Goal-Oriented Task Composition for Bioinformatics

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Abstract

A key application area of semantic technologies is the fast-developing field of bioinformatics. However, a gap exists between the computer literacy of biologists using bioinformatics tools and the computer scientists developing them.

Tools such as Taverna¹ provide a graphical user interface for creating biological workflows using web services and semantic technologies. However, these tools are aimed primarily at bioinformaticists, i.e. those who have an interest in biology, but are also fairly knowledgeable in computing. The level of technical detail required is generally beyond that possessed by most biologists.

The work illustrated in this poster aims to bring the biologist closer to being able to create and run their own workflows by using principles from Hierarchical Task Network (HTN) planning and plan recognition. The aim is to identify the goals or questions in which a researcher may be interested, and show how these goals can be broken down into simple tasks which the computer can subsequently run.

This work was carried out in the context of the Sealife project, part of which allows a user to click on semantically-linked biological terms to add them to a 'shopping cart'. Each term is assigned a semantic type which can then be used in the system described here to find goals of relevance to the user. The HTN domain model is central to the process, allowing goals to be discovered by working up the tree from simple tasks to more complex goals. Once a user has chosen a goal from the list of possibilities it can be broken down into sub-goals and subsequent basic tasks to produce a workflow. This is then executed by the myGrid² workflow execution engine.

The system uses a variety of techniques that together allow a biologist to discover the possibilities of the Semantic Web, as well as providing an efficient way of achieving goals that would previously have been undertaken manually.

Acknowledgments Funding for this work has been provided by the EU project Sealife (FP6-2006-IST-027269).

¹ http://www.taverna.sourceforge.net

² http://www.mygrid.org.uk