

E-BioSci

Semantic networks of biological information

Les Grivell European Molecular Biology Organisation

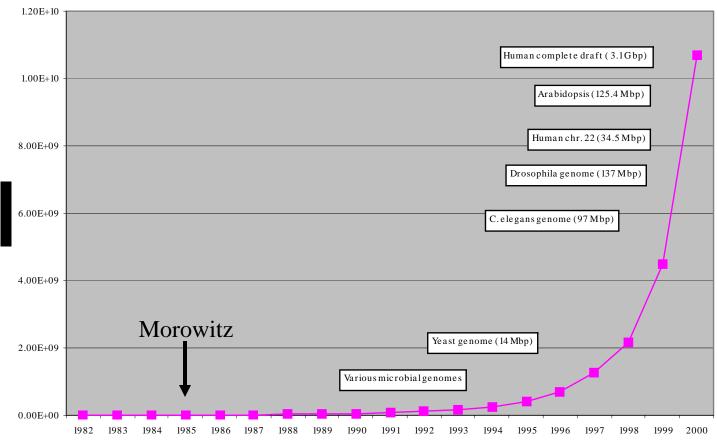




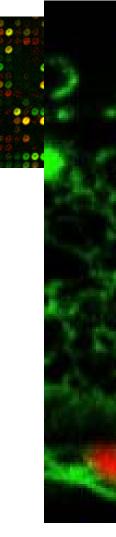
"Biological research has reached a point where new generalizations and higher order biological laws are being approached, but may be obscured by the simple mass of data"

> Harold Morowitz, 1985 Report to the U.S. National Academy of Sciences

One part of the information explosion



Sequences are not the only form of digital information



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ICEBERG: A Novel Inhibitor of Interleukin-1β Generation

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Summary

ProIL-1 β is a proinflammatory cytokine that is proteolytically processed to its active form by caspase-1. Upon receipt of a proinflammatory stimulus, an upstream adaptor, RIP2, binds and oligomerizes caspase-1 zymogen, promoting its autoactivation. ICEBERG is a novel protein that inhibits generation of IL-1 β by interacting with caspase-1 and preventing its association with RIP2. ICEBERG is induced by proinflammatory stimuli, suggesting that it may be part of a negative feedback loop. Consistent with this, enforced retroviral expression of ICEBERG inhibits lipopolysac(Thornberry et al., 1992). The zymogen has low but detectable enzymatic activity. Upon receipt of a proinflammatory signal, caspase-1 is thought to oligomerize and autoprocess to generate the active p10/p20 heterodimeric protease (Walker et al., 1994; Wilson et al., 1994; Ghayur et al., 1997). The N-terminal prodomain appears to play a critical role in this oligomerization-based activation of caspase-1 since its removal prevents processing (Van Criekinge et al., 1996).

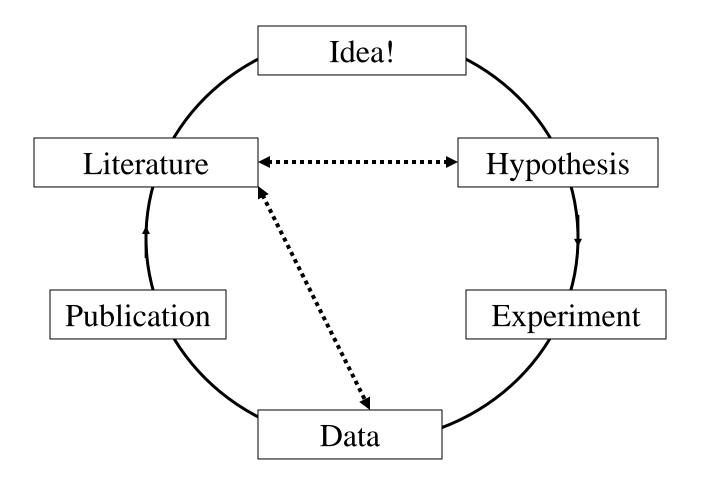
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At least one potential mechanism by which caspase-1 is regulated became evident with the identification of a serine/threonine kinase RIP2/CARDIAK/RICK (Inohara et al., 1998; McCarthy et al., 1998; Thome et al., 1998) that binds caspase-1 and promotes its processing (Thome et al., 1998). RIP2 engages caspase-1 through a direct protein-protein interaction involving corresponding caspase recruitment domains (CARDs) present at the C terminus of RIP2 and within the prodomain of caspase-1 (Hofmann et al., 1997; Thome et al., 1998). The CARD module mediates the interaction between a number of large prodomain caspases and their corresponding upstream activator adaptors, the prototypical examples being caspase-9 and Apaf-1 (Zou et al., 1997, 1999; Day et al., 1999; Qin et al., 1999). Structurally, the CARD motif resembles the death domain (DD) and the

