Survival or time-to-event data arise in various research areas such as medicine, epidemiology, genetics, engineering, econometrics, and sociology. Survival data have unique features including incomplete observation such as censoring and/or truncation. Use of semi-parametric models and potential correlation among time-to-events from the same cluster can make the statistical inference further complicated.

Broad classes of multivariate models using random effects have been developed. For inferences about unobserved random variables, the hierarchical (or h-)likelihood has been proposed by Lee and Nelder (1996). This book presents recent works on h-likelihood for the analysis of survival data. The h-likelihood method has been used to make inferences on the random effects models, especially for the frailty model for time-to-event data, where the frailties are treated as unobserved yet realized in the data. The h-likelihood allows an extension to the frailty models under competing risks as well as to the models for joint outcomes, e.g., longitudinal and event time outcomes. The h-likelihood method estimates the population parameters and the random effects simultaneously, with the random effects being updated from the observed data. This book covers the state-of-the-art h-likelihood methods, which include interval estimation of the individual frailty and variable selection of the covariates in the general class for the frailty models with or without competing risks. A beauty of the h-likelihood is that once the statistical model is specified parametrically or nonparametrically, the required inference procedures can be made.

A systematic presentation of the h-likelihood procedures and identification of future directions in survival analysis would be meaningful contributions to the field. Although most of the examples in this book came from biomedical sciences, the methodology is also applicable to engineering, econometrics, and other fields, whenever event times are collected and used for statistical inference.

The targeted audience includes researchers in medicine, graduate students, and Ph.D. (bio)statisticians, interested in working with clustered survival data with or without competing risks. Knowledge of survival analysis at an introductory graduate level is the minimum prerequisite to read this book. To be reader-friendly, the
technical details including derivations and proofs are given in the Appendix of each chapter. Real data examples are furnished with R codes to provide readers with useful hands-on tools such as \texttt{frailtyHL} in Comprehensive R Archive Network (CRAN). The majority of data sets used in the book are available at URL \url{http://cran.r-project.org/package=failtyHL} for the R package \texttt{frailtyHL} (Ha et al. 2018).

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Busan, Korea
Pittsburgh, USA
Seoul, Korea
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Il Do Ha
Jong-Hyeon Jeong
Youngjo Lee
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