imaging, at rest and during dipyridamole vasodilation.

Data Analysis MBF maps were created using both B-spline and this new method. Global MBF values were measured by drawing a ring over entire LV wall of the MBF maps.

RESULTS

At moderate noise levels (CNR>10), both algorithms overestimated simulated MBF by approximately 7%, and had a standard deviation less than 0.1 ml/min/g. It was found that the new algorithm was less noise-sensitive at CNR<8, probably because of it uses few parameters (n=3). In dog study, microsphere data from two dogs during the dipyridamole vasodilation were not available. Fig. 1 demonstrates examples of similar MBF maps created by both mapping algorithm. Correlations between MR and microsphere data were similar (R^2=0.91 for B-splines and R^2=0.92 for the new methods) (Fig. 2). MBF mapping with the new algorithm required less than 3 seconds, comparing to 3-5 min with the B-spline method.

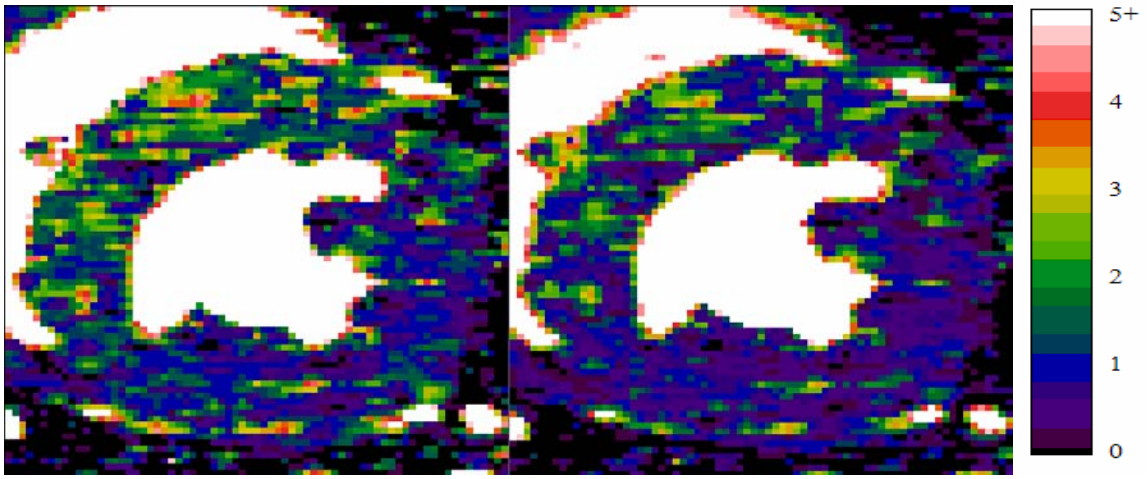
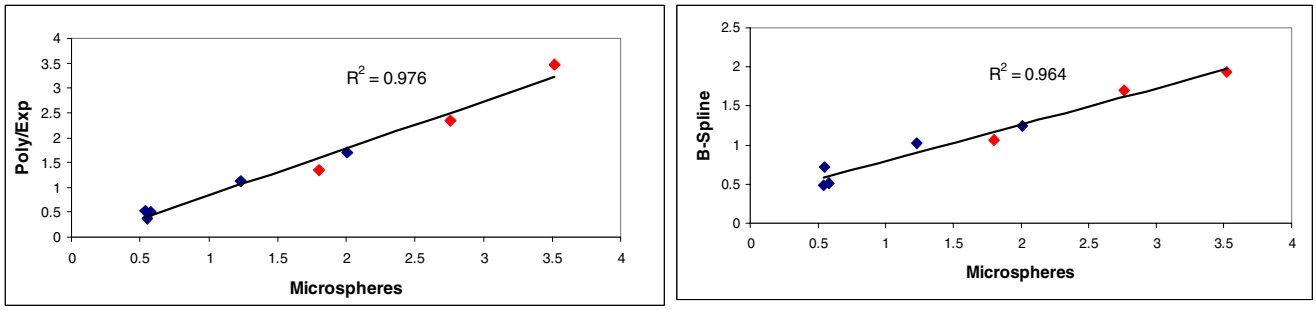


Figure 1. MBF(ml/g/min) maps using both the B-Spline (left) and novel (right) method. Both maps appear similar. The B-Spline map required 2 min and 13 seconds to compute, while the novel map required 2 seconds.

Discussion and Conclusion: Because this new method has a very small number of parameters and does not require regularization or user inputs, it can create pixel-by-pixel MBF data rapidly, making it more suitable for mapping in a clinical setting.



(a) (b)

Figure 2. Correlations of MBF values between MR and microsphere data for the new (a) and B-Spline (b) algorithms. Data points represent average blood flows over the entire myocardial ring of each dog in both rest (blue) and hyperemia (red) conditions.