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Nota di contenuto	<ul> <li>Cover; Title Page; Copyright; Contents; Foreword; Chapter 1. Symbolic Representation and Inference of Regulatory Network Structures; 1.1. Introduction: logical modeling and abductive inference in systems biology; 1.2. Logical modeling of regulatory networks; 1.2.1.</li> <li>Background; 1.2.2. Logical model of signed-directed networks; 1.2.2.1.</li> <li>Prior knowledge; 1.2.2.2. Rule-based underlying model; 1.2.2.3.</li> <li>Integrity constraints; 1.2.2.4. Inferring signed-directed networks and explanatory reasoning; 1.3. Evaluation of the ARNI approach; 1.3.1.</li> <li>ARNI predictive power</li> <li>1.3.1.1. Prediction under biological and experimental noise1.3.1.2.</li> <li>Prediction under incomplete data; 1.3.2. ARNI expressive power;</li> <li>1.3.2.1. Network motif representations; 1.3.2.2. Representing complex interactions; 1.4. ARNI assisted scientific methodology; 1.4.1. Testing biological hypotheses; 1.4.1.1. Testing cross-talk between signaling pathways; 1.4.2. Informative experiments for networks discrimination;</li> <li>1.5. Related work and comparison with non-symbolic approaches;</li> <li>1.5.1. Limitations and future work; 1.6. Conclusions; 1.7. Bibliography</li> </ul>

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	Chapter 2. Reasoning on the Response of Logical Signaling Networks with ASP2.1. Introduction; 2.2. Answer set programming at a glance; 2.3. Learn and control logical networks with ASP; 2.3.1. Preliminaries; 2.3.2. Reasoning on the response of logical networks; 2.3.3. Learning models of immediate-early response; 2.3.4. Minimal intervention strategies; 2.3.5. Software toolbox: caspo; 2.4. Conclusion; 2.5. Acknowledgments; 2.6. Bibliography; Chapter 3. A Logical Model for Molecular Interaction Maps; 3.1. Introduction; 3.2. Biological background; 3.3. Logical model 3.3.1. Activation and inhibition3.3.1.1. Activation and inhibition capacities; 3.3.1.2. Relations between the activation and inhibition causes and effects; 3.3.1.3. Relations between causal relations; 3.3.2. Model extension; 3.3.2.1. Phosphorylation; 3.3.2.2. Autophosphorylation; 3.3.2.3. Binding; 3.3.3. Causality relations redefinition; 3.3.3.1. Activation axioms; 3.3.3.2. Phosphorylation axioms; 3.3.3.3. Autophosphorylation axioms; 3.3.3.4. Binding axioms; 3.3.3.5. Inhibition axioms; 3.4. Quantifier elimination for restricted formulas; 3.4.1. Domain formulas; 3.4.2. Restricted formulas; 3.4.5. Quantifier elimination procedure; 3.5. Reasoning about interactions in metabolic interaction maps; 3.6. Conclusion and future work; 3.7. Acknowledgments; 3.8. Bibliography; Chapter 4. Analyzing Large Network Dynamics with Process Hitting; 4.1. Introduction/state of the art; 4.1.1. The modeling challenge; 4.1.2. Historical context: Boolean and discrete models; 4.1.3. Analysis issues; 4.1.4. The process hitting framework; 4.1.5. Outline; 4.2. Discrete modeling with the process hitting; 4.2.1. Motivation 4.2.2. The process hitting framework
Sommario/riassunto	Systems Biology is the systematic study of the interactions between the components of a biological system and studies how these interactions give rise to the function and behavior of the living system. Through this, a life process is to be understood as a whole system rather than the collection of the parts considered separately. Systems Biology is therefore more than just an emerging field: it represents a new way of thinking about biology with a dramatic impact on the way that research is performed. The logical approach provides an intuitive method to provide explanations based on an expres