Oncology over Internet: integrating data and analysis of oncology interest on the net by means of workflows

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Introduction

The Human Genome Project has transformed biology by providing a list of all genes and proteins, but the field has since then expanded to the management, processing, analysis and visualization of large quantities of data from genomics, proteomics, medicinal chemistry and drug screening. This huge amount of data and the heterogeneity of software tools that are used for its distribution make the tasks of searching, retrieving and integrating the information very difficult. Data is retrieved and analysed by hand by accessing several bioinformatics servers and transferring the data by FTP clients or web browsers by the "cut and paste" technique.

The need is felt for a system that is able to improve the information accessibility. Such a system should be able to automate the accesses to the remote sites, in order to retrieve the information from the specific database or for using the appropriate software tools to achieve the desired analysis. At the same time, it should be able also to "understand" the information that it is managing. Among current ICT technologies, workflow management systems in connection with Web Services seem to be the most promising ones. Workflows are defined as "computerized facilitations or automations of a business process, in whole or part" (Workflow Management Coalition). Their goal is the implementation of data analysis processes in standardized environments and their main advantages relate to effectiveness, reproducibility, reusability of intermediate results and traceability.

Some workflow management systems have already been proposed and are being increasingly applied in the biomedical domain. Some of them are add-ons to other tools, like biopipe [1], a perl module designed to be used with bioperl, and GPipe, an extension of the Pise interface [2]. Other systems are autonomous applications that are being developed either by industries, like the Bioinformatic Workflow Builder Interface – BioWBI from IBM [3], and Pipeline Pilot from SciTegic, or by academic and research institutes, like Wildfire from the Singapore Bioinformatics Institute, and Taverna Workbench [4] from the European Bioinformatics Institute (EBI).

Web Services (WS) are software oriented network services which communicate usually by using SOAP (Simple Object Architecture Protocol, a framework for the distribution of XML structured information) over HTTP. They offer a good, standard solution for automated retrieval of information. Standards are available or have been proposed for their retrieval and identification, description and composition [5]. They allow software applications to access data in a semantic- aware way since being in the form of XML documents their contents can be made visible and when metadata is given, interpretation of semantic information becomes possible..

Many WS and WS deployment tools have recently been set up in the biomedical domain and perspectives for their widespread use has been proposed [6,7]. Among

the providers of biology oriented WS are some of the most important network service providers such as the USA National Center for Biotechnology Information (NCBI), which has implemented API interfaces for accessing so-called e-utilities [8], the Bioinformatics Center of the National Cancer Institute [9], the Bioinformatics Center of Kyoto University, which has implemented the KEGG API [10], and the European Bioinformatics Institute (EBI).

We present here a prototype system which can support researchers in the execution of predefined and tested workflows of oncology interest by transparently accessing Web Services. A user-friendly web interface has been developed thus simplifying access to public in-silico analysis.

