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	Nota di contenuto	pt. I. Foundation of systems biology, integrative biology and issues of biosystem complexity, redundancy and of other network properties -- pt. II. Modeling of ill-defined, lack of knowledge (experimental) problems in the field of complex biosystems including identification and validation : a review of enabling technologies -- pt. III. Critical analysis of multi-scale computational methods and tools, computational tools for crossing levels and applications.
	Sommario/riassunto	Growth in the pharmaceutical market has slowed down – almost to a standstill. One reason is that governments and other payers are cutting costs in a faltering world economy. But a more fundamental problem is the failure of major companies to discover, develop and market new drugs. Major drugs losing patent protection or being withdrawn from the market are simply not being replaced by new therapies – the pharmaceutical market model is no longer functioning effectively and most pharmaceutical companies are failing to produce the innovation needed for success. This multi-authored new book looks at a vital strategy which can bring innovation to a market in need of new ideas and new products: Systems Biology (SB). Modeling is a significant task of systems biology. SB aims to develop and use efficient algorithms, data structures, visualization and communication tools to orchestrate

the integration of large quantities of biological data with the goal of computer modeling. It involves the use of computer simulations of biological systems, such as the networks of metabolites comprise signal transduction pathways and gene regulatory networks to both analyze and visualize the complex connections of these cellular processes. SB involves a series of operational protocols used for performing research, namely a cycle composed of theoretical, analytic or computational modeling to propose specific testable hypotheses about a biological system, experimental validation, and then using the newly acquired quantitative description of cells or cell processes to refine the computational model or theory.