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Sommario/riassunto	Repetitive structures in biological sequences are emerging as an active focus of research and the unifying concept of "repeatome" (the ensemble of knowledge associated with repeating structures in genomic/proteomic sequences) has been recently proposed in order to highlight several converging trends. One main trend is the ongoing discovery that genomic repetitions are linked to many biological significant events and functions. Diseases (e.g. Huntington's disease) have been causally linked with abnormal expansion of certain repeating sequences in the human genome. Deletions or multiple copy duplications of genes (Copy Number Variations) are important in the aetiology of cancer, Alzheimer, and Parkinson diseases. A second converging trend has been the emergence of many different models and algorithms for detecting non-obvious repeating patterns in strings with applications to in genomic data. Borrowing methodologies from combinatorial pattern, matching, string algorithms, data structures, data mining and machine learning these new approaches break the limitations of the current approaches and offer a new way to design better trans-disciplinary research. The articles collected in this book provides a glance into the rich emerging area of repeatome research, addressing some of its pressing challenges. We believe that these contributions are valuable resources for repeatome research and will stimulate further research from bioinformatic, statistical, and biological points of view.