Activity Report 2014

Team M3DISIM

Mathematical and Mechanical Modeling with Data Interaction in Simulations for Medicine

RESEARCH CENTER
Saclay - Île-de-France

THEME
Modeling and Control for Life Sciences

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Team M3DISIM

Keywords: Scientific Computation, Finite Elements, Data Assimilation, Inverse Problem, Virtual Physiology, Fluid-structure Interaction

Creation of the Team: 2013 January 01.

1. Members

Research Scientists

Dominique Chapelle [Team leader, Inria, Senior Researcher, HdR]
Sébastien Imperiale [Inria, Researcher]
Philippe Moireau [Inria, Researcher (Secondment from Corps des Mines)]

Engineer

Sébastien Gilles [Inria]

PhD Students

Annabelle Collin [Inria, until Oct 2014]
Bruno Burtschell [Inria, supported by FP7 VPH-SHARE project]

Post-Doctoral Fellows

Matthieu Caruel [Inria, until Aug 2014, supported by FP7 VP2HF project]
Karine Mauffrey [Inria, until Aug 2014, supported by FP7 VP2HF project]

Visiting Scientist

Alexandre Laurin [Inria, from Jun 2014 until Jul 2014]

Administrative Assistant

Hélèna Kutniak [Inria]

Other

Alessandro Felder [Inria, Internship, until Apr 2014]

2. Overall Objectives

2.1. Overall Objectives

The research carried out in the M3DISIM team has a rather global methodological perspective oriented towards biomechanics, encompassing mathematical modeling and analysis, inverse problems arising from model-data coupling, and the formulation and analysis of effective and reliable numerical procedures adapted to this overall program. We are also very keen on demonstrating the effectiveness and relevance of these methods in actual applications, usually by proof-of-concept studies carried out within various collaborations.

3. Research Program

3.1. Multi-scale modeling and coupling mechanisms for biomechanical systems, with mathematical and numerical analysis

Over the past decade, we have laid out the foundations of a multi-scale 3D model of the cardiac mechanical contraction responding to electrical activation. Several collaborations have been crucial in this enterprise, see below references. By integrating this formulation with adapted numerical methods, we are now able to represent the whole organ behavior in interaction with the blood during complete heart beats. This subject

was our first achievement to combine a deep understanding of the underlying physics and physiology and our constant concern of proposing well-posed mathematical formulations and adequate numerical discretizations. In fact, we have shown that our model satisfies the essential thermo-mechanical laws, and in particular the energy balance, and proposed compatible numerical schemes that – in consequence – can be rigorously analyzed, see [5]. In the same spirit, we have recently formulated a poromechanical model adapted to the blood perfusion in the heart, hence precisely taking into account the large deformation of the mechanical medium, the fluid inertia and moving domain, and so that the energy balance between fluid and solid is fulfilled from the model construction to its discretization, see [16].

3.2. Inverse problems with actual data – Fundamental formulation, mathematical analysis and applications

A major challenge in the context of biomechanical modeling – and more generally in modeling for life sciences – lies in using the large amount of data available on the system to circumvent the lack of absolute modeling ground truth, since every system considered is in fact patient-specific, with possibly non-standard conditions associated with a disease. We have already developed original strategies for solving this particular type of inverse problems by adopting the observer stand-point. The idea we proposed consists in incorporating to the classical discretization of the mechanical system an estimator filter that can use the data to improve the quality of the global approximation, and concurrently identify some uncertain parameters possibly related to a diseased state of the patient, see [6], [7], [8]. Therefore, our strategy leads to a coupled model-data system solved similarly to a usual PDE-based model, with a computational cost directly comparable to classical Galerkin approximations. We have already worked on the formulation, the mathematical and numerical analysis of the resulting system – see [3] – and the demonstration of the capabilities of this approach in the context of identification of constitutive parameters for a heart model with real data, including medical imaging, see [1].

