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# Towards a global biological information infrastructure

## Challenges, opportunities, synergies, and the role of entomology

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# Preface

## Towards a global biological information infrastructure: Challenges, opportunities, synergies, and the role of entomology

We have now enetered the 21st century. The world is going towards Information Society. For entomologists this time is particularly challenging because of the wealth of data that is potentially available in this field. Being able to share data efficiently would allow entomologists to make a major contribution to the conservation of biodiversity. The combination of new technologies with systematics and collections based research may offer an opportunity to strengthen such activities in the future. There are many good ways of framing the activities such as the Clearing House Mechanism (CHM) and Global Biodiversity Information Facility (GBIF).

This all calls for a new approach. Biodiversity informatics and taxonomy are emerging as information sciences. We believe that if we are able to create a useful information infrastructure for entomology, it should directly address the burning questions of the time, such as the slow rate of discovery of new species, and extinction that follows from lack of knowledge and value on biodiversity. If data, information, and knowledge could be shared more efficiently than has been the case in the past, it would increase the credibility of the taxonomic community in the eyes of funding organisations, and have a positive snowball effect over a wide range of activities.

The papers in this volume are results of a one-day symposium that was held during the XXI International Congress of Entomology in Iguassu Falls, Brasil, on 24 August 2000. The symposium was called upon to make an inventory of the ongoing activities and possibly to lay down some foundations for further cooperation among the various projects. Twelve presentations were made. Seven of them were turned into papers during the Autumn of 2000 and are printed in this volume. Four other papers that covered 1) Entomology at the Costa Rican InBio, 2) Beetles and beetle larvae of the world: An interactive identification and information systems for families and subfamilies, 3) Developing and sharing data globally: The Global Butterfly Information System GLOBIS, 4) The BioSystematic Database of World Diptera: the first global master species database, are available as abstracts in the Congress volumes. There also is a website that links to all the presented systems ([1]).

Looking at the list of projects and the systems presented, it all looks very exiting. Yet the bigger picture might be still missing. Is there interoperability between the systems? If we compare entomological information management with other areas, such as plant information, it is easy to realise that we still have some way to go. How these challenges will be met was covered by Ebbe Nielsen in the opening speech on the GBIF.

En route to the first meeting of the GBIF Governing Board, the co-editor of this volume Ebbe Nielsen passed away on 7 March 2001. The worldwide entomology and biodiversity informatics communities sustained a huge loss. We dedicate this small work to his memory.

April 2001
Hannu Saarenmaa

[1] http://www.eionet.eu.int/Topic_Areas/Nature_Protection_Biodiversity/Biodiversity/GBII

# The Tree of Life project

## A multi-authored, distributed Internet project containing information about phylogeny and biodiversity

David R. Maddison ([2]), Wayne P. Maddison ([3]), Jeremy Frumkin ([4]), and Katja-Sabine Schulz ([2])

## Abstract

The Tree of Life project (ToL) is a collaborative effort among biologists to portray the relationships and characteristics of organisms. Experts on groups of organisms synthesize available information and portray their view of the phylogeny of that group, including discussion of evidence and alternative hypotheses, alongside additional information about the organisms' characteristics. The ToL is currently a series of static HTML web pages, but in the near future it will be converted into a dynamic, database-driven system. Presentations of the information in the ToL database will then be customizable, allowing the project to better serve a diversity of audiences. The ToL database will be able to communicate with other databases, serving phylogenetic and other information about a group of organisms to other databases, and in turn receiving additional information about taxa from other databases.

**Keywords**: evolutionary tree; organismal characteristics; database.

The affinities of all the beings of the same class have sometimes been represented by a great tree… As buds give rise by growth to fresh buds, and these, if vigorous, branch out and overtop on all sides many a feebler branch, so by generation I believe it has been with the great Tree of Life, which fills with its dead and broken branches the crust of the earth, and covers the surface with its ever branching and beautiful ramifications.

*(Darwin, 1859)*

## Introduction

Organisms we see today are but leaves on the tips of Darwin's Tree of Life. The diversity of species arose by the branching of the evolutionary tree, and the diversity in form of these species by evolutionary change along those branches. As the evolutionary tree is the conduit along which the genes (and therefore traits) of organisms flowed, it is not surprising that knowledge of the shape of this phylogeny can be critical for understanding modern biodiversity (e.g., Ridley, 1983; Felsenstein, 1985; Harvey and Pagel, 1991; Maddison and Maddison, 1992; Martins, 1996; Pagel, 1999).

The Tree of Life Project (http://phylogeny.arizona.edu/tree/phylogeny.html) uses phylogeny as the central organizing principle for information about organisms and biodiversity. It is a collaborative effort among biologists providing a collection of information, available over the Internet, about the phylogeny and diversity of life on Earth. It consists of a series of web pages, each illustrating and discussing an individual species or a group of species, linked together in the form of a current view of the evolutionary tree of life. Along with pictures and introductory information of interest to the general public and students of all levels, Tree of Life pages feature specialized sections (on morphology, phylogeny, biogeography, etc.) addressing the needs of researchers in the field. There are currently over 300 biologists in 21 countries authoring pages of the Tree.

The Tree of Life Project (ToL) currently has three primary goals: (1) to provide comprehensive and authoritative information on the phylogenetic relationships among all species of organism, living and extinct (a goal that will never be fully achieved); (2) to provide information about the characteristics of groups of organisms; (3) to provide information on every species of organism.

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Although initial thoughts of creating an electronic system to organize biological information in a phylogenetic framework were formulated in the late 1980s by DRM, it was not until 1994 that action was taken to create the ToL. DRM and WPM designed the project and built the tools to create it in late 1994, and wrote the first skeletal branch pages. In January of 1995, the project was announced. During 1995 and 1996 progress was made by DRM and WPM in making the tools for authors easier to use and in providing better documentation, as well increasing participation by other systematists. DRM has served as coordinator, editor, designer, and program since that time. In 1997 KS began work on the ToL, helping authors create pages and writing much of the technical documentation on the home site; she now serves as managing editor and technical assistant. Although there has been relatively little change in the technical structure or design of the ToL in the last five years, many new pages have been added. Growth of the ToL has been sporadic, with bursts of growth along particular branches, and stasis in others. In 1999 JF joined the project to help turn the ToL into a database.

In this paper, we will first describe the current ToL. A description of the plans for future changes in the ToL will be followed by a discussion of the place of the ToL among active biodiversity database projects, and its interactions with other projects.

## Current form of the ToL

### *Leaf, branch, and accessory pages*

The portion of the ToL that is visible on the Web is a collection of about 1600 static HTML files with associated graphics files.

The 1600 pages fall into two categories. About 300 of these are *leaf pages*, that focus on individual species, describing the characteristics of the species and any other information the authors deem relevant (geographic distribution, ecological relationships, conservation status, etc.) As there are millions of living species of organisms (plus a much smaller number of known, extinct forms), the ToL's representation of species diversity is still very incomplete. The remaining 1300 pages are *branch pages* that describe groups of species (genera, families, orders, etc.). For the time being, the core effort of the project is the creation of branch pages.

Branch pages provide general information about each group, such as diversity and habitat information, defining characteristics, maps showing where the organisms live, literature references, links to other sources of information on the Internet, etc. Their key elements are a phylogenetic tree (or a simple classification if the phylogeny has not yet been elucidated) depicting the current hypothesis about the relationships of subgroups and a discussion of the evidence for the relationships proposed. Based on the hierarchical structure provided by these trees, the pages for different groups of organisms are then linked together to reflect the shape of the evolutionary tree of life. The pages focusing on groups of species represent the internal branches of the ToL, and chains of such branch pages connect the pages for individual species, which represent the tips of the ToL.

As an example, an excerpt of the page for beetles (Coleoptera) is shown in Figure 1. At the top of the page is a navigational tool bar. The tree diagram below the pictures of beetles shows the current hypothesis for the phylogeny of major lineages of beetles. Below this are several text sections: Introduction, Characteristics, The Suborders of Coleoptera, Discussion of Phylogenetic Relationships, and References. (Other sections can be included; for example, the page for Fungi includes sections on the fossil record and biogeography of fungi, and notable fungi.) These sections are followed by information about the authors, including contact information, links to other relevant sites on the Internet, and another navigational tool bar.

The phylogeny near the top of the page serves as the navigational center. It is from this local tree that one can move down to deeper branches in the Tree of Life (by clicking on the local tree's root), or up to descendent clades (by clicking on the terminal taxa in the local tree). For example, if one clicked on the terminal taxon Adephaga in the beetle page, one would be taken to the page for the beetle suborder Adephaga. On that page, the local tree depicts the relationship of adephagan families; clicking on the terminal taxon Carabidae would take one to the page for the beetle family Carabidae. Continuing in this fashion up the branches of the ToL would eventually lead one to leaf pages for individual species of beetles. If one moved down the branches, to more inclusive groups, one would eventually reach the page for all life.

In order to cover all groups of living things, we will need a total of at least 150 000 branch pages; thus, at present less than 1% of all eventual branch pages are represented. The ToL's branches vary in their completeness. While there are complete pages on some fungi, some archaebacteria, frogs, extinct jawless fishes, beetles, jumping spiders, crayfish, and cephalopods, among others, some regions of the ToL are but buds, and some contain only temporary pages. Notably lacking are mammals (except for bats and some rodents), lizards, many birds, most flowering plant groups, and most unicellular organisms.

In addition to branch and species pages, the project contains linked pages that are not part of the primary tree structure. These accessory pages provide additional information that would not reasonably fit on a branch or species page. For example, the Terrestrial Vertebrates page has four accessory pages attached to it, which contain discussion of variation in life history, breathing, hearing in terrestrial vertebrates, as well as a detailed discussion of the controversies about relationships of the major lineages of terrestrial vertebrates. On other branches there can be a type of accessory page called a Treehouse, which is a web site for children about that particular group of organisms.

The ToL itself is distributed, with different branches on different computers. Current pages are distributed on 20 computers in four countries (U.S.A., United Kingdom, Canada, Brasil), with the largest and root portion on the home computer in Arizona.

### *Constructing pages*

The HTML files that constitute the branch and leaf pages of the ToL are currently created with a special version of the phylogenetics program MacClade (Maddison and Maddison, 2000a). Raw data for ToL pages are stored in text files in the NEXUS format (Maddison et al., 1997), a tagged format designed for housing systematic data that is shared among a number of programs. This special version of MacClade contains editors for manipulating the ToL information contained in the NEXUS file (as described at http://phylogeny.arizona.edu/tree/sep/usingmacclade.html). When an author has completed editing the information, MacClade creates the HTML file, which is the actual web page that will be placed on a web server. MacClade's creation of the HTML file ensures that the pages are of uniform format, and that the author does not need to learn details of HTML.

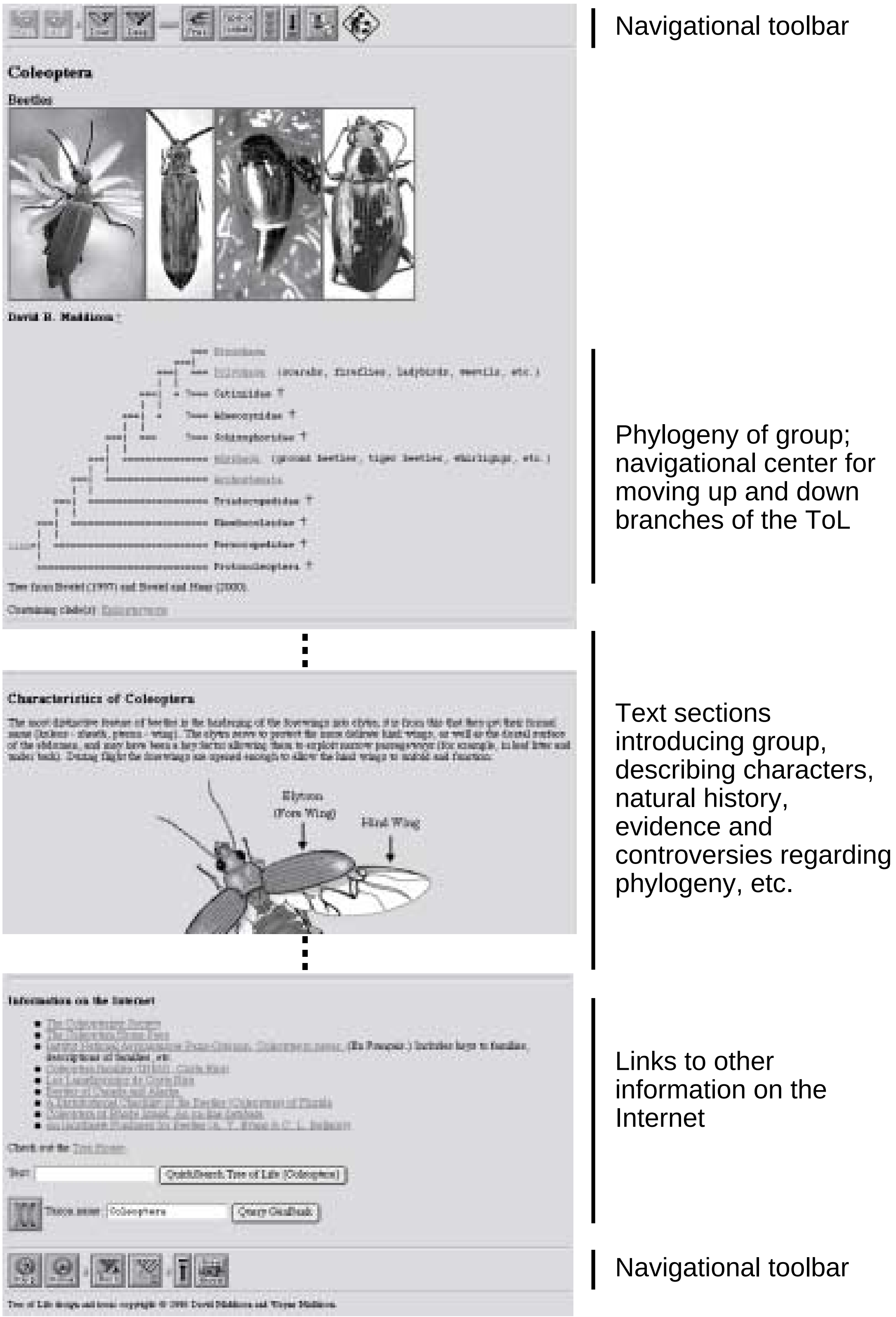
In the HTML pages it creates, MacClade embeds codes containing information about the taxa on a page, images, and so on. This information is gathered by a web crawler that wanders up the branches of the ToL, through the 20 computers containing the various pages, and harvests the information contained in the embedded codes. The database produced by the web crawler is then used to build the searchable index.

MacClade's editing system, while functional, has a number of disadvantages. For example, the editing tools are available only for the MacOS®. While Macintosh® computers are common among evolutionary biologists, the MacOS-only editor does make it more difficult for some biologists to contribute to the project. Authors using the editing tools see the information in a format very different from its eventual appearance on a ToL page, making it more difficult for some authors to easily imagine the consequences of their efforts.

### *Administration and quality control*

David Maddison currently serves as lead coordinator and editor of the project and makes final decisions about design, policy, contributors, and acceptance or rejection of pages. (The administrative structure is likely to change as the project grows.) The project is hierarchically managed, with coordinators of particular groups of organisms serving as associate editors for subgroup pages, coordinators for subgroup pages serving as associate editors for sub-subgroups, and so on.

Figure 1. **Portions of the current branch page for Coleoptera (beetles) in the Tree of Life project**



**Coleoptera**

Beetles

David R. Maddison

```
                    === [illegible]
                 ===|
            ===|    === Polyphaga  (scarabs, fireflies, ladybirds, weevils, etc.)
         ===|  |  + ==== [illegible] †
      ===|  |    ==== [illegible] †
   ===|  ===     ==== [illegible] †
===|  ============= Adephaga  (ground beetles, tiger beetles, whirligigs, etc.)
      ============= Archostemata
   ================ Triadocupedidae †
   ================ [illegible] †
   ================ Permocupedidae †
   ================ Protocoleoptera †
```

Tree from Beutel (1997) and Beutel and Haas (2000).

Containing clade(s): [illegible]

**Characteristics of Coleoptera**

The most distinctive feature of beetles is the hardening of the forewings into elytra; it is from this that they get their formal name (koleos - sheath, pteron - wing). The elytra serve to protect the more delicate hind wings, as well as the dorsal surface of the abdomen, and may have been a key factor allowing them to exploit narrow passageways (for example, in leaf litter and under bark). During flight the forewings are opened enough to allow the hind wings to unfold and function.

**Information on the Internet**

- [illegible]
- [illegible]
- [illegible] (En Français.) Includes keys to families, descriptions of families, etc.
- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]

Check out the [illegible]

Text: [ ] QuickSearch Tree of Life (Coleoptera)

Taxon name: Coleoptera Query GenBank

Tree of Life design and icons copyright © 1995 David Maddison and Wayne Maddison.

Navigational toolbar

Phylogeny of group; navigational center for moving up and down branches of the ToL

Text sections introducing group, describing characters, natural history, evidence and controversies regarding phylogeny, etc.

Links to other information on the Internet

Navigational toolbar

Each Tree of Life page is authored by one or more biologists, who are chosen and invited to contribute by the coordinators of a given group of organisms, in conjunction with the editor. Coordinators are advised to base their selection of authors on a detailed list of criteria including relevant research in recent years, willingness to represent diverse approaches and views of their group's evolution, and ability to coordinate efforts within subgroups. For each individual page, we aim to enlist the cooperation of the world experts of the given group, and if a field is characterized by controversies, communication between different schools of thought is encouraged.

