Section VII and include reviews of genomics and proteomics, HACCP, predictive microbiology, risk analysis, and molecular source tracking. All five chapters are quite relevant and timely for food microbiology, but in comparison to previous editions, this newer version no longer includes a chapter devoted to rapid microbiological methods. The development of rapid methods is currently a very dynamic area of research that would surely justify a chapter in the future.

In summary, Food Microbiology: Fundamentals and Frontiers is a text that is highly appreciated in the field and has continued to improve and expand. The publishers, however, will have to consider for the next edition to divide it into at least two volumes or consider an electronic version, given the somewhat impractically large weight and size. Despite the suggestions for improvement provided in this review, this textbook is highly recommended for anyone with an interest in food microbiology.

Francisco Diez-Gonzalez
University of Minnesota, St. Paul

Metagenomics: Current Innovations and Future Trends

The back cover of Metagenomics: Current Innovations and Future Trends informs us that “metagenomics is one of the fastest advancing fields in biology.” This statement captures both the strengths and weaknesses of this collection of reviews and commentaries on this emerging field. This book will be attractive to scientists from diverse backgrounds, as it discusses a wide range of topics related to metagenomics, including single-cell approaches, community ecology, and functional analyses, as well as applications to virology and mycology. For example, a chapter on the broadly used metagenomic analysis platform CAMERA provides an “under-the-hood” view of how annotation, raw sequence, and metadata can be merged in these analyses. Another strength is the inclusion of chapters that concern conceptual issues, such as bacterial genealogy and species, and those that consider “future trends,” including stable isotope probing, which provides an exciting opportunity to merge metagenomics with microbial community ecology.

The growth and dynamic nature of this field presents a challenge for the book format. The chapters that discuss general themes and the potential connections between fields are more successful than those that dedicate space to now-obsolete technical issues, such as comparisons of appraisals of sequencing read lengths and capacities, sequencing platforms, and the statistics of genome and metagenome databases. Moreover, many important new developments, such as the role of crowdsourcing in metagenomics (e.g., the American Gut Project, the Earth Microbiome Project, and uBiome) are not mentioned because they were initiated after this book went to press. In addition, several chapters focus on the use of microarrays in metagenomics, although this technology has been largely abandoned in favor of the more widely used sequencing-based approaches.

The fault with this compilation does not lie with the authors: most were diligent to their task of supplying a readable and informative chapter. Sure, the editor should have eliminated the pervasive redundancy and repetition among chapters that invariably arises when each contributor toils independently; however, the real problems rest with the publisher. Most of the material is stale, with few references to papers published after 2010. In this fast-moving, data-rich field, even earnest discussions of the most “recent” topics, literature, or technical advancements can be rendered obsolete in the time it takes to generate a book of this sort. Next, the production quality is rather low, with little attention to the resolution, readability or comprehensibility of display items. The final insult is its price ($319), out-of-reach for many researchers and an indicator of the marketing strategy being played by this publisher.

Andrew L. Goodman
Howard Ochman
Yale University
New Haven, Conn.