4. Application Domains

4.1. Clinical applications

After several validation steps – based on clinical and experimental data – we have reached the point of having validated the heart model in a pre-clinical context where we have combined direct and inverse modeling in order to bring predictive answers on specific patient states. For example, we have demonstrated the predictive ability of our model to set up pacemaker devices for a specific patient in cardiac resynchronization therapies, see [9]. We have also used our parametric estimation procedure to provide a quantitative characterization of an infarct in a clinical experiment performed with pigs, see [1].

5. New Software and Platforms

5.1. FELISCE

Participants: Dominique Chapelle, Sébastien Gilles [correspondant], Sébastien Imperiale, Philippe Moireau.

FELISCE – standing for “Finite Elements for LIfe SCiences and Engineering” – is a new finite element code which the MACS and REO teams have decided to jointly develop in order to build up on their respective experiences concerning finite element simulations. One specific objective of this code is to provide in a unified software environment all the state-of-the-art tools needed to perform simulations of the complex cardiovascular models considered in the two teams – namely involving fluid and solid mechanics, electrophysiology, and the various associated coupling phenomena. FELISCE is written in C++, and may be later released as an opensource library. See https://gforge.inria.fr/projects/felisce/.

In FELISCE we have prepared a branch called HappyHeart, which aims at providing a user-friendly interface able to deal efficiently with complex cardiovascular simulations. Started in 2013, the code is already quite large (about 55 000 lines of code in almost 700 different files) and its core is about to be complete in early 2015. It includes among others full HPC functionalities, high-order finite elements, physics coupling and topology capabilities. Our purpose will then be to use the library to implement the sophisticated cardiovascular models of the team and couple them with Verdandi (data assimilation library) to provide patient-specific simulations.

- Software benefit: HappyHeart is a multiphysics HPC FEM Library with cardiac simulation concerns
- Type of human computer interaction: Command line and configuration files.
- OS/Middleware: MacOS, Linux.
- Required library or software: OpenMpi (parallelism), Petsc (linear algebra), Seldon (linear algebra), Parmetis (partitioner), Mumps (solver), Ops (input parameter file management), STL and Yuni (generic C++ libraries).
- Programming language: C++ 11/14.
- Documentation: Doxygen and user's manual in English.

5.2. HeartLab

Participants: Matthieu Caruel, Dominique Chapelle, Alessandro Felder, Philippe Moireau [correspondant].

The heartLab software is a library written in (64-bit compatible) Matlab and C (mex functions) designed to perform both simulation and estimation (based on various types of measurements, e.g. images) of the heart mechanical behavior. Started in 2006, it is already quite large (about 60,000 lines), and is used within various collaborations.

The code relies on OpenFEM – to which the team has previously contributed, see http://www.openfem.net – for the finite element computations, and the implementation was performed with a particular concern for modularity, since modeling and estimation use the same finite element operators. This modularity also allows to couple the code with other FEM solvers, such as LifeV and Mistral developed in the Reo team-project. In particular, we are now able to include perfusion and electrical coupling with LifeV using PVM, and fluid-structure interaction using Mistral.

We also included geometric data and tools in the code to define cardiac anatomical models compatible with the simulation requirements in terms of mesh quality, fiber direction data defined within each element, and the referencing necessary for handling boundary conditions and estimation, in particular. These geometries are analytical or come from computerized tomography (CT) or magnetic resonance (MR) image data of humans or animals.

We incorporated numerous non-linear data assimilation observation operators based on medical imaging post-processing to be able to now perform estimation with a large variety of medical imaging modalities. And recently we have worked on generalized micro-macro cardiac law using stochastic formulations.

5.3. Verdandi

Participants: Aurora Armiento [Mamba team], Dominique Chapelle, Annabelle Collin, Vivien Mallet [Clime team], Karine Mauffrey, Philippe Moireau [correspondant].

Verdandi is an opensource (LGPL) software library aiming at providing data assimilation methods and related tools. Mainly targeted at large systems arising from the discretization of PDEs, it is intentionally devised as generic, which allows for applications in a wide range of problems (biology and medicine, environment, image processing...). See also the web page http://verdandi.gforge.inria.fr/, with a complete documentation in English. The first stable version (1.0) was released in June 2012 and contains most of the major data assimilation algorithms of both variational and sequential types. The current version (1.6) contains additional estimation algorithm and parallel capabilities. Note that some specific developments are performed with particular regard to cardiac modeling applications, as Verdandi is partly funded by – and distributed within – the VPH-Share and VP2HF projects and is now referenced in the peer-reviewed article [4].

