

1. Record Nr.	UNISA996466285603316
Titolo	Data Integration in the Life Sciences [[electronic resource] ] : 7th International Conference, DILS 2010, Gothenburg, Sweden, August 25-27, 2010. Proceedings // edited by Patrick Lambrix, Graham Kemp
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	1-280-38833-1 9786613566256 3-642-15120-5
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (X, 215 p. 82 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 6254
Disciplina	570.285
Soggetti	Life sciences Computer engineering Computer communication systems Application software Artificial intelligence Information storage and retrieval Life Sciences, general Computer Engineering Computer Communication Networks Information Systems Applications (incl. Internet) Artificial Intelligence Information Storage and Retrieval Goteborg <2010>
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Invited Talks -- Provenance Management for Data Exploration -- High-Performance Systems for in Silico Microscopy Imaging Studies -- Ontology Engineering -- Discovering Evolving Regions in Life Science Ontologies -- On Matching Large Life Science Ontologies in Parallel -- A System for Debugging Missing Is-a Structure in Networked Ontologies -- Web Services -- On the Secure Sharing and Aggregation

of Data to Support Systems Biology Research -- Helping Biologists Effectively Build Workflows, without Programming -- A Data Warehouse Approach to Semantic Integration of Pseudomonas Data -- Data Mining and Text Mining -- The Cinderella of Biological Data Integration: Addressing Some of the Challenges of Entity and Relationship Mining from Patent Sources -- Algorithm for Grounding Mutation Mentions from Text to Protein Sequences -- Handling Missing Features with Boosting Algorithms for Protein-Protein Interaction Prediction -- Instance Discovery and Schema Matching with Applications to Biological Deep Web Data Integration -- Information Management -- Integrative Information Management for Systems Biology -- An Integration Architecture Designed to Deal with the Issues of Biological Scope, Scale and Complexity -- Quality Assessment of MAGE-ML Genomic Datasets Using DescribeX -- Search Computing: Integrating Ranked Data in the Life Sciences.

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## Sommario/riassunto

The development and increasingly widespread deployment of high-throughput experimental methods in the life sciences is giving rise to numerous large, complex and valuable data resources. This foundation of experimental data underpins the systematic study of organisms and diseases, which increasingly depends on the development of models of biological systems. The development of these models often requires integration of diverse experimental data resources; once constructed, the models themselves become data and present new integration challenges for tasks such as interpretation, validation and comparison. The Data Integration in the Life Sciences (DILS) Conference series brings together data and knowledge management researchers from the computer science research community with bioinformaticians and computational biologists, to improve the understanding of how emerging data integration techniques can address requirements identified in the life sciences. DILS 2010 was the seventh event in the series and was held in Göteborg, Sweden during August 25–27, 2010. The associated proceedings contain 14 peer-reviewed papers and 2 invited papers. The sessions addressed ontology engineering, and in particular, evolution, matching and debugging of ontologies, a key component for semantic integration; Web services as an important technology for data integration in the life sciences; data and text mining techniques for discovering and recognizing biomedical entities and relationships between these entities; and information management, introducing data integration solutions for different types of applications related to cancer, systems biology and microarray experimental data, and an approach for integrating ranked data in the life sciences.

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