

1. Record Nr.	UNINA9910458612303321
Autore	Wariboko Nimi <1962->
Titolo	The principle of excellence [[electronic resource]] : a framework for social ethics / / Nimi Wariboko
Pubbl/distr/stampa	Lanham, Md., : Lexington Books, c2009
ISBN	1-282-56165-0 9786612561658 0-7391-3640-2
Descrizione fisica	1 online resource (253 p.)
Disciplina	179/.9
Soggetti	Excellence Social ethics Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Pt. I: What is excellence? -- The making of a new meaning of excellence -- Exegeting excellence -- The core features of excellence -- New being : participation and imitation-- Justice, love, and hope -- Pt. II: Social-ethical framework -- A framework for social ethics -- Social practice as boundary of possibilities -- Excellence and economic development.
Sommario/riassunto	This book is a bold attempt to reconceptualize excellence. It is no longer the virtue of doing something well or the mean of two extremes, but a clearing which allows humans to manifest their potentialities and creatively resist obstacles. The concept of excellence is emancipated from the excessive concern with order and good citizenry to become a libratory principle for interrogating all social institutions in the name of a better future.

2.	Record Nr.	UNISALENTO991001403009707536
	Autore	Thomas, Hugh <1931- >
	Titolo	La guerre d'Espagne / Hugh Thomas ; traduit de l'anglais par Jacques Brousse et Lucien Hess
	Pubbl/distr/stampa	Paris : Robert Laffont, 1961
	Descrizione fisica	697 p. : 12 c. di tav. ; 23 cm
	Collana	L'histoire que nous vivons
	Altri autori (Persone)	Brousse, Jacques Hess, Lucien
	Lingua di pubblicazione	Francese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
3.	Record Nr.	UNISALENTO991002910539707536
	Autore	Vitruvius Pollio
	Titolo	On architecture : in two volumes / Vitruvius ; edited from the Harleian manuscript 2767 and translated into english by Frank Granger
	Pubbl/distr/stampa	London : W. Heinemann Cambridge : Harvard University press, 1962-1970
	Descrizione fisica	2 v. ; 17 cm
	Collana	The Loeb classical library
	Altri autori (Persone)	Granger, Frank
	Disciplina	720
	Lingua di pubblicazione	Molteplice Latino
	Formato	Materiale a stampa
	Livello bibliografico	Monografia

4. Record Nr.	UNINA9910830486903321
Titolo	Symbolic Approaches to Modeling and Analysis of Biological Systems / / edited by Cedric Lhoussaine and Elisabeth Remy
Pubbl/distr/stampa	London, England : , : ISTE Ltd and John Wiley & Sons, Inc., , [2023] ©2023
ISBN	1-394-22908-9 1-394-22906-2
Edizione	[First edition.]
Descrizione fisica	1 online resource (397 pages)
Disciplina	570.11
Soggetti	Biological systems
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Cover -- Title Page -- Copyright Page -- Contents -- Preface -- Part 1. Models and Data -- Chapter 1. Inference of Gene Regulatory Networks from Multi-scale Dynamic Data -- 1.1. GRN and differentiation -- 1.1.1. The coordination of gene expression by GRNs -- 1.1.2. The process of differentiation -- 1.2. Inference of GRN from population data -- 1.2.1. Population expression data -- 1.2.2. Bayesian approaches -- 1.2.3. Information theory approaches -- 1.2.4. Boolean approaches -- 1.2.5. ODE approaches -- 1.3. Inferring GRNs from single-cell data -- 1.3.1. Single cell expression data -- 1.3.2. Adaptation of GRN inference algorithms for single-cell data analysis -- 1.3.3. Using single-cell stochastic models for GRN inference -- 1.4. Alternative strategies for GRN inference -- 1.5. Performance and limitations of GRN inference -- 1.6. Inference based on the wave of expression concept -- 1.6.1. The differentiation process seen as a dynamic process of signal processing by GRNs -- 1.6.2. Experimental demonstration of waves of expression -- 1.6.3. Using waves of expression for GRN inference -- 1.6.4. Scaling up the distributed computing approach -- 1.7. Conclusion -- 1.8. References -- Chapter 2. Combinatorial Optimization Problems for Studying Metabolism -- 2.1. Dynamics and functionality of a metabolic network -- 2.1.1. Metabolic networks -- 2.1.2. Reconstruction of metabolic networks -- 2.1.3. From the dynamics of a metabolic network to its function -- 2.2.