- ACM: Mathematical software
- AMS: System theory; control
- Software benefit: Verdandi is the only *generic* data assimilation library
- License: LGPL (2.1 or any later version)
- Type of human computer interaction: Command line and configuration files
- OS/Middelware: Linux, MacOS ou Windows
- Required library or software: Seldon (LGPL, http://seldon.sourceforge.net/)
- Programming language: C++, ISO/IEC 14882: I998(E) Python, version 2.6
- Documentation: Doxygen and utilisation manual in English

Moreover a Matlab module called VerdandinMatlab is developed in the team for pedagogical and test purposes.

6. New Results

6.1. Highlights of the Year

- Radomir Chabiniok recruited in starting research position (start Febr 2015);
- PhD Defense of Annabelle Collin;
- "Usine Nouvelle" article.

6.2. Modeling

6.2.1. Mechanics of collective unfolding

Participants: Matthieu Caruel [correspondant], Jean-Marc Allain [LMS], Lev Truskinovsky [LMS].

Mechanically induced unfolding of passive crosslinkers is a fundamental biological phenomenon encountered across the scales from individual macro-molecules to cytoskeletal actin networks. In this work we study a conceptual model of athermal load-induced unfolding and use a minimalistic setting allowing one to emphasize the role of long-range interactions while maintaining full analytical transparency. Our model can be viewed as a description of a parallel bundle of N bistable units confined between two shared rigid backbones that are loaded through a series spring. We show that the ground states in this model correspond to synchronized, single phase configurations where all individual units are either folded or unfolded. We then study the fine structure of the wiggly energy landscape along the reaction coordinate linking the two coherent states and describing the optimal mechanism of cooperative unfolding. Quite remarkably, our study shows the fundamental difference in the size and structure of the folding-unfolding energy barriers in the hard (fixed displacements) and soft (fixed forces) loading devices which persists in the continuum limit. We argue that both, the synchronization and the non-equivalence of the mechanical responses in hard and soft devices, have their origin in the dominance of long-range interactions. We then apply our minimal model to skeletal muscles where the power-stroke in acto-myosin crossbridges can be interpreted as passive folding. A quantitative analysis of the muscle model shows that the relative rigidity of myosin backbone provides the long-range interaction mechanism allowing the system to effectively synchronize the power-stroke in individual crossbridges even in the presence of thermal fluctuations. In view of the prototypical nature of the proposed model, our general conclusions pertain to a variety of other biological systems where elastic interactions are mediated by effective backbones.

6.2.2. Thermodynamical framework for modeling chemical-mechanical coupling in muscle contraction - Formulation and validation

Participants: Matthieu Caruel, Dominique Chapelle [correspondant], Philippe Moireau.

Muscle contraction occurs at the nanoscale of a hierarchical multi-scale structure with the attachment of so-called cross-bridges within sarcomeres, namely, the creation of chemical bonds between myosin heads and specific sites on actin filaments. A cross-bridge in itself can be seen as a special chemical entity having internal mechanical variables - or degrees of freedom - pertaining to the actual geometric configuration, which implies that the free energy of the cross-bridge - whether in an attached or unattached state - must be made dependent on these internal variables (T.L. Hill, Free Energy Transduction And Biochemical Cycle Kinetics, Dover, 2004). This provides a thermodynamical basis for modeling the complex interplay of chemical and mechanical phenomena at the sarcomere level. Within this framework we propose a muscle model with two mechanical variables associated with a cross-bridge. For the action of individual cross-bridges occurring at the nanometer scale, the energy provided by the Langevin thermostat cannot be neglected, and we therefore propose to endow the internal mechanical variables with stochastic dynamics. Important motivations for this modeling choice include the ability to represent (i) the so-called power-stroke phenomenon and (ii) short-time responses of a muscle, e.g. to load steps. Our approach allows for systematic treatment of the model energetics, and in particular one goal of the proposed description is to investigate the potential benefit in mechanical efficiency with systems including - in addition to chemically-induced transformations - thermally-induced conformational changes such as the power-stroke.

