A First Course in “In Silico Medicine”

Volume 3

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Computational Biomechanics

Theoretical Background
and Biological/Biomedical Problems

Springer
Preface

Computational biology and system biology are bases for in silico medicine, which consists of two main activities. The first is the development of mathematical models describing structures and functions of biological systems across a multiple scale augmented with experimental data from wet and dry biological and medical measurements. The second is the development of a simulator of biological functions in physiological and pathological situations to provide us with the behavior of components at multiple scales in a quantitative manner and to enable us to apply that information to medical problems. This book is the third volume of the textbook series A First Course in “In Silico Medicine”. The first volume gives an introduction to computational physiology, and the second volume is devoted to computational electrophysiology. The main physical quantities discussed in these two volumes are electric/ionic currents and potentials related to electrical phenomena in biology. Other important physical quantities in biological systems are forces and deformations studied in mechanics, and these are the topics of this third volume.

Biomechanics is an area that deals with mechanical aspects, especially structures and functions, of hardware and software constructing biological systems of a living body. It is considered a relatively new area compared to mechanics, biology, and physiology, in spite of its long history at least from the ancient Greeks with Aristotle’s treatises. In these decades, the area covered by biomechanics has expanded tremendously in accordance with rapid developments in life science. In fact, the dynamics of biomolecules such as DNA and proteins, mechanics of the whole cell and an intercellular structure, and so on are recent major subjects of biomechanics at a smaller scale, in addition to the advanced subjects of tissue and organ biomechanics of the musculo-skeletal system, the cardiovascular system, and other systems at a relatively larger scale. Qualitative advancement is another important direction in biomechanics because of rapid developments in biological/biomedical measurement and imaging technologies as well as development of computer analysis and information technologies. The quantity of data nowadays is so huge that it results in a qualitative change in the meaning of data as a whole.
The quantitative increase in data, such as structural geometry obtained with CT and MR images, enables us to deal with a target body entirely as it is, and invites us into a virtual computer world that represents realistic biological tissue and/or organ structures, while classical studies focus on essential phenomena by simplification necessitated by the limited availability of fundamental data and solvable scale-problems. This direction is common in biomedical imaging supported by computer graphics and virtual reality technologies. Computational biomechanics lies in the same direction towards computational biology and medicine. The essences of computational biomechanics are mathematical and computational modeling of phenomena concerning deformations and forces.

In this textbook, mathematical fundamentals are limited to continuum mechanics, and no attention is paid to statistical, quantum, and relativistic mechanics. Therefore, a biological body is assumed to be a continuum body, because the continuum assumption is reasonable in many scales of size and time for biomedical problems except for molecule size, although any body is composed of atoms. Computational modeling is thus for discrete representation of a continuum within the scale of continuum mechanics. This is not limited to the geometrical modeling of an object body but also involves the mechanical modeling of phenomena under consideration. The degree of discretization is determined of course based on the objective of computational analysis in general, and it governs the adequacy of results of analyses. These are sometimes limited by the resolution of fundamental data available for analysis. These days, there are many powerful and function-rich engineering tools available in mechanics analysis on the software market. These are applicable to biomechanics problems as well, but this does not mean that computational biomechanics analysis is ready for every researcher or student. To be a reasonable user and become a smart user, it is essential to understand what the software tools are able to do and are doing for your problem. Biomechanics problems need mechanical modeling for biological bodies and environments, which are essentially different from common problems in mechanical, civil, and other engineering fields. For these reasons, the theoretical bases and assumptions should be understood and therefore this textbook is self-contained, covering both the basics of continuum mechanics of biosolids and biofluids and the theoretical core of computational methods for continuum mechanics analyses. Several biomechanics problems in orthopedic and cardiovascular biomechanics and other areas are provided for better understanding of computational analysis background and modeling issues in biomechanics problems. These are mainly direct analyses but include back or inverse analyses as well.

A standard direct analysis is the first key of computational biomechanics in \textit{in silico} medicine that gives us much quantitative information for biological and biomedical phenomena in practical problems in medicine. A back/inverse analysis extended from a direct one is the promising second key as expected for the model-based prediction towards \textit{in silico} medicine. We hope readers will be interested in the further development of biomechanics and contribution to predictive medicine.
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