EDITORIAL

Special Issue: Imaging-based methods in computational medicine

Adrian Buganza Tepole[1] · Johannes Weickenmeier[2] · Maria Holland[3] · Rafael Grytz[4]

Being able to peek into the human body during development, physiological processes, and in disease has revolutionized medicine since the end of the nineteenth century and continuing today. Imaging modalities that are routinely used to gather anatomical and (patho)physiological information include ultrasound, X-ray, and magnetic resonance (MR) imaging. In addition to the development of imaging technologies to visualize internal organ systems, optical imaging methods have also contributed to the analysis of tissues and organs such as the skin, which is conveniently exposed to the outside environment. An example of recent progress in three-dimensional (3D) geometry reconstruction with optical imaging is multi-view stereo, which yields accurate 3D geometry from a collection of two-dimensional (2D) pictures. Medical imaging has shed light on the structure and function of arguably all organ systems, from the heart and the spine, to the airways, the brain and the eyes.

Yet, despite how revolutionary, images alone are not enough to fully understand the (patho)physiology of human tissues. Not surprisingly, another stream of research in biomedical engineering, especially during the last four decades, is the mechanistic modeling of human organ systems in their physiological setting as well as in disease. Within the computational approaches, we would like to distinguish between two main categories, computational biology and computational biophysics. Broadly speaking, computational biology can be associated with the modeling of cellular populations and cellular processes as the core element. In contrast, this special issue is primarily focused on computational biophysics methods, which focus on processes somewhat independently of cellular populations, for instance fluid flow,

tissue deformation, mechanical and transport properties, and how they can change over time in development, aging, and disease.

Computational models allow for hypothesis testing, experimental design, and mechanistic understanding. However, biophysics modeling crucially depends on the domain geometry over which the equations are solved, and on boundary conditions, both of which are specific to individuals. While many insights can be gained from simplified models with modeling assumptions regarding geometry and boundary conditions, there is no question that personalized models are needed to improve diagnostic and treatment of disease in the clinical setting. This special issue on Imaging-based Methods in Computational Medicine showcases cutting-edge research on integrating imaging information and biophysics models to elucidate disease mechanisms across different organ systems and impact personalized medicine.

Perhaps the most natural integration of medical imaging and for computational biophysics models is the use of images to inform individualized geometries for the solution of the partial differential equations (PDE) governing the problem, or to directly collect kinematic information, e.g., deformation and flow. This is particularly true in the case of cardiovascular systems. Some of the existing problems, however, derive from the low resolution or relatively high noise-to-signal ratio in dynamic imaging modalities. This special issue shows how to integrate multiple imaging modalities, i.e., ultrasound and MR imaging, to obtain high-fidelity personalized models of blood flow in arteries [4]. Another article in this collection shows how to constrain the kinematic analysis of determining fluid velocities for blood flows from MR images by concurrently solving the Navier–Stokes equations, overall increasing the fidelity of the analysis [6].

Inverse problems, to identify parameters with physical or mechanistic interpretation, is another open area of research that relies on combining imaging data and physics-based modeling. For example, MR imaging can be used to infer properties of tissue, such as transport parameters of tumors, which is needed to determine if drugs are having an effect or

✉ Adrian Buganza Tepole
abuganza@purdue.edu

1   Purdue University, West Lafayette, IN, USA

2   Stevens Institute of Technology, Hoboken, NJ, USA

3   University of Notre Dame, South Bend, IN, USA

4   University of Alabama at Birmingham, Birmingham, AL, USA

not on reducing tumor growth [11]. Another inverse problem showcased in this collection is the identification of activation maps of the heart, with implications for intervention design. This inverse problem is highly sensitive to patient specific geometries and heterogeneous parameter distributions, requiring new methods as shown in Ruiz Herrera et al. [10]. Yet another inverse problem in this issue is outlined by Olson and Throne [7], to infer heterogeneous mechanical properties of the breast from optical imaging and indentation data, providing a noninvasive and accessible method for breast cancer identification.

Registration is another important class of image processing techniques, used to analyze longitudinal data to understand development and disease progression. Traditionally, registration is performed based solely on geometry. For example, by relying on landmarks or other geometric features, e.g., curvature or closest distance between geometries, a map of how a geometry changes over time can be inferred. This type of method ignores the role of physics constraints and therefore can result in inaccurate mapping between geometries, as well as limiting our understanding of a given disease to fully geometric indicators, ignoring other sources of information. The work reported in Pawar et al. [8] and Cox et al. [2] shows how to pose registration problems constrained by PDEs describing tissue deformation. As a result, PDE-constrained registration can uncover not just geometric changes, but also strain maps, which are mechanistic inputs for models of tissue growth and remodeling.

This special issue lays out key areas of active technology development for numerical and image analysis. Not surprisingly, machine learning (ML) methods are one of the fastest evolving fields for medical image analysis. Here we find examples of how ML can be combined with both imaging data and physics-based modeling to enhance computational models. For instance, ML methods can enhance prediction of scoliosis progression given longitudinal data for patients at risk by integrating these data with the modeling of bone biomechanics and growth [15]. ML is suitable for posing inverse problems such as the identification of cardiac activation maps [10], or imputation of missing longitudinal data in an image sequence [9]. Undoubtedly, work in ML that specifically fuses image analysis and biophysics modeling will continue to play a central role in computational medicine.

