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BOOK REVIEW

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Review of: *Advanced Topics in Forensic DNA Typing: Methodology*

REFERENCE: Butler JM. Advanced topics in forensic DNA typing: methodology. Waltham, MA: Elsevier, 2012, 704 pp.

The author of this text, John Butler, is a well-known research scientist with extensive experience in forensic DNA analysis. Through his well-integrated research program at NIST, he benefits from frequent interactions, collaborative projects, and training/troubleshooting sessions with current casework practitioners. Additionally, Dr. Butler has well over 100 peer-reviewed publications related to the subject material of this text and has been widely recognized as one of the world's leading experts in the field since the release of his first book (*Forensic DNA Typing: Biology & Technology Behind STR Markers, 1st edn.*) in 2001 and its follow-up, *Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers, 2nd edn.* (2005). Together, these qualities allow him to offer a uniquely broad perspective of the field, which makes him perfectly suited to author an advanced text on the topic. A more recent text, *Fundamentals of Forensic DNA Typing* (2010), replaces portions of the original volumes providing a basic text that is perfect for beginners or undergraduate-level students studying the topic. *Advanced Topics in Forensic DNA Typing: Methodology* complements the *Fundamentals* text by providing advanced technological information and critical updates on developing topics within the field. This text is most appropriate for practicing professionals and/or advanced graduate-level students in molecular forensic academic programs. Ultimately, a third volume focusing on interpretation and statistics will be released. Rapid growth in the research literature in the field of forensic DNA analysis coupled with the recent proliferation of related university courses, curricula, and professional training programs have fueled a need for up-to-date textbooks of this nature.

Although the history and basic background included in the *Fundamentals* text has been omitted from the *Advanced Topics* text, there is significant overlap in several other topics. However, where overlap exists, the *Advanced Topics* chapters include updated references, recent technological improvements, and methodology modifications designed to improve assay success. Chapters 1–6 work sequentially through the major analytical processes required for routine human identification from biological evidence samples. Chapter 1 begins with the rudimentary steps of sample collection, storage, and serological characterization and includes new content on RNA-based body fluid identification and contamination concerns. Chapters 2–3 include comprehensive information on contemporary forensic methods for DNA extraction and quantitation, including the newer solid-phase extraction methods (silica columns and magnetic bead technology), small-scale automated platforms for extractions, laser-capture microdissection, and an expanded section on real-time PCR quantitation chemistries and instrumentation. Chapter 4 contains a familiar review of basic PCR and multiplex development with new material on reagent and consumable contamination, stochastic effects, and recent modifications designed to improve speed and robustness of multiplex STR amplification. Chapters 5–6 include added content related to the anticipated expansion of the CODIS core loci, the most recently released commercial multiplex STR kits, and modern capillary electrophoresis platforms (ABI 3130, 3500, and all "xl" models). Readers of earlier editions of textbooks from this author will notice the absence of antiquated technologies, including the FMBIO gel imaging system.

The primary purpose of the mid-section of this text is to cover issues and topics that are tangentially related to traditional STR-based forensic DNA typing including QA and validation, DNA databases, missing person and mass disaster victim identification, and issues encountered when typing degraded DNA and low-level DNA samples. While most of the information from the previous text (*Forensic DNA Typing*, 2005) has been retained, Chapters 7–8 have been substantially updated with new content. This includes the addition of "performance checks" for previously established procedures, recommendations for internal validation study design, and ENFSI recommendations for database development and management. Sections on DNA databases and laws around the world, the U.S. CODIS database, partial matches, and concerns of DNA database critics have been widely expanded. Overall, Chapter 9 is the most similar to the previous text but does include added introductory information and content on NamUS, ISFG DVI recommendations, and a brief review of international identification projects for identifying human remains from mass graves. Chapter 10 provides a concise overview of degraded DNA analysis, with an updated section on mini-STR typing and a discussion of newer technical approaches. The chapter covering low-level DNA testing (Chapter 11) has been significantly updated moving from a three-page introduction (in the previous text) to a separate 35-page chapter, which accurately reflects the explosion in the research literature on this topic since 2005. New content includes critics' perspectives and the CADDY report, as well as information on admissibility rulings and technical strategies to improve sensitivity including, but not limited to, LCN-PCR. Further, the chapter includes a unique, highly informative section on the special features necessary for high-sensitivity laboratory facilities as well as associated validation considerations.

The final chapters of the text cover an assortment of topics, including new technologies/automation, legal aspects and expert testimony, single nucleotide polymorphisms, nonhuman DNA-based testing, and comprehensive altogether new or updated chapters on

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nonautosomal DNA testing (mitochondrial DNA, Y chromosome, and X chromosome). Professionals and academics alike will most appreciate the new Chapter 18, Legal Aspects of DNA testing and the Scientific Expert in Court, which provides a succinct overview of the critical general information needed by any scientist preparing to testify in a court of law (*Daubert/Frye*, discovery, courtroom procedures, and preparation of expert witnesses). Unlike other texts covering the topic, this chapter is offered from the perspective of Dr. Butler (as a scientist), with help from other distinguished forensic scientists and lawyers, which readers will find most relatable. Last, bonus material is included at the end of the book in Appendices 1–4, which readers will find very practical. Appendices contain an updated compilation of the sizes and sequences of STR alleles, issues related to familial searching, a list of DNA-related supplies, and interview transcripts from the experts referenced in Chapter 18.

In conclusion, this text provides an easy-to-read, well-organized reference book for trainees, working professionals, and advanced graduate-level students. Compared to previous Butler texts, the chapters have been rearranged allowing for better flow from chapter-to-chapter. Additionally, the writing covers material that is scientific and complex, but uses language and style that freely engages the reader. While the content of this text is similar to the author's earlier version (2005), the added chapters, updated discussions, and the addition of many new, striking color graphics make this a must-have reference book. Further, the referencing at the end of each chapter provides an up-to-date list of resources that is conveniently organized by topic. There are several STR typing- and interpretation-related topics noticeably absent from this book. However, the author clearly states his intention to cover these in a forthcoming volume. This, along with the frequent referencing to the introductory book (*Fundamentals*) throughout the text, means that the reader will be best served by acquiring all three volumes. Together, these texts will, undoubtedly, serve as *the* authoritative textbooks in the field of forensic DNA analysis for years to come.