

Preface

Machine learning is a novel discipline concerned with the analysis of large data and multiple variables. It involves computationally intensive methods, is currently mainly the domain of computer scientists, and is already commonly used in social sciences, marketing research, operational research, and applied sciences.

It is virtually unused in clinical research. This is probably due to the traditional belief of clinicians in clinical trials where multiple variables are equally balanced by the randomization process and are not further taken into account. In contrast, modern computer data files often involve hundreds of variables like genes and other laboratory values, and computationally intensive methods are required for their analysis.

The book *Machine Learning in Medicine* published in March 2013 by Springer, Dordrecht, the Netherlands, was written as an introduction to the medical community, and consists of 20 chapters relevant to clinical research. It addresses subjects like optimal scaling, neural networks, factor analysis, partial least squares, discriminant analysis, canonical analysis, and fuzzy modeling.

Why are these methods so convenient for clinical data analysis? This is so because (1) they can handle a large amount of or complex data is no problem, (2) they are more flexible than traditional statistical methods, (3) software programs based on these methods offer user friendly menus without a lot of syntax.

Prior to the completion of the first volume of this publication the authors came to realize that additional methods accounting the effects of potential biases of the reported methods were available. Also, some of the methods not reported so far might provide a better fit for some clinical data sets. These points were the main reasons for writing the current volume *Machine Learning in Medicine: Part Two*. Like the first volume it consists of 20 chapters, and it reviews methods like various clustering models, support vector machines, Bayesian networks, discrete wavelet analysis, genetic programming, association rule learning, and anomaly detection.

We as authors believe that, together with the first book, this book is unique in its field, because the medical community, although increasingly involved in large and complex data, is lacking adequate knowledge for in-depth analyses. Each chapter of the novel book is written in a way much similar to that of the first volume and

(1) will describe a novel method that has already been successfully applied in the authors' own research, (2) will provide the analysis of medical data examples, (3) will provide step-by-step analyses for the benefit of the readers, (4) will provide the commands to be given to the software programs applied (mostly SPSS), (5) can be studied without the need to consult other chapters, and (6) will be written in an explanatory way for a readership of mainly nonmathematicians.

We should add that the authors are well qualified in their field. Professor Zwinderman is president of the International Society of Biostatistics (2012–2015), and Professor Cleophas is past-president of the American College of Angiology (2000–2002). From their expertise they should be able to make adequate selections of modern methods for clinical data analysis for the benefit of physicians, students, and investigators. The authors have been working and publishing together for 14 years, and their research can be characterized as a continued effort to demonstrate that clinical data analysis is not mathematics but rather a discipline at the interface of biology and mathematics.

The authors are not aware of any textbook in the field of machine learning in medicine, and, therefore, believe that the current two-volume publication entitled *Machine Learning in Medicine Parts One and Two* does fill a need.

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Part Two

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