6.2.3. Mechanical modeling and numerical methods for poromechanics: Applications to cardiac perfusion

Participants: Bruno Burtschell, Dominique Chapelle [correspondant], Philippe Moireau.

We have previously formulated a rather general modeling framework of poromechanics – formulations that combine solid and fluid components to represent the behavior of a porous medium – to take into account large deformations and rapid fluid flows, see [16]. This allows to consider, in particular, the application of blood perfusion within the cardiac tissue, which features these specific complex phenomena, out of the scope of classical poromechanical models. One of our major objectives now, within the PhD of Bruno Burtschell, is to propose and assess some associated relevant numerical schemes.

Some existing algorithms of fluid-structure interaction, with which our poromechanics formulations feature deep similarities, have been implemented – in FreeFEM++, both in axisymmetric configuration and in 3D – and compared. Their numerical and theoretical analysis – consistency, convergence – has been performed. Then, the adaptation of these algorithms to our poromechanics formulations enabled us to propose a time discretisation well-fitted to our framework, and to present its energy stability analysis. Further perspectives include implementation and numerical validation of this scheme, including special care regarding space discretisation, then integration into FELISCE (“HappyHeart” module).

6.2.4. Personalized modeling for cardiac amyloidosis diagnosis

Participants: Alessandro Felder, Dominique Chapelle, Philippe Moireau, Jean-François Deux [Hôpital Henri Mondor], Thibault Damy [Hôpital Henri Mondor].

Cardiac amyloidosis is a condition induced by pathological deposition of amyloid proteins within muscle tissue and nerves, thus severely impairing the cardiac function and often requiring cardiac transplantation as the only available treatment. Our objective here in a first stage is to use our previously developed patient-specific modeling methodologies to analyse some clinical cases – based on actual patient data – to better apprehend the impact of the pathology on biomechanical properties. Further perspectives include the modeling of the protein deposition and associated tissue remodeling in order to predict the disease evolution in a patient-specific context. This work is performed in collaboration with medical doctors from Hôpital Henri Mondor (Créteil).

6.3. Numerical Analysis

6.3.1. Fourth-order energy-preserving locally implicit discretization for linear wave equations

Participants: Juliette Chabassier [Magique-3d], Sébastien Imperiale [correspondant].

A family of fourth-order coupled implicit-explicit time schemes has been developed. The spatial coupling is done at the boundaries of several non conforming meshes of regions in which we want to simulate propagating waves. A global discrete energy is shown to be preserved and leads to global fourth-order consistency. Numerical results in 1D and 2D have been produced to illustrate the good behavior of the schemes and their potential for the simulation of realistic highly heterogeneous media and strongly refined geometries, for which using an explicit scheme everywhere can be extremely penalizing. Accuracy up to fourth order reduces the numerical dispersion inherent to implicit methods used with a large time step, and makes this family of schemes attractive compared to second order accurate methods in time.

6.4. Model-Data Interaction

6.4.1. A Luenberger observer for reaction-diffusion models with front position data

Participants: Dominique Chapelle, Annabelle Collin, Philipe Moireau [correspondant].

We propose a Luenberger observer for reaction-diffusion models with propagating front features, and for data associated with the location of the front over time. Such models are considered in various application fields, such as electrophysiology, wild-land fire propagation and tumor growth modeling. Drawing our inspiration from image processing methods, we start by proposing an observer for the eikonal-curvature equation that can be derived from the reaction-diffusion model by an asymptotic expansion. We then carry over this observer to the underlying reaction-diffusion equation by an "inverse asymptotic analysis", and we show that the associated correction in the dynamics has a stabilizing effect for the linearized estimation error. We also discuss the extension to joint state-parameter estimation by using the earlier-proposed ROUKF strategy. We then illustrate and assess our proposed observer method with test problems pertaining to electrophysiology modeling, including with a realistic model of cardiac atria. Our numerical trials show that state estimation is directly very effective with the proposed Luenberger observer, while specific strategies are needed to accurately perform parameter estimation – as is usual with Kalman filtering used in a nonlinear setting – and we demonstrate two such successful strategies.