Quality control is important, and it begins with careful choices of editors, coordinators, and authors. However, a more thorough means of oversight is needed, and for this reason, a standard peer-review process has recently been implemented. It is currently optional, with pages successfully undergoing peer-review being so marked. Eventually it will become mandatory for all major pages, at least. One for coming years is to increase the quality of all existing pages, and to replace those current pages that are out of date or incomplete.

### *Coping with controversy*

There will always be disagreement about some of the information presented in the Tree of Life project, including the shape of the phylogeny for some groups. For this reason we require authors to discuss reasonable alternative phylogenetic hypotheses on their pages. In general the ToL attempts to track the community consensus on a subject, but there is always the danger of thereby choosing overly conservative beliefs based on partial evidence. The other approach, of presenting more novel, less popular ideas, may often cater to radical beliefs that will not stand the test of time. Choosing the right point in the wave of each controversy will hopefully be accomplished with the appropriate combination of associate editors, authors, and peer-review.

To some pages, a moderated forum for discussion will be added, where multiple participants can discuss their views about the phylogenetic relationships of the group. This will allow for a better representation of diverse views than might be accomplished by confining the description of the state of the field to a single contribution.

A forum will not allow competing hypotheses about relationships to be built into the structure of the tree itself, however, and for this reason we will also explore the possibility of allowing multiple trees for a particular group. In some cases, competing trees may not be feasibly contained within the tree's backbone, if they are very different (for example, if they contain different terminal taxa).

## Future form of the ToL

### *Growth in content*

The ToL will grow in several different directions over the next few years. The content of the ToL will be expanded by the addition or completion of numerous pages. First versions of most primary branch pages will be completed, including the major groups of organisms, and the entire paths up to focal groups such as *Homo*, *Mus*, *Escherichia*, *Saccharomyces*, *Caenorhabditis*, *Drosophila*, and *Arabidopsis*. The ToL's use in education and conservation biology will be expanded. Several model Treehouses will be built, in order to explore their use and nature. The format of ToL pages will be redesigned, and new features will be added, such as live analyses of data.

### *The ToL as a database*

In the near future, the Tree of Life will be transformed from a series of NEXUS files and HTML pages into a database, and associated applications for display of the data and their entry will be created. This will have many advantages over its current form.

With a databased ToL, pages can be tailored for different audiences, and flexibility can be given to users in how the data are displayed. We will be able to create several display formats, such that educational users could see the ToL displayed with features specific to their needs, or researchers could choose to have their Tree of Life pages displayed with sections specific to their research field. Others will be able to create new display formats as well. We will develop the applications that are used to access the database using the open source model, thereby not only making it possible for others to create modules or accessing the data in the ToL, but encouraging it as well.

Many new features will eventually be possible with the ToL reconstructed as a database. The administration of the ToL will be much more efficient, as we will be able to track the status of pages more effectively; for example, applications associated with the database could easily generate lists of pages completed some time ago, and thus potentially requiring revision. Cataloguing and archiving previous versions of peer-reviewed pages will be easier. A ‘you are here’ view can be created, which shows a bird's eye view of a larger portion of the phylogenetic tree than is evident on a standard page, thus allowing users to get a better sense of their location in the entire Tree of Life. The veracity of any links on a page can automatically be checked, automatic glossary systems can be incorporated, and so on. As a major goal of our data model is to ensure flexibility for future expansion, many other novel elements might eventually be added to the ToL.

### *Movement of the current data into the new database*

As the current data resides in tagged NEXUS files, it will be fairly simple to convert and import the information from those files into the ToL database. MacClade can easily be modified to take each NEXUS file and export the data in a format designed to be easily imported into the database.

### *Data entry tools*

The first step in adding a new branch to the ToL will be creation of the tree-node structure in the database (Figure 2, upper right). For this a cross-platform, client-side application will be built with a graphical interface for editing the tree. In this manner, the user will not need to know about the internal database structure to build a portion of the ToL's structure; the client-side application translates their manipulations of a graphically displayed tree into values that can be placed into the ToL database.

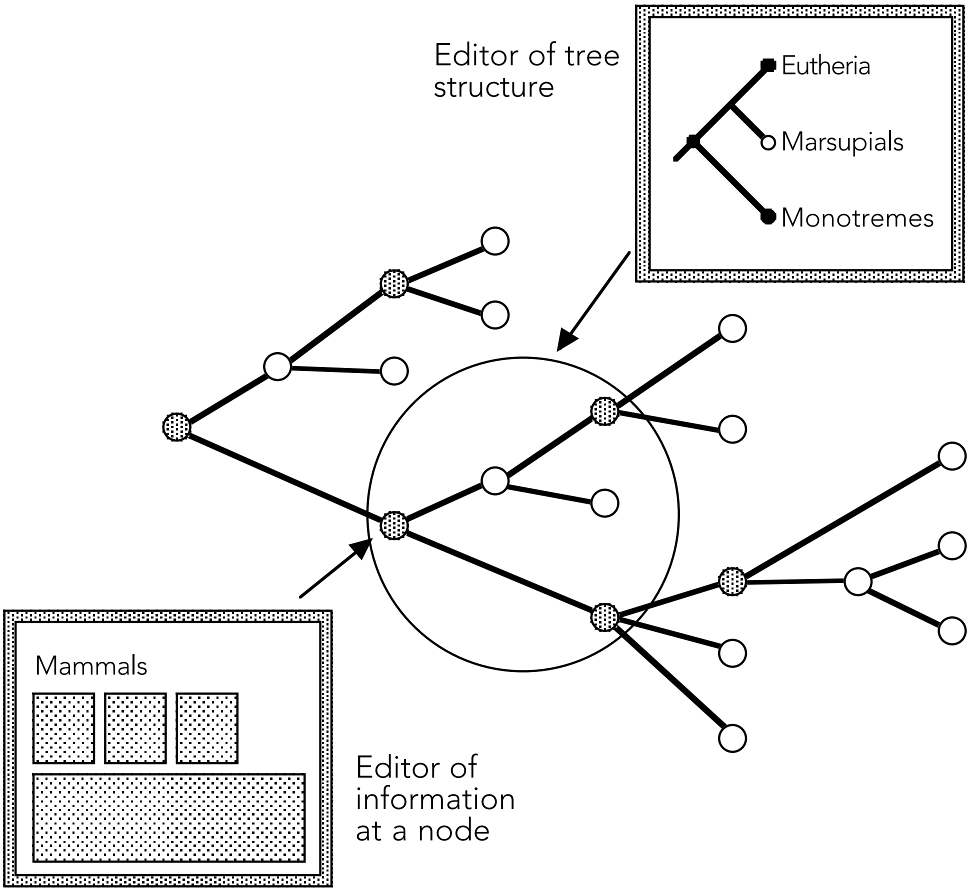
Once the tree structure has been established using this client-side application, contributors can then designate that a particular node has a page attached, and can begin editing that page in the page editor (Figure 2, lower left). The cross-platform page editor will present to the author a view of their page-in-progress that matches, as closely as possible, the view of the completed page as it might be displayed in a browser.

### *Data presentation system*

If ToL content resides in a database, presentation becomes dynamic and configurable; in the current ToL, presentation is the result of a static design. The ToL database will provide additional possibilities when it comes to presentation and dissemination of the ToL’s phylogenetic data. In order to take advantage of many new possibilities, a presentation system will be developed that will allow not only recreation of the current ToL's general appearance, but development of alternative presentation styles that will add function and variety to the ToL.

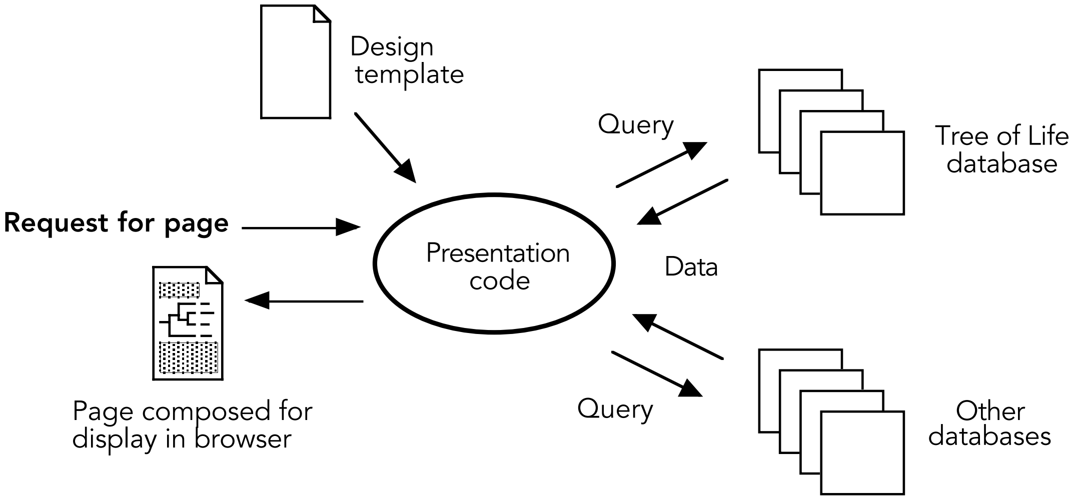
To streamline creation of specialized presentations of the ToL, a system using design templates will be created (Figure 3). In particular, the presentation code will be able to read a design template, which will be a text file, likely written in XML. The template will specify the layout of the page, including which elements of the ToL's database are to be displayed in which location. The presentation code will then query the database for the requested elements, and will compose the page based upon the design template's specifications. Notably, the template itself needn't specify use of data only in the Tree of Life database; it could specify information present in other databases with which the ToL can communicate.

**Data entry tools for the Tree of Life project** Figure 2.



**Note**: A cross-platform, graphical editor of the tree structure (upper right) will allow an author to create the phylogenetic structure underlying the ToL and to designate those nodes containing additional information such as pages. These pages can then be edited using an editing application (lower left).

**The presentation system for the Tree of Life project** Figure 3.



**Note:** When a request for a page is received by the presentation code (center), this code queries an XML text file containing the design template for the page to be created. This tells the presentation code which data to request from the ToL database and other databases (right); the presentation code then composes this information into a page as specified by the design template, and returns the page to the browser for display (left)

Another foreseeable advantage of the presentation system is that it can eventually be developed to allow for user-specific ToL designs. That is, a particular user could tailor the presentation of the ToL to their own personal preferences, without affecting standard ToL presentation(s). For example, an instructor teaching a high school biology course could modify a template to reflect the needs of the class being taught.

### *Communication with other databases*

The ToL's database will be built to allow communication with other databases through various means (such as SQL commands, XML files, and an API). This will allow the ToL to serve its data (phylogenetic structure, images, introductory text, references, etc.) to other databases. In addition the presentation code to be developed will be designed to communicate with other databases, allowing elements of other databases to be incorporated in ToL pages (with appropriate credit given).

Many elements might be added to ToL pages through communication with other databases. Species distribution maps might be retrieved from another database and included in a ToL page. Lists of GenBank sequences might be displayed on a page. Specification of which elements would be included would be built into the design template used by the presentation system.

The ability of others to pick specific, identified pieces of content out of the ToL provides many possibilities for the use of the ToL's content. While we can imagine other databases accessing the image database, or the list of references for a group of organisms, or a text description of the characteristics of the group, at its core the ToL's role may be to serve the shape of the phylogenetic tree to other databases. Included with the phylogenetic tree may be information about peer-review, authorship, and so on, which would allow the user to judge the tree within the context of the display presented by the remote database.

While many systems will be able to access the ToL's content directly by SQL queries into the database, there may be systems that cannot, or circumstances in which accessing the ToL's data through a live connection is inefficient. To accommodate communication and interoperability with those systems, we will build an XML-based export / import module. This module will export portions of the ToL's content to an XML file, which can then be downloaded via a browser or ftp. Likewise, we will then be able to import XML data files from other projects into the ToL. Addtionally, with the creation of an API into the ToL, other systems will be able to access and use Tree components in an object-oriented manner.

It is likely that communication between the ToL and other databases will need to be routed through a name server that will allow resolution of taxonomic synonyms and homonyms.

### *Data analysis*

The ToL database will not only be able to communicate with other databases and the ToL's presentation system, but its information will be accessible to special-purpose applications, including those that conduct data analysis. For example, one might imagine an application requesting the phylogeny of a large group from the ToL, and then using this tree for a phylogenetic analysis of the evolution of a particular character. Data on the distribution of the character's states might reside locally on the same computer as the application conducting the analysis, or they might be in some other database on the Internet. We plan to modify Mesquite (Maddison and Maddison, 2000b), a cross-platform system for phylogenetic analysis, to be able to access the phylogenetic information contained in the ToL, and others could build analytical applications as well.

### *Open source and intellectual property rights*

There are three primary portions of code created in this project: the database structure, the presentation code, and the data entry tools. These will be treated as open-source (Perens et al., 2000; Raymond, 2000) projects. By providing these as open source, we allow others who are interested to enhance and improve the code.

The data themselves will all include the name of the owner of the intellectual property rights, and any database or other presentation engine accessing the data would be required (by the license granting authorized access to the data and the open-source license) to present relevant copyright information, and respect any restrictions. We currently maintain information about copyright owners for all images and text in the project; this information will be transferred into the ToL's new database.

## Relationship to other projects

The ToL, at its core, contains information about groups of organisms, and their phylogeny, synthesized and resolved from available data by experts. There are other projects that contain phylogenetic trees contained in the literature (most notably TreeBase, http://herbaria.harvard.edu/treebase/), but the ToL uniquely presents a synthetic review authored by researchers on each taxon.

The purpose of the ToL is not merely to depict the phylogenetic tree, but also to describe the characteristics of groups of organisms, such as their structural features, life history, geographic distribution, and so on. In addition to the summary information provided on the ToL branch pages themselves, we anticipate that the links to information on other web sites will enable the ToL to serve as a phylogenetic organizer for information beyond its own boundaries.

As information contained on branch pages about groups of organisms is the central feature of the Tree of Life project, the status of the project as repository of information about individual species is less clear. There are other projects that contain or will contain information about individual species, such as Species2000 (http://www.sp2000.org/) and INBio (http://www.inbio.ac.cr/), or that coordinate such efforts (GBIF, http://www.gbif.org/). It may be that the ToL plays a prominent role in the storage of species pages, or it may be that increasingly that role will be played by other projects. If the future favors the latter course, the ToL may contain fewer species pages, with many of the species pages served to the ToL by other databases. Wherever species information will be stored, theTree of Life project will continue to serve information about the phylogeny and characteristics of organisms.

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# Issues of quality control in large, mixed-origin entomological databases

Jorge Soberón ([5]), Laura Arriaga ([5]), Liliana Lara ([5])

## Abstract

This paper analyzes the problems of working with large, mixed-origin taxonomic databases. The analyses were based in an example of a database that included more than 50 000 specimens of Papilionidae and Pieridae butterflies of Mexico, obtained from *ca.* twenty different museums. The major problems and errors present in this database were classified as errors of structure, consistency, and content. Errors of structure referred to faulty normalization or lack of referential integrity. Lack of consistency referred to contradictions among data fields, while errors of content included mistakes found from mere typos to factual errors like misidentified specimens, faulty taxonomy or imprecise and equivocal georeferencing. Several ways of identifying and correcting errors are presented and discussed.

**Keywords**: Butterflies, Papilionidae, Pieridae, databases, bioinformatics, quality control.

## Introduction

The data contained in the labels of the museums and herbaria of the world is one of the largest repositories of biological information available today. It is estimated that collections worldwide contain in the order of a few billion specimens (Hawksworth *et al.*, 1995). Unfortunately, access to this wealth of information has been severely hindered by the distributed nature of the collections and by lack of efficient methods for information retrieval. However, in recent times an increasing amount of labels in museum's specimens is being computerized (ICBP, 1992; Scott, Tear and Davies, 1996; Miller, 1994; Soberón, Llorente and Benítez, 1996; Umminger and Young, 1997; Bisby, 2000; Edwards et al., 2000) and often made accessible through the Internet (REMIB, http://www.conabio.gob.mx/remib/remib.html, and Species Analyst, http://habanero.nhm.ukans.edu/TSA/, represent the two best examples of distributed data of museums labels). This opens the door to the creation of databases in the orders of $10^4$ to $10^6$ records that can be used (and are being used) for applications that include basic science, like the study of evolutionary questions (Peterson *et al.*, 1999; Zhong, 1999); management issues, like biodiversity exploration (Jones *et al.*, 1997; Lobo *et al.*, 1997) and the assessment of the potential damage of pests (Sanchez Cordero and Martinez Meyer, 2000) or routes for invasive species (Higgins et al., 1999), to name just a few examples.

Most recently created databases tend to be implemented as a relational model expressed as in entity-relationship diagrams. Many taxonomic databases are composed by from one to 15 or 20 tables (entities), often with several thousand georeferenced localities and from tens of thousands to hundred of thousand of specimens (Pankhurst, 1991). The requirements of the relational model (maintenance of referential integrity and normalization, among other things) are not always followed: by pooling together data that come from a variety of sources, mixed-origin taxonomic databases are created that often degrade the original relational model, if it was present.

Such mixed databases present several challenges in terms of their quality. For example: the degree of taxonomic expertise used in their curation may be variable or the taxonomy may be

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unstable (McNeill, 1993; Solow et al., 1995) and georeferencing may be imprecise or equivocal (Chapman and Busby, 1994). Data quality control becomes indispensable as an integral part of the compilation and use of such databases (Chapman and Busby, 1994; Soberón and Koleff, 1997).

To establish links and share information among biological databases standards might be required (Williams 1997). Several tools have already been developed to analyze database and to identify errors and inconsistencies in data, using statistical analysis and knowledge-based systems technology (Ricciuti, 1993), but no integrated software has been developed yet to address data quality of taxonomical/biogeographical information. In the present, this task still requires the direct participation of experts, supervising any work that it is done by the computer.

