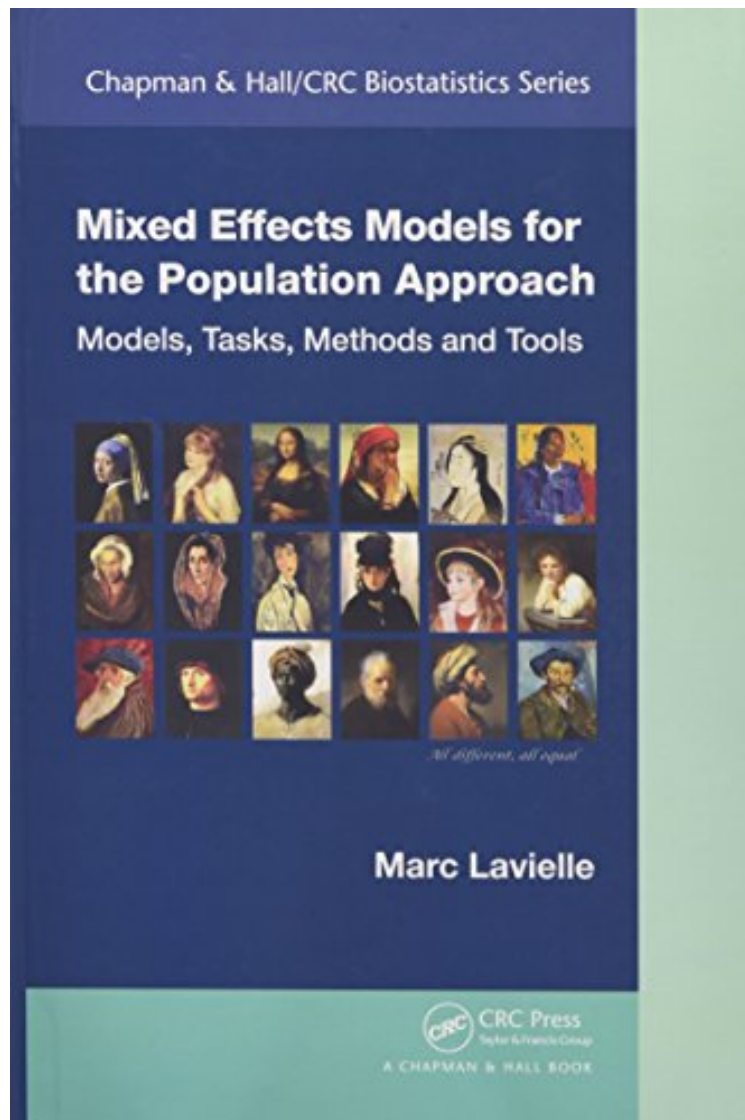


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Mixed Effects Models for the Population Approach: Models, Tasks, Methods and Tools (Chapman Hall/CRC Biostatistics Series)

Marc Lavielle

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Wide-Ranging Coverage of Parametric Modeling in Linear and Nonlinear Mixed Effects ModelsMixed Effects Models for the Population Approach: Models, Tasks, Methods and Tools presents a rigorous framework for describing, implementing, and using mixed effects models. With these models, readers can perform parameter estimation and modeling across a whole population of individuals at the same time. Easy-to-Use Techniques and Tools for Real-World Data ModelingThe book first shows how the framework allows model representation for different data types, including continuous, categorical, count, and time-to-event data. This leads to the use of generic methods, such as the stochastic approximation of the EM algorithm (SAEM), for modeling these diverse data types. The book also covers other essential methods, including Markov chain Monte Carlo (MCMC) and importance sampling techniques. The author uses publicly available software tools to illustrate modeling tasks. Methods are implemented in Monolix, and models are visually explored using Mixplot and simulated using Simulx. Careful Balance of Mathematical Representation and Practical ImplementationThis book takes readers through the whole modeling process, from defining/creating a parametric model to performing tasks on the model using various mathematical methods. Statisticians and mathematicians will appreciate the rigorous representation of the models and theoretical properties of the methods while modelers will welcome the practical capabilities of the tools. The book is also useful for training and teaching in any field where population modeling occurs.

"Although there are many excellent books available on mixed linear models and generalized linear mixed models, few provide broad coverage of nonlinear models. The strength of this text is the extensive coverage of the modeling of nonlinear trajectories in a wide variety of forms." (Journal of the American Statistical Association) " the text contains much of interest to the applied statistician who may be working as a consultant. I found the text useful to explain the difference between individual and population models so I have no hesitation in recommending this book for applied statisticians who may need a few well-developed examples from which to explain, and explore, statistical concepts and hierarchical modeling with non-statistical clients. In addition to model formulation and parameter estimation, the author addresses topics in model selection and diagnostic tools, too. a valuable text that is well-worth reading "International Statistical , 2015 " it is very precise I was pleasantly surprised at how readable it was a very good addition to the books of Davidian and Giltinan and Bonate. an essential companion to the Monolix software I would highly recommend it to all practitioners of the population approach for the systematic and thorough way it presents the subject."CPT: Pharmacometrics Systems Pharmacology, 2015"... the first combination of a 'how-to' framework for statisticians and mathematicians with a thorough description of the statistical and mathematical models for users with a clinical background. ... an excellent book on how to model biopharmaceutical data with a very good structure and solid lecture materials."Julie Bertrand,Journal of Biopharmaceutical StatisticsAbout the AuthorMarc Lavielle is a statistician specializing in computational statistics and healthcare applications. He holds a Ph.D. in statistics from University Paris-Sud, Orsay. He was named professor at Paris Descartes University and joined Inria as research director in 2007. Creator of the Monolix software, he led the Monolix software development project at Inria between 2009 and 2011. He created the CNRS Research Group "Statistics and Health" in 2007. Since 2009, Dr. Lavielle has been a member of the French High Council of Biotechnologies, where he promotes the use of sound statistical methods to evaluate health and environmental risks related to genetically modified organisms (GMOs).