Understanding the metabolism of non-model organisms: metabolic gap-filling algorithms -- 2.2.1. Metabolism of non-model organisms -- 2.2.2. Reconstruction of the metabolism of non-model species and gap-filling problems -- 2.2.3. Added-value and limitations of metabolic gap-filling problems: example of biotic interactions -- 2.3. Microbiota metabolism: new optimization problems. 2.3.1. Genomics of microbiota -- 2.3.2. From merged models to compartmentalized models -- 2.3.3. Completion problem for community selection in non-compartmentalized microbiota -- 2.3.4. Completion problem for selecting compartmentalized communities with minimal exchanges -- 2.4. Discrete semantics: a Boolean approximation of metabolic producibility -- 2.4.1. Topological accessibility of compounds and reactions in a metabolic network -- 2.4.2. Activation and cycles -- 2.4.3. Applications -- 2.5. Flux semantics -- 2.5.1. Modeling the response of a metabolic network with fluxes -- 2.5.2. Steady-state cycles -- 2.5.3. Application to the completion of metabolic networks -- 2.6. Comparing semantics: toward a hybrid approach -- 2.6.1. Complementarity of Boolean and stoichiometric abstractions -- 2.6.2. Hybrid completion of metabolic networks -- 2.7. Solving gap-filling problems with answer set programming -- 2.7.1. Model the Boolean activation of a reaction in ASP -- 2.7.2. Non-compartmentalized selection of communities -- 2.7.3. Compartmentalized selection of communities -- 2.8. Conclusion -- 2.9. References -- Chapter 3. The Challenges of Inferring Dynamic Models from Time Series -- 3.1. Challenges of learning about time series -- 3.2. Reconstruction of a regulation network (Boolean network) and its logical rules -- 3.2.1. Multi-valued logic -- 3.2.2. Learning operations -- 3.2.3. Dynamical semantics -- 3.2.4. GULA -- 3.2.5. PRIDE -- 3.3. Modeling Thomas networks with delays in ASP -- 3.3.1. Formalisms used -- 3.3.2. Networks -- 3.3.3. ASP technology -- 3.3.4. Description of the problem -- 3.3.5. Implementation -- 3.3.6. Results -- 3.3.7. Synthesis -- 3.4. Promise of machine learning for biology -- 3.4.1. Learning about biological regulatory networks modeling complex behaviors -- 3.4.2. Review of models -- 3.5. References. Chapter 4. Connecting Logical Models to Omics Data -- 4.1. Introduction -- 4.2. Logical models: objectives, nature and tools -- 4.2.1. Objectives and biological questions addressed -- 4.2.2. Logical modeling -- 4.2.3. Tools and resources for logical modeling -- 4.3. Building an influence graph using biological data -- 4.3.1. Defining the outline of the model -- 4.3.2. Construction of the regulation network -- 4.4. Defining logical rules and refining model parameters using biological data -- 4.4.1. Determining logical rules locally -- 4.4.2. Define or modify the logical model as a whole -- 4.5. Data to validate models and predict behaviors -- 4.6. Conclusion -- 4.7. References -- Part 2. Formal and Semantic Methods -- Chapter 5. Boolean Networks: Formalism, Semantics and Complexity -- 5.1. Introduction -- 5.2. Classical semantics of Boolean networks -- 5.2.1. Definitions -- 5.2.2. Examples -- 5.2.3. Properties -- 5.3. Related formalisms -- 5.3.1. Cellular automata -- 5.3.2. Petri nets -- 5.4. Guarantees against quantitative models -- 5.4.1. Boolean network refinements -- 5.4.2. Counterexample for classical semantics -- 5.4.3. MP Boolean networks -- 5.5. Dynamic properties and complexities -- 5.5.1. Fixed points -- 5.5.2. Reachability between configurations -- 5.5.3. Attractors -- 5.6. Conclusion -- 5.7. Acknowledgments -- 5.8. References -- Chapter 6. Computational Logic for Biomedicine and Neurosciences -- 6.1. Introduction -- 6.2. Biomedicine in linear logic -- 6.2.1. Introduction -- 6.2.2. Logical frameworks, linear logic -- 6.2.3. Modeling in LL -- 6.2.4. Modeling breast cancer progression -- 6.2.5. Verifying