In the past eight years, CONABIO, the Mexican national commission on biodiversity has assembled data (obtained from museums in Mexico and abroad) in about 300 databases, to obtain more than 5 millions of specimen labels in electronic formats (Soberon and Koleff, 1997). This has lead to an acute realization of the importance of quality control for taxonomic databases. In our experience, problems and errors in mixed-origin taxonomic databases can be reduced to a few major categories, like logical structure and scheme encoding, consistency, and content errors. Errors of structure in the relational model, like faulty normalization or lack of referential integrity are discussed in basic books on the relational model for databases (Hogan 1990, Bobak 1997, Date 1997, Celko 1999). Essentially, they refer to poor logical design that often is conducive to commitment of other errors. Bad scheme encoding (Celko 1999) is discussed less often than referential integrity and normalization, but years of experience tells us that encoding schemes that do not allow the growth of the model, include ambiguous fields or lack codes for ‘missing’, ‘unknown’ and ‘not applicable’ states tend to be hard to translate, difficult to interpret and in time become useless.

Consistency means lack of ‘contradictions’ among data fields. Examples of inconsistent data might be specimens of the same genus assigned to two different families, or the geographical coordinates of a locality appearing in a province different from the one in the label. Of course data may be thoroughly consistent and at the same time contain factual errors.

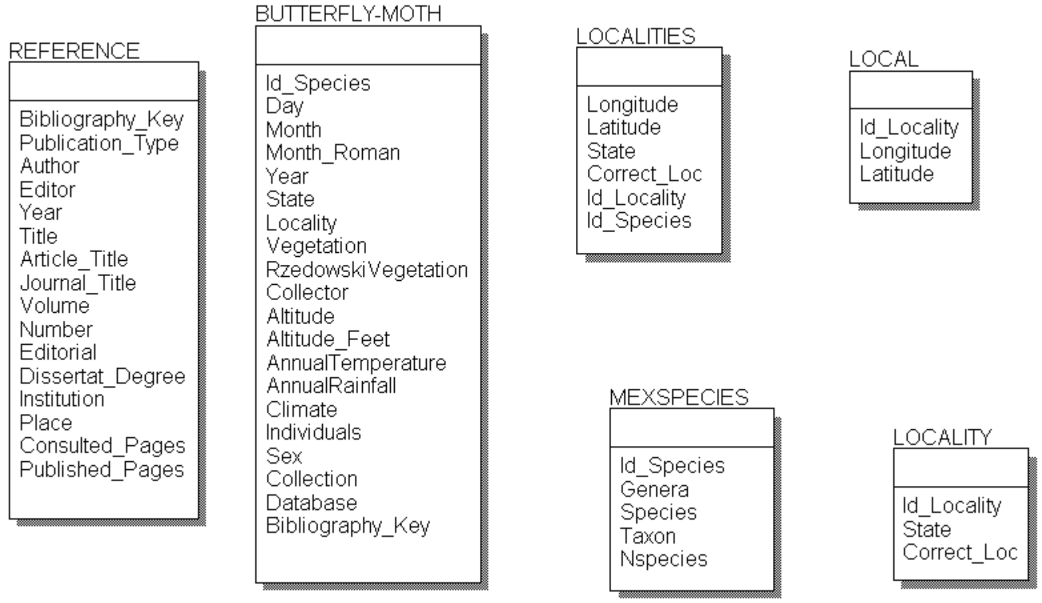
Errors of content mean the existence of mistakes, from mere typos to factual errors like misidentified specimens, faulty taxonomy or sloppy georeferencing. These are the most difficult to detect, and in fact, many of them cannot be identified without an expert actually checking the original data (the specimen or the field books). However, as we shall see, consistency analysis very often leads to spotting factual errors.

In this work we will use an example of a database of about 55 000 records of Papilionidae and Pieridae butterflies of Mexico, obtained from nearly twenty different museums, to explore some of the major problems of such databases and ways of identifying and correcting them. The thesis of the work is that although probably all large, mixed-origin databases are fraught with problems, techniques already exist to deal with some of those problems and to extract useful knowledge from the databases.

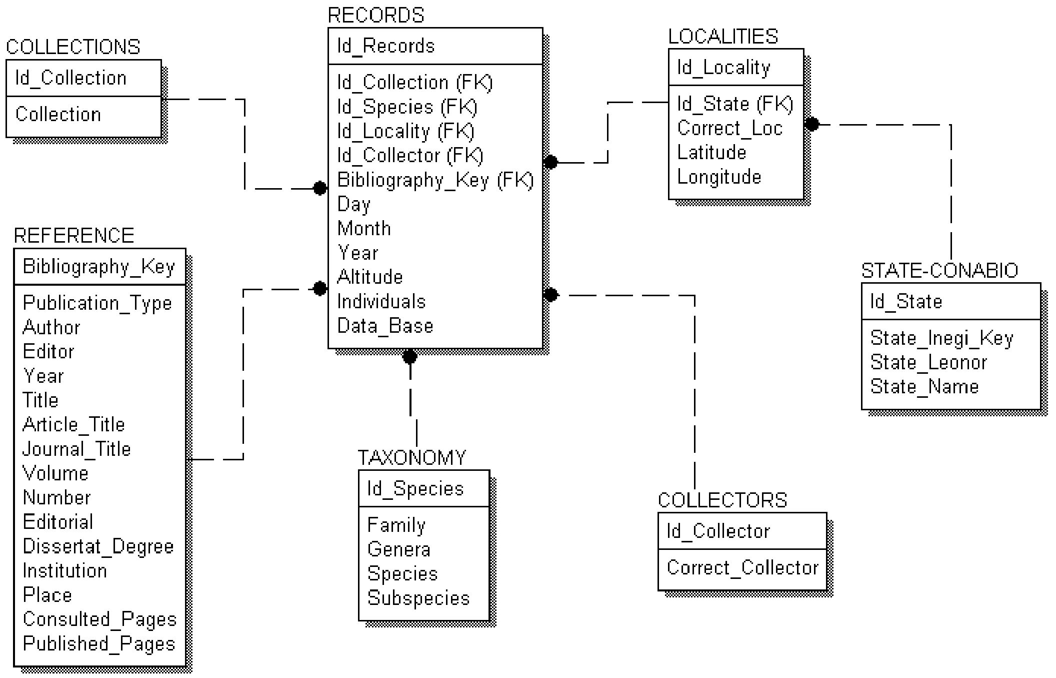
## Description of the database

Between the years of 1978 and 1995 (Llorente *et al.*, 1997) a compilation was made of the data in about 55 000 specimens in major American and Mexican butterfly collections. This work served to create a database of the Mexican Pierids and Papilionids (sulphur and swallowtail butterflies). The institutions consulted appear in Llorente *et al.* (1997). This database contains the largest amount of specimen data available in the world for these two families in Mexico, with the exception of the collection at the Instituto de Biología, UNAM, which at that time was not yet computerized. A significant part of the data in the private de la Maza family collection was included using the extensive literature published by the de la Mazas (see Llorente and Luis, 1993 and Llorente *et al.*, 1997 for reviews).

**Data model of the original database, including 6 unlinked tables and 43 data fields** Figure 1.

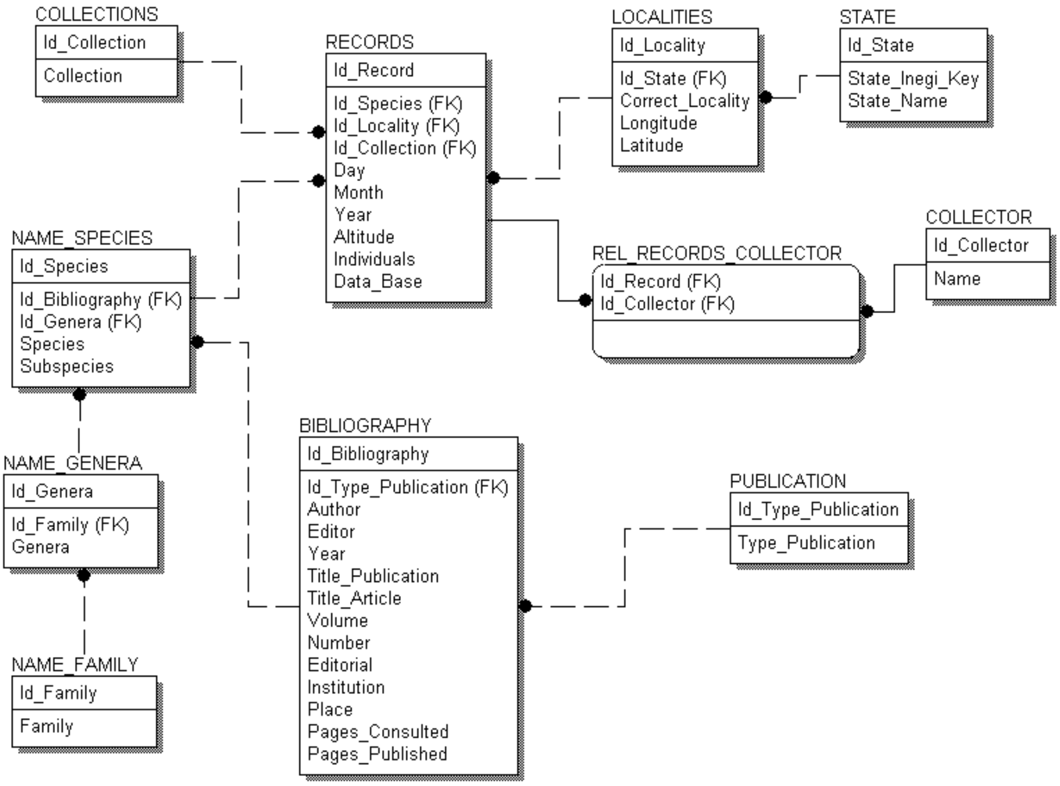


**Data model of the database used by Llorente et al. (1997), including 7 linked tables and 33 data fields** Figure 2.



The taxonomy follows Tyler et al. (1994) and Llorente *et al.* (1997). Different subspecies were regarded as different entities for a total of 176 different subspecies, 70 of the Papilionidae and 106 of the Pieridae. The 55 000 specimens were aggregated into 36,685 *registers*, that is, groups of specimens with the same name, date, collector and associated georeferenced locality.

Figure 3. **Data model of the revised database (RD), including 29 data fields and 20 identification (ID) fields to build the keys and foreign keys in 11 tables**



The original database consisted of a main flat file (39 301 records by 20 data fields), with some auxiliary tables with the names and the coordinates of 2 330 localities and bibliographic and information about collectors and collections. Some of the localities were easily identified and represent well-defined sites (field stations, for example) but others are more subject to interpretation. All localities were georeferenced to the next minute using extensive geographic gazetteers and 1:250 000 charts of Mexico. The process of georeferencing the localities was time consuming and difficult. A report on a previous version of the database, together with a detailed printout of all the geographical information as well as illustrations of each species appear in Llorente *et al.* (1997).

The original database was created over a period of several years of visiting museums to capture the data in the labels, and often by obtaining printed or electronic catalogues of the collections. Despite this effort the database was not properly modeled and was full of problems due to lack of referential integrity and normalization. The main problems are described below.

### *Logical structure problems*

The original database was not modeled as a relational database. Altogether six unlinked tables or entities with a total of 43 data fields or attributes composed it. Not being relational, the model was not normalized (i.e., there were many types of redundancies in the data, leading to higher chances of introducing errors). These redundancies appeared in the following attributes: number of georeferred records, records associated to localities, collected specimens, records of species and subspecies, collections and collectors. The model also lacked referential integrity. For example, the identity keys for some bibliographic references were empty (Figure 1).

A first attempt to convert the database to a relational model yielded six linked tables, 33 data fields and 36,685 records (Figure 2). This process unveiled the fact that some tables were full of redundancies and that literally hundreds of thousands of fields were empty, since in the original database the bibliographical fields were almost empty. This was due in good part to an overenthusiastic design of the first database that left too many fields unpopulated. In this model (Llorente *et al.* 1997) referential integrity was established.

A third model was obtained to correct the lack of normalization (Figure 2) so that the data inconsistency was reduced (Figure 3). This revised database yielded eleven linked tables, 29 data fields and 20 identification (ID) fields to build the keys and foreign keys, all this with 36 685 records. The comparisons between some of the attributes showing numerical differences among these three models are presented in Figure 4.

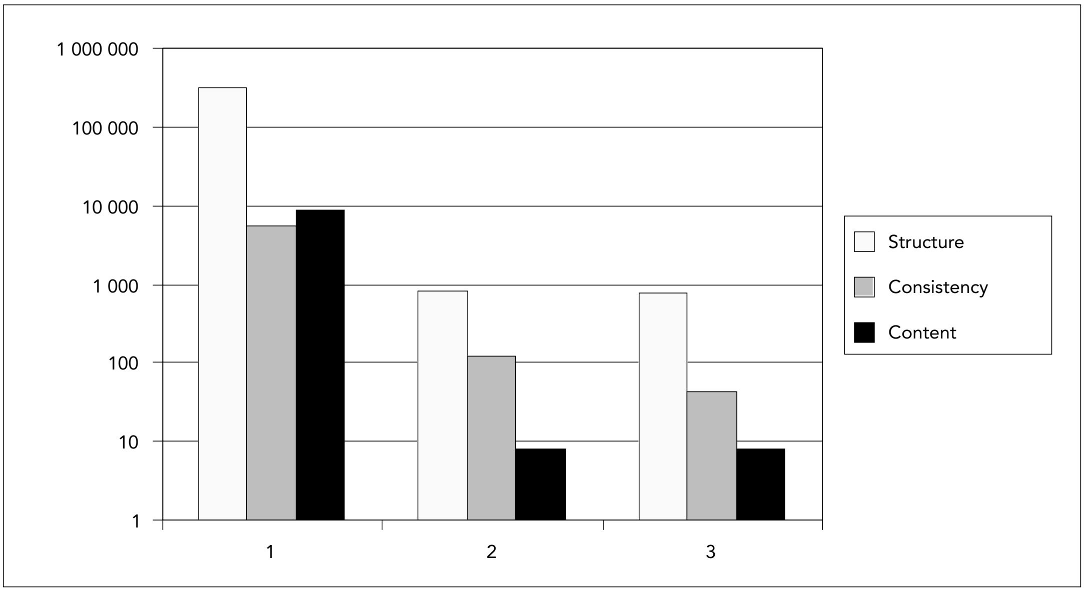
The greatest structural problems that were presented in the first two models (Figure 1 and 2) were completely solved in the RD model (Figure 3 and 4). Among other things, this means that logically equivalent queries produced the same results. This is not necessarily the case in databases lacking integrity or not correctly normalized.

### *Inconsistencies*

The first database contained numerous inconsistencies among fields, which were drastically reduced in Llorente *et al.* (1997) database. The comparison between the types of errors associated to both databases is shown also in Figure 4. The greatest problems in the original database were the amount of empty fields and typing errors in the Reference and Butterfly-Moth tables; geographical inconsistencies were also identified in the Localities table (Figure 1).

The standard procedure for detecting geographical inconsistencies is to check the coordinates of the locality of each specimen in relation to other fields in the labels, like municipality, state or vegetation type. Thus, a label with a locality in state X, must have coordinates lying within (up to a certain error) the polygon representing state X. Notice that whether a ‘point’ lies within the borders of a given polygon, depends on the precision at which the point and the polygon were created. In other words, a country border or state polygons obtained from 1:4 000 000 maps may be spatially quite different to the polygons for the same entities but obtained at a scale of 1:250 000, to give an example. Checking for these problems unveiled 115 inconsistent localities. Most of these inconsistencies were due to ‘typing errors’ during the georeferencing (Figure 4) and therefore inconsistency checking lead to the detection of many errors of content.

**Comparison of structure, consistency and content errors** Figure 4.



Notice the logarithmic scale. Number 1 corresponds to the original database, number 2 corresponds to Llorente´s *et al.* (1997) database, and number 3 corresponds to the revised database (RD). Structure errors include empty fields, most of which are due to ‘underpopulation’ of the original database. The remaining errors in the RD database are empty fields. that will be corrected by populating some fields in the database and consistency and content problems that cannot be corrected without expert participation.

The original database also presented a high number of records that were ambiguous due to lack of standardization in the names of the states of Mexico (Figure 4). For example, both the states of Chiapas and Chihuahua might be abbreviated to CHI. by different authors. These ambiguities might lead to inconsistencies, if, for example, a set of coordinates for Chiapas, are labeled as inconsistent because they appear outside Chihuahua. These problems were avoided with the normalization.

### *Problems with content*

For this particular database, taxonomical problems were few, since the providers of the database (Llorente *et al.*, 1997) gave special consideration to this issue. The only taxonomy problems we spotted were three species for which subspecies were not determined (*Catasticta ochracea* ssp., *C. teutila* ssp1, *C. teutila* ssp2) and a genus that had no specimens determined to species level (*Catasticta* sp1).

A necessary requisite to detect certain kinds of errors is to have the taxonomy fields checked against authority dictionaries, which in its simplest form consist of validated orthography for all the names, and may in the other extreme consist of full checklists, with the synonyms labeled as such. Of course, these dictionaries are difficult to obtain and very difficult to maintain updated. An example of a web-based dictionary of names is the ITIS catalogue of the United States, Canada and Mexico Government http://www.itis.usda.gov/itis).

All the taxonomical names in this database were correctly spelled and used and no taxonomic inconsistencies were found.

A difficult content problem is faulty but consistent georeferencing. For certain taxonomic groups (butterflies, cacti, orchids), it is not uncommon to have specimens collected by amateurs and by commercial providers. In certain cases this may lead to specimens being labeled carelessly and in some extreme cases, with false information.