Methods

We have designed a general architecture of a system (see figure 1) for the remote execution of workflows of biomedical interest that are intended to access to and to retrieve data from various Web Services.
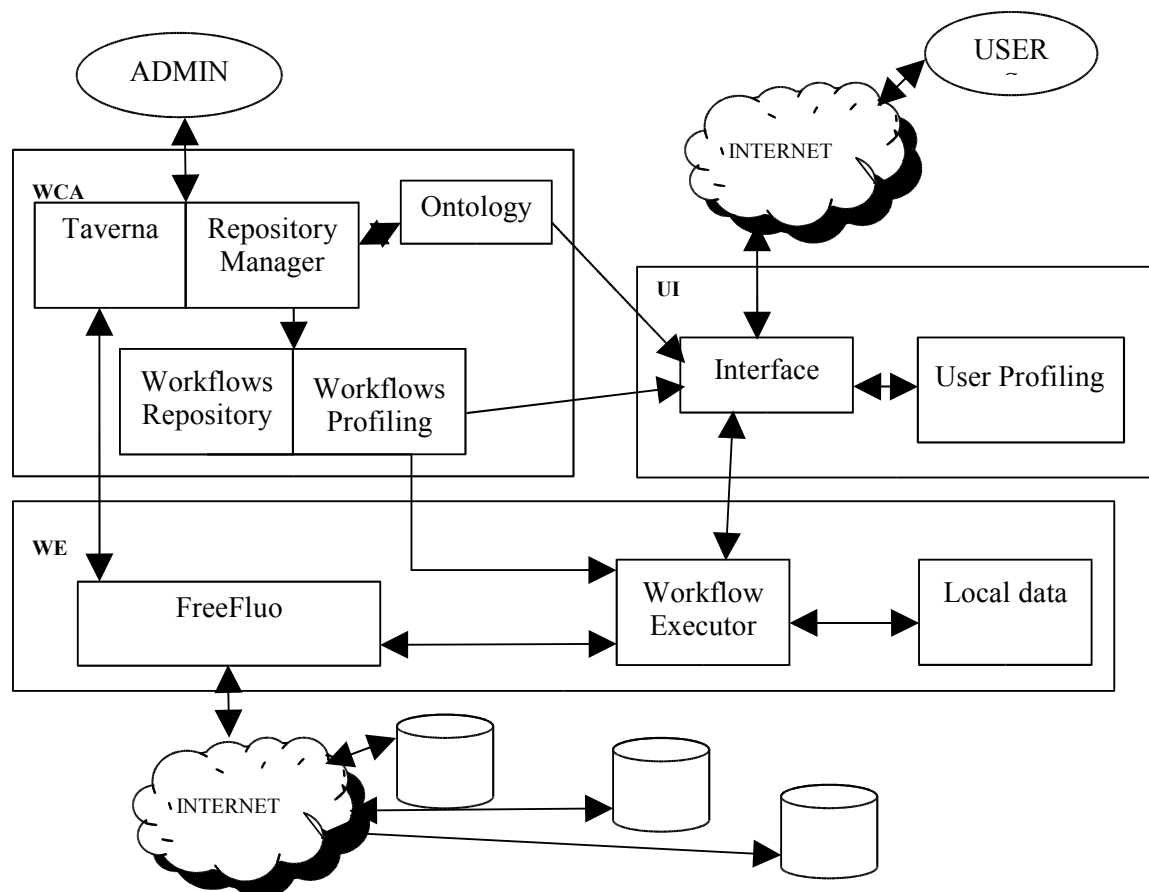

Figure 1: General architecture of the system.

The system is partially based on open source software tools. The Taverna Workbench is a workflow management system developed at the European Bioinformatics Institute (EBI) as part of the ^{my}Grid project [11]. It allows skilled end users to create complex analysis workflows, to access both remote and local processors of various kinds, to run workflows and to display results in different formats. In Taverna workflow execution is carried out by an associated tool, FreeFluo. Taverna also includes an ontology for bioinformatics data. Its only requirement is the availability of Java Run-time Environment (JRE) on a Windows XP

or Linux box. A MySQL data management system [12] can optionally be used for local data storage.

The system includes three main blocks: the workflow manager, the user interface and the workflow executor. Workflows are created and tested by an administrator using the Taverna Workbench. They are then stored in a repository by adopting the Taverna Simple conceptual unified flow language (Scufl) format. At the same time, their main processing steps are annotated in workflows profiles by using a specially designed ontology. This ontology describes bioinformatics tasks on the basis of their input and output data, processing type and application domain. These main processing steps may actually represent more real tasks grouped to achieve a functionally significant processing step. The user interface supports end users authentication and profiling and allows for the selection and launch of workflows. Workflow selection can be assisted by the user profile and by searching through significant processors of annotated workflows. Workflows are executed by the third block that is based on FreeFluo and it is also able to store input and output data of actual workflow executions, so that they can later be analysed and possibly reused.

