

Preface

Patients are not alike! This simple truth is often ignored in the analysis of medical data, since most of the time results are presented for the “average” patient. As a result, potential variability between patients is ignored when presenting, e.g., the results of a multiple linear regression model. In medicine there are more and more attempts to individualize therapy; thus, from the author’s point of view biostatisticians should support these efforts. Therefore, one of the tasks of the statistician is to identify heterogeneity of patients and, if possible, to explain part of it with known explanatory covariates.

Finite mixture models may be used to aid this purpose. This book tries to show that there are a large range of applications. They include the analysis of gene expression data, pharmacokinetics, toxicology, and the determinants of beta-carotene plasma levels. Other examples include disease clustering, data from psychophysiology, and meta-analysis of published studies.

The book is intended as a resource for those interested in applying these methods. So the main focus is on introducing the ideas of finite mixture models and their ideas in various applications. The author hopes that this material is accessible to an audience with some quantitative background, such as (bio)statisticians, epidemiologists, pharmacokineticists, and interested physicians. The book assumes knowledge of statistics at an intermediate level; hence, familiarity with maximum likelihood estimation is assumed, since such methods are the basis for the statistical inference and estimation used throughout the book. The chapter on theory and algorithms is perhaps mathematically a bit more demanding. This chapter follows the idea to provide the necessary background in convex optimization necessary to understand the algorithms available for finite mixture models.

To provide easy to use software, the book is accompanied by the R (<http://www.r-project.org>) package CAMAN, which can be used to carry out many of the analyses performed in this book. The package and data sets available to the public may be found at <http://www.charite.de/biometrie/schlattmann/book>. Some of the analyses may also be performed with SAS. The corresponding code may also be found on the appropriate Web page.

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