In our example, we spotted 5 examples of such 'impossible' localities by visual inspection of the maps displaying the localities of each species. All were cases of species very strictly associated to certain types of vegetation or biogeographic regions, but labeled to localities completely outside their normal ranges. For example, *Parides sesostris sestos*, which is a strictly tropical rainforest species, had reports by a commercial collector for localities in the pine highlands of the Oaxacan plateau. People experienced in the taxa in question can spot this kind of very unlikely georeferencing. However, there might be many non-obvious georeferencing mistakes that can be very difficult to detect. A tool that may help is bioclimatic modeling. A bioclimatic surface can be generated for each species and outliers may be studied specifically (Chapman and Busby, 1994).

Thousands of other errors were spotted (Figure 4). Most of them are obvious typos that can be corrected by non-experts, like a space character at the beginning of a field, or lack of spacing between words, but others require the participation of the expert for their correction, for example, variations in the name of a collector (R. de la Maza; Roberto de la Maza; de la Maza, R.; R. de la Maza E. and so on). These problems can be spotted but are not corrected, since this is a task for the experts responsible for the database.

## Conclusion

The creation of large, mixed-origin databases is becoming very common mainly because: 1) the growing interest of many countries to computerize and repatriate data about specimens collected in their territories (Soberón, Llorente and Benítez, 1996) and, 2) increasing Internet accessibility to museum holdings (Soberón, 1999; Bisby, 2000; Edwards et al., 2000).

Without proper quality control of those mixed-origin databases, their use is fraught with potential mistakes. However, the experience of the Australian Environmental Resources Information Network (ERIN, Chapman and Busby, 1994; Austin, 1998) as well as the Mexican Comisión Nacional de Biodiversidad (CONABIO, Soberón and Koleff, 1997) clearly show that a very large percentage of such errors can be detected and corrected, and the resulting databases can be used to tackle both basic scientific questions as well as applied ones. In this contribution we discussed some of the most basic categories of problems. These can be disaggregated in a very detailed way, which depends to an extent on the specifics of the data model one is using. The CONABIO data model currently requires 83 different checks in its quality control process.

One of the responsibilities of future data providers, especially if they are going to distribute information using the Web, would be to be very specific about the type of quality control steps the database has undertaken. Without such metadata information, it may be very difficult to assess the quality of a database. Another possibility is the development and widespread use of taxonomic data managers with built-in quality control routines. Such software is becoming increasingly available. Examples are CONABIO´s Biotica® (http://www.conabio.gob.mx/biotica_ingles/acerca_biotica.html) and CSIRO´s Biolink (http://www.ento.csiro.au/biolink/).

The existence of such large amounts of good-quality, on-line data will encourage a multiplicity of users. Many will be taxonomists, biogeographers and ecologists, but probably many more will be NGOs and the general public. This trend should be welcomed, but it also will impose an extra responsibility on the data providers and distributors. Developing tools and procedures to spot and correct problems in the type of data we have discussed here will have to become a priority for the near future.

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# Interactive identification using the Internet

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## Abstract

Computer-based interactive keys have several advantages over conventional keys: characters can be used, and their values changed, in any order; a correct identification can be made in spite of errors by the user or in the data; errors which were circumvented by the error-tolerance mechanism can be located; the user can express uncertainty by entering more than one state value, or a range of numerical values; numeric characters can be used directly, without being divided into ranges. Other features important for efficient and reliable identification include: advice on the most suitable characters to use at any stage of an identification; notes on the interpretation of characters; illustrations of characters and taxa; finding the differences and similarities between taxa; finding diagnostic descriptions. Interactive identification can be made available over the Internet in the following ways:

1. A stand-alone program.
2. A program (Java or JavaScript) running in a Web browser.
3. Cooperating programs running in a Web browser and server.
4. A program running on a Web server, and generating HTML pages.

Programs of type 1 must first be installed, and most are available for only one operating system (usually MS-Windows). Programs of types 1 and 2 download the data matrix at the start of a session. The user cannot proceed until the downloading is completed, but afterwards response is fast, and there is no further load on the network and server, except when subsidiary files, such as images, are required. The programs can also be used off line. In programs of types 3 and 4, the data matrix is not downloaded. Each operation requires an Internet transaction, so responses tend to be slow, and a continuing load is placed on the network and server. The programs cannot be used off line. In programs of type 4, the user interface is familiar to Web users, but may become cumbersome for some operations, particularly with large data sets. Programs of types 2–4 are potentially independent of the user's operating system and browser, but in practice there may be problems. Currently available programs of types 2–4 lack many of the features required for efficient and reliable identification.

**Keywords**: DELTA, Intkey, keys, interactive, identification, Internet.

## Introduction

Identification is the process of finding the taxon to which a specimen belongs. Several methods are available for aiding this process (e.g. Pankhurst 1991). The most important are conventional identification keys and interactive keys.

A conventional identification key is a tree with characters at the internal nodes and taxon names at the terminal nodes. Each branch corresponds to a state of the character or characters at the node from which it arises. The user starts at the root of the tree, and follows the branches corresponding to the character states exhibited by the specimen until the taxon name is reached.

Authors of conventional keys try to provide some flexibility for the user by placing alternative characters at each node, but the possibilities for doing this are limited, because the characters must have identical distributions of their states among the taxa remaining in contention at that node. An error by the user in assigning a character state to the specimen inevitably leads

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to a wrong identification, unless the author has allowed for the possibility of this error by placing the taxon name in the subtree corresponding to the wrongly assigned state, as well as in the subtrees corresponding to states actually exhibited by the taxon. The author's use of this mechanism must also be limited, because each possible error (taxon/character-state combination) treated in this way adds a terminal node to the tree. This increases the size of the printed key (proportional to the number of terminal nodes), and the average number of characters which must be used to obtain an identification (proportional to the logarithm of the number of terminal nodes).

After any identification, it is good practice to check its accuracy by comparing the specimen with a description or illustrations of the taxon, or with other specimens known to belong to the taxon. When a conventional key is being used, the only way to recover from a wrong identification due to an error by the user is to guess where the error was made, return to that node, and try following another branch. If the error is in the key itself (that is, an error was made by the author), recovery is not possible.

An interactive key is an interactive computer program in which the user enters attributes (character-state values) of the specimen. The program eliminates taxa whose attributes do not match those of the specimen. This process is continued until only one taxon remains. The taxon attributes are usually stored as a characters-by-taxa 'matrix'. It is also possible to store the attributes as 'rules', but this kind of program is generally less satisfactory (Dallwitz 1992).

Dallwitz et al. (2000) give a comprehensive discussion of the principles of interactive keys. Dallwitz (1996) gives a list of available interactive-key programs, and contact information for them, and Dallwitz (2000) gives a detailed comparison of several of these programs.

We will use the program Intkey (Dallwitz et al. 1993, 1995) to exemplify some of the features of interactive keys.

## Advantages over conventional keys

A well designed interactive key has several advantages over a conventional key.

*Unrestricted character use.* Any characters can be used, in any order. Characters which are not available on the specimen, or whose interpretation is not clear to the user, can be avoided (provided that there is sufficient redundancy in the data).

*Character deletion and changing.* The values of any character can be changed at any stage of the identification, or any character deleted from the identification.

*Error tolerance.* A correct identification can be made in spite of errors by the user or in the data. Taxa are normally eliminated when they differ from the specimen in any way. If it is known or suspected that an error has been made, the program can be instructed to eliminate taxa only if they differ from the specimen in more than one attribute. It is immaterial where the error occurred, and whether it was made by the user or by the author of the data.

In Intkey, this function is controlled by the 'Tolerance' parameter, whose value may be 0 or any positive integer. Taxa are eliminated if they differ from the specimen in more attributes than the current value of 'Tolerance'. The parameter may be set to any permitted value at any time in the identification process, but typically it would be incremented by 1 when an identification has been made and found to be incorrect. The identification process is then continued, exactly as before. If *all* the taxa are eliminated, the program can increment 'Tolerance' automatically. If a single taxon remains, the program has no way of knowing whether this is the correct identification, and it is up to the user to check the identification, and, if necessary, increment 'Tolerance' manually.

*Locating errors.* The program should be able to locate user and/or data errors which were circumvented by the error-tolerance mechanism. The identification of user errors helps to improve the user's interpretation of characters. Data errors can be reported to the author for correction in later versions.

In Intkey, errors can be located by using the 'Differences' command to display the differences between the specimen and the remaining taxon.

*Expressing uncertainty.* The user can express uncertainty by entering more than one state value, or a range of numerical values. A user who is not sure which character-state value applies to the specimen may nevertheless sometimes be confident that some state values *do not* apply. Entering all the values which may conceivably apply to the specimen eliminates those taxa which never exhibit any of those values.

*Numeric characters.* Numeric characters can be used directly, without being divided into ranges. In conventional keys, numeric characters such as lengths must be divided into ranges before being incorporated in the key, that is, they are expressed as multistate characters. This usually results in loss of information. In an interactive key, the actual range of values exhibited by each taxon can be recorded in the data, and the taxon eliminated if the specimen's value does not fall within this range.

*Easy updating.* The key is maintained simply by making corrections and additions to the data matrix. Updating of conventional keys is relatively difficult. Even when the key is generated by computer from a data matrix, major changes to the matrix, particularly the addition of new characters and taxa, can have a large effect on the key structure, which has to be checked and possibly re-optimized.

## Important features for interactive keys

Interactive keys require other features for efficient and reliable identification. A few of the most important are described here; see Dallwitz *et al.* (2000) for a comprehensive list.

*Advice on the most suitable characters to use at any stage of an identification.* The program should be able to advise the user on the most suitable characters for use at any stage of an identification. Because of the very large number of paths which may be taken through an interactive key, the ranking of the characters should be calculated directly from the data matrix for the set of taxa actually remaining at each stage of the identification. It is unsatisfactory to pre-assign rankings for a relatively small number of cases, as, for example, in a rule-based expert system.

The character-ranking algorithm used in Intkey is the same as that used in the key-generation program, Key (Dallwitz 1974). Unlike most such algorithms, it has a theoretical basis and gives sensible results for characters with three or more states, and for numeric characters. The relative weight of the separating power and the 'reliability' of the character (a subjective measure, usually supplied by the author, of the character's accuracy and/or ease of use) can be controlled by both the author and the user.

Ranking of the characters can take a considerable time in large data sets, so it is important that the computation is as efficient as possible, and that the user does not have to wait for the ranking to be completed before choosing a character.

'Best' algorithms should be able to handle numeric characters, as these often have high separating power. For example, the data set '*Festuca* of North America' (Aiken et al. 1996) has 29 numeric characters and 67 multistate characters. When Intkey ranks these characters by their separating power, the top 17 characters are numeric. A similar tendency is shown in 'The Families of Flowering Plants' (Watson and Dallwitz 1992), which has 39 numeric characters and 459 multistate characters (excluding 'characters' used to define the classification). When the characters are ranked by separating power, 4 of the top 5, and 14 of the top 30, are numeric.

The high separating power of numeric characters is surprising to most taxonomists, as numeric characters are generally not very useful in conventional keys. There are two reasons for this. (1) Conventional keys must use multistate characters for numeric data, and this causes a loss of separating power. (2) Numeric characters often show a large amount of overlap between taxa; in conventional keys, this results in multiple occurrences of taxa, and an increase in the *printed* length of the key. Neither of these factors apply to interactive keys.

*Notes on the interpretation of characters.* Extensive text to aid interpretation of characters should be conveniently available.

*Illustrations of characters.* Illustrations to aid interpretation of characters should be conveniently available. State selection, and changing of the selections, should be possible from the illustration screens (that is, it should not be necessary to return to a text-based screen for these operations). There should be no restrictions on the number of illustrations for each character and/or character state.

*Illustrations of taxa.* Taxon illustrations are useful for confirming identifications. Display of these illustrations should be flexible: there should be no limits on the number of illustrations of a taxon, the illustrations should be selectable by subject (e.g. habit, habitat, flowers, fruits, distribution map), and it should be possible to display illustrations of different taxa simultaneously.

*Finding the differences and similarities between taxa.* The program should be able to find the differences between members of a set of taxa, in terms of a selected set of characters. There should be no restrictions on the size of the set of taxa.

*Finding diagnostic descriptions.* The program should be able to find diagnostic descriptions, which distinguish a given taxon from all the other taxa. These provide a quick way of confirming the identity of a specimen. The characters should be chosen from those which have not been used in the current identification, in order to provide an independent confirmation.

Intkey has a parameter, 'DiagLevel', which specifies the minimum number of characters for which the diagnostic description should differ from all the other taxa. Another parameter, 'DiagType', distinguishes between specimen-diagnostic and taxon-diagnostic descriptions. The latter are allowed to contain characters which may sometimes be inapplicable to specimens belonging to the taxon.

## Interactive identification over the Internet

Interactive identification can be made available over the Internet in several ways, which differ in whether the processing is done on a Web server or the user's machine, and in the method of loading and running the software on the user's machine. Each method has advantages and disadvantages, particularly in the times taken for various operations. The times given below are for a 133MHz Pentium, with an Internet connection running at about 15Kbytes per second.

### *A stand-alone program*

Programs of this type must be downloaded and installed before their first use. This process usually takes a few minutes, depending on the size of the program and the speed of the Internet connection. Most are available for only one operating system (usually MS-Windows). The programs download the data matrix at the start of a session. The user cannot proceed until the downloading is completed, but afterwards response is fast, and there is no further load on the network and server, except when subsidiary files, such as images, are required. (The images can be downloaded with the data matrix (e.g. Dallwitz et al. 1997), but this would usually make the downloading time prohibitively large). The user interface can be compact and simple, and can utilize the full capabilities of the operating system. The programs can (potentially) be set up as 'helper applications', so that they can automatically run a specified data set by clicking on a link in a Web page. They can also be used off line. Powerful programs are already available.

Examples of this type of program are:

| | |
|---|---|
| Intkey | http://biodiversity.uno.edu/delta/ |
| LucID | http://www.lucidcentral.com/ |

Intkey is free for non-commercial use and is available at the above URL by following the links 'Programs and documentation > Intkey'. A complete, annotated example of an identification using Intkey is also available by following the links 'Overview of the DELTA System > An Intkey example: identification'.

The full version of LucID is commercial, but there is a free version with some of the features disabled. Both versions lack many features important for efficient, accurate identification (see Dallwitz 2000).

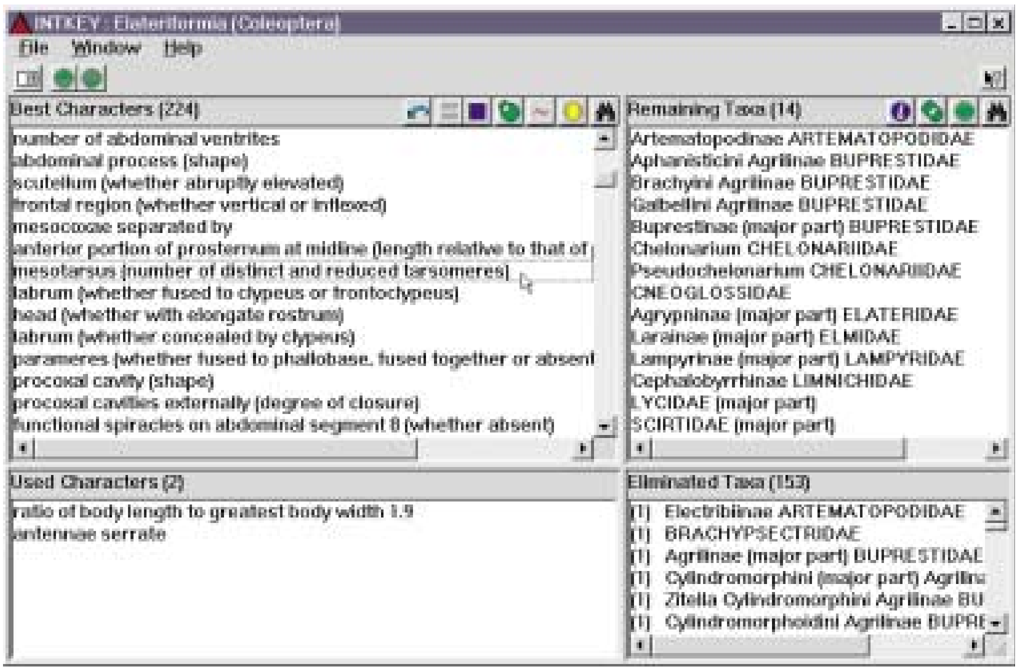
The Intkey installation file is about 2.1MB in size. It takes about 150 seconds to download, and a further 60 seconds to install. The installed files occupy about 2.3MB (not counting the installation file, which can be deleted after installation), and are placed entirely in a separate directory — no files are added or overwritten in the Windows directories.

The Web site also has links to many Intkey data sets. One of these, 'The Families of Flowering Plants' (Watson and Dallwitz 1992), was used for timing tests. It contains 582 characters and 585 taxa. When running the data from the Internet, program startup and downloading of the data took 50 seconds. Thereafter the program works entirely locally, except for downloading images and description files when required (descriptions can also be generated from the data without reference to external files). Simple operations such as using a character in an identification take less than 0.5 seconds. When calculating the 'Best' characters for an identification, the characters found so far are displayed after 2 seconds, and the rest after the calculation is complete. The characters are examined in descending order of character reliability, so a suitable character is almost always available within the first 2 seconds. About 320 characters were processed in this initial period.

The following Intkey sample screens were taken from 'Elateriformia of the World', also available at the above site.

Figure 1 shows the main screen, part way through an identification. Two characters have been used, reducing the number of possible taxa from 167 to 14. The characters that can separate the remaining taxa have been automatically displayed in the 'Best Characters' pane, ranked as described above. One of these is about to be selected.

