but methodologically distinct disciplines. The use of population genetics in "Archaeogenetics" or "Anthropological Genetics" is not the sole application of this discipline. Establishing a formal population-genetics framework in molecular epidemiology and disease-predisposition studies is, without doubt, a challenging and highly profitable aspect of what sometimes is perceived as "just dissecting gene pools at a population level." The definition and comparison of present-day patterns of genetic variation not only offer unique insights for a deep study of human evolutionary history but also provide the necessary population-genetic backdrop that constitutes an important prerequisite for understanding the genetics of complex traits.

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*RNA Binding Proteins: New Concepts in Gene Regulation.* Edited by Kathryn Sandberg and Susan E. Mulroney. Norwell, MA: Kluwer Academic Publishers, 2002. Pp. 308. $165.

The editors compiled this book on the basis of the expanding interest in and understanding of post-transcriptional events that regulate mRNA stability, location, and translation. Their second stated purpose is to provide a book that not only can be used as an outline for teaching graduate students and young investigators but also contains enough information to be useful to the seasoned researcher. Having set this lofty goal, they recruited a group of authors to write chapters that included background information, data analysis, and study questions. The 17 resulting chapters were then grouped into three focus areas: translational control, mRNA metabolism, and hormonal and homeostatic regulation.

The first chapter adheres closely to the stated purpose outlined by the editors and allows anticipation that this pattern would be repeated in the subsequent chapters. That anticipation is quickly shattered, since the style and information provided vary significantly as one proceeds through the chapters. One gets the impression that there was a lack of editing, since there exists considerable redundancy both within and between chapters. If this book is to be a learning guide for the student, there needs to be a glossary or a more complete definition of terms. Some chapters assume an esoteric knowledge of the material presented, making them difficult to follow without a significant amount of background in the area. Unfortunately, there is misinformation in a few of the chapters.

The last chapter, authored by the editors, returns to the purpose of the book and looks much like Chapter I in style. It summarizes the recurring theme in all chapters: that mRNA stability and expression are controlled by linear nucleic acid sequence within the 5′ UTR, the coding region, and the 3′ UTR, as well as by the secondary structure of the molecule. Proteins that specifically bind to these regions are being characterized by standard methods, and most of the authors illustrate or describe these procedures in their chapters about their favorite mRNA. Cells from different tissues handle the mRNAs in a variety of ways, and the response can be affected by external stimuli.

The idea of study questions at the end of each chapter addresses the goal of using the text as a course outline. The problem, again, is the inconsistency of these questions. Some simply ask for regurgitation of information that was presented in the chapter, whereas others are thought provoking and encourage understanding of the experimental design and data interpretation. A course outline could come from the first and last chapters alone.

Initially, I was excited about the potential for this text and the reasons given for its writing. In the end, my reaction was disappointment for its falling far short of the expectation. Chapters were repetitious in describing methods. Part of the problem might be that we are still in the early stages of understanding mRNA synthesis and expression. One area omitted from these chapters was the advancing understanding of how other RNA species help in the regulation of mRNA production and use.

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