



NETTAB 2007

*A Semantic Web for Bioinformatics:
Goals, Tools, Systems, Applications*

June 12 - 15, 2007

Department of Computer Science,
University of Pisa, Italy



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Biological data integration

Biological information is increasing at an impressive rate.

Its integration is needed and it is concerned with how to:

link data, select and extract information, pipe retrieval and analysis steps.

Integrated access to information requires.

The integrated and automated access to information requires complex searching and retrieval software that can be achieved by adopting new technologies and tools.

A possible methodology:

use XML schemas for information models' specification,
define XML based languages for data representation and exchange,
implement Web Services for access to analysis tools and data,
create and execute computerised pipelines and workflows.

What about **semantic integration**?





Semantic integration

What we need are:

shared definitions of knowledge domains, i.e. ontologies,
association of concepts to existing data,
metadata information describing information sources and contents,
search tools able to make the best use of this additional information.

Ontologies and their use to support software and databases is useful to
organize the information, overcoming heterogeneity of data structures.

Associating information sources and their huge contents with concepts defined
in these ontologies is a big problem. Adding semantics to current databases
would give an essential contribution to the best integration of distributed
biological information.

The development of metadata for biological information, on the basis of
Semantic Web standards, and its definition for all information sources can
also be seen as a promising approach for a semantic based integration of
biological information.

What about **Semantic Web** tools?





Semantic Web

This workshop aims at getting together biologists, bioinformaticians, computer scientists and linguists to try to answer the following questions:

- Is the Semantic Web of some use for Bioinformatics?
- Which goals should have a Semantic Web for Bioinformatics?
- Which standards, technologies and tools of the Semantic Web can most profitably be used in Bioinformatics?
- Which application did the Semantic Web already find in Bioinformatics?
- Which current Bioinformatics research problems can be solved by the Semantic Web?
- Which are the short, medium and long term perspectives in applying Semantic Web technologies to Bioinformatics?

The **panel discussion** will discuss these issues.





Workshop Agenda

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Final Agenda

Wednesday June 13, 2007

Morning		Afternoon	
09:15	Opening Lecture	14:30	'From component to processes'
10:45	Coffee break	16:00	Coffee Break
11:15	Focus Session 1 (Goals)	16:30	'Algorithm in Bioinformatics'
13:00	Lunch	18:00	Flash Posters Session

Thursday June 14, 2007

Morning		Afternoon	
09:15	Network Tools and Applications	14:30	'Formal Methods for Systems Biology'
10:30	Coffee break	16:30	Poster Session
10:50	Focus Session 2 (Tools)	18:30	Guided Tour Visit to San Rossore Park
13:00	Lunch	20:30	Social Dinner

Friday June 15, 2007

Morning		Afternoon	
09:00	Focus Session 3 (Applications)		
10:30	Coffee break		
11:00	Panel Discussion		
13:00	Farewell & Closure		





We wish you a fruitful workshop!

<http://www.nettab.org/2007/>

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