Another technology for numerical analysis that appears in several of the articles in this collection is iso-geometric analysis (IGA). Finite element methods have been the default option of numerical solution of PDEs for decades. However, IGA has emerged as a powerful alternative, particularly in image analysis applications, for its ability to represent accurate geometries while also relying on locally supported, complete, and high-continuity basis functions. In this issue, the work by [2, 4, 8, 14] illustrate new developments in IGA methods for imaging-based biophysics models.

From an organ systems perspective, the special issue covers a wide variety of applications to show just how versatile image-based computational medicine methods are. The more mature field of cardiovascular biomechanics is represented by several contributions including work by [2, 4–6, 10, 13].

Several papers of this special issue stress the need for high-fidelity personalized models. The musculoskeletal system is the focus of Tajdari et al. [15], who created personalized models of spine growth in scoliosis, and that of Crutison and Royston [3], who obtained material parameters from different MR imaging modalities on muscles. Meanwhile, skin [8] and tumors are also studied [7, 11].

Finally, we would like to emphasize the study on brain biophysics, an emerging area of study which is very well-represented among the papers of this issue. High-fidelity personalized models of brain are needed to understand the heterogeneous damage patterns in traumatic brain injury [14], or those during aging and neurodegeneration [1]. Population-level modeling of reaction–diffusion systems of key proteins in the brain are useful to understand neurodegeneration patterns and improve early detection of disease [12].

In summary, we have assembled a representative collection of the latest research on imaging-based computational medicine, showcasing new technological developments and emerging applications. We anticipate that this special issue will serve as a good snapshot, not just to understand the current landscape in the area, but to drive the next generation of methods that continue to bring computational biophysics modeling into day-to-day clinical practice.

References

1. Caçoilo A, Rusinek H, Weickenmeier J (2022) 3D finite-element brain modeling of lateral ventricular wall loading to rationalize periventricular white matter hyperintensity locations. Eng Comput. https://doi.org/10.1007/s00366-022-01700-y

2. Cox A, Ortiz-Puerta D, Sotelo J et al (2022) Mechanics-informed snakes isogeometric analysis (MISIGA): an image-based method for the estimation of local deformation and strain in blood vessels. Eng Comput. https://doi.org/10.1007/s00366-022-01738-y

3. Crutison J, Royston T (2022) The design and application of a diffusion tensor informed finite-element model for exploration of uniaxially prestressed muscle architecture in magnetic resonance imaging. Eng Comput. https://doi.org/10.1007/s00366-022-01690-x

4. Horn JD, Starosolski Z, Johnson MJ et al (2022) A novel method for improving the accuracy of MR-derived patient-specific vascular models using X-ray angiography. Eng Comput. https://doi.org/10.1007/s00366-022-01685-8

5. Mathur M, Meador WD, Malinowski M et al (2022) Texas TriValve 1.0 : a reverse-engineered, open model of the human tricuspid valve. Eng Comput. https://doi.org/10.1007/s00366-022-01659-w

6. Naudet CJ, Töger J, Zahr MJ (2022) Accurate quantification of blood flow wall shear stress using simulation-based imaging: a synthetic, comparative study. Eng Comput. https://doi.org/10.1007/s00366-022-01723-5

7. Olson LG, Throne RD (2022) Stiffness mapping for early detection of breast cancer: combined force and displacement measurements. Eng Comput. https://doi.org/10.1007/s00366-022-01741-3

8. Pawar A, Li L, Gosain AK et al (2022) PDE-constrained shape registration to characterize biological growth and morphogenesis from imaging data. Eng Comput. https://doi.org/10.1007/s00366-022-01682-x

9. Raad R, Patel D, Hsu CC et al (2022) Probabilistic medical image imputation via deep adversarial learning. Eng Comput. https://doi.org/10.1007/s00366-022-01712-8

10. Ruiz Herrera C, Grandits T, Plank G et al (2022) Physics-informed neural networks to learn cardiac fiber orientation from multiple electroanatomical maps. Eng Comput. https://doi.org/10.1007/s00366-022-01709-3

11. Sainz-DeMena D, Ye W, Pérez MÁ et al (2022) A finite element based optimization algorithm to include diffusion into the analysis of DCE-MRI. Eng Comput. https://doi.org/10.1007/s00366-022-01667-w

12. Schäfer A, Chaggar P, Goriely A et al (2022) Correlating tau pathology to brain atrophy using a physics-based Bayesian model. Eng Comput. https://doi.org/10.1007/s00366-022-01660-3

13. Shidhore TC, Cebull HL, Madden MC et al (2022) Estimating external tissue support parameters with fluid–structure interaction models from 4D ultrasound of murine thoracic aortae. Eng Comput. https://doi.org/10.1007/s00366-022-01735-1

14. Shim V, Tayebi M, Kwon E et al (2022) Combining advanced magnetic resonance imaging (MRI) with finite element (FE) analysis for characterising subject-specific injury patterns in the brain after traumatic brain injury. Eng Comput. https://doi.org/10.1007/s00366-022-01697-4

15. Tajdari et al (2022) Next-generation prognosis framework for pediatric spinal deformities using bio-informed deep learning networks. Eng Comput. https://doi.org/10.1007/s00366-022-01742-2