TAMBIS Online: A Bioinformatics Source Integration Tool

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1. Introduction

Conducting bioinformatic analyses involves biologists in expressing requests over a range of heterogeneous information sources. The TAMBIS (Transparent Access to Multiple Bioinformatics Information Sources) project seeks to make the diversity in data structures, call interfaces and locations of bioinformatics sources transparent to users. TAMBIS is available at `http://img.cs.man.ac.uk/tambis`. The TAMBIS query processor is described elsewhere in this proceedings [1].

Figure 1. Browsing the concept model.

2. Facilities

In TAMBIS, users view the world as a collection of concepts in an ontology. To write queries, users must identify concepts of interest in the ontology, and express queries
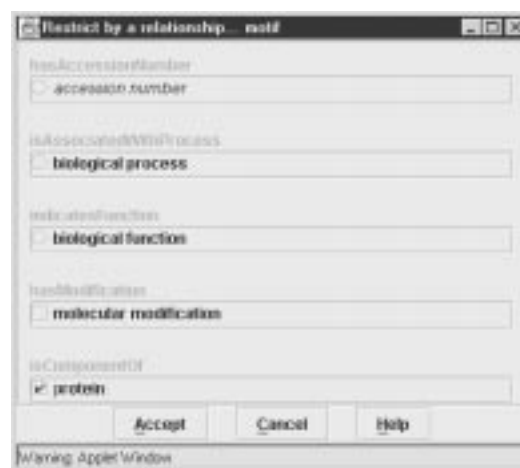

Figure 2. Restricting the concept `motif`.

over these concepts. The two principal tasks performed by users are thus *ontology exploration* and *query construction*.

The ontology of bioinformatics concepts is explored using a range of browsers. For example, figure 1 shows the concept `motif` surrounded by the concepts to which it is related.

Queries are constructed by selecting concepts within the model, and imposing restrictions on those concepts. For example, figure 2 shows how a query over `motif` is being refined so that only motifs that are involved in specific relationships are included in the result of the query.

References

[1] N. Paton, R. Stevens, P. Baker, C. Goble, S. Bechhofer, and A. Brass. Query Processing in the TAMBIS Bioinformatics Source Integration System. In *Proc. SSDBM*, 1999.