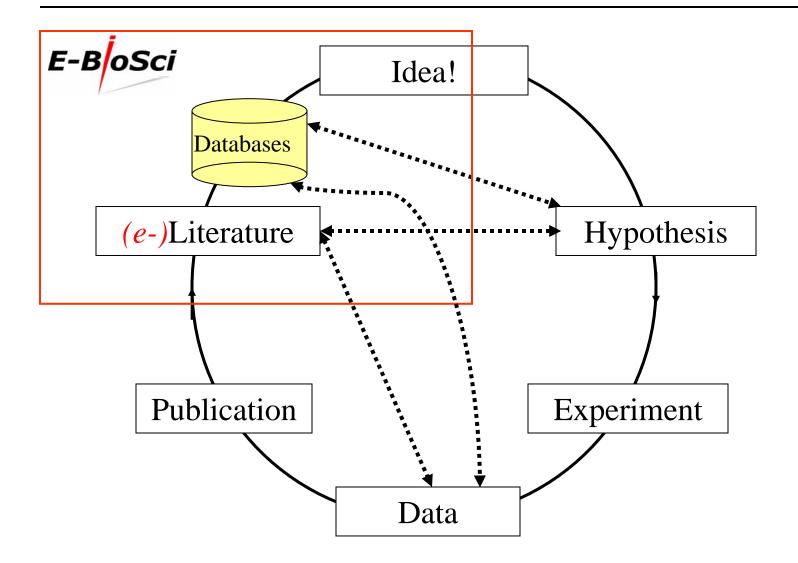
The digital revolution is

- driving dramatic changes in the way research is conducted and in the way knowledge is being generated
- exposing limitations in current mechanisms for disseminating and sharing information
- driving changes in publication strategies

The knowledge cycle (traditional)



The knowledge cycle (extended)



Biological information: current reality

- Hundreds of different databases, many in flat-file format
- Non-uniform or lack of external identifiers
- Lack of interoperability at the level of syntax and semantics
- Knowledge scattered across the literature in many thousands of non-computer readable journal articles

Information retrieval from text

- There is increasing need for the use of literature as a computer-readable resource (intelligent search / retrieval)
- There is a need to apply computational methods to text as well as data analysis (mining / analysis; literature as discovery resource)
- There is a need for new methods of integration and visualization of this information
- There is a need for a scale-up in the rate of *curated* database growth through integration with the literature

Dealing with the data deluge: what do researchers need?

- Intuitive interfaces to web resources
- Advanced search / retrieval facilities
- Smooth navigation from one resource to another
- Immediate availability of authoritative information; free of charge at the point-of-use
- Information that can be integrated / manipulated / visualized /output in another form



A new information service for the life sciences that will interlink factual and image data repositories with the research literature

EU Quality of Life research infrastructure: platform under construction

Closely linked to **ORIEL**, an EU-funded research project in information technology







