

Yongjie Jessica Zhang
João Manuel R.S. Tavares (Eds.)

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Computational Modeling of Objects Presented in Images

Fundamentals, Methods, and Applications

4th International Conference, ComplIMAGE 2014
Pittsburgh, PA, USA, September 3–5, 2014
Proceedings



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Preface

The 4th CompIMAGE conference (<http://jessicaz.me.cmu.edu/CompImage2014/>) aimed to bring together researchers in the area of computational modeling of objects represented in images. Different approaches, such as level set methods, deformable models, optimization, geometric modeling, principal component analysis, stochastic methods, machine learning and fuzzy logic, among others, were discussed by experts to address problems from different applications, including medicine, biomechanics, biometrics, material science, robotics, surveillance, and defense. The CompImage 2014 conference was held in Pittsburgh, USA, during September 3–5, 2014. The previous CompIMAGE conferences were held in Rome, Italy (2012), Buffalo, USA (2010), and Coimbra, Portugal (2006).

There were 54 papers submitted to CompIMAGE 2014, and each paper was carefully reviewed by several Program Committee members and/or external reviewers. Papers were individually reviewed and subsequently opened for discussion by their reviewers to encourage debate and finding a consensus among reviewers. Eventually, 29 full papers were accepted. In addition, we solicited and accepted ten short or position papers. The proceedings are published by Springer in *Lecture Notes in Computer Science* and the authors of the best ranked papers were invited to submit extended versions to the journal *Computer Methods in Biomechanics and Biomedical Engineering: Imaging & Visualization*. The conference also featured six invited talks by Profs. Michael Sacks from The University of Texas at Austin, Jelena Kovačević from Carnegie Mellon University, Andrew D. McCulloch and Jiun-Shyan (JS) Chen from the University of California San Diego, Ross Whitaker from the University of Utah, and Marc Thiriet from the Université Pierre et Marie Curie.

We would like to thank the authors and participants at the conference, the international Program Committee members, and the external reviewers, all of whom made their best effort to ensure the high quality of the CompIMAGE 2014 technical program. We further thank Christine Lambrou, Keri Baker, and Mike Scampone from the Department of Mechanical Engineering, Carnegie Mellon University, for their very hard effort in organizing and handling all the events at CompIMAGE 2014.

July 2014

Yongjie Jessica Zhang
João Manuel R.S. Tavares

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Keynote Talks

On Development of an Anatomical, Structural, and Mechanical Integrated Model of the Mitral Valve

Michael Sacks

Professor of Biomedical Engineering

W.A. "Tex" Moncrief, Jr. Simulation-Based Engineering Science Chair I
Director of the ICES Center for Cardiovascular Simulation-based Engineering
Institute for Computational Engineering and Sciences
The University of Texas at Austin, USA

Abstract. The mitral valve (MV) is one of the four heart valves which locates in between the left atrium and left ventricle and regulates the unidirectional blood flow and normal functioning of the heart during cardiac cycles. Alternation of any component of the MV apparatus will typically lead to abnormal MV function. Currently 40,000 patients in the United States receive MV repair or replacement annually according to the American Heart Association. Clinically, this can be achieved iteratively by surgical repair that reinstate normal annular geometry (size and shape) and restore mobile leaflet tissue, resulting in reduced annular and chordae force distribution. High-fidelity computer simulations provide a means to connect the cellular function with the organ-level MV tissue mechanical responses, and to help the design of optimal MV repair strategy. As in many physiological systems, one can approach heart valve biomechanics from using multiscale modeling (MSM) methodologies, since mechanical stimuli occur and have biological impact at the organ, tissue, and cellular levels. Yet, MSM approaches of heart valves are scarce, largely due to the major difficulties in adapting conventional methods to the areas where we simply do not have requisite data. There also re-mains both theoretical and computational challenges to applying traditional MSM techniques to heart valves. Moreover, existing physiologically realistic computational models of heart valve function make many assumptions, such as a simplified micro-structural and anatomical representation of the MV apparatus, and thorough validations with in-vitro or in-vivo data are still limited. We present the details of the state-of-the-art of mitral valve modeling techniques, with an emphasis on what is known and investigated at various length scales.

