Biomedical Signal Analysis: Contemporary Methods and Applications

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Preface

If we knew what we were doing, it wouldn't be called research, would it?
Albert Einstein (1879–1955)

Our nation's strongest information technology (IT) industry advances are occurring in the life sciences, and it is believed that IT will play an increasingly important role in information-based medicine. Nowadays, the research and economic benefits are found at the intersection of biosciences and information technology, while future years will see a greater adoption of systems-oriented perspectives that will help change the way we think about diseases, their diagnosis, and their treatment. On the other hand, medical imaging is positioned to become a substantial beneficiary of, and a main contributor to, the emerging field of systems biology.

In this important context, innovative projects in the very broad field of biomedical signal analysis are now taking place in medical imaging, systems biology, and proteomics. Medical imaging and biomedical signal analysis are today becoming one of the most important visualization and interpretation methods in biology and medicine. The period since 2000 has witnessed a tremendous development of new, powerful instruments for detecting, storing, transmitting, analyzing, and displaying images. These instruments are greatly amplifying the ability of biochemists, biologists, medical scientists, and physicians to see their objects of study and to obtain quantitative measurements to support scientific hypotheses and medical diagnoses.

An awareness of the power of computer-aided analytical techniques, coupled with a continuing need to derive more information from medical images, has led to a growing application of digital processing techniques for the problems of medicine. The most challenging aspect herein lies in the development of integrated systems for use in the clinical sector. Design, implementation, and validation of complex medical systems require not solely medical expertise but also a tight collaboration between physicians and biologists, on the one hand, and engineers and physicists, on the other.

The very recent years have proclaimed systems biology as the future of biomedicine since it will combine theoretical and experimental approaches to better understand some of the key aspects of human health. The origins of many human diseases, such as cancer, diabetes, and cardiovascular and neural disorders, are determined by the functioning and malfunctioning of signaling components. Understanding how individual

components function within the context of an entire system under a plentitude of situations is extremely important to elucidate the emergence of pathophysiology as a result of interactions between aberrant signaling pathways. This poses a new challenge to today's pharmaceutical industry, where both bioinformatics and systems biology/modeling will play a crucial role. Bioinformatics enables the processing of the enormous amount of data stemming from high-throughput screening methods while modeling helps in predicting possible side effects, as well as determining optimal dosages and treatment strategies. Both techniques aid in a mechanistic understanding of both disease and drug action, and will enable further progress in pharmaceutics by facilitating the transfer from the "black-box" approach to drug discovery.

The goal of the present book is to present a complete range of proven and new methods which play a leading role in the improvement of biomedical signal analysis and interpretation.

Chapter 1 provides an introduction to biomedical signal analysis. It will give an overview on several processing and imaging techniques that will disambiguate mixtures of observed components being observed in the biomedical analysis. Chapter 2 contains a description of methods for spectral transformations. Signal processing techniques that extract the information required to explore complex organization levels are described . Methods such as continuous and discrete Fourier transforms and derived techniques as discrete cosine and sine transform will be elucidated. Chapter 3 deals with principal component analysis, representing an important step in demixing groups of components. The theoretical aspects of blind source separation or independent component analysis (ICA) are described in chapter 4. Several state-of-the-art ICA techniques are explained and many practical issues are presented, since the mixture of components represents a very important paradigm in biosignal processing. Chapter 5 presents a new signal processing technique, the dependent component analysis and practical modeling of relevant architectures. Neural networks have been an emerging technique since the 1980s and have established themselves as an effective parallel processing technique in pattern recognition. The foundations of these networks are described in chapter 6. Besides neural networks, fuzzy logic methods represent one of the most recent techniques applied to data analysis in medical imaging. They are always of interest when we have to deal with imperfect knowledge, when a precise modeling of a system is difficult,
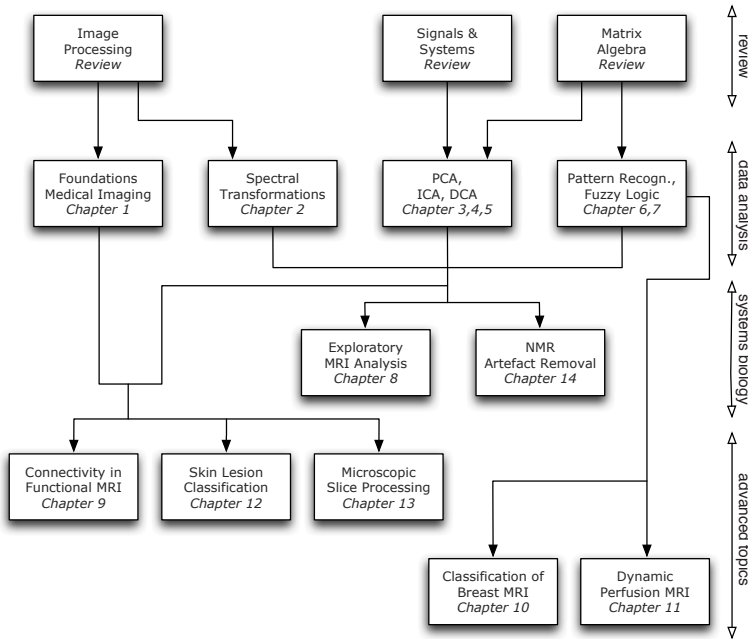
Figure 1
Overview of material covered in this volume and a flow diagram of the chapters.

