Web-Based Virtual Lab for Taxonomic Description

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ABSTRACT
The taxonomic description of a specimen is an essential task carried out by biologists aimed to identify and study living beings. The usual approach involves analysing and describing a given specimen in a physical laboratory. Nevertheless, several tasks are being virtualized. Images, sounds, and videos of living beings are being digitalized; records are stored in spreadsheets and databases and the description task itself are being supported by specialized software. This work investigates a step beyond, where the laboratory itself becomes virtual.

Categories and Subject Descriptors
D [Software]: [Miscellaneous]; J.3 [Life and Medical Sciences]: [Biology and genetics]

General Terms
Experimentation

Keywords
virtual lab, software component, taxonomic description, web

1. INTRODUCTION
Virtual laboratories simulate physical equipments and the infrastructure of a physical laboratory by using computational techniques. They can represent experiments by graphical interfaces and offer interactive simulations.

Virtual labs can be tooled to afford learning experiences comprising exercises, theoretical explanations, and interactive assistants that explain experiments step by step. In many cases, they can be used any time and from anywhere. This kind of laboratories are also known as simulated laboratories or e-laboratories [4].

By handling and combining visual software components, users can describe specimens in a virtual laboratory. This paper presents our work of such a tool involving the description of living beings. In this work we investigate a specific kind of Biology virtual laboratory to support taxonomic description of specimens, in which the basic lab elements are virtualized as visual software components.

This is an ongoing work and, in order to validate our proposal, we have implemented a preliminary prototype with components to describe monitor lizards of the genus Varanus. The lab is based on a system called Varan-ID.

Varan-ID is an online determination system for monitor lizards. It is based on a morphological knowledge base of a group on carnivorous lizards, the genus Varanus. The system is based on the idea that not only experts are involved with monitor lizards. Students, curious, breeders, keepers are either interested in this subject, but may not have the necessary knowledge to work with the specimen. The process of identification in the Varan-ID system is based on descriptors.

In this paper we present a prototype of our virtual web laboratory to describe and to identify living beings. It is based on visual components handled by direct manipulation, which play roles of building blocks for descriptions and lab tools. Therefore, when a user inserts a component that represents a tail in the composition, he/she will add a related tail descriptor in the lizard description. The entire lab runs over the web on top of the Componere authoring environment[8], which explores the Rich Internet Application (RIA) approach to provide an interactive interface.

The remaining of the paper is organized as follows: Section 2 presents a taxonomic description model of the context of the developed tool. Section 3 presents implementation details of the tool. Section 4 presents future works and conclusions.

2. TAXONOMIC DESCRIPTION MODEL
The starting point for designing our lab was the software Xper2 (http://lis-upmc.snv.jussieu.fr/lis/?q=en/resources/software/xper2/). This tool supports the identification and description of specimens. It follows the character/character state (C,CS) [5] approach, organized in three phases:

(i) to define descriptors and possible states;
(ii) to relate descriptors/states to species;
(iii) to identify a given specimen by recognizing values for each descriptor.
The Varan-ID system was developed over the Xper2. Its descriptors are organized in two distinct groups, easy-to-see descriptors and expert descriptors. Table 1 shows an example of some easy-to-see descriptors and their respective states.

<table>
<thead>
<tr>
<th>Lizard Part</th>
<th>Descriptor</th>
<th>States</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tail</td>
<td>transversal section of the tail</td>
<td>roundish or laterally compressed</td>
</tr>
<tr>
<td>Head</td>
<td>position of nostrils between eyes and tip of snout</td>
<td>same distance from eyes than from tip of snout or nearer the eyes than the tip of snout or nearer the eyes than the tip of snout</td>
</tr>
<tr>
<td>Tongue</td>
<td>tongue coloration</td>
<td>red, light pink or whitish or blue, purple or black</td>
</tr>
</tbody>
</table>

Our tool is able to interact with Xper2 by accessing SDD files it can export. The Structure Descriptive Data format (SDD) is an open standard endorsed by the TDWG (Taxonomic Database Working Group) and DELTA (Descriptive Language for Taxonomy) for representing taxonomic descriptions in a XML format (http://wiki.tdwg.org/SDD/).

Figure 1 shows a diagram representing a fragment of a SDD file containing data to describe Varanus lizards. The hexagons represent elements, the rectangles represent texts and the ovals represent attributes. The CategoricalCharacter element defines a descriptor and possible states. In this example it defines the tongue coloration element and three possible states: red, light pink or whitish and blue, purple or black.

The States element aggregates all possible states: StateDefinition elements. As can be seen in the diagram, the Representation element can be applied in many levels of the schema, containing textual and multimedia descriptions. This element is formed by a label, a detailed description (Detail) and references to multimedia resources (MediaObject).

In our tool we map these SDD description blocks in the following way:
(i) each CategoricalCharacter becomes a description component;
(ii) the set of states that the CategoricalCharacter can assume is transformed in a set of possible states that the component can assume;
(iii) every time the description component assumes a state it provides a visual feedback.

These description components transform the task of describing specimens in selecting and customizing components, which are combined in compositions.

