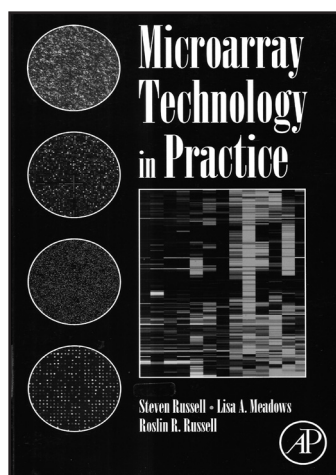identification including immune (Chapters 4-7), lectin (Chapter 8), hybridization (Chapter 9), histochemical staining and microscopy (Chapters 10 and 11), and specific methods for identification of hypoxia in situ (Chapter 12) and apoptosis (Chapter 13), are described. In the third part, the authors conclude the book with advanced imaging techniques (Chapters 14-16) and image analysis (Chapter 17). This book is recommended to students and researchers using the laboratory techniques on histology described. Updated protocols are described by renowned scientists in the area using understandable language while details of possible interference are given for each technique. Tim D. Hewiston and Ian A. Darby have undertaken several studies on histology, many of which were conducted in collaboration with the authors contributing to this book.

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MOLECULAR BIOLOGY

RUSSEL, S.; MEADOWS, L. A.; RUSSEL, R.R. *Microarray technology in practice*. London: Academic Press, 2009. 449 p.

The publication of the book "Microarray technology in practice" represents an important contribution to practical technical information on both DNA and protein microarrays. The work is relevant for basic and applied research in genome-related field of knowledge. The volume comprises 13 chapters and was overseen by authors Steven Russel, Lisa A. Meadows and Roslin R. Russell. Chapters 1 to 5 outline the principles of the methodology, a brief background, and the experimental bases for carrying out experimental design for measurements on nucleic acid and protein microarrays. From chapter 3, the selection of probes and obtention of cDNA and amplicons are addressed as well as the preparation of the arrays. Chapter 4 highlights the importance of obtaining samples, extraction of nucleic acids, especially RNA, production of cDNA, and the staining methods, as well as RNA amplification. The chapter includes a critical assessment of a range of methods, with emphasis on quality control focusing on fluorescence staining. In Chapter 5, hybridization procedures are described, followed by bioinformatics procedures for system data acquisition, methods of comparison and data obtention. The importance of quality control in these procedures is emphasized as are basic precautions for performing analysis. Chapter 6 introduces the applied bioinformatics procedures characterizing the treatment of data obtained, and the application of selection concepts using filters which normalizing data based on internal quality controls. Concepts of normalization, consortium systems of internal and external quality control of microarrays, data reprocessing, system noise correction and final normatization for application of statistical methods. Chapters 7 and 8 outline concepts of general and applied statistical methods for both parametric and non-parametric microarray data. Classification by gene groups, introduces the concept of supervised method quality, and quality control of the data analyzed. Chapter 9 provides details on databases at various sites. Chapter 10 describes the application of microarrays in genomic analysis whereas Chapter 11 addresses the application of microarrays in medical sciences such as: investigation of pathogens, profile of nucleic acids in human metabolic diseases, study of single-base polymorphism, and its relationship with diseases. Chapter 12 provides a succinct description of other applications of abundant protein binding arrays, and protein microarray technology. Finally, Chapter 13 contains suggestions on new perspectives of microarrays besides their technical evolution and analysis. This book represents an important source for updating knowledge on high-performance technologies, and is applicable to research and translational medicine.

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