

Correspondence

## Annotations for all by all - the BioSapiens network

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Published: 10 February 2009

*Genome Biology* 2009, **10**:401 (doi:10.1186/gb-2009-10-2-401)

The electronic version of this article is the complete one and can be found online at <http://genomebiology.com/2009/10/2/401>

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### Abstract

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The BioSapiens network has developed a distributed infrastructure for genome and proteome annotation by laboratories anywhere in the world.

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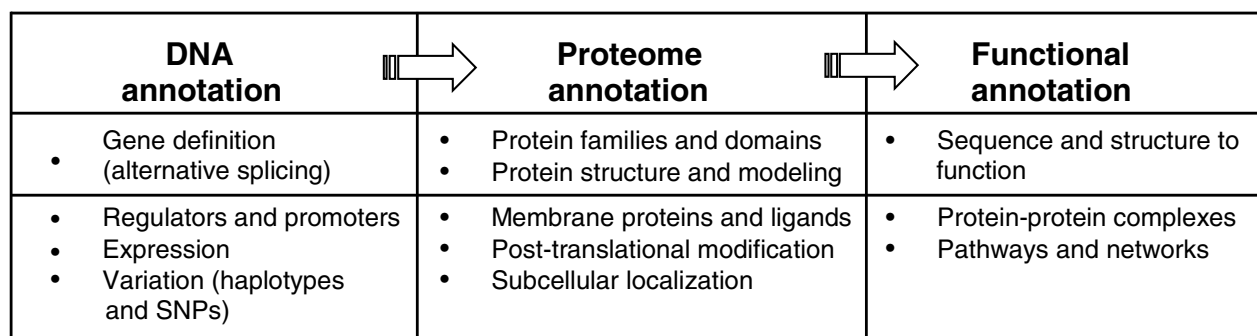
Over the last five years, the BioSapiens network has developed a distributed infrastructure to facilitate the combined annotation of genomes and proteomes by laboratories scattered throughout Europe. In a series of four review articles, published in *Genome Biology* [1-4], members of the consortium have collaborated to provide an overview of current methods and challenges for the future.

In total, there are now thousands of completed genomes in the public domain and with the second revolution in DNA sequencing technology, many, many more will be determined. However, DNA sequence is merely a string of letters; it must be interpreted in terms of the RNA and proteins that it encodes and the promoter and regulatory regions that control transcription and translation. Annotation can be described as the process of 'defining the biological role of a molecule in all its complexity' and mapping this knowledge onto the relevant gene products encoded by genomes (Figure 1).

The main objective of BioSapiens, a Network of Excellence funded by the European Commission, is to provide an infrastructure and tools to support a large-scale, concerted effort to annotate genome and proteome data by laboratories distributed around Europe. The Network brought together 26 laboratories in Europe to create a Virtual Institute for Genome Annotation, divided into nodes, each focused on one aspect of genome annotation. The network provides a focus for annotation and through the organization of meetings and workshops encourages cooperation, rather than duplication of effort. The annotations generated are all available in the public domain and easily accessible through a single portal on the web [5].

The review by Harrow *et al.* [1] tackles the challenge of identifying protein-coding genes from genomic sequences. Even the concept of a 'gene' is under revision. The review focuses on the strategies being applied to delineate a number of reference human gene sets - the ones most widely used by researchers in biology - and to assess their quality and completeness. Once the genes are defined, the next challenge is to unravel how regulatory information is encoded in the genome. Gene-expression data has illuminated the consequences of transcriptional activation and propelled the quest to find common regulatory sequences in coexpressed groups of genes. Vingron *et al.* [2] attempt to summarize progress in integrating these approaches for the purpose of identifying regulatory sequence elements and their function. The other two reviews focus on annotating the proteins and their functions. As reviewed by Juncker *et al.* [3], these tasks include identifying functionally important residues, such as those involved in catalysis or binding, and predicting post-translational modifications and cellular localization. Finally, Loewenstein *et al.* [4] show how both sequence and structural data can be used to illuminate the function of the protein by recognizing a homolog. A recent trend is that many prediction tools are combined in complex workflows and pipelines that facilitate the analysis of feature combinations and use a variety of data and methods.

A key to integrated annotation is the ability to combine annotations of different types from different laboratories. Within BioSapiens, the Distributed Annotation System (DAS) is used as a lightweight data-integration infrastructure. Originally developed by Dowell *et al.* [6] for genomic sequences, DAS defines a framework for the annotation of reference

**Figure 1**

Steps in the analysis and annotation of genomes.

sequences by multiple independent sites. The DAS concept was extended [7] from genomic sequences to protein sequences, structures, and protein interactions. DAS clients such as DASTY [8,9] now visualize the results of many different approaches for functional protein annotation in a consistent framework. One consequence of this was the need to develop an ontology for annotating sequences [10], so that annotations from different laboratories are consistent.

This infrastructure is open to all, allowing any laboratory to generate its own annotations for proteins or genes, and to view their results in the light of other annotations, derived in other laboratories. More detail is available in a book, written by the consortium [11].

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### Acknowledgements

The BioSapiens project is funded by the European Commission within its FP6 Programme, under the thematic area 'Life sciences, genomics and biotechnology for health', contract number LSHG-CT-2003-503265.

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