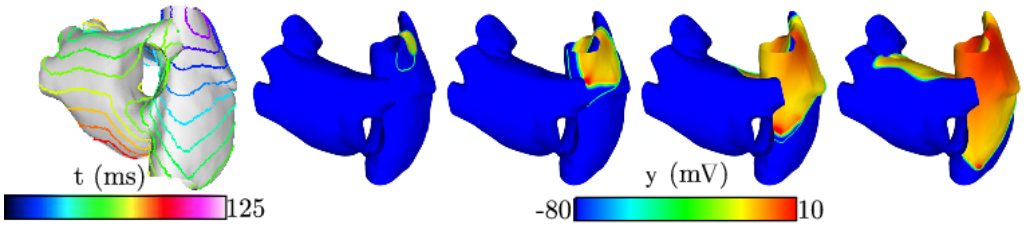

Figure 1. Collocated front data on an atria (left), and observer of the atrial electric activation pursuing the green front from a wrong initial condition (right, 4 time-steps)

6.4.2. Identification of weakly coupled multiphysics problems. Application to the inverse problem of electrocardiography

Participants: Cesare Corrado [Reo team], Jean-Frédéric Gerbeau [Reo team], Philippe Moireau [correspondant].

This work addresses the inverse problem of electrocardiography from a new perspective, by combining electrical and mechanical measurements. Our strategy relies on the definition of a model of the electromechanical contraction which is registered on ECG data but also on measured mechanical displacements of the heart tissue typically extracted from medical images. In this respect, we establish in this work the convergence of a

sequential estimator which combines for such coupled problems various state of the art sequential data assimilation methods in a unified consistent and efficient framework. Indeed, we aggregate a Luenberger observer for the mechanical state and a Reduced-Order Unscented Kalman Filter applied on the parameters to be identified and a POD projection of the electrical state. Then using synthetic data we show the benefits of our approach for the estimation of the electrical state of the ventricles along the heart beat compared with more classical strategies which only consider an electrophysiological model with ECG measurements. Our numerical results actually show that the mechanical measurements improve the identifiability of the electrical problem allowing to reconstruct the electrical state of the coupled system more precisely. Therefore, this work is intended to be a first proof of concept, with theoretical justifications and numerical investigations, of the advantage of using available multi-modal observations for the estimation and identification of an electromechanical model of the heart.

6.4.3. Data assimilation for hyperbolic conservation laws. A Luenberger observer approach based on a kinetic description

Participants: Anne-Céline Boulanger [Ange team], Benoît Perthame [Mamba team], Philippe Moireau [correspondant], Jacques Sainte-Marie [Ange team].

Developing robust data assimilation methods for hyperbolic conservation laws is a challenging subject. Those PDEs indeed show no dissipation effects and the input of additional information in the model equations may introduce errors that propagate and create shocks. We propose a new approach based on the kinetic description of the conservation law. A kinetic equation is a first order partial differential equation in which the advection velocity is a free variable. In certain cases, it is possible to prove that the nonlinear conservation law is equivalent to a linear kinetic equation. Hence, data assimilation is carried out at the kinetic level, using a Luenberger observer also known as the nudging strategy in data assimilation. Assimilation then amounts to the handling of a BGK type equation. The advantage of this framework is that we deal with a single "linear" equation instead of a nonlinear system and it is easy to recover the macroscopic variables. The study is divided into several steps and essentially based on functional analysis techniques. First we prove the convergence of the model towards the data in case of complete observations in space and time. Second, we analyze the case of partial and noisy observations. To conclude, we validate our method with numerical results on Burgers equation and emphasize the advantages of this method with the more complex Saint-Venant system.

6.4.4. Optimal observer for parabolic problems

Participants: Karine Mauffrey, Philippe Moireau [correspondant].