In order to automatically derive SDD CategoricalCharacters to description components, a process was created to get all information on the SDD file and use it to fetch the respective description components, customizing them with the respective values. Figure 3 illustrates the creation process of lizard components and their use during a composition. A proxy reader component accesses a SDD file (step 1). This information is delivered to a component generator that creates all the description components (step 2 and 3) – lizard description components in the example. Therefore, the categorical element will be used to identify a specimen characterization – a lizard in the example – to generate its respective composition. The State element will generate the value that the parameter assume.

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data from XML files in the base (step 7); which uses the HTTPXMLRequest API (step 8).

In our proposal, a description component is one type of the available components. Another type comprises tool components, a group that will be responsible to support the authoring process. The classification based on this two types of components is illustrated in Figure 4.

As mentioned before, our laboratory is built over the Componere environment. In the original Componere authoring environment all components play the role of building blocks. Our lab, on the other hand, introduces this new kind of component - the tool component - to assist the authoring task itself.

3. IMPLEMENTATION

The implementation of the proposed laboratory involved two steps: the construction of description components and the construction of the laboratory on Componere. As mentioned before, this first prototype is focused on a specific practical scenario involving the identification of Varanus lizards, based on the Varan-ID database.

3.1 Construction of Lizard Components

The Varan-ID base is composed by 7 knowledge bases: the Main base, V. indicus-group base, V. prasinus-group base, V. timorensis-group base, V. gouldii-group base, V. salvator-group base, and the Australian spiny-tailed base. Each base can be exported as an SDD file. To build the components, we analysed the available descriptors in these bases.

A component builder engine was developed to extract information from the exported database and to use them to build each one of the lizard components.

There are two ways to build Componere compositions. The first is by using a javascript code to instantiate and to connect components. The second is by embedding compositions in HTML pages through microformats based specifications [8]. During the authoring process the laboratory uses the first dynamic approach. Resulting compositions can be further materialized as HTML embedded compositions.

3.2 The Laboratory on Componere

As mentioned before, Componere is a framework based on javascript components that works over web browsers.

Thus, the Lizard Lab is an environment totally based on javascript, mainly directed to beginners in the monitor lizard identification process. An overview of the system is illustrated in Figure 5.

Figure 3: The Creation of Lizard Components and Composition Process

Figure 4: The Component Classification for the Lizard Lab

Our lab is designed to afford any kind of description component for living beings. However, in our prototype we have produced only description components representing each part of the Varanus lizard. They are visual components derived from Varan-ID easy-to-see descriptors. The tool components can be visual or not. For example, the button is a visual component that starts the execution process. The table is a visual component that contains data organized as rows and cols. The proxy is a non visual component that brings data stored in a database to the composition.

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Figure 5: The Model of the Lizard Lab

The environment is organized in four areas: description components, settings, composition and result area. The description components area is where the components representing parts of the lizard are placed. Each one is independent and has its own set of parameters to be configured.

In order to produce a description the author drags description components to the Composition Area where they are
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5. CONCLUSIONS
The main contribution of this paper is our unified approach
to produce a virtual lab for taxonomic description, combining
the perspective of tools to describe specimens with the
virtual laboratory model. It involved the design of a
new component based description approach, in which com-
ponents work as basic descriptive building blocks.
Future works include to expand the laboratory features, en-
abling it to better integrate with real world resources, i.e.,
fetching images and other kinds of media of real world spec-
imens, including them in the description process. We are
also working to generalize the process of building description
components, enabling smooth expansion to new descriptors
and other domains.
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During the description/identification process the author can
access the base containing available descriptions of existing
species – lizard in this case – whose descriptor/states match
with those already assigned in the lab. For example, if the
author assigns a specific tongue color and tail shape, the sys-
tem will record these settings in the Settings area; whenever
the author clicks in the “Candidates” button, available in the
environment (see Figure 5), the system fetches and presents
all lizards in the base which have the informed tongue color
and tail shape. The steps to execute this process is illus-
trated in Figure 3. This technique to present progressive
candidates is based in Xper2 approach to describe spec-
imens.
The prototype is available at http://fluidweb.sourceforge.net.
The page has many experiments using different kind of soft-
ware components. To access the work proposed in this pa-
paper, click on the link “Lizard Prototype”.

4. RELATED WORK
Our work combines two approaches: virtual laboratories and
tools to describe and identify specimens.
According to [6] the laboratories can be classified in three
categories: real, remote and virtual. Real labs are physical
rooms, having concrete equipments and infrastructure. Re-

treme labs enable access to physical resources of real labs by
networks – as the Internet – through a simulation software,
which replicates the remote environment. Virtual labs have
the goal of offering a simulation environment to support vir-
tual experiments. Our proposal can be considered a mixture
of the three contexts, since it is a virtual lab that grabs data
from the real world and is built over the web.

Laboratories usually offer specialized resources according to
the context they are inserted. [1] proposes an educational
environment for electronics and electrical engineering. [5]
presents an environment for genetics learning. [4] presents
a virtual lab of Chemical Vapor Deposition aimed to com-
plement a physical laboratory in the undergraduate course
curriculum. [7] proposes a virtual laboratory for medical
digital analysis based on grids.

The tool to describe specimens – as Xper2, detailed before,
and Lucid (http://www.lucidcentral.org) – are designed for
specialists and does not follow a laboratory approach. As far
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