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Nota di contenuto	Preface -- 1 MicroRNAs in human cancer -- 2 Bioinformatics, non-coding RNAs and its possible application in personalized medicine -- 3 MicroRNA target prediction and validation -- 4 MicroRNA-regulated networks: the perfect storm for classical molecular biology, the ideal scenario for systems biology -- 5 The p53/microRNA network in cancer: experimental and bioinformatics approaches.-6 MicroRNAs in melanoma biology -- 7 MicroRNA in the lung -- 8 The E2F1-miRNA cancer progression network -- 9 Modeling of microRNA-transcription

factor networks in cancer -- 10 Coordinated networks of microRNAs and transcription factors with evolutionary perspectives -- 11 Mathematical modeling of microRNA-mediated mechanisms of translation repression -- 12 Web resources for microRNA research -- 13 Discovery of microRNA regulatory networks by integrating multidimensional high-throughput data -- 14 Discovering the functional microRNA-mRNA regulatory modules in heterogeneous data -- 15 Elucidating the role of microRNAs in cancer through data mining techniques -- 16 Working together: Combinatorial regulation by microRNAs. .

Sommario/riassunto

This book reflects the current state of knowledge about the role of microRNAs in the formation and progression of solid tumours. The main focus lies on computational methods and their applications in combination with cutting edge experimental techniques that are used to approach all aspects of microRNA regulation in cancer. The use of high-throughput quantitative techniques makes an integrative experimental and computational approach necessary. This book will be a resource for researchers starting out with microRNA research, but is also intended for the experienced researcher who wants to incorporate concepts and tools from systems biology and bioinformatics into his work. Bioinformaticians and modellers are provided with a general perspective on microRNA biology, and the state-of-the-art in computational microRNA biology.