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Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Simulation of the Benchmark Datasets -- A Panel of Learning Methods for the Reconstruction of Gene Regulatory Networks in a Systems Genetics Context -- Benchmarking a simple yet effective approach for inferring gene regulatory networks from systems genetics data -- Differential Equation based reverse-engineering algorithms: pros and cons -- Gene regulatory network inference from systems genetics data using tree-based methods -- Extending partially known networks -- Integration of genetic variation as external perturbation to reverse engineer regulatory networks from gene expression data -- Using Simulated Data to Evaluate Bayesian Network Approach for Integrating

	Diverse Data.
Sommario/riassunto	This book presents recent methods for Systems Genetics (SG) data analysis, applying them to a suite of simulated SG benchmark datasets. Each of the chapter authors received the same datasets to evaluate the performance of their method to better understand which algorithms are most useful for obtaining reliable models from SG datasets. The knowledge gained from this benchmarking study will ultimately allow these algorithms to be used with confidence for SG studies e.g. of complex human diseases or food crop improvement. The book is primarily intended for researchers with a background in the life sciences, not for computer scientists or statisticians.