The current E-BioSci - ORIEL partnership



- Distributed network of information resources
- Europe-based; world-wide role





The platform

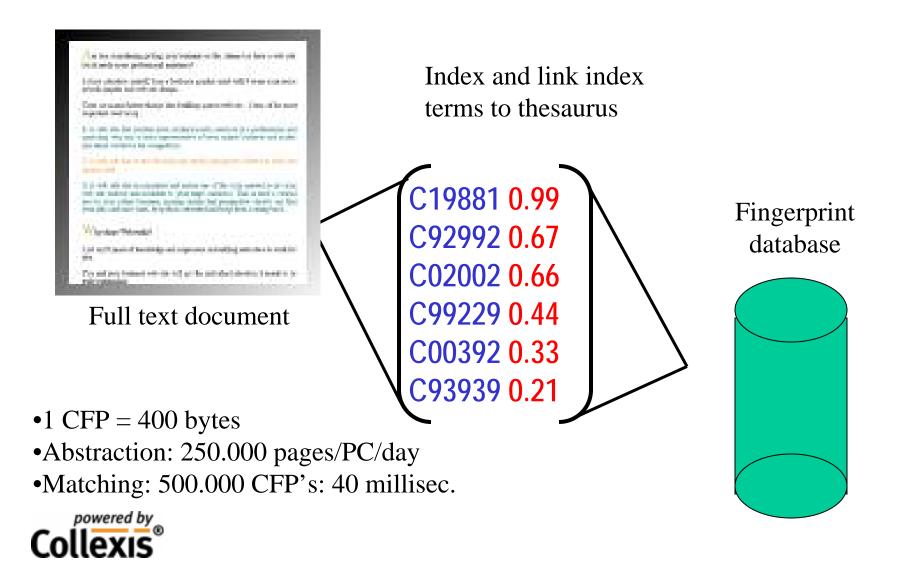
- Services freely accessible to the academic research community
- Set of *distributed* resources (literature, sequence- and image- databases)
- Full-text search
 - across document repositories
 - using cross-language queries (e.g. English French, German etc)
 - 2-way navigation links between literature and molecular datasets via gene symbol recognition

Features implemented via conceptual fingerprinting





Conceptual fingerprints

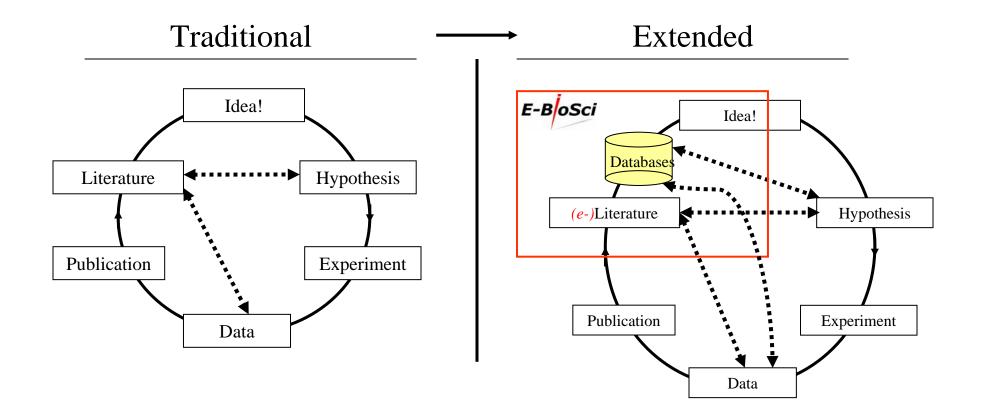


E-BioSci – distinguishing features

- Is a free academic access to services
- Places strong emphasis on concept searching of full text – a discovery tool
- Uses conceptual fingerprints to semantically link text with different data types (in particular genomic and image data)
- Links only to refereed material that meets criteria of editorial control
- Welcomes principles of free access, but respects existing restrictions of (commercial) content providers