**Intkey main screen** Figure 1.



Best Characters (224)

number of abdominal ventrites
abdominal process (shape)
scutellum (whether abruptly elevated)
frontal region (whether vertical or inflexed)
mesocoxae separated by
anterior portion of prosternum at midline (length relative to that of
mesotarsus (number of distinct and reduced tarsomeres)
labrum (whether fused to clypeus or frontoclypeus)
head (whether with elongate rostrum)
labrum (whether concealed by clypeus)
parameres (whether fused to phallobase, fused together or absent
procoxal cavity (shape)
procoxal cavities externally (degree of closure)
functional spiracles on abdominal segment 8 (whether absent)

Remaining Taxa (14)

Artematopodinae ARTEMATOPODIDAE
Aphanisticini Agrilinae BUPRESTIDAE
Brachyini Agrilinae BUPRESTIDAE
Galbellini Agrilinae BUPRESTIDAE
Buprestinae (major part) BUPRESTIDAE
Chelonarium CHELONARIIDAE
Pseudochelonarium CHELONARIIDAE
CNEOGLOSSIDAE
Agrypninae (major part) ELATERIDAE
Larainae (major part) ELMIDAE
Lampyrinae (major part) LAMPYRIDAE
Cephalobyrrhinae LIMNICHIDAE
LYCIDAE (major part)
SCIRTIDAE (major part)

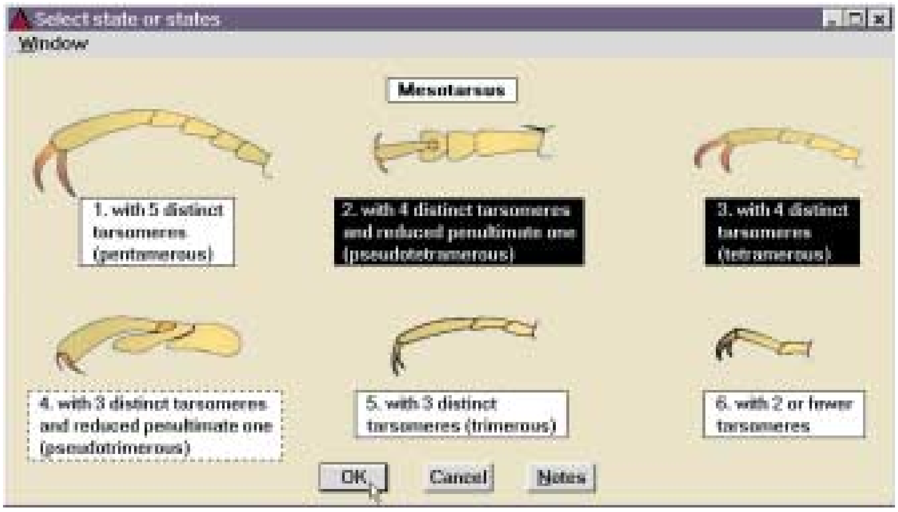
Used Characters (2)

ratio of body length to greatest body width 1.9
antennae serrate

Eliminated Taxa (153)

(1) Electribiinae ARTEMATOPODIDAE
(1) BRACHYPSECTRIDAE
(1) Agrilinae (major part) BUPRESTIDAE
(1) Cylindromorphini (major part) Agrilina
(1) Zitella Cylindromorphini Agrilinae BU
(1) Cylindromorphoidini Agrilinae BUPRE

Figure 2. **Intkey character-state selection screen**


Select state or states
Window
Mesotarsus
1. with 5 distinct tarsomeres (pentamerous)
2. with 4 distinct tarsomeres and reduced penultimate one (pseudotetramerous)
3. with 4 distinct tarsomeres (tetramerous)
4. with 3 distinct tarsomeres and reduced penultimate one (pseudotrimerous)
5. with 3 distinct tarsomeres (trimerous)
6. with 2 or fewer tarsomeres
OK
Cancel
Notes

The screen shown in Figure 2 is then automatically displayed. Pressing the 'Notes' button would display notes on the interpretation of the character. States 2 and 3 have been selected, because it is difficult to distinguish between them in the specimen.

After using this character, a single taxon remains. Pressing the 'Information' button gives access to descriptions and illustrations, as shown in the screen shown in Figure 3. In this example, a diagnostic description and the single illustration of the taxon have been selected to be displayed. The 'Web Search' button can be used to search for the selected taxon using a nominated general-purpose search engine (e.g. Google) or taxonomic database (e.g. ITIS).

Figure 3. **Intkey taxon information screen**

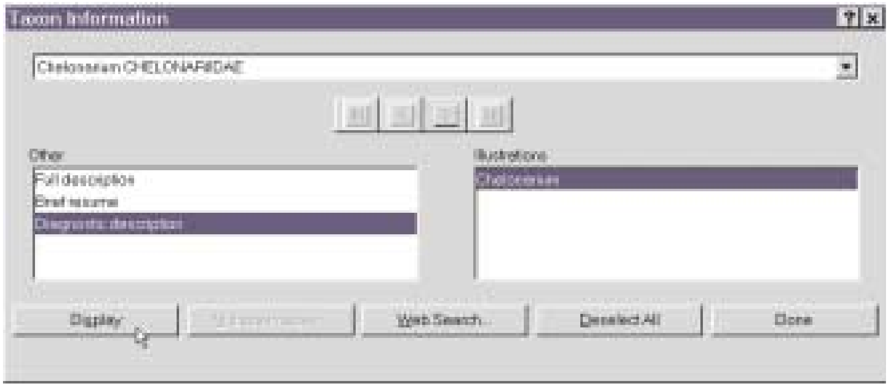
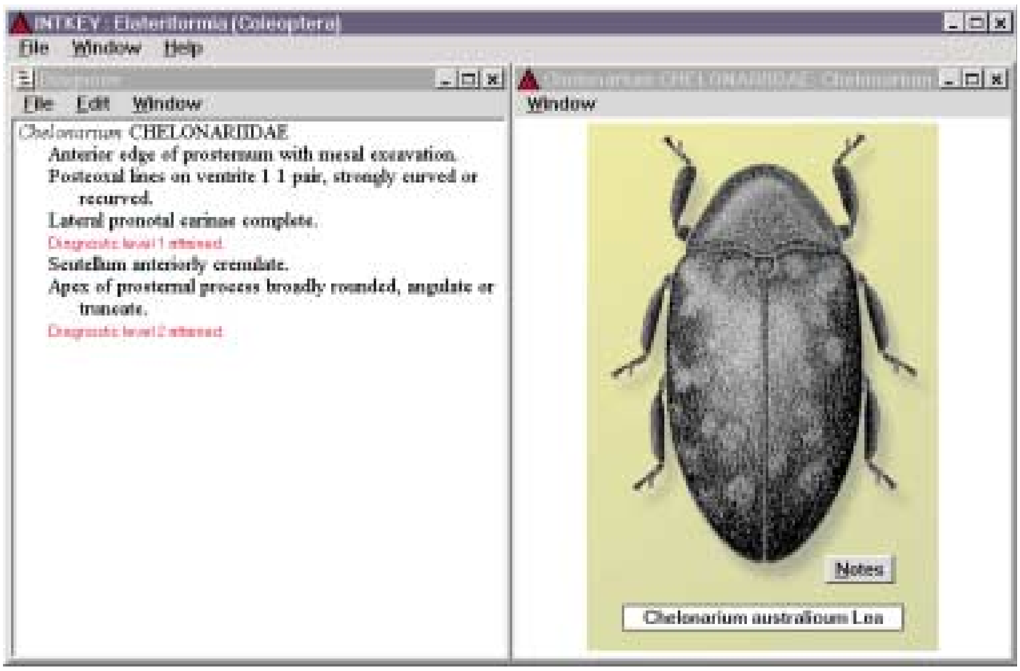


Figure 4 shows the requested information. The diagnostic description contains only characters not used in the identification, and separates the taxon in at least 2 respects from every other taxon in the database.

Intkey diagnostic description and taxon illustration Figure 4.


INTKEY : Elateriformia (Coleoptera)
File Window Help
File Edit Window
Window
Notes
Chelonarium australicum Lea

Chelonarium CHELONARIIDAE
Anterior edge of prosternum with mesal excavation.
Postcoxal lines on ventrite 1 1 pair, strongly curved or recurved.
Lateral pronotal carinae complete.
Diagnostic level 1 attained.
Scutellum anteriorly crenulate.
Apex of prosternal process broadly rounded, angulate or truncate.
Diagnostic level 2 attained.

### *A program (Java or JavaScript) running in a Web browser*

Programs of this type do not have to be installed before use — they are downloaded and run automatically by the Web browser. For Java programs, the browser must also load the Java interpreter. Downloading and starting the program can take a significant time, depending on the size of the program, the speed of the Internet connection, whether the program is cached from a previous use, and the speed of the user's computer. Java and Javascript programs should be independent of the user's operating system and browser, but in practice there can be compatibility problems. The programs download the data matrix at the start of a session, and the user cannot proceed until the downloading is completed. There is no further load on the network and server, except when subsidiary files, such as images, are required. Response times may be slow owing to inefficient computation in the browser. The user interface can be compact and simple, but design may be somewhat restricted by the limitations of the programming language and by compatibility considerations. The programs can also be used off line. Currently available programs lack many important features.

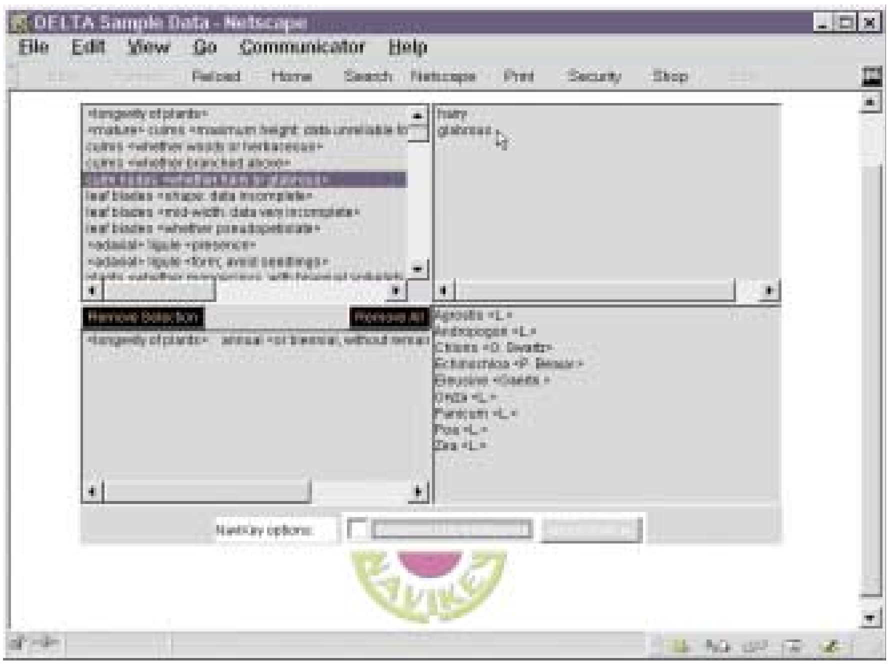
An example of this type of program is:

| | |
|---|---|
| NaviKey | http://www.herbaria.harvard.edu/software/navikey/ |

NaviKey is free for non-commercial use. It uses Java applets, and loads the data from DELTA files (Dallwitz 1980; Dallwitz et al. 1993) when the program is started. Working from a local hard disk, loading the applets and the 'Families of Flowering Plants' data (582 characters and 585 taxa) took 105 seconds. Working from the Internet, the same operations took 230 seconds. Other operations take the same time whether running locally or from the Internet. The program has a feature, 'Selection List Intelligence', which removes redundant characters from the list. With this feature off, using a character took 10 seconds; with it on, it took 65 seconds.

The NaviKey screen shown in Figure 5 uses the sample data supplied with the DELTA programs (Dallwitz et al. 1993). An identification is in progress. The state 'annual' of the character 'longevity of plants' has been selected, leaving 9 taxa remaining from the original 14. The character 'culm nodes' has been selected, and its state 'glabrous' is about to be selected.

Figure 5. NaviKey main screen


DELTA Sample Data - Netscape
File Edit View Go Communicator Help
Reload Home Search Netscape Print Security Shop
Remove Selection
Remove All
NaviKey options:
NAVIKEY

<longevity of plants>
<mature> culms <maximum height: data unreliable fo
culms <whether woody or herbaceous>
culms <whether branched above>
culm nodes <whether hairy or glabrous>
leaf blades <shape: data incomplete>
leaf blades <mid-width: data very incomplete>
leaf blades <whether pseudopetiolate>
<adaxial> ligule <presence>
<adaxial> ligule <form; avoid seedlings>

hairy
glabrous

<longevity of plants> annual <or biennial, without rena

Agrostis <L.>
Andropogon <L.>
Chloris <O. Swartz>
Echinochloa <P. Beauv.>
Eleusine <Gaertn.>
Oryza <L.>
Panicum <L.>
Poa <L.>
Zea <L.>

### *Cooperating programs running in a Web browser and server*

Programs of this type do not have to be installed before use. The ‘client’ — the program running in the Web browser — is downloaded and run automatically by the browser. For Java programs, the browser must also load the Java interpreter. Downloading and starting the program can take a significant time, depending on the size of the program, the speed of the Internet connection, whether the program is cached from a previous use, and the speed of the user’s computer. Java and Javascript programs should be independent of the user’s operating system and browser, but in practice there can be compatibility problems. The division of work between the server and client programs could be done in various ways, with the extremes approaching type 2 (data downloaded at the start, most of the work done by the client) and type 4 (no data downloaded, most of the work done by the server). The most useful division would probably be to:

- download the character descriptions and taxon names at the start (because these are typically displayed repeatedly during a session)
- carry out the data-matrix computations on the server (e.g. ‘best’ characters, taxa possessing a given attribute)
- use character, state, and taxon numbers to exchange information between the server and the client (e.g. the user’s selections, and the results of the server’s computations)

There is a continuing load on the network and server. The load on the network may be small compared with programs of type 4, because the information can be exchanged in a compact form. The load on the server may be comparatively large, because of the amount of computation required (e.g. for ‘best’ characters, differences, diagnostic descriptions). The response time is the time taken for a small Web transaction, plus the computation time on the server, plus the time taken for the client to interpret and display the results. The user interface can be compact and simple, but design may be somewhat restricted by the limitations of the programming language and by compatibility considerations. The programs cannot be used off line. Currently available programs lack many important features.

Examples of this type of program are:

| | |
|---|---|
| FloraSearch | http://www.reticule.co.uk/flora/index.html |
| NaviKey (client-server version) | http://www.herbaria.harvard.edu/software/navikey/ |

All are free for non-commercial use. No tests have been carried out on these programs.

### *A program running on a Web server, and generating HTML pages*

Programs of this type do not have to be installed before use, as they reside entirely in the server. The Web browser handles only standard HTML pages generated by the server. Typically, many of the HTML pages contain the whole character list or a substantial part of it, which may have to be downloaded afresh after a transaction. There is therefore a continuing heavy load on the network and server. Response times may be slow because of the amount of information downloaded at each transaction, and because of slow computation in the server if it is also carrying out tasks for other users. The user interface tends to be cumbersome, because of the limitations of HTML. The programs cannot be used off line. Currently available programs lack many important features.

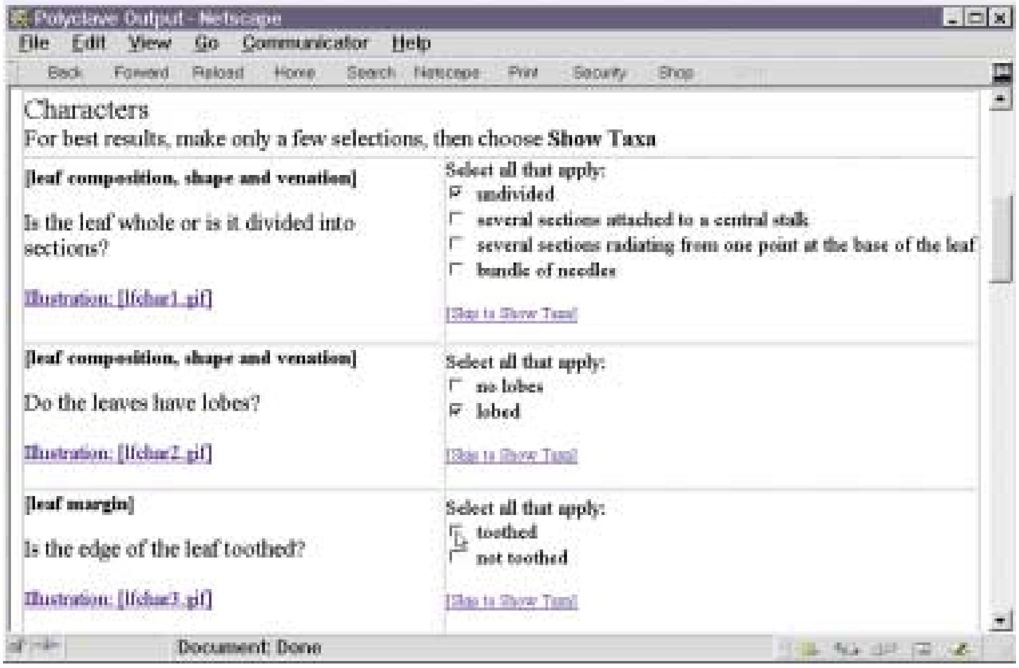
Examples of this type of program are:

| | |
|---|---|
| DAP (Delta Access Perl) | http://www.axel-findling.de/programs/dap/ |
| DAWI (Delta Access Web Interface) | http://www.axel-findling.de/programs/dawi/ |
| PollyClave | http://prod.library.utoronto.ca/polyclave/index.html |

All are free for non-commercial use. There are examples of keys using DAP and DAWI at http://www.mycology.net/lias/index.cfm, and examples of keys using PollyClave at above site.

