PhD course

Title:

Introduction to imaging-based computational forecasting of tumor growth and treatment response

Teacher:

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Duration:

24 hours (10 hours of lectures + 14 hours of hands-on coding), corresponding to 6 CFU

Schedule:

November 28, 29, 30 & December 5, 6, 7: 11-13 h and 14.30-16.30 h

Venue (tentative):

Aula MS1, Dipartimento di Ingegneria Civile e Architettura (ground floor)

Abstract:

The computer simulation of personalized mechanistic models of tumor growth and treatment response has enabled the prediction of clinical outcomes for multiple types of cancers and provides a promising approach to optimize their clinical management. Mechanistic models of cancer usually consist of a set of partial differential equations describing the key mechanisms involved in cancer growth and treatment. Longitudinal clinical and imaging data collected from an individual patient enable the personalized calibration of these mechanistic models, hence accounting for the unique heterogeneity of each patient's tumor. In particular, quantitative medical imaging (e.g., multiparametric magnetic resonance imaging, positron emission tomography) can provide spatiotemporally-resolved measurements of key biological features of tumors, such as their morphology, architecture, metabolism, and supporting vasculature. The resulting personalized model can then be leveraged to forecast tumor progression, the therapeutic outcome of prescribed therapies, and the response to alternative treatments to optimize tumor control.

This course will begin by reviewing the main approaches of organ-scale, patient-specific mechanistic modeling of tumors using different imaging data types for model initialization and calibration. We will also describe standard computational technologies enabling model simulation, model calibration, model selection, and treatment optimization. We will focus on the use of isogeometric analysis (IGA) to solve mechanistic models of cancer and hence run computer simulations to forecast tumor dynamics. IGA extends the classical finite element method by representing geometry with functions which are typically used by CAD systems (e.g., B-splines, NURBS). Hence, the computational domain exactly reproduces the CAD description of the physical domain. Numerical testing in different situations has shown that IGA holds great promises, with a substantial increase in the accuracy per degree of freedom with respect to standard finite elements. These geometric and numerical advantages are also of interest in computational oncology, where IGA has been leveraged to run accurate simulations over patient-specific anatomic meshes matching the tumor host organ segmentation over imaging data.

The course will cover the derivation of the standard isogeometric Galerkin formulation of the model, an outline of the main numerical algorithms for their resolution, and several technical details for code implementation (e.g., isoparametric mapping, numerical quadrature, boundary conditions). Additionally, the course includes a series of hands-on coding sessions using MATLAB. These sessions will begin with the resolution of a collection of introductory problems using standard isogeometric Galerkin methods, which will ultimately serve as a basis to construct an elementary code to solve a standard imaging-based reaction-diffusion model of cancer growth.