Short Bio: Professor Michael Sacks is the W.A. "Tex" Moncrief, Jr. Simulation-Based Engineering Science Chair and a world authority on cardiovascular biomechanics. His research focuses on the quantification and modeling of the

structure-mechanical properties of native and engineered cardiovascular soft tissues. He is a leading authority on the mechanical behavior and function of the native and engineered heart valves. He is also active in the biomechanics of engineered tissues, and in understanding the in-vitro and in-vivo remodeling processes from a functional biomechanical perspective.

His research includes multi-scale studies of cell/tissue/organ mechanical interactions in heart valves and is particularly interested in determining the local stress environment for heart valve interstitial cells. Recent research has included developing novel constitutive models of right ventricular myocardium that allow for the individual contributions of the myocyte and connective tissue networks.

Selected Recognitions:

Fellow, American Society of Mechanical Engineers

Fellow (Inaugural), Biomedical Engineering Society

Fellow, American Institute for Medical and Biological Engineering

Van C. Mow Medal, American Society for Mechanical Engineers Bioengineering Division

Chancellor's Distinguished Research Award, University of Pittsburgh

Ph.D., Biomedical Engineering, University of Texas Southwestern Medical Center at Dallas

M.S., Engineering Mechanics, Michigan State University

B.S. Engineering Mechanics, Michigan State University

Image Based Modeling of Biomaterials Based on Galerkin and Collocation Meshfree Method

Jiun-Shyan (JS) Chen

William Prager Chair Professor
Structure Engineering
University of California San Diego, USA

Abstract. This work introduces meshfree method for image based modeling of biomaterials. The proposed approach allows a direct construction of simulation model based on pixel data obtained the MRI images. The pixel points serve for dual purposes in the meshfree modeling: they are used to define the geometry of the subject and are employed as the discrete points to obtain approximate solution of the governing partial differential equations. The material properties and the fiber orientation information in the DTI data are stored at each pixel point, and the displacements, stresses and strains are solved at each pixel point as well. The meshfree approximation with smooth kernel allows a representation of material heterogeneity with smooth transition across the material interfaces. The point based reproducing kernel (RK) approximation also avoids the complexity in construction of the well shaped mesh in the conventional finite element method. Two types of meshfree method for image based modeling of biomaterials are introduced, one based on Galerkin type weak formulation and the other based on a direct collocation of differential equations. In conjunction with the level set based image segmentation technique, we apply the proposed meshfree methods to multiscale modeling of bone materials as well as simulation of skeletal muscles under contraction.

Short Bio: Prof. Jiun-Shyan (JS) Chen is the William Prager Chair of Structural Engineering at UCSD. He earned his undergraduate degree from National Central University in Taiwan, and Master's and Ph.D. from Northwestern University. Before moving to UCSD in October 2013, he was the Chancellor's Professor of UCLA and has served as the Department Chair of Civil & Environmental Engineering Department (2007-2012). His research is in computational mechanics and multiscale materials modeling with specialization in development of meshfree methods. He is one of the original developers of the meshfree Reproducing Kernel Particle Method (RKPM). He has applied meshfree methods to large deformation and contact mechanics, geomechanics, shock waves, high strain rate fragment-impact problems, biomechanics, molecular mechanics, quantum mechanics, as well as multi-scale mechanics and materials.

He is the past President of US Association for Computational Mechanics (USACM) and is currently serving on the Executive Council of the International

Association for Computational Mechanics (IACM), the Executive Council of the USACM, the Executive Council of the International Chinese Association for Computational Mechanics (ICACM), and the Board of Governors of ASCE Engineering Mechanics Institute (EMI). He has received numerous awards, including GenCorp Technology Achievement Award; James Lightners Faculty Fellowship and The Faculty Scholar Award from The University of Iowa; Outstanding Alumnus of National Central University (Taiwan); Tongji Chair of Tongji University (China); the ICACM Award from International Chinese Association for Computational Mechanics; the Computational Mechanics Award from International Association for Computational Mechanics, among others. He is the Fellow of USACM, IACM, ASME, EMI, ICACM. He is serving as the Editor-in-Chief, Associate Editor, or Editorial Board member for nine international journals.