Preliminary results

At present, the general architecture, a preliminary version of the user interface and a set of new Web Services are available. Web Services implement access to IARC TP53 Mutation Database [12,13] and to CABRI catalogues of biological resources [14]. Workflows are being created and tested in various application domains. The ontology is being created starting from the Taverna bioinformatics data ontology.

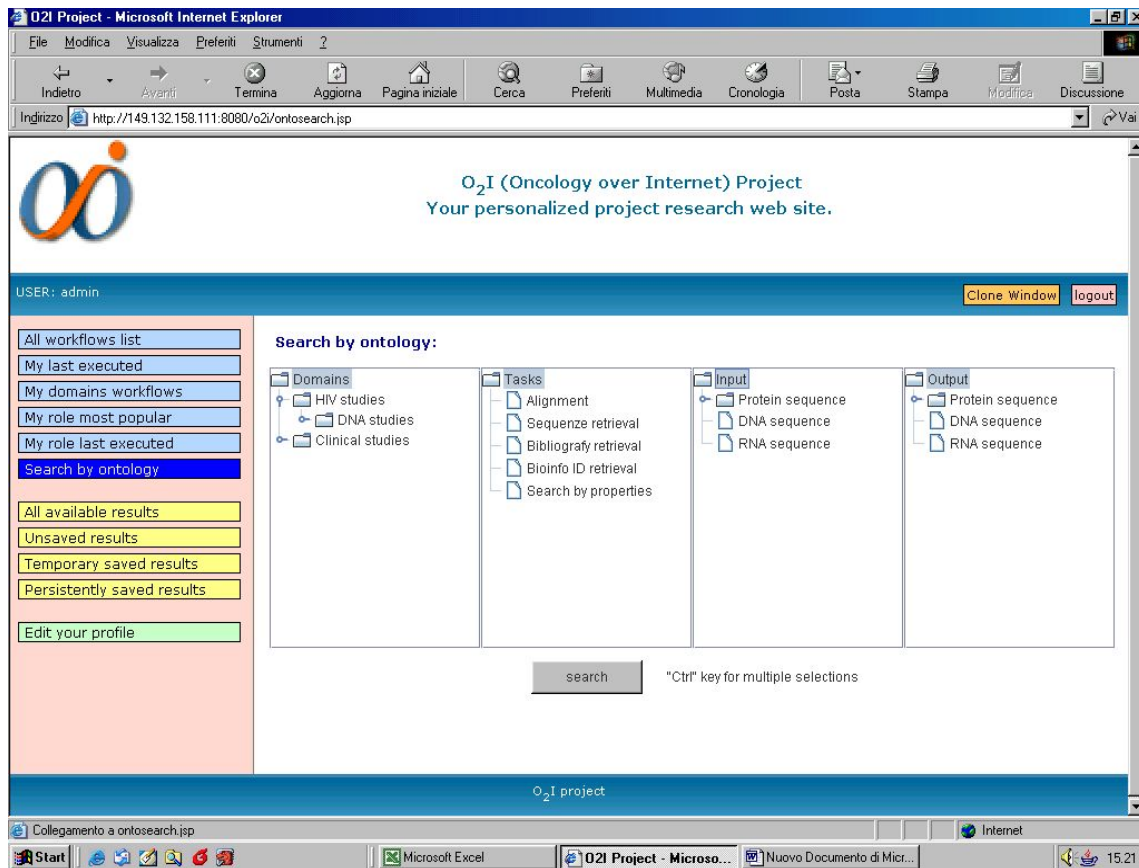**Figure 2: list of most recently executed workflows**

