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| Altri autori (Persone) | LambrixPatrick<br>KempGraham |
| Disciplina | 570.285 |
| Soggetti | Data mining<br>Web usage mining |
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| Livello bibliografico | Monografia |
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| 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.

Sommario/riassunto

The development and increasingly widespread deployment of high-throughput experimental methods in the life sciences is giving rise to numerous large, c- plex and valuable data resources. This foundation of experimental data und- pins 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 sequence 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 Goth- burg, 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 - cro array experimental data, and an approach for integrating ranked data in the life sciences.