Only small PollyClave data sets are available on the Internet. The response times for these are typical of small Web transactions — about 2–4 seconds. With a data matrix of about 500 characters and 500 taxa, I estimate that loading the character list would take about 20 seconds. This operation may be required at each cycle of the identification, but the browser's 'back' button can be used in some circumstances (even that would take 8 seconds). In each cycle, states may be selected from 1 or more characters, though using several characters without the guidance of 'Best' will increase the chance of errors. After states have been selected, it would take about 7 seconds for the program to respond with the list of remaining taxa.

PollyClave main screen Figure 6.


Polyclave Output - Netscape
File Edit View Go Communicator Help
Back Forward Reload Home Search Netscape Print Security Shop
Document: Done

Characters

For best results, make only a few selections, then choose **Show Taxa**

**[leaf composition, shape and venation]**

Is the leaf whole or is it divided into sections?

Illustration: [lfchar1.gif]

Select all that apply:
☑ undivided
☐ several sections attached to a central stalk
☐ several sections radiating from one point at the base of the leaf
☐ bundle of needles

[Skip to Show Taxa]

**[leaf composition, shape and venation]**

Do the leaves have lobes?

Illustration: [lfchar2.gif]

Select all that apply:
☐ no lobes
☑ lobed

[Skip to Show Taxa]

**[leaf margin]**

Is the edge of the leaf toothed?

Illustration: [lfchar3.gif]

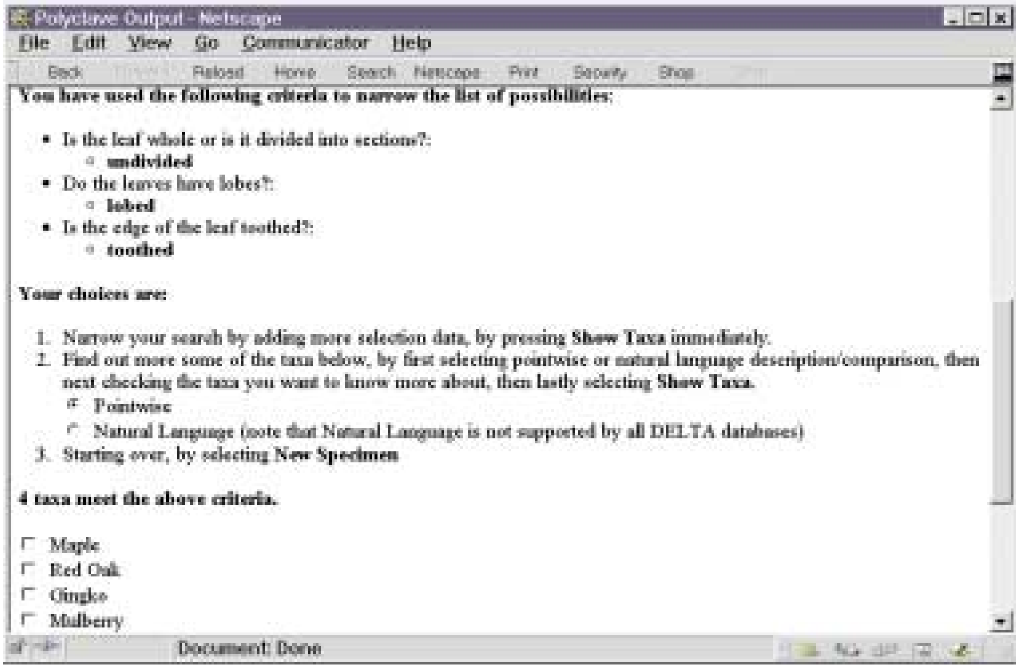
Select all that apply:
☐ toothed
☐ not toothed

[Skip to Show Taxa]

Figure 6 shows a PollyClave screen at the start of an identification. The state ‘undivided’ of the character ‘Is the leaf whole or is it divided into sections?’ and the state ‘lobed’ of the character ‘Do the leaves have lobes?’ have been selected. The state ‘toothed’ of the characters ‘Is the edge of the leaf toothed?’ is about to be selected. The user then moves to the bottom of the page (not visible in this screen) by means of the scroll bar or the link ‘Skip to Show Taxa’, and presses the button ‘Show Taxa Matching Selections’.

The screen shown in Figure 7 is displayed. It shows that 4 taxa remain. The user can then return to the previous screen by using the browser’s ‘Back’ button, or obtain the best characters to separate the remaining taxa by pressing the ‘Rank Characters’ button at the bottom of the page (not visible on this screen).

Figure 7. **PollyClave ‘Taxa Matching Selections’ screen**



Polyclave Output - Netscape
File Edit View Go Communicator Help
Back Forward Reload Home Search Netscape Print Security Shop

**You have used the following criteria to narrow the list of possibilities:**

- Is the leaf whole or is it divided into sections?:
  - **undivided**
- Do the leaves have lobes?:
  - **lobed**
- Is the edge of the leaf toothed?:
  - **toothed**

**Your choices are:**

1. Narrow your search by adding more selection data, by pressing **Show Taxa** immediately.
2. Find out more some of the taxa below, by first selecting pointwise or natural language description/comparison, then next checking the taxa you want to know more about, then lastly selecting **Show Taxa.**
   - ● Pointwise
   - ○ Natural Language (note that Natural Language is not supported by all DELTA databases)
3. Starting over, by selecting **New Specimen**

**4 taxa meet the above criteria.**

□ Maple
□ Red Oak
□ Gingko
□ Mulberry

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# New approaches to creating global species databases in entomology

Malcolm J. Scoble [7]

## Abstract

Global species databases are, broadly speaking, computerised taxonomic catalogues. Databases have, however, the capacity to be more extensive than catalogues, and they are much more effectively searched. They can also be networked. It is increasingly evident that the kind of information inherent in traditional taxonomic catalogues is of value beyond the systematics community. In particular, it forms the basis for such products as life-lists, biodiversity surveys and inventories, which are needed to meet certain requirements under the Convention on Biological Diversity. The main difference between creating global species databases for insects and most other groups of organisms is that of the size of the task. In this paper I give an example of the steps in creating one such database (on geometrid moths) and the hardcopy catalogue that was derived from it. Although a great deal of effort was required to complete the database in a timely fashion, such large compilations are quite possible given appropriate facilities and the right people. Key features in the production of the work, both material and in terms of human effort, will be discussed. Attempts are now being made by the University of Essex and The Natural History Museum, London, to build a Versatile Interactive Archive Document System (VIADOCS). The project will use modified optical character recognition (OCR) software to convert species data on index card archives. A demonstration system utilizing a particular Lepidoptera index-card archive (on Pyraloidea) will be developed and evaluated against current manual conversion methods. The data will be made accessible, interactively, over the Internet. The aim of producing this system is to provide a means of making extensive quantities of data available, which are currently trapped in typed and hand-written archives. All these efforts should be seen in the broader context of computerising biological data typically associated with biological collections.

**Keywords**: taxonomic information, catalogues, archival data.

## Introduction

Entomological catalogues have been printed for a wide variety of taxa. They are durable products based on data that form the bedrock of museum biodiversity information. They have been built from details gleaned from card indexes, from descriptions in publications, from centralized compilations, such as the *Zoological Record*, and from information in collections of specimens themselves. Traditionally they have been published on paper. But while the value of that medium arguably has still an important role in conveying fundamental information, the advent of desktop computers has changed our view of these traditional products for two main reasons. First, computers can be loaded with software for constructing relational databases thus enabling data to be searched flexibly. Second, the Internet allows (actually or potentially) both shared access to live data-sets and, increasingly, added value through interoperability across distributed data-sets.

Taxonomists are now open to new conceptual levels. They realize that while the net is a wonderful, if flawed, mechanism for communication its value rests on the quality of the input. They know that this situation will persist. But they appreciate also that flexible searching methods across any single database provides a new dimension to using data, for now questions can be asked that are impossible of a simple index in a printed book. Furthermore, they see

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that taxonomic names can be used, in effect, as hypertext links. At present these links mainly allow access to species web-pages, but interoperable systems are evolving to provide instantaneous access to data across multiple servers. This, in turn, creates the possibility of new opportunities for analysis of these data.

Suddenly taxonomic catalogues, which were never noted, nor indeed ever compiled, for their capacity to excite, have gained, potentially, a wider role. They act as a source for biodiversity inventories, required by most governments as national contributions towards the Convention on Biological Diversity. Futhermore, lists of names can act as thesauri permitting access to a growing body of information in global digital space.

The present account is written with this wider perception of the value of databases in mind, although it deals specifically with examining the process of data input. Two projects are featured, both involving lepidopteran data stored on archives of index cards. In the first of these, an account is given of the logistics of how a particular database (and the catalogue derived from it) was produced for a group of moths, the resources on which it was based, and the value of teamwork in its production. In the second I outline a recent collaborative initiative to computerise, semi-automatically, taxonomic data stored in index card archives using another large group of moths as a demonstrator of the system. In both cases, the broader aim has been to make taxonomic information trapped in museum archives more widely available.

## A global taxonomic facility for geometrid moths

The first of these databases is to a species-rich family of Lepidoptera – the Geometridae, which are the moths with ‘looper’ caterpillars. This project involved the production of a printed catalogue (Parsons *et al.*, *in* Scoble, 1999) and a computerised database to all available species- and genus-group names of Geometridae.

The Geometridae were selected for several reasons. Geometrid moths are currently being studied in The Natural History Museum, London (BMNH). The resources for this group of insects within the institution are the most comprehensive in the world, which makes the location the most appropriate one in which to compile the work. The museum houses the most extensive collection of these insects taxonomically and geographically, and it has a comprehensive library with access to virtually all original descriptions for the species. Associated with the collection is a card index to all genus- and species-group names of the family within which is contained the kind of data that typically goes into creating taxonomic catalogues. Furthermore, the Geometridae are species-rich, so the group provided a good basis for testing our ability to create large databases to a timetable. From the wider standpoint, lepidopteran caterpillars are primary consumers of plants and, as a species-rich group, have a significant, although unmeasured, impact in ecosystems. This is true particularly of tropical ecosystems, which is where most geometrid species occur.

The participants preferred to refer to this project as a *global taxonomic facility* rather than simply a catalogue. In this way the dual catalogue/database output of the work was emphasized, as was the fact that fundamental taxonomic information on a world basis was included, and that the compilation would act as a tool for collections management and research. Moreover, given the flexibility of modern relational databases, the capacity for expansion with the addition of images and specimen records was made possible.

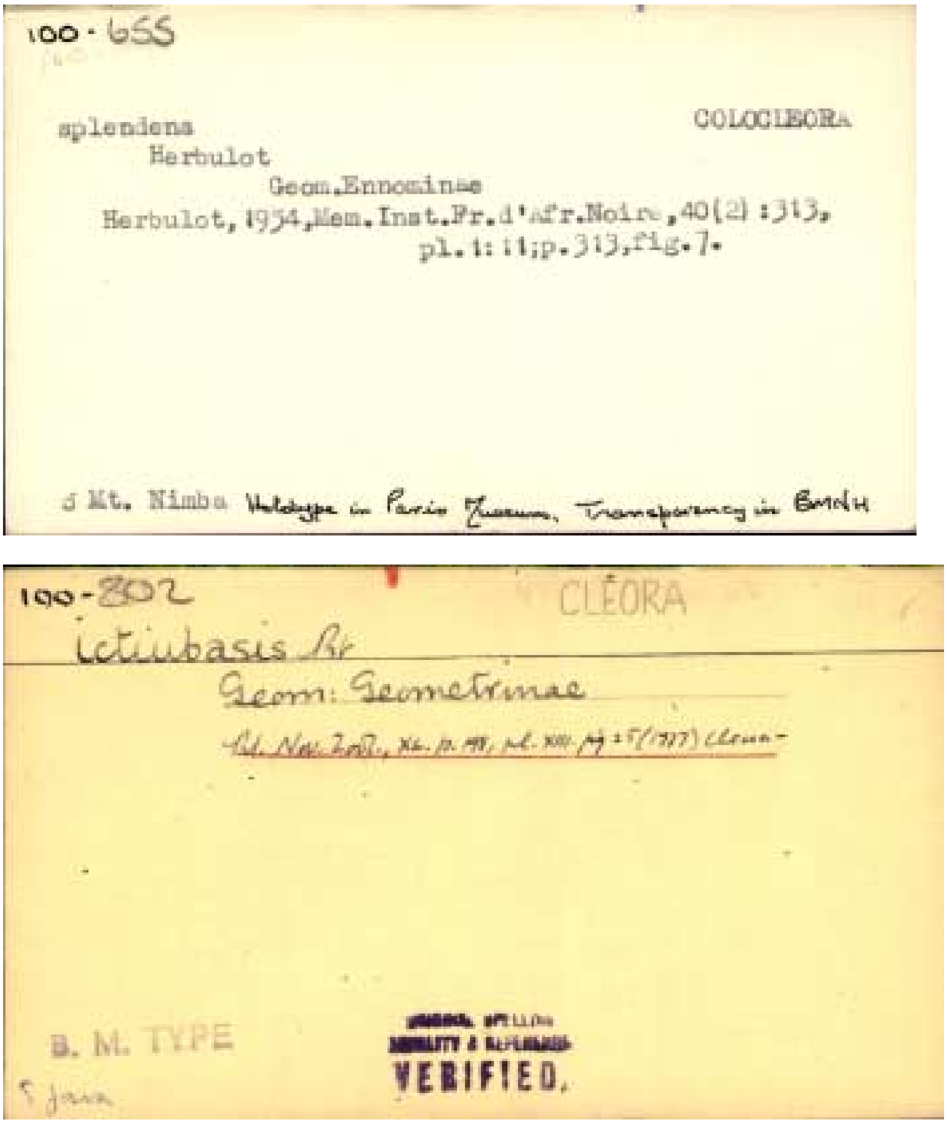
### *The card archive*

The basic information on each of the 35 000 cards in the archive, two examples of which are shown in Figure 1 on the following page. The cards are divided first by subfamily. Within each subfamily they are indexed alphabetically by genus, within each genus alphabetically by species, and within each species alphabetically by subspecies. Junior synonyms and homonyms are arranged alphabetically following the senior name. Many of the genus/species combinations are unpublished having been incorporated during detailed curation of the collection. As no indication was given when new combinations or synonymys were made, it was considered wiser not to flag any of them as new since, without searching all the literature subsequent to the original descriptions, we could not be sure that they were, in fact, unpublished.

The index also contains many infrasubspecific names. These were not added to the database on a comprehensive basis since they fall outside the regulations of the *International Code of Zoological Nomenclature* and are of very limited value biologically. Time was better spent concentrating on the available names.

It should be emphasized, therefore, that the catalogue was not constructed directly from original descriptions, for much of the information needed already existed in the card archive. The geometrid moth archive forms a part of a much larger set of cards, which covers all the Lepidoptera, and which were compiled over many decades. For the Geometridae, L.B. Prout (1864-1943), who made such an impact on the classification of the family, was responsible for the early development of the archive. This work was continued, expanded and refined by D.S. Fletcher and his collaborators who curated the archive alongside the collection of an estimated one million specimens of the family. So although the current collaborators have made the archival data more accessible by means of the published catalogue, much of the original information was incorporated in the index by the earlier curators. As with so much of taxonomy, our knowledge has developed accumulatively.

Figure 1. **Two index cards from the geometrid moth archive at The Natural History Museum, London**



100 · 655

splendens COLOCLEORA
Herbulot
Geom.Ennominae
Herbulot,1954,Mem.Inst.Fr.d'Afr.Noire,40(2):313,
pl.1:11;p.313,fig.7.

♂ Mt. Nimba Holotype in Paris Museum, Transparency in BMNH

100-802 CLÉORA
ictiubasis Pr
Geom: Geometrinae
Nov. Zool. [illegible] (1913) Cleora-

B. M. TYPE
♀ Java

[illegible]
VERIFIED.

Nevertheless, the project did not involve simply converting the card archive to a database. Many errors were corrected and additional information was added, particularly by reference to original species-group descriptions, nearly all of which were examined during the course of the study. Deciding on whether names were subspecific (and thus available) or infrasubspecific (and thus unavailable) was a particularly time-consuming process. Efforts were made to resolve as many as possible of the nomenclatural issues that became evident during the project. Numerous taxonomic changes that were not in the index, but that were present in the literature subsequent to the original description (i.e., in revisions), were incorporated in the database. A considerable research effort was therefore required.

### *Purpose*

The purpose of the project was to produce both a computerised database for research and collections management and a hardcopy version for publication. Although databases are more flexible for searching different fields, paper versions of catalogues provide users with certain advantages. The pages of books (personal copies at least) can be annotated, and volumes are rather more easily moved around collections even than laptop computers. The further advantage of a hardcopy publication is that it provides a fixed reference – a brick in the taxonomic literature. With the growing impact of dynamic information on the Internet, it is by no means clear just what the future of hardcopy publications for large taxonomic datasets will be, but we are not quite at the stage where a complete switch from static hardcopy to dynamic electronic information has been made. The dual media of hardcopy and database seem highly complementary each having their own virtues.

Large taxonomic catalogues are compiled typically by individuals, or perhaps two collaborators, often over a long period whereas a further aim of the present project was to see if we were able to produce a catalogue to the Geometridae in a relatively short period. Speed should not, ideally, be the primary criterion in assembling taxonomic works, but taxonomists are, reasonably enough, under pressure to produce their work in a timely fashion, notably for demands to inventory the species of the world.