We aim at proposing optimal observers strategies for reconstructing the solution of general systems of PDEs using available observations, including both wave-type equations and heat-like equations. The main objective of this work is to present a self-contained analysis. For a general parabolic system, we have established the exponential stability of the operator occurring in the equation satisfied by the error between the target and the optimal observer. The proof relies on two major hypotheses: an observability inequality satisfied by the observation operator and a controllability property for the modeling error operator by which model noises enter the dynamics (controllability property which is related to the invertibility of the solution of the associated infinite dimensional Riccati equation). Then we have tackled the discretisation questions and demonstrated that the discrete-time Kalman filter is an adequate discretization of the continuous-time Kalman filter. Finally we have also studied the strong formulation of the Kalman observer using a kernel representation of the Riccati operator.

6.4.5. Elastography by magnetic resonance imaging

Participants: Guillaume Bal [Columbia Unviersity], Cedric Bellis [LMA Marseille], Sébastien Imperiale [correspondant], Francois Monard [University of Washington- Seattle].

We have studied the potential application of elastography by Magnetic Resonance Imaging (MRI) within the framework of linear elasticity. We assume given internal full-field MRI measurements of the deformations of a non-homogeneous isotropic solid, and the aim is the quantitative reconstruction of the associated physical parameters. Upon using polluted measurements, a variational formulation is constructed, its inversion enabling the recovery of the parameters. The analysis of this inversion procedure provides existence and uniqueness results while the reconstruction stability with respect to the measurements is investigated. As the inversion procedure requires differentiating the measurements twice, a numerical differentiation scheme has been proposed and analyzed. It is based on a regularization that allows an optimally stable reconstruction of the sought parameters.

7. Partnerships and Cooperations

7.1. Regional Initiatives

The team is part of the Mechanics and Living Systems Initiative (Opération Mécanique et Systèmes du Vivant), a joint operation – focused on biomechanical modeling – between the LadHyx and LMS labs (CNRS and Ecole Polytechnique), and Inria-M3DISIM.

7.2. European Initiatives

7.2.1. FP7 & H2020 Projects

7.2.1.1. VPH-Share

Type: FP7

Defi: Towards sustainable and personalised healthcare

Instrument: Integrated Project

Objectif: Virtual Physiological Human

Duration: March 2011 - February 2015

Coordinator: Univ. Sheffield (UK)

Other partners: Cyfronet (Cracow), University College London, Istituto Ortopedico Rizzoli (Bologna), NHS, IBM Israel, Univ. Auckland, Agència d'Informació, Avaluació i Qualitat en Salut (Barcelona), Biocomputing Competence Centre (Milano), Universitat Pompeu Fabra (Barcelona), Philips Research, TUE (Eindhoven), Sheffield Teaching Hospitals, Atos Origin (Madrid), the Open University (UK), Univ. Vienna, King's College London, Empirica (Bonn), Fundació Clínic (Barcelona), Univ. Amsterdam

See also: http://vph-share.org/

Abstract: VPH-Share aims at developing the organisational fabric (the infostructure) and integrating the optimised services to expose and share data and knowledge, to jointly develop multiscale models for the composition of new VPH workflows, and to facilitate collaborations within the VPH community. Within this project, the M3DISIM team is in charge of developing some high-performance data assimilation software tools.

7.2.1.2. VP2HF

Type: FP7

Defi: ICT for Health, Ageing Well, Inclusion and Governance

Instrument: Specific Targeted Research Project

Objectif: Virtual Physiological Human

Duration: October 2013 - September 2016

Coordinator: King's College London (UK)

See also: http://vp2hf.eu/

Abstract: Heart failure (HF) is one of the major health issues in Europe affecting 6 million patients and growing substantially because of the aging population and improving survival following myocardial infarction. The poor short to medium term prognosis of these patients means that treatments such as cardiac re-synchronisation therapy and mitral valve repair can have substantial impact. However, these therapies are ineffective in up to 50% of the treated patients and involve significant morbidity and substantial cost. The primary aim of VP2HF is to bring together image and data processing tools with statistical and integrated biophysical models mainly developed in previous VPH projects, into a single clinical workflow to improve therapy selection and treatment optimisation in HF.