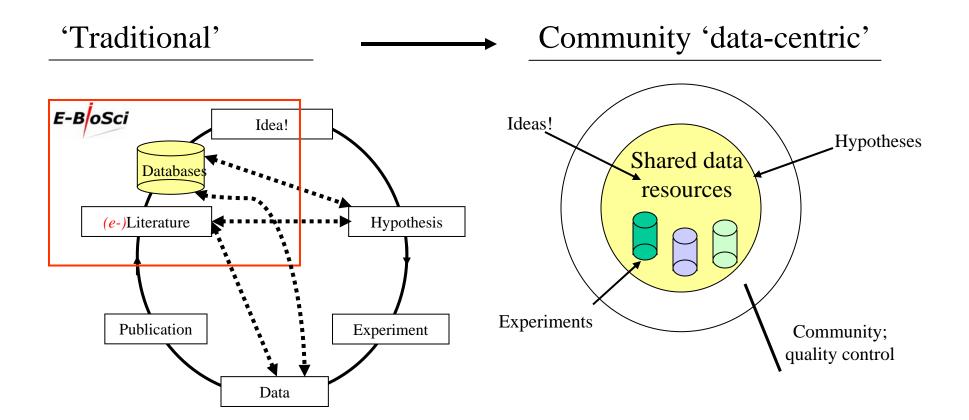
Community-driven *e*-science (1)

•The growing importance of interactive databases



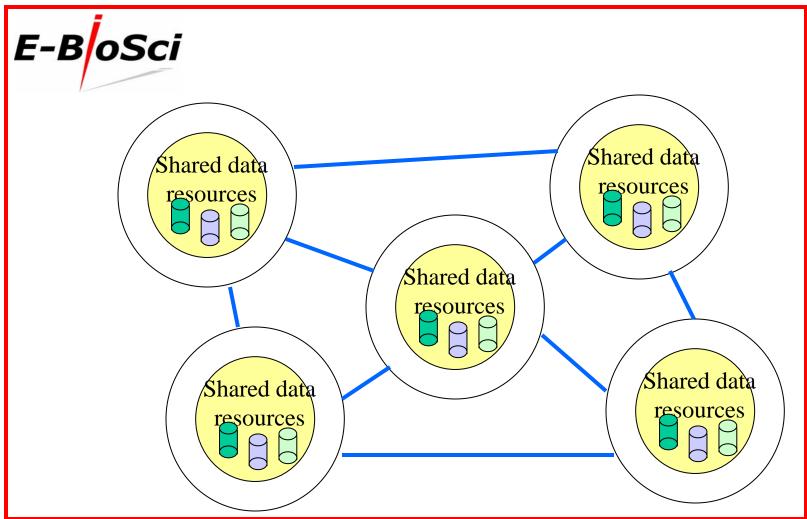
Community-driven *e*-science (2)

• Large-scale projects will drive further changes in communication and publishing practice



Community-driven *e*-science (3)

•Proliferation of community knowledge networks raises new challenges of semantic interconnectivity

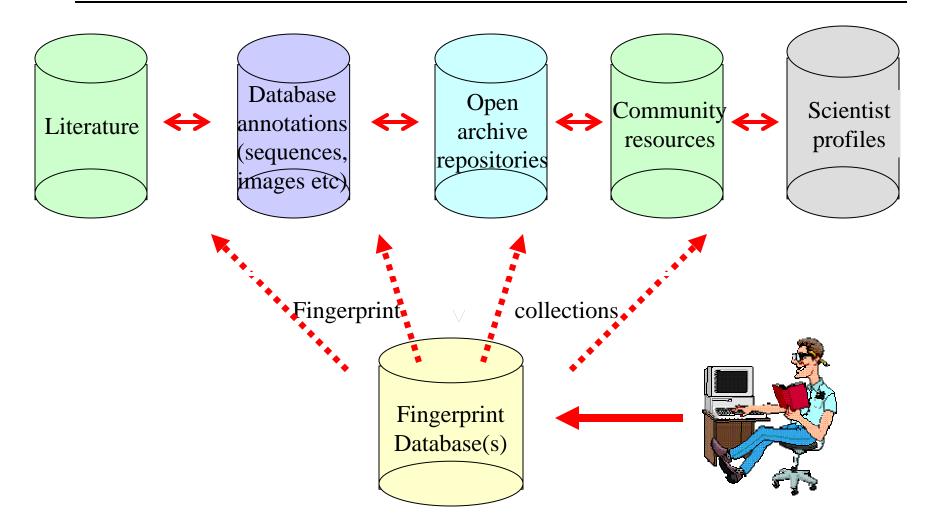






of searchable resources

E-BioSci and semantic interconnection



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E-BoSci

