Adaptive Interface and BiODS Tools

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Adaptive Interface and `BiODS` tools

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ABSTRACT

To fully exploit the **Oriel** integrative vision, we developed `BiODS`, a "biology-centered" interactive system driven by ontologies. In our opinion, biologists urgently need global systems that offer transparent access to a variety of public resources (databases and/or analysis tools). Consequently, `BiODS` is taking advantage of some basic tenets (simplicity, ease-of-use, user-centered, transparency, knowledge model driven...) to give a simple, straightforward view and allow use of a number of biological resources. `BiODS` can therefore be described as a "semantic" adaptive system. The `BiODS` central paradigm is that systems have to operate at a knowledge level in order to maximize their interconnectivity. Consequently, `BiODS` is offering a description logics-based interpreter (advanced shell), and a semantic file system to facilitate the right communication acts between users and systems.

Context and objectives
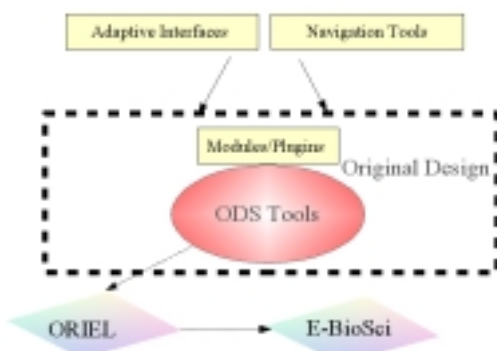
In **Oriel** context, our objective is to have a tool that help experts to design and build `ODS` modules to get a desktop environment that may assist a biologist to manage *ressources* (data and tools).

Problems to overcome

- To efficiently manage heterogeneous ressources.
- To take benefit of specific tools with their own software and user interface.

Our approach

Our idea is to prototype a kind of programming environment with an *Adaptive interface* in which user side aspect in the same way that the user desktop is an extension of the operating system.
So, in this point of view, interface is related to users but also to software components in an interaction.

About `ODS`

`ODS` stands for Operating Description System, is entirely written in `Java` and requires some extra packages such as a compiler tool `MORK` and a web-service toolbox `Axis`.
`ODS` will be distributed under the GNU General Public License and is available on `http://www.lirmm.fr/~oriel`.
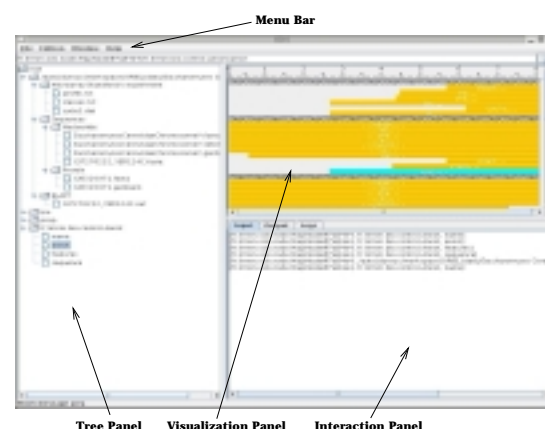
Architecture

`ODS` is mainly supported by 3 different layers. The first one corresponds to the memory management with a very similar approach to a Virtual File System or conceptually speaking a Knowledge Tree. The second layer is typicaly a session manager that executes a collection of instructions provide by a client w.r.t. a syntax analyzer. Finally, the third layer is dedicated to the development of the user interface components:

- a shell interface that is directly built on the top of the session manager with a very limited syntax (head-first) and instructions set (`cat`, `rm`, `load`, `quit`, ...).
- a graphical user interface that is also conceived on a set of instructions but they are embedded in GUI components which may take part of the memory management.

Extensions to `ODS` are obtained with a mix of specific modules and plugins. Then `BiODS` is equipped with a number of services and queries that are respectively nodes and arrows of the biological scenario dataflow.

General graphical interface

Currently, the user interface is a Java Swing application that is very similar to an internet navigation tool. The information is distributed thru different panels according to their type and the graphical interface provides also a link to the shell command line.

Dataflow of the biological scenario

The biological scenario under consideration is expected to provide interactive ways (chains of in-silico tasks) to characterize gene expression data generated by microarray experiments.
In the dataflow, nodes represent in-silico tasks and arrows indicate how information flows from one processing unit to another.

Applet service illustration

We are taking benefit of existing tools such a graphical annotation tool available as a `Java` applet. It consists of a tool editing sub-sequence area and adding tags to it.
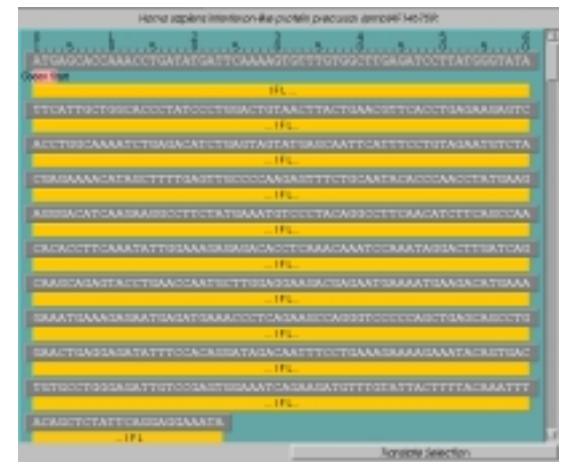
Web-service illustration

The Webservice `BLAST` (Basic Local Alignment Search Tool) is dedicated to biological sequences local or global alignment. Basically, two different fonctionnalities are available, an interaction through:

- an HTML form,
- a Java client.

A screenshot of the HTML form is shown here, the user may choose between different versions of BLAST and may select a whole of criteria: data bank, matrix, gap penalities...

Next steps

`BiODS` and its underlining kernel design `ODS` are a first step to provide a extensible framework that will provide a better interaction between data and tools belonging in a unique interface system.
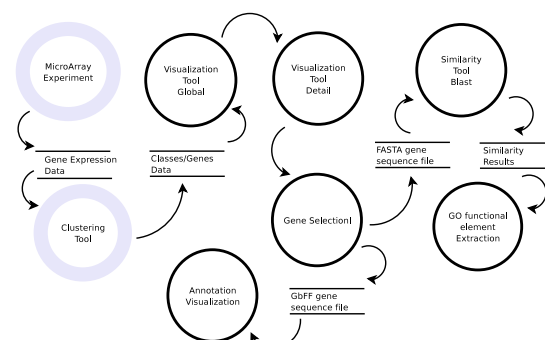On a technical aspect, we intend to introduce :

- level of usage based on user registration or account,
- more generic graphical components or views.

On a more scientifical point of view, we intend to develop a symbolic learning component to provide semi-automatic script completion (such value-type abstraction, type-type conversion) to help the user to combine protocols with more tasks.