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Projet HeartIC: Image-based data assimilation for an HPC model of the heart.

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Abstract. The aim of the proposed project is to couple a high-performance implementation of a 3D model of cardiac function [2] with clinical data acquired by magnetic resonance imaging, by using the data assimilation library Verdandi [1], in order for such personalized (patient-specific) models to bring additional information compared to pure image processing. While the 3D heart model "HappyHeart" and the data assimilation library Verdandi have been developed and implemented by the Inria M3DISIM research team, the expertise of processing the magnetic-resonance image (MRI) data is brought into the project by Philips Research, Hamburg. The cardiac MR images of patients and healthy volunteers will be provided by St Thomas' hospital, King's College London, and the Institute for Clinical and Experimental Medicine, Prague.

1 Scientific Context

It has been already demonstrated that the MΞDISIM heart model can be calibrated to represent cardiac cycles of patients with various pathologies [7]. Moreover, data assimilation strategies have been proposed in [6] to register this type of model on actual data extracted from medical images – typically Cine-MRI. An important aspect of this strategy is the definition of an adequate discrepancy measure between the data and the model. Indeed, data processing techniques are able to extract contours of cardiac chambers, but do not provide trajectories of material points of the myocardium (the observations are in essence Eulerian), and the inner myocardial points of the myocardium cannot be tracked at all. Therefore, in [6] a data assimilation feedback is computed from a discrepancy based on the distance between the model contours and the contours of segmented images.

However, this initial work suffers from two drawbacks: (1) it requires a segmentation step of the data and (2) it is based on a simple definition of the distance between contours to compute the discrepancy. In this project, by using the expertise of Philips Hamburg [4], we propose a new discrepancy measure that can be constructed without prior segmentation of the image data. The idea is to construct a distance map from the simulated contour directly to the image as it is performed in the state-of-the-art segmentation algorithm used by Philips in the clinics. This will therefore allow the data assimilation strategy to be directly interfaced with cine-MRI data.

Moreover, in [6], the results were obtained using a research code of the Team MΞDISIM based on Matlab. Over the last two years, the team has made a great effort in refactoring this initial research code in a C++ HPC version. This allows to use much larger models and to be transferred in general architectures.

Our objective is thus that the resulting coupled model-data implementation will then benefit from state-of-the-art components from the cardiac modeling community and from the image community and bring new perspectives to the respective communities.

For the modeling community, we will finally have a robust implementation of a model registered over clinical data. For the clinical community, we will bring additional information compared to pure image processing, and we will assess our results based on a "ground truth" provided by tagged-MRI, while also comparing our results with dynamic segmentations of cine-MRI, the current state-of-the-art for direct image processing, provided by Philips as well. For instance, our model can recover the circumferential component of displacements (heart twisting) of clinical value [5].

Another benefit is then to use the registered model in processing yet another type of magnetic resonance imaging data such as in reconstructing a map of T1-relaxation times from the so-called Modified Look-Locker inversion recovery (MOLLI), and in the quantitative analysis of perfusion MRI. The former has raised a keen interest in the recent years in clinical cardiac MRI, as it allows to locally assess some myocardial tissue properties, e.g. tissue fibrosis. Here, a set of 10-15 2D images are acquired over a relatively long breath-hold period. While the reconstruction of the T1 map requires all these 2D images to exactly cover the same part of the organ, the cardiac cycle variations during the long breath-hold often causes the heart not to be in the same phase of cardiac cycle (i.e. various wall thickness over these 10-15 samples). Correction of this non-rigid misregistration can be based on the 3D+time information obtained from the cine-MRI coupled with the biomechanical model performed in our previous step. The perfusion MRI consists of a set of 2D images periodically acquired (typically every heart beat) during a period of 30–60 seconds. In order to perform any quantitative analysis based on this data, the whole dynamical image series needs to be well registered in 3D space and, similarly to the MOLLI samples, the coupled biophysical model and cine-MRI will serve as a 3D template. The approach of employing cine-MRI in reconstructing the T1- and perfusion maps would be entirely compatible with clinical practice, since the cine-motion data are always acquired prior / with the cardiac T1-relaxation or perfusion data.

Finally, the quantitative values of T1 relaxation time and of perfusion map have important diagnostic value (the former reflecting passive stiffness tissue properties, the latter the active contractility), and could be also taken as an initialization for a second detailed parameter estimation study employing the same model. This would be indeed well in the spirit of applied cardiac modeling and data assimilation: first, less computationally intensive state estimation is run using relatively routine data with the advantage of no need of image data pre-processing, as proposed in our project. A decision is made depending on the more detailed motion indicators, T1 relaxation and perfusion maps (all based on the state estimator) wether – typically in the patients with suspected and hard-to-diagnose specific cardiac disease – a more detailed parameter estimation should be employed.

2 Objective and tasks

Objective

Coupling an HPC cardiac simulator with a state-of-the-art model-image discrepancy based on the original distances implemented by Philips in their clinical segmentation tool.

Main tasks

- **T1 Algorithm (18-25/07)** – Adapt the existing algorithm based on the simple distance to contours to the Philips-based distance
- **T2 Implementation (25-01/08)** – Integrate the Philips library into the HPC code, and compute the variational term that assimilates the discrepancy
- **T3 First Test (01-15/08)** – Evaluate the implementation by comparison with the MΞDISIM legacy code.
- **T4 Validation (15-26/08)** – Validate the method by comparison with existing outputs provided by Philips in the clinical context.