### *The database*

The fields in the database (Table 1) include information typically found in entomological taxonomic catalogues. For nearly all species-group names we were able to give original and current genus, the author and date and the reference and page. Infrasubspecific names were omitted and several other names in the card archive were excluded because they were deemed likely to be manuscript names, no literature source having been traced. Besides the basic fields, we also added type status, the depository of the primary type (or of syntypes if no primary type had been designated) and the type locality. Foodplant information was provided where we were able to gain access to it, the most comprehensive source being *HOSTS - a database of World Lepidoptera hostplants* (Robinson *et al.*, in prep, - NHM internal research document - see also http://www.nhm.ac.uk/entomology/hostplants).

Table 1. **Fields in Geometridae database**

| |
|---|
| Subfamily |
| Genus |
| Original genus |
| Species |
| Subspecies [if appropriate] |
| infrasubspecific [some] |
| Author |
| Year of publication |
| Journal title [in standardized abbreviated form] |
| Journal series [if existing] |
| Journal part [if existing] |
| Volume |
| Page + plate + figure |
| Comments [for notes on nomenclatural issues] |
| Junior synonym? [Yes or No] |
| Synonym of genus [if Yes] |
| Synonym of species [if Yes] |
| Synonym of subspecies [if Yes] |
| Original reference checked? [Yes or No] |
| Type depository |
| Type status [holotype, lectotype, neotype, syntype(s)] and sex |
| Type locality: country |
| Type locality: state |
| Type locality [place] |
| Zoogeographical area |
| Drawer number [in BMNH collection] |

### *Project logistics*

The process of keyboarding the data, checking original references to species-group descriptions, resolving nomenclatural issues, editing the final manuscript derived from the original database, and dealing with our publishers took about five years with the catalogue being published in 1999. This can be accounted for as follows:

- 20 months to keyboard the data in the archive
- 16 months to check references to original descriptions
- 24 months to edit and publish

These figures do not represent person-months, but rather the approximate periods taken for aspects of the work to be completed. The compilation took about four and a half years of staff time, which may be divided thus:

- 3 years keyboarding and checking references by one person working full-time
- advisers (on nomenclatural issues) and people checking references: 6 months
- editing: 1 year.

The size of the task may be understood by appreciating that for each of the 35 000 species-group names, there were data on an index card to be converted, and that maximally 26 fields were filled on the database. The six month period of work estimated under 'advisers' (see immediately above), involved the sum of efforts by at least seven people. It is impossible to give an accurate measure of this time since much of the work took place by the research assistant, whose time was entirely dedicated to the project, discussing problems with colleagues and eliciting advice from them on demand.

The museum team included a supervisor responsible for the project funding, management and editing; a research assistant working full-time for three years; and six others who variously provided advice, helped with checking original references and also in editing. Those involved in the project were from both research and collections management divisions of the Entomology department at the BMNH.

In addition to the in-house staff, we received a great deal of help from key colleagues at other museums, notably the American Museum of Entomology, New York, where a specialist checked entries to all the New World taxa and provided a great deal of extra advice. Nomenclatural problems on certain European species were discussed by e-mail with colleagues at other museums.

Funds to cover the costs of the full-time research assistant for three years were granted by The Leverhulme Trust, and this support enabled the project to be carried out.

### *Limiting factors*

For a project of this size inevitably there were limiting factors. The first was the validity of the taxonomic system. A great deal has been achieved in constructing a classification of the Geometridae, but much has yet to be done. Many of the genera still require revision and we can expect there to be numerous new species combinations, species and genus synonymies, and descriptions of new species.

Second, we were intent on making the catalogue available within a reasonable period of time. Resolving complex issues of nomenclature can take a considerable amount of work, so a balance had to be achieved between resolution and completion. Finally, in a data-set of this size, there remain errors.

### *Conclusions*

Despite the demands of producing global species databases, production of the geometrid moth catalogue demonstrated that compilations of this magnitude really can be achieved in a timely way, provided that access is available to the basic resources of information, staff time and team-work. The card archives, collections and library resources at the BMNH made the project one that could be carried out on a single site with little in the way of *material* outside sources (i.e., discounting advice from willing colleagues). Undoubtedly without the card archive the task would have been much more time-consuming: information would have to have been extracted from original descriptions and modified by assessing changes in revisions published subsequently.

Nevertheless, for most taxa there are likely to be published checklists or catalogues at least for parts of the groups. There are, furthermore, many card archives in museums around the world, so, with better networking, compilations of a similar size should not be impossible to achieve given the will, sufficient finance and time. A much larger initiative, Fauna Europapaeae, which is already in progress, and which aims by means of pan-European collaboration to list all species of animals in Europe, is a good example of how a managed approach can make an impact in recording a significant number of species across a large geographical area. Certainly if we are to help overcome the taxonomic impediment in a reasonably timely way, taxonomic information is likely to have to be made more accessible more quickly.

Although it is obvious that catalogues can be as good only as the existing taxonomy from which they are derived, the great advantage of computer databases is that they are relatively easily to update. So although hardcopy publications start to become outdated as soon as they are published, modification and addition can still continue electronically. The combination of hardcopy with computerised databases provides therefore a complementary system combining the permanence of publication with a flexible (computerised) means of updating. It is desirable, therefore, that at some stage the database will be made accessible on the Internet so that static and dynamic versions of the data are accessible. Since we have excellent working relationships with our publishers, who have taken a considerable commercial risk in publishing a two-volume work of over 1000 pages, Internet access will need to be agreed with them.

## Versatile Interactive Archive Document Conversion System (VIADOCS)

Compiling the geometrid database was achieved by manually keyboarding the card archive. With IT collaborators from the University of Essex, we are currently exploring ways of converting card archives from digital images using modified OCR software. The exemplar for the project is an archive to moths of the superfamily Pyraloidea, which is roughly equivalent in size to that of the Geometridae. The archive of approximately 30 000 cards has been digitised using a SEAC BANCHE RDS 3000 document reader scanner. There are a series of problems to be addressed if the data are to be transferred within the card archive to a database containing several fields, but good quality images have already been derived from the scanner. Major aims of the work will be to recognize the characters and parse the data into fields for incorporation to a database. The type-written script on the cards takes the form of courier font from old mechanical typewriters, for, as with the geometrid archive, that to the pyraloids was compiled prior either to the use of electric typewriters or to modern printers linked to computers.

Although OCR of type-written script might be expected to be a relatively straightforward process, problems arise with touching characters. Off-the-shelf OCR software fails to give an accurate conversion, and modifications are required. The problem of character recognition is at its most extreme for dealing with handwriting on the cards. In some cases, characters are difficult to interpret even by a human observer. Nevertheless, we expect to make progress with interpreting some of the handwritten emendations to the archive.

Dictionaries (partial or relatively complete) for comparing text are already available from various sources. For example, a set of authors names for many Lepidoptera is available from the HOSTPLANTS database (see above). A computerised list of many journal titles in standard abbreviated form were compiled during the geometrid database project and during work on providing digital access to the generic names of moths of the world (B.R. Pitkin & P. Jenkins, *in prep.*). These dictionaries should allow inconsistencies in archive citations to be resolved and enable the standardization and recognition of textual elements.

Perfect conversion is not expected and many corrections will need to be made manually. But through a series of iterations we aim both to deal with editorial matters and to improve the archive conversion system. Furthermore, we intend to upgrade the data in the pyralid moth card archive where possible by checking original references to key sections, by incorporating element of the latest research on the group, and by resolving nomenclatural issues. By providing Internet access to the images of the cards, pyralid moth taxonomists will be in a position to feed information back to the compilers enabling constant upgrading to occur.

The archive to the Pyralidae (including Pyraliformes and Crambiformes) was targeted for the VIADOCS project both because it provides a substantial demonstrator for the system and also because it is the main lepidopteran taxon the names of which have yet to be digitised. Two other large families of Lepidoptera have been catalogued recently, the Geometridae, as described above, and the Noctuidae (Poole, 1989). The fact that the names to parts or the whole of many other families are already digitised means that once the Pyralidae are catalogued, we shall be close to having a digitised databank to all the names of the order Lepidoptera, which is itself, a major insect group.

Given that the broader aim of VIADOCS is to create a system by which card archives in general can be converted, it is hoped that the system will be of value to paper archives in natural history collections and also to those institutions housing cultural artefacts.

## Wider issues

The data being gathered for catalogues/databases to the groups of Lepidoptera discussed above, are of the kind that will eventually populate broader initiatives to catalogue the living resources of the world. Notable is 'Species 2000' (Bisby, 1994; http://www.sp2000.org), which provides interoperability software to query various databases on different servers (see also http://litchi.biol.soton.ac.uk and http://www.systematics.reading.ac.uk/spice/ for associated technical developments).

Other programmes are in various stages of development, but while the development of interoperability software is clearly being made increasingly effective, the limiting factor appears to be that of getting the Global Species Databases to populate the systems. Gaining funding to compile these databases is more difficult than obtaining support for innovative software development.

## Epilogue

Global Species Databases should be perceived as one part of a biological information system constructed from resources existing within collections-based institutions. The other major component of such a system is specimen data. Ways of digitising text and images of specimens are in a state of evolution, and management systems for prioritizing the selection of data to be digitised are unsophisticated. Although total digitisation is a worthy eventual goal, the huge number of specimens makes prioritization essential. One approach to providing access to specimen (unit) information is via descriptions of collections (metadata), as suggested by the BioCISE project (the Biological Collections Information Service for Europe, http://www.bgbm.fu-berlin.de/biocise/). Descriptions of collections are easier to compile in a more comprehensive way and in a much shorter time than unit data, and access to information about collections provides users with a means of knowing where to seek the latter. For a comprehensive model addressing questions of access to biological collections see Berendsohn et al. (1999). Access to specimen data is, however, being addressed through ENHSIN (the European Natural History Specimen Information Network, http://www.nhm.ac.uk/science/rco/enhsin/

The digitisation of museum resources, whether from archival data on species of the kind described above, or from the labels of specimens, already shows signs of adding a further dimension to natural history museums and other physical 'memory institutions' (Dempsey, http://www.ariadne.ac.uk/issue22/dempsey). This new dimension is not simply the sum of information made accessible on the Internet. Rather, it is the creation of new and complementary places existing in digital space. The coexistence of the physical and the digital, so elegantly described by Dempsey (loc. cit.), provides an enormous opportunity for natural history museums if they will reaffirm their position as custodians (collectively) of the best stored sample we have of biodiversity, while at the same time creating dynamic access to their very considerable resources.

## Acknowledgements

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# An information infrastructure for German insect collections including multimedia and GIS tools

Karl-Heinz Lampe [8] and Klaus Riede [8]

## Abstract

The German Ministry of Science and Education has launched the EDIS-project (Entomological Data and Information System) to digitise and harmonise the rich, but scattered entomological collections housed at various German institutions. The concept is illustrated for the DORSA-subproject, which will integrate German Orthoptera collections within one 'Virtual Museum', accessible by an internet-based user interface. DORSA is a network project, connecting expertise in data-basing, collection management, systematics, geographical information systems and neuroinformatics. The core of DORSA is a specimen-based database of important grasshoppers and crickets in German collections. The taxonomic backbone will be the 'Orthoptera Species File', a global species register already available on the World Wide Web. DORSA integrates specimen-based pictures and sound recordings. The species-specific songs will be used as a knowledge base for the development of song recognition algorithms and bio-acoustic 'Rapid assessment tools'. In addition, all localities will be geo-referenced, resulting in a huge data-set of point data, which can be intersected with other GIS-maps (e.g. on rainforest distribution). A customised Java-tool allows geographic depiction and retrieval of taxonomic data.

**Keywords**: Orthoptera, species database, specimen database, collection management, GIS, song recognition

## Introduction

The number of insect species on earth and their actual extinction rates is a matter of speculation for several years already, but exact numbers are still not available (Stork et al. 1997). This is mainly due to the lack of an efficient information infrastructure. Complete registers of valid taxa only exist for few insect groups, and much of the information stored within museum collections is not readily accessible, because most of it is not digitised. In many institutions it is common notion that 'computerisation' of collections might be possible for the vertebrate departments, but that the mission will be impossible for invertebrate sections due to the overwhelming number of species and specimens, compared to the lack of staff and money. Further difficulties for insect collection managers are the high number of undetermined specimens or undescribed (new) species ('taxonomic impediment').

Nevertheless, an impressive demonstration of feasibility has recently been accomplished by the Insect@thon project (Komen & Marais 2000), where around 21 000 insect inventory records of the Namibian National Museum have been entered by 92 schoolkids on 1 weekend. The project managers stress the need for digital access to the hand-written catalogues of huge first-world collections such as the Natural History Museum London, with 65 million insect specimens: 'We estimate that some 70% of these collections originate in the third world. Inasmuch, we strongly believe that first-world museums are urgently accountable to us…' (http://www.natmus.cul.na/biodive/insectresults.html). Other initiatives such as CONABIO or InBio show that biodiversity-information management in developing countries is much more advanced than in many developed countries. Especially European institutions seem to have severe difficulties in adopting the new information technologies.

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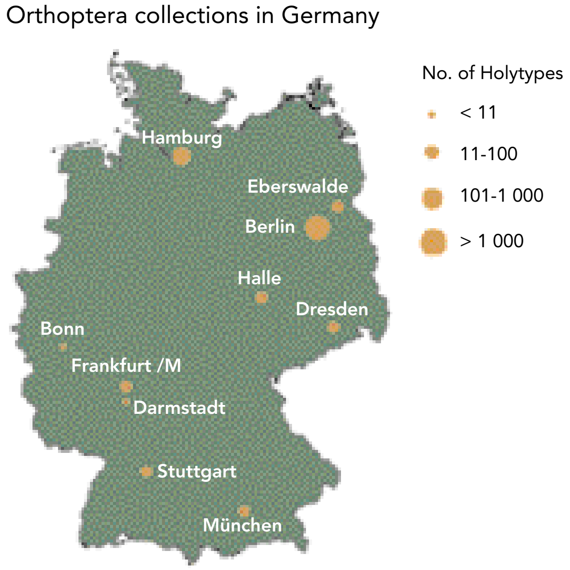
This asymmetry was part of the rationale for the establishment of the Global Biodiversity Information Facility (GBIF) (Edwards et al. 2000). As part of this initiative, the German Ministry of Science and Education (BMBF) has launched the EDIS-project (Entomological Data Information System) to digitise and harmonise the rich, but scattered entomological collections housed at various German institutions within one specimen-based collection database (http://www.insects-online.de/).

The EDIS-project consists of separate and self-dependent subprojects including 'global species registers' (cf. GLOBIS, this volume) and collection databases of specimens with a connection to geographical information systems (GIS). Further projects are rapid assessment tools for automatic identification at the molecular level, by optical analysis of bee's wing venation and sound recognition of crickets and grasshoppers (http://www.insects-online.de). The respective databases will be pooled by an Oracle-based database, which will provide Internet-access (SYSTAX: see http://www.biologie.uni-ulm.de/systax).

This paper deals with the subproject ‘German Orthoptera collections’ (DORSA, according to the German acronym). Germany harbours rich collections including material from tropical countries dating back to the 19th century (Figure 1). Most of this material is not data-based. The DORSA project will digitise specimen-specific information for crickets and grasshoppers and integrate them within one ‘Virtual Museum’, accessible by an internet-based user interface.

Figure 1.

**German research collections with estimated numbers of Orthoptera holotypes. Most of the material is not data-based**



## Databasing and collection management

In practice the overall efficiency of data-basing the inventory of traditional entomological collections depends on two factors: suitable software, and management measures to ensure the highest possible data quality already during the input process. All data entry is based on determined specimens (systematic label information), but ‘determination’ is not limited to the species level - it can be any higher taxon (e.g. ‘Acrididae’ for an unknown grasshopper). In our institution we introduced a lock-step programme for ergonomic and efficient data entry consisting of the following steps:

1. primary data capture of systematic label information
2. validity check of the systematic information against a current catalogue
3. set up of a collection based catalogue of taxa (consisting of the updated systematic information including synonyms, hierarchy of taxa, authors, year, etc.)

4. secondary data capture of sampling information (such as locations, collectors, determinators etc.)
5. validity check of the geographic information against a current gazetteer (by adding geographical attributes such as latitude, longitude and in a hierarchy such as province/ area, state, country, continent/ocean and a link to the zoogeographical region)
6. set up of a collection based catalogue & completion of lists (e.g. collectors, determinators)
7. final data entry of existing specimens into the database

Each step of the procedure is clearly separated from the next. Therefore, everyone involved in this work can clearly see his own area of responsibility as well as the progress of his work. A nice side effect is the allocation of the various jobs involved where they are most welcome. Someone who is interested in working with catalogues by looking for further geographical or systematic information can work easily together with someone who is more interested in doing an accurate data capture. That means a single person is no longer forced to complete all the various tasks alone. Yet another advantage is that any of these procedures can be stopped or interrupted and even taken over by a third party with very little extra effort.

## Systematic backbone

The ‘Orthoptera Species File’ (OSF) will be used as a taxonomic backbone. The OSF is an electronic catalogue of named grasshoppers and crickets, including pictures and sounds, and is available on the WorldWide Web (OSF: Otte and Naskrecki 2000). The OSF is one of the few fully functional global species registers. Queries allow searching for valid names as well as synonyms, their taxonomic reference and the depository place of the holotype. This means that one can ask for all holotypes for a certain museum, as known from the type descriptions. DORSA will realise the next step: a link between species names and existing specimens in German collections. In the future, a simple mouse click on a taxon should produce a list of specimens, together with a map of point data.