and when we have to cope with both uncertain and imprecise knowledge. Chapter 7 develops the foundations of fuzzy logic and of several fuzzy c-means clustering and adaptive algorithms. Chapters 8 through 14 show the application of the theoretical tools to practical problems encountered in everyday biosignal processing. Challenging topics ranging from exploratory data analysis and low frequency connectivity analysis in fMRI, to MRI signal processing such as lesion detection in breast MRI, and cerebral time-series analysis in contrast-enhanced perfusion MRI time series are presented, and solutions based on the introduced techniques are outlined and explained in detail. In addition, applications to skin lesion classification, microscopic slice image processing, and automatic labeling, as well as mass spectrometry, are described.

An overview of the chapters is given in order to provide guidance through the material, and thus to address specific needs of very diverse audiences. The basic structure of the book is depicted in figure 1.

The selected topics support several options for reference material and graduate courses aimed to address specific needs of a very diverse audience:

• **Modern biomedical data analysis techniques:** Chapters 2 to 7 provide theoretical aspects and simple implementations of advanced topics. Potential readers: graduate students and bioengineering professionals.

• **Selected topics of computer-assisted radiology:** chapters 1, 2, 3, 4, 6, 7 (section 7.5) and 10 to 14. Potential readers: graduate students, radiologists, and biophysicists.

The book is also designed to be accessible to the independent reader. The table of contents and end-of-chapter summaries should enable the reader to quickly determine which chapters he or she wants to study in most depth. The dependency diagram in figure 1 serves as an aid to the independent reader by helping him or her to determine in what order material in the book may be covered.

The emphasis of the book is on the compilation and organization of a breadth of new approaches, modelling, and applications from signal processing, exploratory data analysis, and systems theory relevant to biosignal modeling. More than 300 references are included and are the basis of an in-depth study. The authors hope that the book will complement existing books on biomedical signal analysis, which focus primarily on time-frequency representations and feature extraction.

Only basic knowledge of digital signal processing, linear algebra, and probability is necessary to fully appreciate the topics considered in this book. Therefore, the authors hope that the book will receive widespread attention in an interdisciplinary scientific community: for those new to the field as a novel synthesis, and as a unique reference tool for experienced researchers.

Acknowledgments

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We end with some remarks about the form of this book.

Conventions   We set technical terms in italics at first use e.g. *new definition*.

Exercises   At a number of places, particularly at the end of each theoretical chapter, we include exercises. Attempting the exercises may help you to improve your understanding. If you do not have time to complete the exercises, just making sure that you understand what each exercise is asking will be of benefit.

Experiments and intuitions   Often we want you to reflect on your opinion on a particular claim, or to try a small psychological experiment on yourself. In some cases, reading ahead without thinking about the problem or doing the experiment may spoil your intuition about a problem, or may mean that you know what the "correct" result is.

Citations and References   As we mentioned above, we have kept citations in the running text to an absolute minimum. Instead, at the end of each chapter, we have included a section titled Further Reading, where we give details of not only the original references where content presented in the chapter first appeared, but also details of how one can follow up certain topics in more depth. These references are also collected in a bibliography at the end of the book.

Index   An integrated index is supplied at the end of the book. This is intended to help those who do not read the book from cover to cover to come to grips with the jargon. The index gives the page reference where the term in question was first introduced and defined, as well as page references where the various topics are discussed.

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