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	Nota di contenuto	Keynote Presentations -- Enabling the Molecular Medicine Revolution Through Network-Centric Biomedicine -- Phyl-O'Data (POD) from Tree of Life: Integration Challenges from Yellow Slimy Things to Black Crunchy Stuff -- New Architectures and Experience on Using Systems -- Automatically Constructing a Directory of Molecular Biology Databases -- The Allen Brain Atlas: Delivering Neuroscience to the Web

on a Genome Wide Scale -- Toward an Integrated RNA Motif Database -- B-Fabric: A Data and Application Integration Framework for Life Sciences Research -- SWAMI: Integrating Biological Databases and Analysis Tools Within User Friendly Environment -- Grid and UTOPIA: An Integrated Approach to Enacting and Visualising in Silico Experiments in the Life Sciences -- Managing and Designing Scientific Workflows -- A High-Throughput Bioinformatics Platform for Mass Spectrometry-Based Proteomics -- Bioinformatics Service Reconciliation by Heterogeneous Schema Transformation -- A Formal Model of Dataflow Repositories -- Project Histories: Managing Data Provenance Across Collection-Oriented Scientific Workflow Runs -- Mapping and Matching Techniques -- Fast Approximate Duplicate Detection for 2D-NMR Spectra -- Ontology – Supported Machine Learning and Decision Support in Biomedicine -- Instance-Based Matching of Large Life Science Ontologies -- Modeling of Life Science Data -- Data Integration and Pattern-Finding in Biological Sequence with TESS's Annotation Grammar and Extraction Language (AnGEL) -- Inferring Gene Regulatory Networks from Multiple Data Sources Via a Dynamic Bayesian Network with Structural EM -- Accelerating Disease Gene Identification Through Integrated SNP Data Analysis -- Annotation in Data Integration -- What's New? What's Certain? – Scoring Search Results in the Presence of Overlapping Data Sources -- Using Annotations from Controlled Vocabularies to Find Meaningful Associations -- CONANN: An Online Biomedical Concept Annotator.

Sommario/riassunto	Understanding the mechanisms involved in life (e. g. , discovering the biological functionofasetofproteins, inferringtheevolutionofasetofspecies)isbecoming increasinglydependent onprogressmade inmathematics,computer science,and molecular engineering. For the past 30 years, new high-throughput technologies have been developed generating large amounts of data, distributed across many data sources on the Web, with a high degree of semantic heterogeneity and di?erentlevelsofquality. However, onesuchdatasetisnot,byitself,su?cientfor scienti?c discovery. Instead, it must be combined with other data and processed by bioinformatics tools for patterns, similarities, and unusual occurrences to be observed. Both data integration and data mining are thus of paramount importance in life science. DILS 2007 was the fourth in a workshop series that aims at fostering d- cussion, exchange, and innovation in research and development in the areas of data integration and data management for the life sciences. Each previous DILS workshop attracted around 100 researchers from all over the world. This year, the number of submitted papers again increased. The Program Committee - lected 19 papers out of 52 full submissions. The DILS 2007 papers cover a wide spectrum of theoretical and practical issues including scienti?c work?ows, - notation in data integration, mapping and matching techniques, and modeling of life science data. Among the papers, we distinguished 13 papers presenting research on new models, methods, or algorithms and 6 papers presenting imp- mentation of systems or experience with systems in practice. In addition to the presented papers, DILS 2007 featured two keynote talks by Kenneth H. Buetow, National Cancer Institute, and Junhyong Kim, University of Pennsylvania.