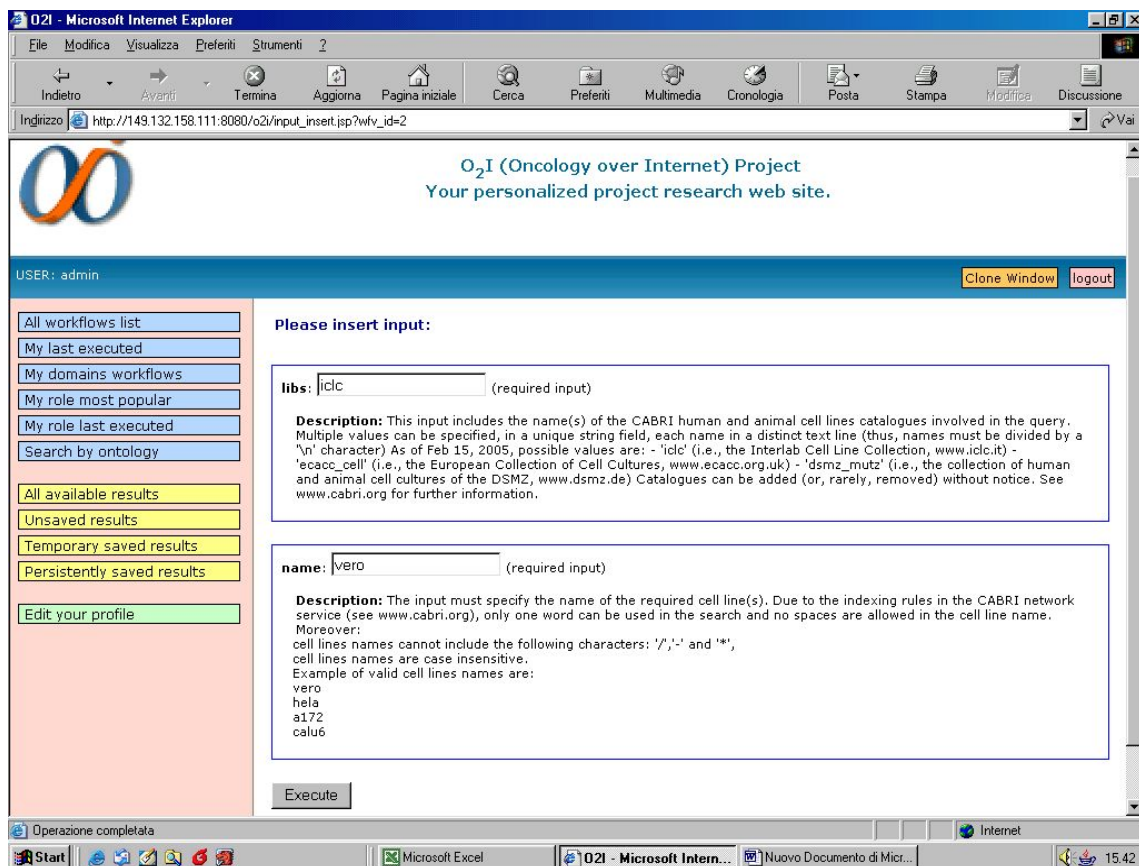**Figure 3: web page allowing search by the annotation of workflows.**