Problems in Biological Imaging: Opportunities for Signal Processing

Jelena Kovačević

Department Head of Electrical & Computer Engineering
Professor in Electrical & Computer Engineering and Biomedical Engineering
Director of Center for Bioimage Informatics
Carnegie Mellon University, Pittsburgh, PA, USA

Abstract. In recent years, the focus in biological sciences has shifted from understanding single parts of larger systems, sort of vertical approach, to understanding complex systems at the cellular and molecular levels, horizontal approach. Thus the revolution of “omics” projects, genomics and now proteomics. Understanding complexity of biological systems is a task that requires acquisition, analysis and sharing of huge databases, and in particular, high-dimensional databases. Processing such huge amount of bioimages visually by biologists is inefficient, time-consuming and error-prone. Therefore, we would like to move towards automated, efficient and robust processing of such bioimage data sets. Moreover, some information hidden in the images may not be readily visually available. Thus, we do not only help humans by using sophisticated algorithms for faster and more efficient processing but also because new knowledge is generated through use of such algorithms.

The ultimate dream is to have distributed yet integrated large bioimage databases which would allow researchers to upload their data, have it processed, share the data, download data as well as platform-optimized code, etc., and all this in a common format. To achieve this goal, we must draw upon a whole host of sophisticated tools from signal processing, machine learning and scientific computing. I will address some of these issues in this presentation, especially those where signal processing expertise can play a significant role.

Short Bio: Prof. Jelena Kovačević received a Ph.D. degree from Columbia University. She then joined Bell Labs, followed by Carnegie Mellon University in 2003, where she is currently Professor and Head of the Department of Electrical and Computer Engineering and a Professor in the Department of Biomedical Engineering. She received the Belgrade October Prize and the E.I. Jury Award at Columbia University. She is a coauthor on an SP Society award-winning paper and is a coauthor of the books “Wavelets and Subband Coding” and “Foundations of Signal Processing”. Dr. Kovacevic is the Fellow of the IEEE and was the Editor-in-Chief of the IEEE Transactions on Image Processing. She was a

keynote speaker at a number of meetings and has been involved in organizing numerous conferences. Her research interests include multiresolution techniques and biomedical applications.

Adaptivity and Conformity in Meshing: A Two Phase Strategy

Ross Whitaker

Professor in School of Computing
Scientific Computing and Imaging Institute
University of Utah, USA

Abstract. Despite a great deal of important research and many fundamental advances, the general problem of tetrahedral meshing remains unsolved and challenging. In particular, the constraints imposed by adaptive element size, good tetrahedral quality (shape measured by some local metric), and material boundaries are often in conflict, and attempts to satisfy these conditions simultaneously frustrate many conventional approaches, particularly those that rely on iterative local updates to the mesh. This talk presents results from a recent body of work where we decouple these problems of adaptivity and geometric conformity. The strategy is to construct an adaptive background mesh that ignores geometric boundaries, and then partition or cleave that mesh, so that the resulting mesh conforms to geometry and maintains certain guarantees on important mesh properties. The resulting algorithm produces high-quality, adaptive meshes relatively quickly, but introduces several interesting and important technical challenges.

Short Bio: Ross Whitaker graduated Summa Cum Laude with B.S. degree in Electrical Engineering and Computer Science from Princeton University in 1986. From 1986 to 1988 he worked for the Boston Consulting Group, entering the University of North Carolina at Chapel Hill in 1989. At UNC he received the Alumni Scholarship Award, and completed his Ph.D. in Computer Science in 1994. From 1994–1996 he worked at the European Computer-Industry Research Centre in Munich Germany as a research scientist in the User Interaction and Visualization Group. From 1996–2000 he was an Assistant Professor in the Department of Electrical Engineering at the University of Tennessee and received an NSF Career Award. Since 2000 he has been at the University of Utah where he is faculty member of the Scientific Computing and Imaging Institute and a Professor and the Director of the School of Computing. He teaches discrete math, scientific visualization, and image processing. Professor Whitaker leads a graduate-level research group in image analysis, geometry processing, and scientific computing, with a variety of projects supported by both federal agencies and industrial contracts. He is an IEEE Fellow and a member of the Computing Community Consortium.