properties of the model -- 6.2.6. Conclusion and future perspectives on the biomedicine section -- 6.3. On the use of Coq to model and verify neuronal archetypes -- 6.3.1. Introduction -- 6.3.2. Discrete leaky integrate and fire model. 6.3.3. The basic archetypes -- 6.3.4. Modeling in Coq -- 6.3.5. Encoding neurons and archetypes in Coq -- 6.3.6. Properties of neurons and archetypes in Coq -- 6.3.7. Conclusions and future work on the archetypes section -- 6.4. Conclusion and perspective -- 6.5. References -- Chapter 7. The Cell: A Chemical Analog Calculator -- 7.1. Introduction -- 7.2. Chemical reaction networks -- 7.3. Discrete dynamics and digital calculation -- 7.4. Continuous dynamics and analog computation -- 7.5. Turing-completeness of continuous CRNs -- 7.6. Chemical compiler of calculable functions -- 7.7. Chemical programming of non-living vesicles -- 7.8. 1014 networked analog computers -- 7.9. References -- Chapter 8. Formal Verification Methods for Modeling in Biology: Biological Regulation Networks -- 8.1. Introduction -- 8.1.1. Illustrative example: the simplified circadian cycle of mammals -- 8.2. Formalization of René Thomas's modeling -- 8.2.1. Static description or influence graph -- 8.2.2. Dynamics of a biological regulation graph -- 8.3. Genetically modified Hoare logic -- 8.3.1. Using experimental observations: an example -- 8.3.2. A language of assertions -- 8.3.3. A language of paths -- 8.3.4. The power of assertions -- 8.3.5. A logic to calculate the weakest precondition -- 8.4. Temporal logic and CTL -- 8.4.1. CTL and model-checking -- 8.4.2. CTL fair path -- 8.5. TotemBioNet -- 8.5.1. Tools -- 8.5.2. Example 1: growth and apoptosis of a tadpole tail -- 8.5.3. Example 2: simplified mammalian cell cycle -- 8.6. Hybrid formalism -- 8.6.1. Hybrid regulation networks -- 8.6.2. Definition of hybrid trajectories -- 8.7. Hybrid Hoare logic -- 8.7.1. Property, path, and assertion languages -- 8.7.2. Hoare triples -- 8.7.3. Weakest precondition calculus -- 8.7.4. Inference rules -- 8.7.5. Holmes BioNet: an implementation of the processing chain. 8.8. General methodology -- 8.9. Acknowledgments -- 8.10. References -- Chapter 9. Accessible Pattern Analyses in Kappa Models -- 9.1. Introduction -- 9.1.1. Context and motivations -- 9.1.2. Modeling languages for molecular interaction systems -- 9.1.3. The Kappa language -- 9.1.4. Abstract interpretation -- 9.1.5. The Kappa ecosystem -- 9.1.6. Content of the chapter -- 9.2. Site graphs -- 9.2.1. Signature -- 9.2.2. Biochemical complexes -- 9.2.3. Patterns -- 9.2.4. Embedding between patterns -- 9.3. Rewriting site graphs -- 9.3.1. Interaction rules -- 9.3.2. Reactions induced by an interaction rule -- 9.3.3. Underlying reaction networks -- 9.4. Analysis of reachable patterns -- 9.4.1. Reachability in a reaction network -- 9.4.2. Abstraction of a set of states -- 9.4.3. Fixed point transfers -- 9.5. Analysis using sets of orthogonal patterns -- 9.5.1. Orthogonal pattern sets -- 9.5.2. Post-processing and visualization of results -- 9.5.3. Study of performance and practical use -- 9.6. Conclusion -- 9.7. References -- List of Authors -- Index -- EULA.

Sommario/riassunto

Systems Biology is an approach to biology that involves understanding the complexity of interactions among biological entities within a systemic whole. The goal is to understand the emergence of physiological or functional properties. Symbolic Approaches to Modeling and Analysis of Biological Systems presents contributions of formal methods from computer science for modeling the dynamics of biological systems. It deals more specifically with symbolic methods, i. e. methods that can establish the qualitative properties of models. This book presents different approaches related to semantics, language, modeling and their link with data, and allows us to examine the

fundamental problems and challenges that biological systems are facing. The first part of the book presents works that rely on various available data to build models, while the second part gathers contributions surrounding issues of semantics and formal methods.
