men) to a more global view (using primarily haplogroups 3 [or M9-G] and 7 [or 92R-7 C]). Zerjal et al.'s male-focused worldview, combined with microsatellite analysis, helps flesh out the recent expansion of certain male lineages in haplogroup 3. However, the chapter by Mehdi et al. discussing present-day Pakistani populations contains a figure that may potentially cause dismay. It portrays genetic relationships as distances for 35 microsatellite loci and depicts African Pygmies in a trifurcation with other all human groups and chimpanzees. I am all for recognizing an African origin of modern humans, but this is an insensitive way to portray that hypothesis.

The uniparental focus also extends to chapters on mtDNA. An attempt by Francalacci et al. to standardize the mtDNA world database is presented for haplogroups, but control-region sequences are restricted to HV1. This is useful for African, European, and some Asian populations but is of limited relevance for tribal populations of southeast Asia and Oceania, as well as for some American Indians. Europeans and central Asians are the primary subject of the contribution of Metspalau et al. on maternal markers. Finally, the chapter by Merriwether et al. on the mtDNAs of the southwest Pacific is a model of clarity and shows just how much information can still be extracted from a single, well-characterized genetic locus.

To complete this set of chapters, Antunez-de Mayolo et al. explore the use of a unique *Alu* insertion in intron G of the progesterone-receptor gene to mark migrations in recent times. Sub-Saharan Africans and most East Asians lack this insertion, which is more common in Europeans and tribal populations from northern and western Asia. When the Americas are assayed, the Maya Campeche of Central America show frequencies comparable to those in modern Germans (.063 vs. .069), which the authors consider evidence of some Caucasian component to American Indian founder populations. This suggestion corroborates the finding of lineage X mtDNA haplotypes in both groups and our inability to map Siberian gene genealogies directly with American Indian ones.

How does this volume stand up to others? It does not give a single worldview on the biogenetic basis of human diversity, as does the recent translation *Genes, People, and Languages* by L. L. Cavalli-Sforza (North Point Press, 2000). However, it is more detailed in many respects and is clearly meant for a different audience. With the recent explosion of haplotypes from the Y chromosome, we have more powerful means of examining who moves where and why. For the next 2 years, however, *Genomic Diversity* will be an excellent place to begin, with signposts to the past for those who seek to learn from the mistakes of others.

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Advances in Twin and Sib-Pair Analysis. Edited by Tim D. Spector, Harold Snieder, and Alex J. MacGregor. London: Greenwich Medical Media. Pp. 266. $39.95 (hardcover)

This book is a useful reference for both the researcher new to the field of twin and sib-pair studies and the seasoned researcher seeking a convenient single source of information about many issues related to this type of research. The book begins with a thorough review of the history of twin and sib-pair studies. The historical review is followed by a chapter that outlines various study designs and the advantages and disadvantages associated with them. Next, the experiences obtained from conducting one of the largest twin studies, the Finnish Twin Cohort, are discussed. There is also a chapter on conducting twin studies in developing countries, which discusses the advantages and pitfalls involved in undertaking such research. Additionally, the chapter discussing the generalizability of twin studies and the assumptions underlying them concisely summarizes the major criticisms of twin studies and the evidence refuting them. These chapters provide a solid introduction to twin and sib-pair studies, one that would benefit anyone thinking about embarking on such research for the first time.

For the researcher already conducting a twin and/or sib-pair study, the methodology chapters offer both basic information regarding methods of analysis—introducing such concepts as concordance rates and the estimation of genetic variance—and more advanced concepts, such as dealing with gene-by-environment and gene-by-gene interactions. Modeling the effects of age and survival analysis methods as they apply to twin and sib studies are additional advanced concepts that are nicely dealt with.

However, perhaps the most appealing chapters to the researcher involved in twin and/or sibling studies are those dealing with the use of such studies for mapping the genetic loci underlying complex traits. Current methods of association and linkage analysis are summarized, and advances, such as the power of multivariate analysis, are presented. There is also a chapter on how to extend the twin and sibling models of genetic variance, which are introduced earlier in the book and are implemented in the program Mx, to performing such analyses of molecular data. Finally, the utility of twins in the field of pharmacogenetics is discussed.

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