Spatio-Temporal Modeling of First-Pass Perfusion Cardiovascular MRI

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INTRODUCTION

First-pass contrast enhanced myocardial perfusion Magnetic Resonance Imaging (MRI) is a promising technique for providing insight into how reduced coronary flow affects the myocardial tissue. It also allows the understanding of microcirculation in the myocardial tissue and myocardial angiogenesis [1]. Clinically, myocardial perfusion MRI plays a major role in the evaluation of ischaemic heart disease beyond situations where there have already been gross myocardial damages such as acute infarction or scarring [2]. In areas affected by collaterals, the maximum blood flow may appear to be normal, but the arrival of contrast agent is delayed [3].
Analysis of myocardial perfusion MRI is typically performed via de-convolution of the myocardial signal response with an Arterial Input Function (AIF) measured in the left ventricle. To date, quantitative analysis of myocardial perfusion MRI has mainly been performed on a *local* level without explicit use of contextual information. However, for analysis of collateral perfusion, the contextual information is important as it indirectly reflects the structure of microcirculation.
The purpose of this paper is to propose a spatio-temporal model for analyzing myocardial perfusion MRI. In normal myocardium, the blood flow in neighbouring segments is largely similar. In the case of collateral flow under coronary obstruction, the response function is expected to be significantly different between segments. The focus of the proposed model is to quantify the dependencies between local kinetic systems. In the proposed framework, all local systems are modelled simultaneously along with their dependencies. It thus allows more robust context-driven estimation of local kinetics, a concept we call "*contextual kinetics*".

METHODS

A hierarchical Bayesian model assumes the existence of unknown, latent variables, which cannot be observed [4]. In the context of myocardial perfusion, the spatial dependencies between different regions of the myocardium are such latent variables. For data analysis, the standard American Heart Association 17 segment model is used [5]. In each segment n of scan k, the observed signal intensity Y_{nkt} at time t is the unknown true signal intensity $S_{nk}(t)$ plus an observation error. In general, the true signal intensity is the convolution of the arterial input function $A_k(t)$, *i.e.*, the signal intensity in the LV blood pool, and a response function $f_{kn}(t)$. We assume the response to be a smooth function and use a B-Spline representation $f_{kn} = \sum \beta_{knp} B_{pj}$, where B is a design matrix of 4*th* order B-splines, and β_{kn} represent the Spline regression parameters.
A typical constraint on β is a first order difference in the temporal dimension [3]. In a Bayesian framework, this constraint is expressed as *a priori* distribution $(\beta_{kn,p+1} - \beta_{kn,p}) \sim N(0,\tau_p)$ [7]. To include contextual information, we assume that spatially adjacent segments share similar properties, *i.e.*, the shape of the response function in neighbouring segments are similar. We therefore impose a stochastic constraint on the spatial differences, $((\beta_{kn,p+1} - \beta_{kn,p}) - (\beta_{km,p+1} - \beta_{km,p})) \sim N(0, \rho_{\{nm\}})$, where n and m are adjacent segments. The spatial distribution parameter $\rho_{\{nm\}}$ describes the similarity between the shapes of the response functions between segments n and m.
For numerical validation, a set of myocardial perfusion images was simulated using the MMID4 model in the JSIM software [8]. For *in-vivo* evaluation, MRI perfusion data from eight patients with coronary artery disease was used. The images were acquired with a 0.1 *mmol/kg* injection of a Gadolinium-based contrast agent on a 1.5-T Siemens Sonata scanner with single-shot FLASH.

RESULTS

Fig. 1 depicts the estimated spatial distribution parameter for the simulated data set. The stenosis simulated in right coronary artery is clearly detected. Segments 9, 10 and, 15, supplied by collateral vessels and therefore with delayed tracer arrival, are clearly detected as different from the adjacent segments. In addition, large differences in maximum blood flow are picked up, for example between segments 11 (MBF= 2) and 12 (MBF= 1).
Fig. 2 shows the MBF estimated both with the local independent and the spatio-temporal model for two of the patients studied. In general, estimated MBF values are similar between both models, but are more robust, *i.e.*, less susceptible to noise for the spatio-temporal model. Fig. 2 also depicts the spatial distribution parameters for both patients. Differences in MBF are reflected by the spatial distribution parameter maps, but in addition differences like a delayed arrival of contrast agent in a segment are detected by the spatio-temporal model.

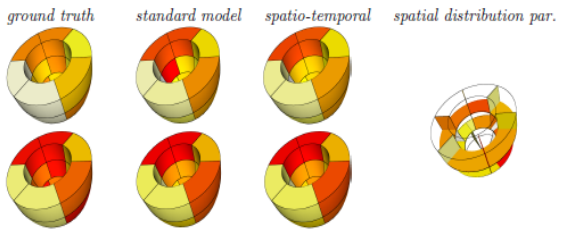

Fig. 1. 3D-visualization of ground truth and estimated MBF and spatial distribution parameters for the simulated data set. Top row: Simulation with conditions at rest, bottom row: Simulation with conditions under stress.

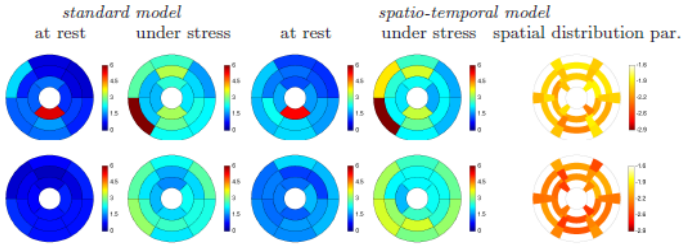

Fig. 2. Bullseye representation of MBF and spatial distribution parameters for two of the patients studied.

DISCUSSION AND CONCLUSION

We have presented a spatio-temporal model for the analysis of myocardial first-pass perfusion MRI scans. The use of a Bayesian framework for estimating the myocardial blood flow form perfusion MRI is a new alternative to the usual de-convolution algorithms [9]. The proposed model includes contextual information to describe the dependencies of the data in the individual segments. Validation with simulated data shows that diseased segments can be detected by depicting the spatial distribution parameter between segments. By taking the complete shape of the response into account, the model highlights differences in delayed enhancement and altered kinetics. Differences in blood flow can result from reduced MBF, and hence stenosis in one of the segments, or from delayed arrival of tracer, hence due to the effect of collateral perfusion. In summary, the proposed method provides additional information to the standard myocardial perfusion index used in cardiovascular MRI, which can further enhance its clinical value.

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