7.3. International Research Visitors

7.3.1. Visits of International Scientists

7.3.1.1. Internships

Alexendre Laurin
[Simon Fraser Univ., Canada]
Sébastien Imperiale
[correspondant]
Philippe Moireau
Dominique Chapelle

In the context of an ongoing collaboration between the Aerospace Physiology lab (Simon Fraser University, Vancouver, Canada) and Inria (M3DISIM and Reo teams), Alexandre Laurin (PhD student) has been awarded some funding for a 2 months internship in the M3DISIM team, with the objective of initiating the modelling of seismocardiography (SCG) measurements. SCG consists in measuring displacements of the sternum and ribs generated by a heart beat using accelerometers placed on the thorax. In this context, linear elastodynamics equations are applicable to account for the transient propagation of motion from the heart to the sternum via the highly heterogeneous underlying materials (cartilage and bone). Specific care has been taken to solve the aforementioned equation in a realistic 3D geometry including the complete thoracic cage. Fully coupled simulations (beating heart with thorax deformation) are planned at the final stage of this modelling work in 2015.

8. Dissemination

8.1. Promoting Scientific Activities

Dominique Chapelle

- Member of the editorial boards of journals *Computers & Structures* and *M2AN*
- Program committee of conference “Functional Imaging and Modeling of the Heart 2015”
- Invited lecturer in workshops “Model Order Reduction and Data” (Jacques-Louis Lions Lab, Paris 6, 6–8 Jan.), and “Modeling and Simulation in Biomechanics” (Graz Univ., 15–17 Sept.)
- Member of the Academic Senate of FCS Paris-Saclay
- Member of the board of directors of the VPH Institute

Philippe Moireau

- Member of the Inria Saclay-Ile de France CR2 Jury
- Reviewer this year for Region Aquitaine Grants
- Reviewer of the PhD Thesis of Atte Alto on *Infinite Dimensional Systems: Passivity and Kalman Filter Discretization*

Sébastien Imperiale

- Reviewer in Inverse problem, SIAM journal on Numerical Analysis, Geophysics, Journal of Computational Physics

8.2. Teaching - Supervision - Juries

8.2.1. Teaching

Dominique Chapelle

Lectures on cardiac biomechanical modeling in Master's programs SIM (Univ. Créteil) and BME (Paris 5 and ParisTech)

Philippe Moireau

Bachelor's degree: "MA103 - Introduction aux EDP et à leur approximation numérique", 14h, M1, ENSTA ParisTech, France

Master's: "MA201 - La méthode des éléments finis", 14h classes , M2, ENSTA ParisTech, France

Master's: "Data assimilation module", 6h lectures, Paris VI University, France

Sébastien Imperiale

Master's: "MA201 - La méthode des éléments finis", 12h, M2, ENSTA ParisTech, France

Master's: "Simnum - Simulation numérique en C++", 36h, M1, ENSTA ParisTech, France

Annabelle Collin

Oral examination:"Algebra and Geometry", Paris 6 University, spring 2012

Bachelor's degre:"Multivariable Calculus", Paris 6 University, fall 2012

8.2.2. Supervision

PhD defended in October: Annabelle Collin, "Dimensional reduction and electro-mechanical coupling for the modeling of electrophysiology and muscle contraction", UPMC, started September 2011, advisors D. Chapelle and J.-F. Gerbeau

PhD in progress: Bruno Burtshell, "Mechanical modeling and numerical methods for poromechanics: Applications to cardiac perfusion", Ecole Polytechnique, started October 2013, advisors D. Chapelle and P. Moireau

8.2.3. Juries

Dominique Chapelle: member of PhD committees of J. Mullaert (Paris 6, 17 Dec.) and C. Dupont (Ecole Polytechnique, 18 Dec., chairman)

Philippe Moireau: member of PhD committee of A. Collin

8.3. Popularization

D. Chapelle interviewed for article in "Usine Nouvelle" on cardiac modeling

D. Chapelle invited at "Futur en Seine" event for presentation and debate on predictive systems

P. Moireau presentation for the Inria Direction of Financial Affairs on the "heart forecasting"

9. Bibliography

Major publications by the team in recent years

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