1. Record Nr. UNINA9910261146403321 Autore David A. Rosenblueth Titolo Computational Methods for Understanding Complexity: The Use of Formal Methods in Biology Frontiers Media SA, 2016 Pubbl/distr/stampa Descrizione fisica 1 online resource (111 p.) Collana Frontiers Research Topics Soggetti Genetics (non-medical) Lingua di pubblicazione Inglese Formato Materiale a stampa Livello bibliografico Monografia Sommario/riassunto The complexity of living organisms surpasses our unaided habilities of analysis. Hence, computational and mathematical methods are necessary for increasing our understanding of biological systems. At the same time, there has been a phenomenal recent progress allowing the application of novel formal methods to new domains. This progress has spurred a conspicuous optimism in computational biology. This optimism, in turn, has promoted a rapid increase in collaboration between specialists of biology with specialists of computer science. Through sheer complexity, however, many important biological problems are at present intractable, and it is not clear whether we will ever be able to solve such problems. We are in the process of learning what kind of model and what kind of analysis and synthesis techniques to use for a particular problem. Some existing formalisms have been readily used in biological problems, others have been adapted to biological needs, and still others have been especially developed for biological systems. This Research Topic has examples of cases (1) employing existing methods, (2) adapting methods to biology, and (3)

developing new methods. We can also see discrete and Boolean models,

and the use of both simulators and model checkers. Synthesis is exemplified by manual and by machine-learning methods. We hope that the articles collected in this Research Topic will stimulate new

research.