3 Technical solutions

HappyHeart

Verdandi Verdandi is a generic C++ library for data assimilation. It is currently developed at Inria. It aims at providing methods and tools for data assimilation. It is designed to be relevant to a large class of problems involving high-dimensional numerical models. To guarantee the highest performance, the library is implemented in C++. In addition, Verdandi provides a Python interface generated by Swig. Models implemented in Fortran, C, C++, Python etc. can be plugged to Verdandi using either a C++ or Python interface.

HappyHeart HappyHeart is an object-oriented finite element library for the numerical simulation of partial differential equations. It aims at simulating multiphysics and multiscale problems on parallel platforms. Its interface has been designed to be compatible with Verdandi to use data assimilation methods very easily.

Image distance Library from Philips Tools for automatic extraction of heart shape from 3D image modalities were developed by Philips Research during euHeart FP7 program [3]. The functionality was extended to standard time-resolved MR cine sequences – the type of data used in the proposed model-data coupling – during the FP7 program VP2HF. The C++ written image distance library provided by Philips contains the following main functions: distance computation for any spatial point from the endo- and epicardial surfaces in a given time-snapshot of cine MRI; projection of the point on the surface mesh; and confidence of the distance for the given spatial point. These three functions are used for the discrepancy operator considered in the model-data coupling.

4 Participants

Radomir Chabinok is a researcher at Inria, team MΞDISIM, and a radiologist at St Thomas' Hospital, King's College London. He is an expert in cardiac modeling and data-based personalization of models.

Philippe Moireau and Dominique Chapelle are researchers at Inria, team MΞDISIM, and initially designed the observer using distances to images.

Gautier Bureau is an engineer in the team MΞDISIM. He has developed the cardiac components in the HPC code HappyHeart and he is an expert in Verdandi.

Sebastien Gilles is a senior engineer in the team MΞDISIM. He has in charge of the development of the HPC code HappyHeart.

Alexandra Groth is a senior scientist at Philips Research Hamburg in the group of Jürgen Weese, where she works on developing software technology for automatic generation of personalized anatomical models of heart and other organs from medical images.

Jiri Minarcik and *Katerina Solovska* are 3-rd year undergraduate students of mathematics at Faculty of Nuclear Sciences and Physical Engineering, Czech Technical University in Prague. They participate in a joint grant with Institute for Clinical and Experimental Medicine on "Quantitative mapping of the myocardium using MRI in non-ischemic cardiac disease patients". While the focus and preliminary work of Jiri within the grant is in image processing methods for motion correction in perfusion MRI data, Katerina's interest is in the T1-mapping MRI (correction in the MOLLI sequence) – the topics representing two additional examples for using the information obtained from the cine-MRI – biomechanical model coupling.

References

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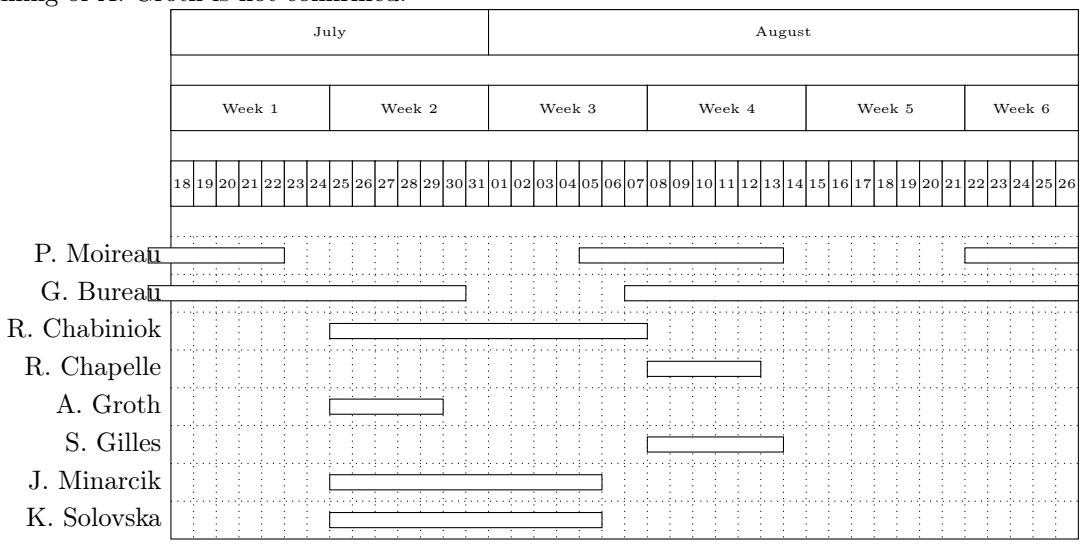
Appendice 1: Planning

The following Gantt diagram 4 gives the list of participants and their planning. Note that the planning of A. Groth is not confirmed.



Appendice 2: Financement

Le Tableau 1 donne pour chaque participant le coût estimé et l'organisme qui le finance.

Table 1: Fundings

	Estimated cost	Fundings
R. Chabiniok	1800 €	King's College London
G. Bureau	4150 €	VP2HF European Project and Inria MΞDISIM
D. Chapelle	800 €	Inria MΞDISIM
P. Moireau	2500 €	Cemracs
S. Gilles	100 € (lunch only for 1 week)	Inria MΞDISIM
J. Minarcik	$\simeq$ 1300 €	Czech Ministry of Health
K. Solovska	$\simeq$ 1300 €	Czech Ministry of Health