
Preface

The earliest descriptions of human chromosomes in the late 1800s by Arnold and Flemming were the beginning of the genomics revolution now upon us. This book on “Array Comparative Genomic Hybridization: Protocols and Applications” explores the scope of what is now possible in documenting abnormalities associated with several types of human cancers. While the technology for interrogating the human genome continues to evolve, refinement of comparative genomic hybridization (CGH) using array CGH and related technologies have provided enormous insight into human cancers at an affordable scale in research and clinical laboratories.

As stated in Chapter 2 by Ewa Przybytkowski and colleagues, “Array CGH is a mature technology with low-cost competitive products, stable commercially produced software, and standardized protocols and therefore provides a low-cost, robust, and more easily accessible technology readily available to most wet lab scientists. In addition, aCGH allows the accurate characterization of gene copy number using as little as 0.5 µg of genomic DNA.” Although costs of next generation sequencing is coming down rapidly, the true cost including bioinformatics support and computing power is daunting for most investigators and clinical laboratories. The challenge for diagnostic laboratories is also to produce results within a clinically meaningful time frame. Array CGH thus is not only cost effective as data analysis is simpler, it can produce clinically relevant data in a timely manner.

Some of the highlights include Chapter 3 in which Martin Hirst discusses the variety of sequence-based DNA methylation techniques to generate DNA methylation maps from normal and abnormal human tissue. Lisa Shaffer and colleagues discuss the two basic types of genomic microarrays in Chapter 4: Comparative genomic hybridization-based arrays (aCGH) and single nucleotide polymorphism-based (SNP) arrays. They describe benefits and challenges of each method in assessing Myelodysplastic Syndrome, and provide guidance in the interpretation of the results and reporting of the diagnostic or prognostic implications to physicians.

A variety of human neoplasia are covered in this book, including breast cancer, acute and chronic myeloid leukemia, chronic lymphocytic leukemia, diffuse large B cell lymphoma, mantle cell lymphoma, malt and marginal zone lymphomas, mycosis fungoides and Sezary syndrome, adult T-cell leukemia/lymphoma, cutaneous anaplastic large cell lymphoma, HIV-related B-cell lymphomas, pediatric osteosarcoma, Wilm’s tumor, childhood myelodysplastic syndromes, adenocarcinoma of lung, and brain tumors.

Finally, two outstanding chapters have been contributed by Oscar Rueda and colleagues and Gavin Ha on computational aspects of assessing copy number alteration and variation.

We are indeed honored by the generous contributions of many of the leaders in the field who have provided overviews of the technologies and many have provided detailed step-by-step protocols to allow the readers to follow and learn these techniques for their own use in research or clinical diagnostic laboratories.

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