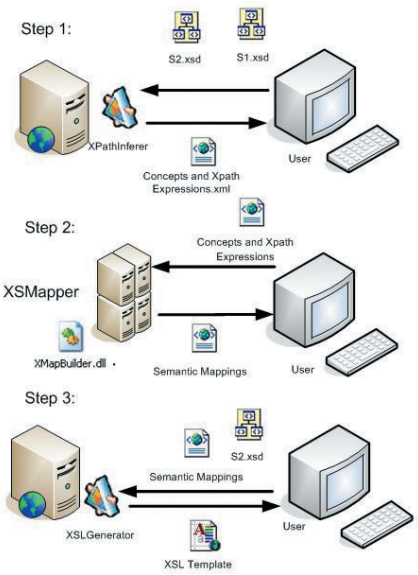
This step is performed automatically by the XPathInferer Web service. This service not only finds the concepts, but also their location within documents in the form of XPATH expressions. This is very important because location in the document can be a key property during the conversion process.

2. Definition of the semantic mappings between the elements of S1 and S2. This step cannot be performed automatically, unless some ontology relating the concepts in both schemas can be used to infer them. XSMapper provides a friendly user interface for defining three kinds of mappings, namely direct, function-based and constant. Direct mappings are used to link one or more concepts of the source schema to one or more concepts of the target schema that are semantically equivalent (eg the 'author' presented above). Function-based mappings are defined in cases where it may be necessary to apply some functions to the source concepts in order to get the equivalent target elements (for instance, splitting one concept like 'author' into two concepts 'first name' and 'surname'). As we are using XSLT to transform documents, we can use the set of functions provided by XPath and XSLT to define our function-based semantic mappings. Finally, the constant mappings are used when we want to assign a constant value to a target concept.
3. Generation of the XSL template. This task is performed automatically by the XSLGenerator Web service. An XSL template has two kinds of elements: structural elements and value-selection elements. The former build the resulting XML tree (composed of elements and their attributes), instantiating the target schema. The latter inserts the source schema values in the resulting XML text following the semantic mappings defined in step 2.



XSL template generation workflow.

Notice that most of the components of XSMapper are available as XML Web services, and can be used at the URLs listed below. We are working on a variety of improvements to the tool, with special emphasis on looking for ways to automate the definition of the semantic mappings that would make XML conversion a fully automated task.

Links:
Bibshare: http://www.bibshare.org
XSMapper:
http://bibshare.dsic.upv.es/XSMapper.exe
XPathInferer Web service:
http://bibshare.org/XPathInferer/XPIWS.asmx
XSLGenerator Web service:
http://bibshare.org/XSLGenerator/XSLGeneratorWS.asmx

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Analysis and Modelling of Genomic Data

by Anna Tonazzini, Francesco Bonchi, Stefania Gnesi, Ercan Kuruoglu and Sergio Bottini

At ISTI-CNR, Pisa, researchers from different areas of computer science are studying an integrated and interdisciplinary approach to various problems in Computational Biology and Bioinformatics.

The achievements of the Human Genome Project and the rapid development of post-genomic technology have dramatically increased the importance of genomics and genetics in disease analysis and diagnosis, novel drug and therapy discovery, and early detection or even prediction of disease. The aim is to improve healthcare strategies and, ultimately, the quality of life of the individual. Due to the enormous flow of heterogeneous biological data that is being made available, powerful tools for storage and retrieval, processing, analysis and modelling are becoming increasingly crucial in order to be able to extract useful knowledge from this data.

Bioinformatics exploits modern computing and communication technology, and is stimulating research that addresses computationally demanding challenges in biology and medicine. This highly interdisciplinary field includes data mining, modelling of complex systems, 2D and 3D visualization, signal and image processing and analysis, 'in silico' modelling and simulation, and algorithms for large-scale combinatorial problems.

Researchers from the ISTI Laboratories for Signal and Images, Knowledge Discovery and Delivery and Formal Methods and Tools form an interdisciplinary group whose comprehensive research in a number of areas of bioinformatics has been recently formalized in a Work Package of the national CNR project on 'Computational Biology'.

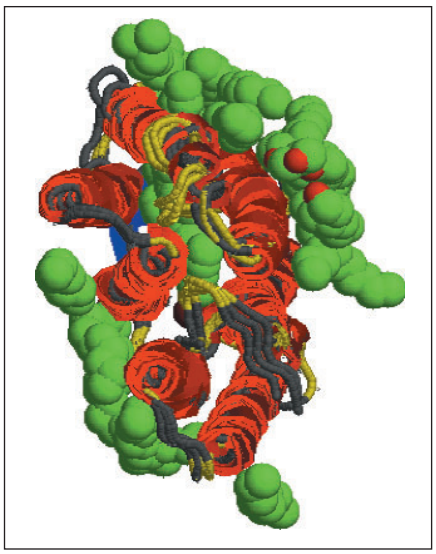
Our main goal is the development of models and analysis methods that can help to describe and understand the spatial characteristics of DNA with a functional value, and the computational

mechanisms behind complex biological systems such as gene regulatory networks. A bottom-up strategy will be adopted, in which low-level processing integrates with high-level classification and modelling. The focus will be on the structural analysis of genomes and proteins, and on the detection and functional analysis of clusters of genes related to underlying biological processes in microarray experiments.

