Book Reviews

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Statistical Methods in Genetic Epidemiology. By Duncan C. Thomas. New York: Oxford University Press, 2004. $65.

The Argentine writer Jorge Luis Borges (1899–1986) once wrote, "Nothing is built on stone; all is built on sand, but we must build as if the sand were stone." The field of genetic epidemiology is no exception. In this constantly mutating field, what was cutting-edge statistical analysis in the 1980s was quickly subverted by the tremendous theoretical and technological advances of the 1990s. However, Thomas' *Statistical Methods in Genetic Epidemiology* reference and textbook expertly extracts what is perennial from what is temporal and describes it in great detail for the current and future generations of individuals interested in genetic epidemiology.

The book is divided into 12 chapters—all well illustrated and with useful examples from the literature—and a glossary. The first four chapters are good reviews of genetic epidemiology, the basics of human genetics, the principles of Mendelian inheritance, and basic epidemiologic and statistical principles. In chapters 5 through 12, Thomas masterfully describes familial aggregation, segregation analysis, linkage analysis, the principles of population genetics, tests for candidate-gene associations, linkage-disequilibrium mapping, and gene characterization and includes a summary "tying it all together: the genetic epidemiology of colorectal cancer" (p. 339).

Since, in the book's preface, Thomas states that the text is "a broad overview written at a level that should be accessible to graduate students in epidemiology, biostatistics, and human genetics" (p. vii), I asked a doctoral student in epidemiology, a doctoral student in bioinformatics, and a biostatistics faculty member for their opinions about the book. These three colleagues perform the statistical analysis of various genetic epidemiological studies for the Genetics Program at Boston University School of Medicine. The doctoral student in epidemiology stated that a graduate student in a discipline with limited use of statistical theory may find the derivations and the theory behind some of the methods difficult to follow. However, she pointed out that a major strength of the book is that the explanations are such that the reader could skip the more statistical explanations and still have at least a basic understanding of the concepts being presented. An additional strength of *Statistical Methods in Genetic Epidemiology* mentioned by this doctoral student is that the text presents many of the modern concepts of epidemiology—for instance, when Thomas discusses control selection for association studies. The graduate student in bioinformatics stated that Thomas' *Statistical Methods* is an insightful and comprehensive reference book. And then he noted, "If I had read this excellent book when I began my studies in bioinformatics three years ago, I would have a much stronger basis in genetic analysis now." Finally, the biostatistics faculty member was impressed by the clarity of the topics covered throughout the book: "The reader is able to choose his/her own difficulty level, from the basics to the advanced statistics; there is much for everybody." She is eager to start using this book in the courses she teaches.

The only weakness that I found in Thomas' *Statistical Methods* is the absence of exercises at the end of the chapters. Their inclusion would have helped readers solidify the concepts and would have ensured that the statistical methods were well understood. This minor criticism aside, *Statistical Methods in Genetic Epidemiology* is a much welcome volume that all readers of *The American Journal of Human Genetics* should consider having on their bookshelves. It seems likely that this will serve as a classic text for many years to come.

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DIEGO F. WYSZYNSKI
Boston University School of Medicine
Boston, MA

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Examining the Farming/Language Dispersal Hypothesis. Edited by Peter Bellwood and Colin Renfrew. Cambridge: McDonald Institute for Archaeological Research, 2002. $85.

This book emerged from a conference of scholars from three different disciplines (archaeology, genetics, and comparative linguistics) that was convened by the book's coeditors. A total of 36 papers written by 43 delegates were circulated before final drafts were prepared, and all the papers focused on the farming/language dispersal hypothesis (FLDH)—namely, that the distributions of some language families resulted from expansions of farming practices from their points of origin. Bellwood introduced the term "triangulation" to refer to the simultaneous focus of evidence from all three disciplines on the hypothesis. The book's 36 chapters are organized into three