A Workflow Service for Biomedical Application

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Introduction

The proposed work has been developed in the O_2I (Oncology over Internet) project context. O_2I aims to develop and prototyping an integrated platform suitable to support the biomedical and clinical research during the retrieval, from Internet, and the integration, in a standard format, of both structured and textual information.
Usually biomedical researchers interact, step by step, with the Web to query, select and integrate information; during the daily work, a bioscientist would benefit from a powerful tool able to execute queries consisting in several interrelated activities. In this scenario, the biomedical research process can be formulated as a workflow of activities, whose execution must be supported by a suitable middleware [1]. We propose a *workflow service agent* to support bioscientist during the creation of their own workflows, by also monitoring their execution. In particular, in the O_2I context, we are experimenting BioAgent an agent-based middleware developed at Camerino University; the middleware can be configurated by plugging-in agent-services to support the tool/services integration for a specific domain [2].

Bioworkflow System for O2I Architecture

1. Application Domains and Use Cases

The proposed *workflow service agent* offers to the biomedical users an environment, with a user-friendly interface, suitable to create a workflow of activities, here named *use cases* with the meaning given by software engineers, i.e. a set of scenarios[1] tied together by a common user goal. Consider as an instance of use case a complex query. Any use case is defined by using a terminology from a specific application domain, and it is parameterized by input data and expected output. In the O_2I context we have considered three application domains: A) *Cell Lines*, B) *Mutations* and C) *Bibliographic Databanks*. We have defined the following use-cases: A1. Find information about the cell line named *x*; A2. Find all cell lines derived from a specific tumour or pathology; A3. Find all Cell Lines producing a specific protein; A4. Given a specific Cell Line, find all related bibliographic references; A5. Given a specific Cell Line, find all information about produced proteins; B1. Find all mutation observed in a specific intron/exon in subjects with specific sex and life habits (i.e. smokers/ drinkers); B2. Find all mutations in subjects affected by a given pathology; B3. Find all subjects affected by a tumoural pathology and without a given protein mutation; B4. Find all mutations observed by using a given cell line; B5. Given a specific mutation, find all abstracts of the correlated bibliographic references; C1. Select all abstracts of bibliographic references, whose text includes a given term; C2. Merge a collection of abstracts. The implementation of the proposed use-cases is still in progress. The **Figure 1** shows a simple bioworkflow aiming to retrieveing all information of a given cell line and to select all related bibliographic references; it consists of two use-cases executed in pipeline.

[1] A scenario is a sequence of steps describing an interaction between a user and a system.

2. Architecture of the BioAgent Component for O2I

BioAgent [2] is an agent-based middleware configurable by services to support the workflow execution into a biological domain. The *workflow service agent,* and all others services, in particular AIXO (Any Input XML Output) service agent, a generalized wrapper for information extraction, interact as shown in **Figure 2.** It is possible, through this link *http://www.bioagent.net/demo* to interact with the demo *Bio-workflow service agent*.

References

[1] F. Corradini, L. Marian and E. Merelli, "A programming environment for global activity based application", WOA04, Cagliari 2004.
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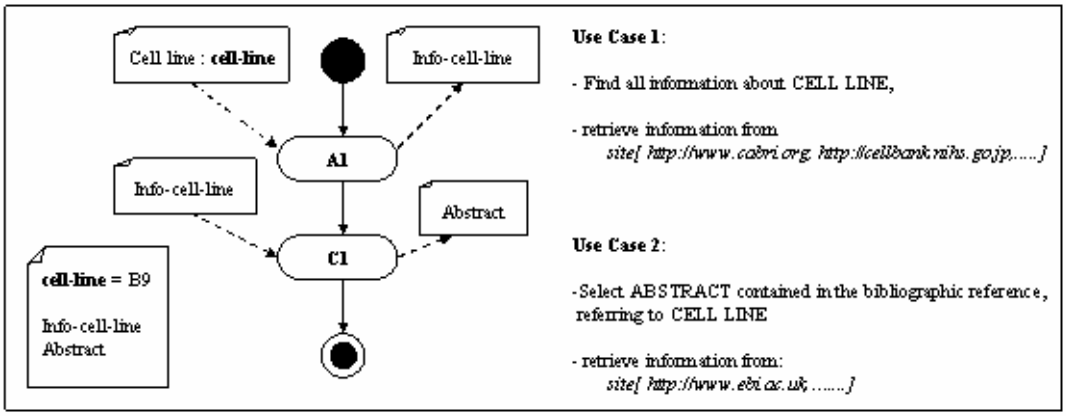

Fig. 1 Bioworkflow example

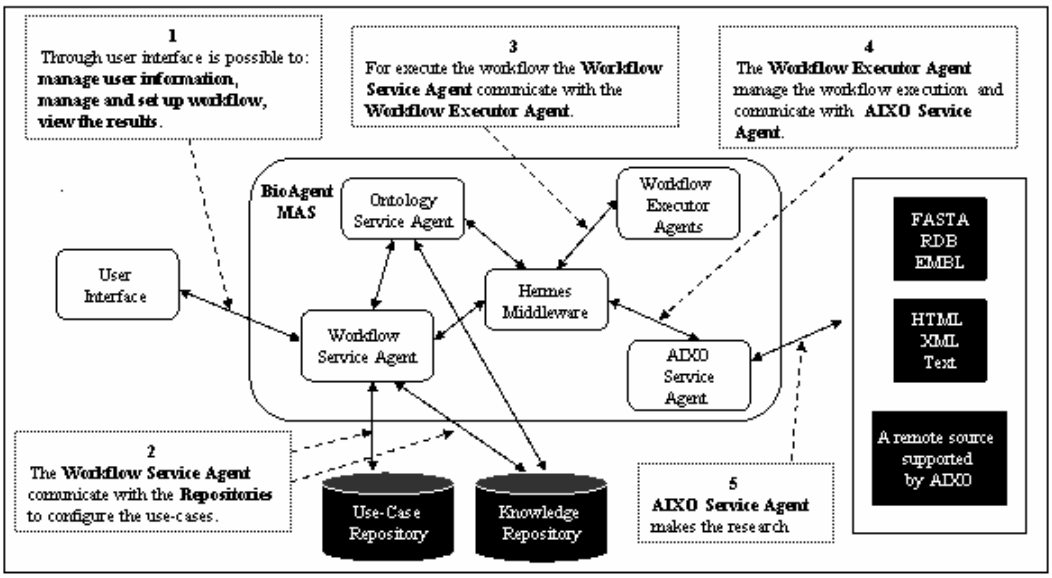

Fig. 2 BioAgent configured for O_2I System Architecture