

Preface

Biostatistics is one of the scientific fields for which the developments during the last decades of the 20th century have been the most important. Biostatistics is a pluri-disciplinary area combining statistics and biology, but also agronomics, medicine or health sciences. It needs a good knowledge of the mathematical background inherent in statistical methodology, in order to understand the various fields of applications. The idea of this book is to present a variety of research papers on the state of art in modern biostatistics.

Biostatistics is interacting with many scientific fields. To highlight this wide *diversity*, we deliberately put these interactions at the center of our project. Our book is therefore divided into two parts. Part I is presenting several statistical models and methods for different biologic applications, while Part II will be concerned with problems and statistical methods coming from other related scientific fields.

This book intends to provide a basis for many people interested in biostatistics and related sciences. Students, teachers and academic researchers will find an overview on modelling and statistical analysis of biological data. Also, the book is meant for practitioners involved in research organisations (pharmacologic industry, medicine, food industry,...) for which statistics is an indispensable tool.

Biology is a science which has always been in permanent interaction with many other fields such as medicine, physics, environmetrics, chemistry, mathematics, probability, statistics On the other hand, statistics is interacting with many other fields of mathematics as with almost all other scientific disciplines, including biology. For all these reasons, biostatistics is strongly dependent on other scientific fields, and in order to provide a wide angle overview we present here a rich *diversity* of applied problems.

Each contribution of this book presents one (or more) real problem. The variation ranges from biological problems (see Chapter 1 and 10), medical contributions (see Chapters 2, 4, 5, 8, 9 or 11) and genomics contributions (see Chapters 3 and 7), to applications coming from other scientific areas, such as

environmetrics (see Chapters 12), chemometrics (see Chapter 13), geophysics (see Chapters 17 and 18) or image analysis (see Chapter 18). Because all these disciplines are continuously taking benefits one from each other, this choice highlights as well how each biostatistical method and modelling is helpful in other areas and vice versa.

A good illustration of such a duality is provided by hazard analysis, which is originally a medical survival problem (see Chapters 4, 9 or 11) but which leads to substantial interest in many other fields (see e.g. the microearthquakes analysis presented in Chapter 17). Another example is furnished by spatial statistics (see Chapters 15 or 18) or food industry problems (see Chapter 13), which are apparently far from medical purposes but whose developments have obvious (and strong) consequences in medical image analysis and in biochemical studies.

Due to the variety of applied biostatistical problems, the scope of methods is also very large. We address therefore the *diversity* of these statistical approaches by presenting recent developments in descriptive statistics (see Chapters 7, 9, 14 and 19), parametric modelling (see Chapters 1, 2, 6 and 18) nonparametric estimation (see Chapters 3, 4, 11, 15 and 17) and semi-parametrics (see Chapters 5, 8 and 10). An important place is devoted to methods for analyzing functional data (see Chapters 12, 13, 16), which is currently an active field of modern statistics.

An important feature of biostatistics is to have to deal with rather large statistical sample sizes. This is particular true for genomics applications (see Chapters 3 and 7) and for functional data modelling (see Chapters 12, 13 and 16). The computational issues linked with the methodologies presented in this book are carried out thanks to the capacities of the XploRe environment. Most of the methodological contributions are accompanied with automatic and/or interactive XploRe quantlets.

We would like to express our gratitude to all the contributors. We are confident that the scope of papers will insure a large impact of this book on future research lines and/or on applications in biostatistics and related fields. We would also like to express our sincere gratitude to all the researchers that we had the opportunity to meet in the past years. It would be tedious (and hardly exhaustive) to name all of them expressly here but specific thanks have to be addressed to our respective teams, will special mention to Anton Andriyashin in Berlin and to the participants of the STAPH working group in Toulouse.

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