A Predictive Mathematical Model of Acupuncture Based on an Explanation Biological Model

Marc Thiriet

Laboratoire Jacques-Louis Lions (LJLL)
Université Pierre et Marie Curie - Paris 6 (UPMC)
France

Abstract. Acupuncture requires a long-term training to handle acupoints. Four techniques exist: (1) development of a local mechanical stress field by needle motions (lifting - thrusting cycle or rotation) at acupoints; (2) development of a local temperature field by directly applying a heating moxa (mugwort herb) stick on the skin or indirectly by applying this stick on the acupuncture needle (moxibustion) at acupoints; (3) development of a local electrical field by applying a small electric current between a pair of acupuncture needles (electroacupuncture, or percutaneous electrical nerve stimulation [PENS]) at acupoints; and (4) laser light excitation independently of heating and other physical means probably via proper G-protein-coupled receptors on the surface of mastocytes.

Acupoints are enriched of mastocytes, among other biological structures and cells. Mastocytes are activation by a mechanical stress field (mechanotransduction), heating (thermotransduction), or a electrical field (electrotransduction). Whatever the operation mode, calcium entry in the mastocyte triggers degranulation and release of chemoattractants, neural stimulants, and endocrine substances. The process is sustained by recruitment of mastocytes (chemotaxis).

Acupuncture effects result from a set of signals sent from activated mastocytes at given acupoints to local nerve endings and capillaries that are transmitted to the brain and heart for processing and augmenting the flow rate, especially in the vasodilated acupoint. Released substances targets their cognate receptors on nerves and lymph and blood vessels. These two types of conduits deliver fast cues (electrochemical waves) and delayed information (blood transport) to the central nervous system, where they are processed for a desired output.

The mathematical model is a system of 5 partial differential equations. Its simplest form describes the evolution of the density of mastocytes and the chemoattractant concentration. A mathematical analysis of a simplified version of the equation set leads to a theorem for blow-up condition (the expected solution) as well as an analytical solution useful for validation. Numerical simulations are also carried out using a finite element method with mesh adaptivity. The computational model based

on the home-made FreeFEM++ software demonstrated the occurrence of a stress field that excite mastocytes. It also shows that only adequate pools of mastocyte, that is, acupoints, must be targeted to have marked effects.

Short Bio: Marc Thiriet was educated at Medicine Faculty of Lille and University Pierre and Marie Curie ([UPMC] MD), and then at Technology University of Compiègne (3rd cycle Doctorate in Biomechanics), and Physics College of University Denis Diderot (Accreditation to Supervise Research). He was assistant physician in the lung disease department of Pontoise hospital. He is currently a member of the INRIA-UPMC-CNRS team REO in Laboratory Jacques-Louis Lions (applied math.) of UPMC. He worked in flows in collapsible tubes applied to airways and veins, 3D unsteady developing laminar flows in bend and branchings, both experimentally and numerically, as well as in models derived from 3D reconstruction of human anatomy. He is now involved in mathematical modeling of biological processes.

Marc Thiriet is the author of *Biology and Mechanics of Blood Flows* (2~Vols.) and the book series “Biomathematical and Biomechanical Modeling of the Circulatory and Ventilatory Systems” (9 Vols., 6 published books). He is associate editor for the medical encyclopedia “Pan Vascular II”. He also wrote the chapter *Biofluid Flow and Heat Transfer* for the next edition of *Handbook of Fluid Dynamics*. He is President of the french committee for Intensive Computation in Biology and Medicine and was involved in European committees for HPC (HPC-Europa-2 and PRACE). He is an Internal Reviewer of several Evaluation Groups of the Canadian Granting Agency (NSERC, mainly Mech. Eng. and also Life Sciences, Chemistry, Material and Chem. Eng., Computer Sci., and Mathematics). He was a Member of the “Biology” Panel of the french National Strategy for Research and Innovation (SNRI). He won the Grand Prix de la Fondation scientifique Franco-Taiwanaise in 2011 from the french Academy of Sciences and Taiwanese Science Council with his colleague Tony WH Sheu for their contribution in high-intensity focused ultrasound (HIFU)-based treatment of liver cancer and the first modeling of acupuncture.