A large number of genomes, ranging from viral and microbial pathogens to higher organisms, have now been fully sequenced and made publicly available for investigations at various levels. Nevertheless, although DNA sequencing is a mature technique and many research efforts to further improve the algorithmic phase are reported in the literature, accurate identification of bases has not yet been fully achieved by the software of available automatic sequencing machines. In this respect, we are currently studying unsupervised statistical techniques to model electrophoresis signals and correct the colour cross-talk and peak-spreading phenomena. At the genome scale, we have developed efficient algorithms for fragment assembly by partial overlap in the shotgun sequencing method. As per high-level processing, we are working on comparative genomics for the identification of conserved and invariant structural elements with functional value within the genomes. Special attention is being paid to the large portion of non-coding regions.

In proteomics, we take advanced techniques for mining complex and high-dimensional information spaces, and apply them to frequent local pattern discovery in protein databases, and to the alignment of proteins at the various structural levels, with the aim of finding common functional characteristics. Knowledge discovery and representation methods will be then exploited as knowledge-based adaptive systems for decision support in medicine and surgery (eg for studying autoimmunity mechanisms and for compatibility testing in organ transplant surgery).

Thanks to recent advances in microarray technology, we are now able to monitor the activity of a whole genome under



by courtesy of Paolo Gualtieri, Istituto di Biofisica CNR, Pisa

Figure 1: 3D structure of a photoreceptor protein of Euglena gracilis.

multiple experimental conditions. Large amounts of data are becoming available, providing simultaneous measurements of expression profiles and of interactions of thousands of genes. The challenge is to discover the complex functional dependencies underlying these data and to identify biological processes driving gene coregulation. At ISTI, techniques for unsupervised clustering of gene expression maps from microarray data are now being investigated. In particular, we are studying statistical techniques of Blind Source Separation, such as Independent Component Analysis –(ICA), nonlinear and constrained ICA, and Dependent Component Analysis, which should provide non-mutually exclusive gene clusters. The results of these analyses will be compared with those of local pattern discovery strategies such as constraint-based mining, and possibly used as input to sophisticated clustering techniques. The ultimate goal is to provide simulations and modelling of molecular interactions and metabolic pathways. In this respect, we are also studying formal methods that can be used to describe complex biological systems and verify their properties. Due to the real and massive parallelism involved in molecular interactions, investigations into the exploitation of biomolecular models as examples of global and parallel computing are also in progress.

The research activity described above is carried out in collaboration with other institutions in the fields of biomedicine and informatics. The biomedical institutions provide us with data and validate the biological significance of the results. Our main collaborations are with the Institute of Biophysics, CNR, Pisa, the National Institute for Applied Sciences (INSA) in Lyon and the Immunohematology Unit, II Pisa Hospital Cisanello. We intend to establish new collaborations with other bioinformatics groups, and in particular we are seeking fruitful interactions within ERCIM.

Link:
http://www.isti.cnr.it/ResearchUnits/Labs/si-lab/ComputationalBiologyGroup.html

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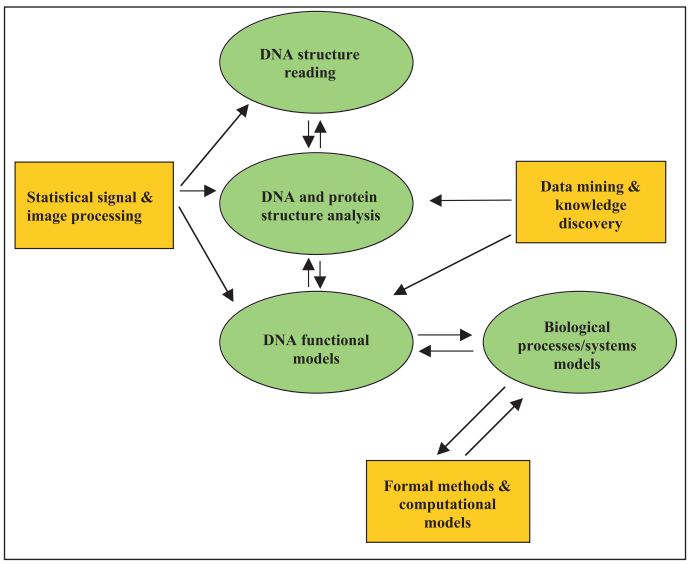

Figure 2: Computational Biology at ISTI-CNR.