DNA Methylation Microarrays: Experimental Design and Statistical Analysis (Chapman & Hall/CRC Biostatistics Series)

Sun-Chong Wang, Art Petronis

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Providing an interface between dry-bench bioinformaticians and wet-lab biologists, **DNA Methylation Microarrays: *Experimental Design and Statistical Analysis*** presents the statistical methods and tools to analyze high-throughput epigenomic data, in particular, DNA methylation microarray data. Since these microarrays share the same underlying principles as gene expression microarrays, many of the analyses in the text also apply to microarray-based gene expression and histone modification (ChIP-on-chip) studies.

After introducing basic statistics, the book describes wet-bench technologies that produce the data for analysis and explains how to preprocess the data to remove systematic artifacts resulting from measurement imperfections. It then explores differential methylation and genomic tiling arrays. Focusing on exploratory data analysis, the next several chapters show how cluster and network analyses can link the functions and roles of unannotated DNA elements with known ones. The book concludes by surveying the open source software (R and Bioconductor), public databases, and other online resources available for microarray research.

Requiring only limited knowledge of statistics and programming, this book helps readers gain a solid understanding of the methodological foundations of DNA microarray analysis.

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