Computer Modeling in Bioengineering

Theoretical Background, Examples and Software





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Miloš Kojić

Harvard School of Public Health, USA University of Kragujevac, Serbia University of Texas Health Science Center at Houston, USA

Nenad Filipović

Faculty of Mechanical Engineering, University of Kragujevac, Serbia

Boban Stojanović

Center for Scientific Research of Serbian Academy of Sciences and Arts and University of Kragujevac, Serbia

Nikola Kojić

Harvard-MIT Division of Health Sciences and Technology, USA Harvard Medical School, USA







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Computer Modeling in Bioengineering

About this Book

This book is comprised of the following entities:

A. The Main Text

Presented in three parts: I II and III

Organized in chapters and sections with reference to other entities on the web.

B. Theory – available at www.wiley.com/go/kojic

Additional details are provided which complement the main text and extend it to give the more complete presentation of the text in the Entity A.

C. Examples - available at www.wiley.com/go/kojic

Additional details are provided for examples from Entity A, and some additional examples are given.

D. Software - the link for the software can be accessed via www.wiley.com/go/kojic

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The Software will continuously be updated by the authors.

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Contributors

Paolo Decuzzi

University of Magna Graecia, Italy The University of Texas Health Science Center, USA

Mauro Ferrari

The University of Texas Health Science Center, USA Rice University, USA

Francesco Gentile

University of Magna Graecia, Italy

Nenad Grujovic

University of Kragujevac, Serbia

Velibor Isailović

University of Kragujevac, Serbia

Miloš Ivanović

University of Kragujevac, Serbia

Nikola Jagić

University of Kragujevac, Serbia

Gareth McKinley

Massachusetts Institute of Technology, USA

Srboljub Mijailović

Harvard School of Public Health, USA

Vladimir Miloradović

University of Kragujevac, Serbia

Božidar Novaković

University of Kragujevac, Serbia

Vladimir Ranković

University of Kragujevac, Serbia

Branko Ristić

University of Kragujevac, Serbia

Mirko Rosić

University of Kragujevac, Serbia

Radovan Slavković

University of Kragujevac, Serbia

Dimitrije Stamenović

Boston University, USA

Daniel Tschumperlin

Harvard School of Public Health, USA

Akira Tsuda

Harvard School of Public Health, USA

Ivo Vlastelica

University of Kragujevac, Serbia

Miroslav Živković

University of Kragujevac, Serbia

Preface

Bioengineering in recent years has become one of the most attractive fields of research and development in industry, education and medicine. The development mainly relies on experimental investigations, which have increasingly been coupled to computer modeling.

The aim of this book is to provide basic information about the methods used in computer modeling and simulation of biological systems and processes and to present typical results of modeling. The book is accompanied by software on the world wide web for studying the representative biomechanical problems in more detail. The primary goal of the book is to serve as a textbook in various bioengineering university courses, as well as a support for basic and clinical research.

The presented text, results and software rely on the work of the authors over a number of years, together with collaborators and contributors from the University of Kragujevac, Serbia and other universities (Harvard University, Boston University, University of Texas Health Science Center at Houston, The Hong Kong Polytechnic University). Most of the topics are presented as an introduction, referring to our modeling results, rather than as an extensive overview of various approaches. On the other hand, we have given in-depth analyses where we considered useful to further elucidate the biomedical problem.

The book is divided into three parts: I Theoretical Background of Computational Methods, II Fundamentals of Computational Methods, and III Computational Methods in Bioengineering. In the first part, Chapters 1–3, the basic relations are summarized for the ease of the presentations in the subsequent chapters and for overall completeness. This summary is accompanied by a rather small number of solved examples to illustrate applications of the theoretical considerations.

Part II, Chapters 4–8, covers computational methods that are subsequently implemented in modeling of bioengineering problems. The basis is the Finite Element (FE) method which is commonly used in engineering, science and medicine. Here, we give the essence of the method, for solids, general field problems and coupled physical fields, in linear and nonlinear domains. Also, we present in Chapter 8 the fundamentals of more recent methods, such as Dissipative Particle Dynamics (DPD), Smoothed Particle Hydrodynamics (SPH), and Element-Free Galerkin (EFG) method, as well as coupling of these methods to the FE method, and a multiscale approach. The last methods are especially well suited for bioengineering applications and are also implemented in the subsequent chapters. The most representative example solutions are shown at the end of sections, and for most of them the software on the web provides a more detailed analysis.

In the last part, Chapters 9–19, the computational methods of Part II are applied to various bioengineering problems. Each chapter contains the following: physiological background and

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significance, description of the computational methods used for modeling of the considered problems, and example solutions. The examples are selected to be representative and the most important results are shown in the form of graphs or fields of the considered physical quantity. The solutions are mainly obtained using the current stage of the computer package PAK (University of Kragujevac, Serbia).

On the web, accompanying the book, the following sections are provided: Theory, Examples, and Software. In Theory, we provide additions to the text in the book in order to make some of the topics more complete and with more detail of certain derivations. In Examples we give further details for some of the examples from the book, or present more example solutions. The Software contains most of examples from the book, with extra examples given. For each of the examples a specific interface is developed so that the model can be generated by the menu with the suitable model parameters. These parameters can be changed within a given range in order to elucidate the effects of various conditions for the considered problem. Post-processing of results can be selected by the menu and results can be displayed by the selected option. Also, a Tutorial is provided for each example where the example is described in detail and guidance through the solution approach is suggested. The Software relies on the current stage of the software package PAK and the size of each example, as well as the range of the model parameters, are limited. Questions about the use of the Software and solutions of problems which are more general or over the prescribed limits, can be sent to the authors: http://www.wiley.com/go/kojic.

The book is prepared mainly as a textbook for upper-level undergraduate or graduate courses in bioengineering, engineering and applied sciences in general, and medicine. For the courses where the computational methods are important, the chapters within Part I and Part II should be used. There, a selection can be made with respect to problems of solids or field problems. In the case of the emphases on solids, Chapters 2, 4, 5, 6 and 8 provide the theoretical background and basics of the computational methods. When the emphasis is on the field problems, then Chapters 2 (with selection of sections), 3, 7 and 8 can be used. After these theoretical background chapters a number of chapters within Part III can be examined. In the case where the fundamentals of the computational methods are not essential, an overview of topics within Part I and Part II can be made, or both parts can be skipped; followed by a selection of Chapters in Part III. We have organized chapters in Part III to be self-sufficient in a way that each chapter has physiological considerations, a presentation of computational methods, and example solutions. Here, also, some of the computer modeling goals and purpose.

We consider that support by the Software on the web should be of great help for lecturers when organizing classes. The theoretical presentations (either from the theoretical background or from bioengineering applications) can be accompanied by use of the Software with menu-driven modeling and solution display. Use of the Software can also aid students when studying various theoretical or bioengineering problems.

The book is also prepared to be useful for researchers in various fields related to bioengineering as well as other scientific fields, including medical applications. The book provides basic information about how a bioengineering (or medical) problem can be modeled, which computational models can be used, and the background of the applied computer models. Each of the bioengineering problems treated in this book has been analyzed elsewhere from different aspects, with more detail and particular theoretical considerations. We have referred to these analyses to a certain extent, but these referrals are far from being complete, since the field of computer modeling in bioengineering is vast and consistently expanding.

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Miloš Kojić, Nenad Filipović, Boban Stojanović, Nikola Kojić

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