1.	Record Nr.	UNINA9910777333203321
	Autore	Armstrong D. M (David Malet), <1926-2014, >
	Titolo	Dispositions : a debate / / D.M. Armstrong, C.B. Martin, and U.T. Place ; edited and with an introduction by Tim Crane
	Pubbl/distr/stampa	London ; ; New York : , : Routledge, , 1996
	ISBN	0-203-00487-6
		1-280-33459-2
		1-134-68898-9
		0-415-17368-X
		1-134-76128-7
		1-134-76129-5
		1-280-33481-9
	Descrizione fisica	1 online resource (206 pages)
	Collana	International library of philosophy.
	Altri autori (Persone)	MartinC. B (Charles Burton)
		PlaceU. T <1924-2000.> (Ullin Thomas)
		CraneTim
	Disciplina	111/.1
	Soggetti	Disposition (Philosophy)
	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.
	Nota di contenuto	1. Dispositions as Categorical States / D. M. Armstrong -- 2. Dispositions as Intentional States / U. T. Place -- 3. Place's and Armstrong's Views Compared and Contrasted / D. M. Armstrong -- 4. A Conceptualist Ontology / U. T. Place -- 5. Properties and Dispositions / C. B. Martin -- 6. Reply to Martin / D. M. Armstrong -- 7. Structural Properties: Categorical, Dispositional or Both? / U. T. Place -- 8. Replies to Armstrong and Place / C. B. Martin -- 9. Second Reply to Martin / D. M. Armstrong -- 10. Conceptualism and the Ontological Independence of Cause and Effect / U. T. Place -- 11. Final Replies to Place and Armstrong / C. B. Martin.
	Sommario/riassunto	Dispositions are essential to our understanding of the world. Dispositions: A Debate is an extended dialogue between three distinguished philosophers - D.M. Armstrong, C.B. Martin and U.T. Place - on the many problems associated with dispositions, which reveals their own distinctive accounts of the nature of dispositions.

These are then linked to other issues such as the nature of mind, matter, universals, existence, laws of nature and causation.

2.

Record Nr.	UNINA9910161648403321
Autore	Reinhard Guthke
Titolo	Computational Systems Biology of Pathogen-Host Interactions
Pubbl/distr/stampa	Frontiers Media SA, 2016
Descrizione fisica	1 online resource (198 p.)
Collana	Frontiers Research Topics
Soggetti	Microbiology (non-medical)
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

Sommario/riassunto

A thorough understanding of pathogenic microorganisms and their interactions with host organisms is crucial to prevent infectious threats due to the fact that Pathogen-Host Interactions (PHIs) have critical roles in initiating and sustaining infections. Therefore, the analysis of infection mechanisms through PHIs is indispensable to identify diagnostic biomarkers and next-generation drug targets and then to develop strategic novel solutions against drug-resistance and for personalized therapy. Traditional approaches are limited in capturing mechanisms of infection since they investigate hosts or pathogens individually. On the other hand, the systems biology approach focuses on the whole PHI system, and is more promising in capturing infection mechanisms. Here, we bring together studies on the below listed sections to present the current picture of the research on Computational Systems Biology of Pathogen-Host Interactions: - Computational Inference of PHI Networks using Omics Data - Computational Prediction of PHIs - Text Mining of PHI Data from the Literature - Mathematical Modeling and Bioinformatic Analysis of PHIs Computational Inference of PHI Networks using Omics Data Gene regulatory, metabolic and protein-protein networks of PHI systems are crucial for a thorough understanding of infection mechanisms. Great

advances in molecular biology and biotechnology have allowed the production of related omics data experimentally. Many computational methods are emerging to infer molecular interaction networks of PHI systems from the corresponding omics data. Computational Prediction of PHIs Due to the lack of experimentally-found PHI data, many computational methods have been developed for the prediction of pathogen-host protein-protein interactions. Despite being emerging, currently available experimental PHI data are far from complete for a systems view of infection mechanisms through PHIs. Therefore, computational methods are the main tools to predict new PHIs. To this end, the development of new computational methods is of great interest. Text Mining of PHI Data from Literature Despite the recent development of many PHI-specific databases, most data relevant to PHIs are still buried in the biomedical literature, which demands for the use of text mining techniques to unravel PHIs hidden in the literature. Only some rare efforts have been performed to achieve this aim. Therefore, the development of novel text mining methods specific for PHI data retrieval is of key importance for efficient use of the available literature. Mathematical Modeling and Bioinformatic Analysis of PHIs After the reconstruction of PHI networks experimentally and/or computationally, their mathematical modeling and detailed computational analysis is required using bioinformatics tools to get insights on infection mechanisms. Bioinformatics methods are increasingly applied to analyze the increasing amount of experimentally-found and computationally-predicted PHI data.

3.	Record Nr.	UNINA9910332059403321
	Titolo	Age
	Pubbl/distr/stampa	Omaha, Neb., : American Aging Association, 1978-1999
	ISSN	2331-3765
	Disciplina	612.67
	Soggetti	Aging
		Older people
		Vieillissement
		Personnes agees
		Periodical
		Periodicals.
		periodicals.
		Periodiques.
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Periodico
	Note generali	Refereed/Peer-reviewed
		Published: Media, PA, -1999.