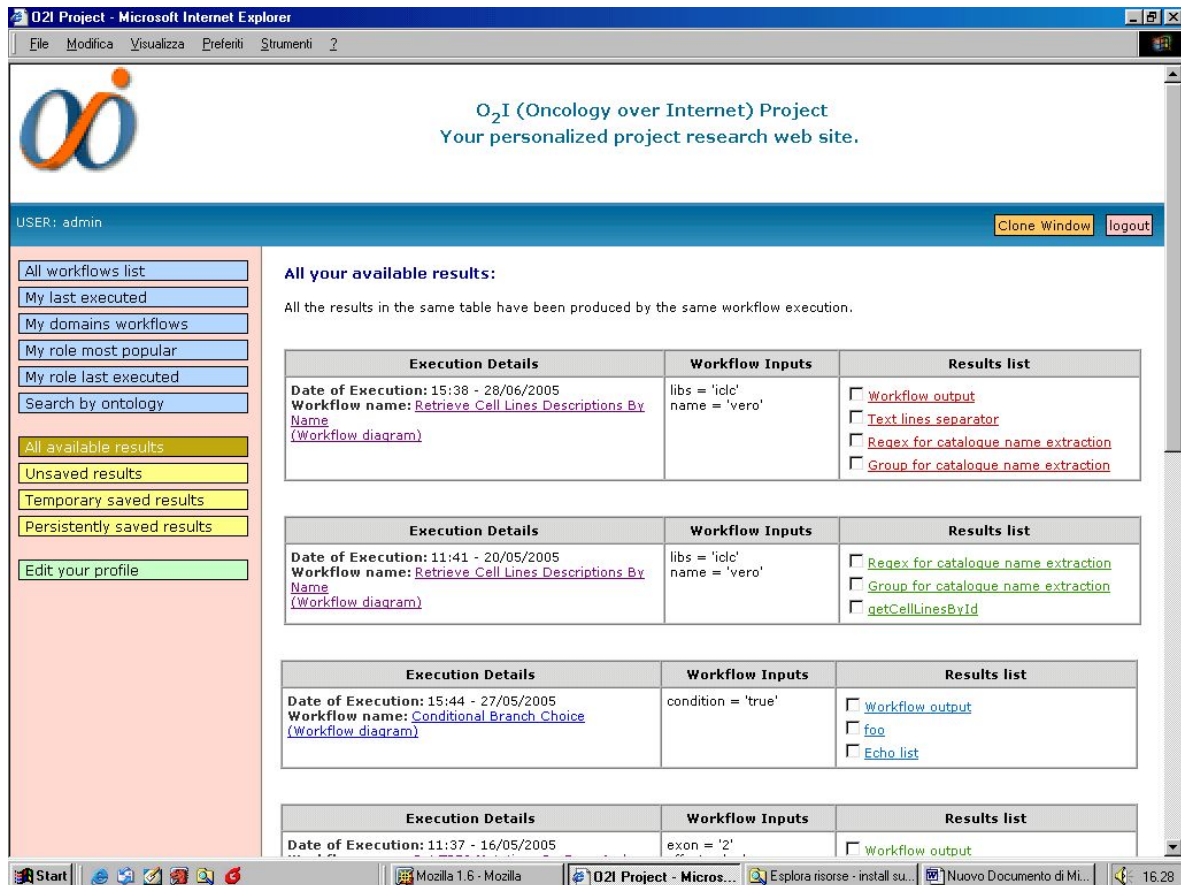**Figure 4: Input form for the execution of a workflow**

Figure 5: web page allowing for the examination of saved results

In figure 2, the web page listing workflows last executed by the user is shown. From this page, the user can launch workflows (button 'run') or retrieve related details (button 'details').

In figure 3, the web page allowing a search of workflows on the basis of their annotation is shown (in this figure, a fictitious ontology is used). Conditions can be set for each column and are linked by a logical AND. Within columns multiple selections are allowed and conditions are linked by a Boolean OR.

In figure 4, the input form for the execution of a workflow is shown. Input fields are described in details and suggestions for possible input values are reported. Required and optional fields are pointed out.

Results are displayed by using Taverna Workbench java applets and can be saved, either temporarily or definitely, and later reanalysed. In figure 5, the web page listing all saved executions' results and allowing for their further visualization is shown.

Conclusions

We have presented in this paper a general architecture for the implementation of a system that is able to execute workflows of biomedical interest remotely. We have presented as well the preliminary user interface.

The further development and implementation of Web Services allowing the access to and retrieval from an exhaustive set of molecular biology and biomedical databases being carried out by many research centres and network service providers in the biological and medical domains and the creation of effective and useful workflows by interested scientists through widely distributed workflows management systems such as those presented in this paper will significantly improve automation of *in-silico* analysis.

Acknowledgements

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