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Sommario/riassunto	Mapping the genomic landscapes is one of the most exciting frontiers of science. We have the opportunity to reverse engineer the blueprints and the control systems of living organisms. Computational tools are key enablers in the deciphering process. This book provides an in-depth presentation of some of the important computational biology approaches to genomic sequence analysis. The first section of the book discusses methods for discovering patterns in DNA and RNA. This is followed by the second section that reflects on methods in various ways, including performance, usage and paradigms.