## Geographical Information System (GIS)

All data sets refer to a locality. To connect them to a GIS, they have to be geo-referenced by their geographic coordinates. In the ideal case, they have been determined exactly, for example by a 'Global Positioning System' (GPS). In most cases, localities are given as geographic names, and coordinates have to be determined afterwards by searching gazetteers or atlasses. In many cases, locality information is vague, which requires coding of imprecision. Geo-referencing is a time-consuming process, but can be speeded up during the project by building up a thesaurus of specific collection sites and major collector's routes.

Once geo-referenced coordinates can easily be exported into a GIS and plotted as a distribution map or analysed by geo-processing. For example, the intersection with borders of states or provinces produces calculated species lists for administrative units. These lists are useful for conservationists and decision makers, but their maintenance is a time-consuming task. There are numerous additional applications for biodiversity maps in GIS-format, among them: Comparison of maps from different sources and different projections; Calculation of biodiversity hotspots; Intersection with other GIS-layers such as eco-regions, land use, population pressure or climate change predictions, to name just a few.

Figure 2 shows an example for the potential of GIS analysis of collection data. Point data based on 3.578 data-sets of a ZFMK Homoptera collection (with 7.969 specimens) are plotted on a satellite view of the world (Figure 2). The original data for each specimen can be requested by simple mouse-click at the locality point.

Figure 2. World map with localities of the ZFMK Homoptera collection, superimposed on a satellite picture

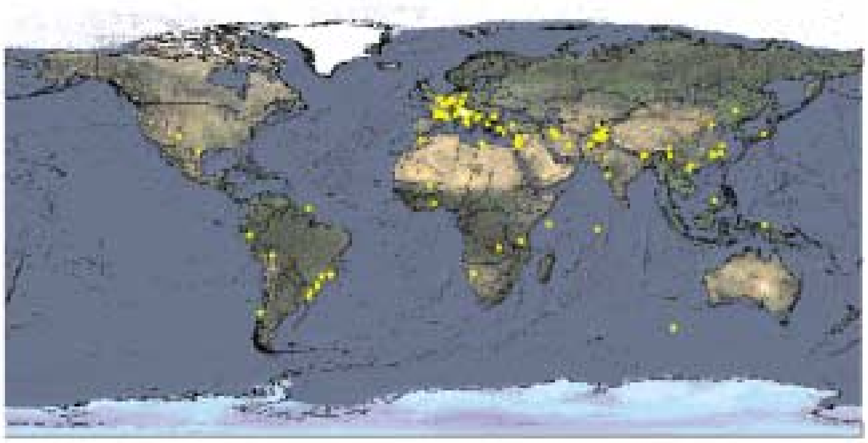
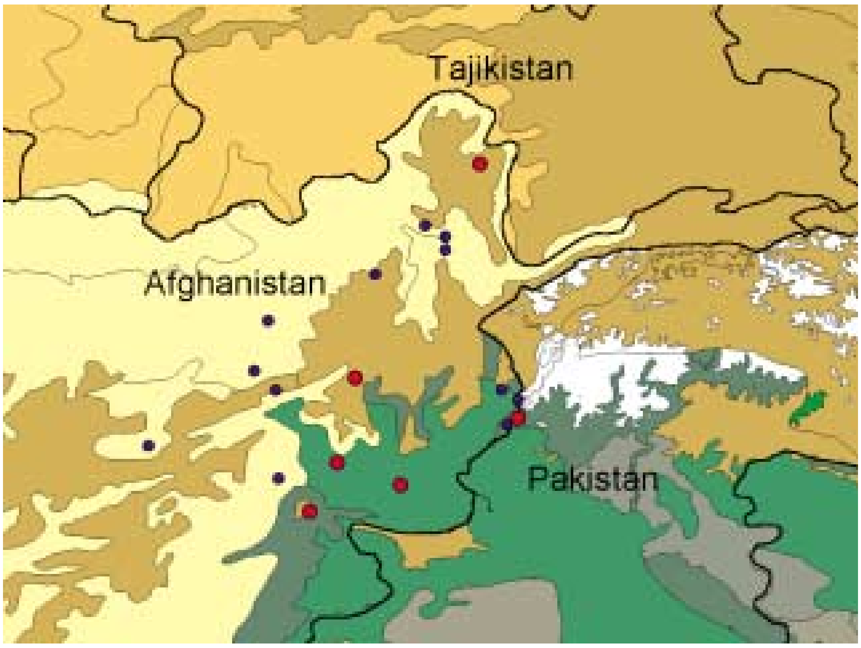


Figure 3. Ecoregions of Central Asia and collection sites (red dots: origin of type material)



With a GIS one can easily zoom into the world map and enlarge special areas and/or change the background information. Figure 3 shows parts of Afghanistan and Pakistan structured by ecological attributes such as the vegetation type. Dots represents collection sites. GIS analysis can be greatly enhanced by pooling data sets from different collections (see Spatial Analyst, this volume).

In spite of these advantages, biologists are still reluctant to use GIS tools. One of the reasons is the user-unfriendlness, such as lack of a standardised query language. The introduction of desktop GIS improved this slightly, but there are still many problems. Even simple questions such as: 'How many species occur within a certain area?' require a number of complex operations. Therefore, a new Graphical User Interface (GUI) has been developed to publish interactive maps on the World Wide Web in cooperation with the Geography Department, Bonn (Fitzke & Friebe 1999). It consists of a platform independent, Java- based information desk for a combined display of geographic and database information (see a pilot version used by the 'Global Register of migratory species': http://www.groms.de). The information desk will be adapted for DORSA to allow queries such as: Show distribution map of a given species! Show maps of non-described species within a higher systematic taxon such as a family! Show material collected during the Kaiserin-Augusta-Fluss-Expedition (Papua-New Guinea 1920). Or even strange sounding queries such as: Show all species singing with a carrier frequency lower than 2 kHz! Results will be depicted as point data maps.

## Multimedia and neuroinformatics

A special feature of crickets and grasshoppers are their species-specific songs which can be used for rapid species identification (cf. Riede 1993). Germany has a long tradition in Orthopteran bio-acoustics and neuroethology, which resulted in several important sound archives (‘phonotheks’) at universities and in private hands (for reviews on Orthopteran communication see Ragge 1998, Riede 1998). At present, the majority of these data is stored on analog media such as magnetic tapes, film or videos. These recordings are now digitised and stored in a standardised format (e.g. wav-files for acoustic data). File names together with data on the original analog data source (tape number, deposit, etc.), recordist and localities are entered into DORSA. Voucher specimens exist for some, but not all of the recordings. Sound files could be used either to analyse inter- and intraspecific song variation, or to provide input for automatic song recognition algorithms. Neural networks for song classification and identification at the species level are presently developed in close cooperation with the Neuroinformatics Department at Ulm University.

The aim is a bioacoustic 'rapid assessment tool' for non-invasive mapping and identification of Orthoptera in the field.

## Perspectives

DORSA will be accessible by Internet from any part of the world as one ‘Virtual Museum Collection’, which is important for potential users in species-rich, but resource-poor developing countries with incipient biodiversity infrastructure. The ‘Virtual Museum Collection’ will help to improve classical taxonomic work such as description of new taxa. Further important functions of this database such as distribution map generation and retrieval of pictures and songs from determined specimens, will be especially useful for ecologists, conservationists and applied entomologists.

At present, types and paratypes are entered into DORSA. The process of databasing is an excellent opportunity for type revision, lectotype designations and eventually repatriation of secondary types. In the case of type loss, re-collection of topotypes should be initiated. Topotypes should also be collected and designated for the country representing the ‘terra typica’, in particular for endemic species. The database will reveal information about historic species distributions which can be compared with actual distributions. Especially in rainforests, such a comparison will form the base for estimates of the actual conservation status and insect extinction rates, which at present are not even informed guesses.

## Acknowledgements

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# Engineering considerations for biodiversity software

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## Abstract

We describe how object oriented design and programming, together with object databases, support applications that require diversity in their data structures reflecting diversity in the description of the data. A three tier web-based architecture permits flexible multiple views on the data. With working instances of an electronic field guide and of applications that federate distributed biodiversity data, we show how XML and object technologies can ease the burden of biologists who must prepare descriptive and diagnostic data for inclusion in web-accessible database.

## Introduction

Biodiversity software encompasses a wide range of applications including the maintenance of specimen records, analysis of phylogenies, examination of biogeographic relationships, and recording of ecological observations (see Biosis, 2000, Geocities, 2000, and Lampinen, 2000 for lists of free and commercial packages). The rapid development in power and sophistication of biodiversity software in the last 15 years mirrors progress in the broader software industry. All software is moving from single user platforms to Web based tools, from text to graphical user interfaces and from custom made software built from the ground up to applications layered on top of commercial or open source components.

Biodiversity software concentrates at the species level because species are the leaves of the hierarchical grouping system called the ‘taxonomic tree’ used by scientists to classify life forms. Despite limitations to the species concept (Futuyma, 1998), the classification system is well established in the scientific community, having been used since Carl Linnaeus invented it over 250 years ago. Therefore is it not surprising that a significant portion of biodiversity software deals with the management of taxonomic information. Examples include programs that help manage collections of specimens such as Biota (Colwell, 1996) and Biolink (Shattuck and Fitzsimmons, 2000) from which taxonomists describe and name species, construct keys to differentiate species (Dallwitz, 2000) or document the tree itself (Maddison, 2000). Common to all of these programs and to many other efforts to share biodiversity information is the species page (also called the homepage, species summary or species treatment) in which biologists present basic information about a species.

Below we describe a biodiversity software application we are developing called the Electronic Field Guide (EFG). The EFG has elements common to biodiversity software listed above but different goals (see below). There are many efforts within scientific and environmental communities to establish standards and way of linking biodiversity information across multiple databases. Among these efforts are those of the Taxonomic Database Working Group http://www.tdwg.org/, the U.S. National Science Foundation’s Long Term Ecological Research Sites http://www.lternet.edu/informatics/, those of governmental agencies such as the National Biological Information Infrastructure, NBII http://www.nbii.gov/ and http://www.nbii.gov/home/partner/bioeco/index.html; the Global Biodiversity Informatics Facility (GBIF) http://www.gbif.org/ ); Cornell’s Laboratory of Ornithology Citizen Science projects http://birds.cornell.edu/citsci/, the Nature Mapping Program http://

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www.fish.washington.edu/naturemapping/; and Discover Life in America http://www.discoverlife.org. In the second part of the paper we discuss how XML (the eXtensible Markup Language) now being adopted in the Web community as a replacement to HTML is likely to help with the federation of information across multiple heterogeneous data sources.

The UMASS-Boston Electronic Field Guide Project, UMB-EFG (Stevenson and Morris, 2000) provides a web-accessible distributed object-oriented database for the identification of biological specimens from field observations. The data, including both taxonomic and environmental or ecological data, will aid in identification by building a context for each observation. As observation data accumulates, larger-scale ecological studies can be carried out using the data. UMB-EFG is being constructed and populated under The EFG project has recently been expanded to encompass investigation of a number of issues and solutions under discussion in the eco-informatics community, including the use of XML for federation of data from disparate distributed database, as well as for more common tasks such as data exchange and system configuration. This paper describes our engineering approach to the building of these systems and reports on their current status.

## Field guides and descriptive data: object-oriented representations

Central to the majority of field studies in biology is the correct scientific identification of species. People learn from others or use field guides if possible, but for most groups identification is accomplished with keys constructed by specialists with knowledge and experience in a taxonomic group. The process begins with the collection of specimens in the field. Taxonomists and systematists then prepare, study and catalogue the specimens, usually in academic institutions or natural history museums. Finally, written descriptions are published and a name given to each new species discovered. Some taxonomists work only in the laboratory, obtaining the specimens from field collectors.

Most paper field guides are devoted either to a specific collection of taxa, e.g. birds, trees, wild-flowers, etc., of a specific geographic region. In most cases, a field guide user who is interested in ecological interactions will require several different field guides. For example, a guide to butterflies may have some narrative identifying the host and nectar plants of a particular butterfly species, but it would give little help in identifying that plant (which might in turn help the reader identify the butterfly). An electronic field guide on contemporary computers (or the web) can easily hold data on a wide variety of taxa, but a data representation issue immediately arises: descriptive characters appropriate to one group of taxa may have little to do with a radically different group. For example, plants have no wing spots since they have no wings, and butterflies have no leaves to be characterized as simple or compound. Therefore, to represent both organisms in a traditional relational database one must either accept large sparse tables or manage very complex joins on the ecological relationships. Essentially, the diversity of life is not amenable to a single description.

Object-oriented Database Management Systems (OODBMSs) (King, 1997) are a solution to the problem of representation of biodiversity, because their data is self-describing. (This is also true of XML, of which more later). Saarenmaa et al. (1995) have observed in detail how object-oriented techniques in general, and OODBMS in particular are well suited to taxonomic databases. However, they reported that with technologies then available, they were unable to usefully create taxa as classes, rather than instances of a single class. In a database with a huge number of taxa, class loading overhead would still make this impractical today. In any case this approach might model specimen collections well, but it does not seem appropriate to a field guide, where it would result in one instance per class. Instead, we model an author's treatments of a large group, e.g. a family, as a class, and model individual taxa as instances. The cost of this is that a species described in an electronic field guide in several different treatments, e.g. by different authors for different locations, are not in the same object-oriented class. We discuss our approach to this issue below. We have implemented the UMASS-Boston Electronic Field Guide (UMB-EFG, or just EFG) on eXcelon Corporation's Object Store product (eXcelon, 2000). This OODBMS is a persistent store for Java (or C++) classes, and we describe next how we create such classes, along with our design requirements for author-friendliness, i.e. criteria by which the authors of descriptive data and keys are kept isolated from the technology. We note in passing that object/relational database management systems (ORDBMSs) (Grimes, 1998) may well provide the support we require, but did not have mature programming interfaces at the time we began coding.

A design requirement of the EFG is that the system should be fundamentally ignorant of the nature of descriptive data. If an author chose to offer characters of restaurants of Boston, our software would produce a meaningful and useful restaurant guide instead of a field guide to the butterflies of Costa Rica, our initial target.

Diverse data such as we described above is called *semi-structured data* in recent literature (see Abiteboul et al., 2000). This means that it need not have a precise database schema such as would be found in a relational database. Pure OODB's are a special case, but of course so is a relational database (Abiteboul et al. *op. cit.*). This property makes it particularly easy for us to import diverse descriptive data and combine it in a single database. The taxon abstraction we use is a software construction called a *JavaBean.* (Sun, 2000a). Beans differ from other Java classes in having particularly convenient *introspection.* The introspection interface allows programs to inquire of the bean — in our case a collection of taxa having a common set of descriptive characters — what its properties and behavior are. This frees us from requiring advance knowledge of that behavior. As a simple example, when the user selects a group of taxa, e.g. butterflies of Costa Rica, we create, on the fly, a biologist-friendly search facility comprising a typical web form with pull-down menus for each character, the names of the character having been gained by introspection and the possible character values by inquiry into the database. (Here we mention 'biologist-friendly' because we will also describe below how our architecture supports flexible user interfaces by separating the UI from the rest of the system. In particular, we'll describe experiments in visual keys more suitable for amateur users.) A JavaBean must be compiled and loaded into the current Java Virtual Machine, so in essence we are generating and compiling source code on-the-fly when we import biological taxon treatments and we do this with some unsupported Java compiler classes available from Sun. This being a somewhat fragile approach, we are presently designing a different mechanism based on Java Map (Sun, 2000b) interfaces, which also can describe and manipulate objects based on their properties, and so are good candidates for a software model of a taxon.

## Architecture overview

We have a typical three-tier Web application with Java servlets as middleware forwarding questions to an eXcelon Corp. ObjectStore OODB. HTML forms and Java Applets pass queries to the servlets, which transform them into queries suitable for the ObjectStore backend. After retrieving the data, the servlets build html pages, or send data to the applets, for presentation to the user. Although we operate our ObjectStore and servlets on the same host, this is completely unnecessary. In addition, ObjectStore is itself a distributed client-server system and various pieces of the database could be scattered around the Internet with no change to our architecture except to add resource discovery mechanism to find the distributed data. In a symmetric fashion, because servlets accept connections on internet IP ports, other clients than our own front end can forward queries to our servlets. See Nakhimovsky and Myers (1999) for an introduction to three-tier applications.

## Importing data

We do not require an author to understand object-oriented technologies. Most biologists keep their descriptive data in software that is, or rests on, standard table-based databases or in a spreadsheet. Typical systems are Excel, Microsoft Access, FileMaker, and specialized systems such as Biota (Colwell, 1996), which uses 4D ODBC support (4D, Inc., 2000)**.** Most of these products can respond to SQL queries along an ODBC connection (Microsoft, 1999) and in turn can be accessed in Java by the JDBC-ODBC bridge (Sun, 1997). More sophisticated systems based on Oracle can use JDBC natively. Our code uses this bridge to import database field names (i.e. character names). We must also attach the data at the appropriate place in the taxonomic tree, because in most cases the author will deliver data about a group of taxa, e.g. a family in a particular locale, without a complete taxonomy. To accomplish the attachment we require a simple XML description of the common taxonomic hierarchy above all the taxa in the data source.

This import strategy is convenient, but leads to several problems. Most notably, the order of the delivery of fields is not determined by the ODBC protocol. Typically the order is that in which the fields were created, but that is often not the order in which the biologist may wish them displayed. Our solution, not fully implemented, is to specify the character order in metadata that is also represented in XML. A second difficulty is that it is possible to specify field names in many databases that do not yield legal Java identifiers (e.g. they contain white space). We convert illegal characters to underscores, but this is not a robust solution, since it may not allow going backwards from the OODB to the original. XML metadata specifying a one-to-one mapping of illegal characters to not-necessarily easily readable Unicode characters in Java identifiers would suffice, but would probably require tools to make the Java identifiers readable for software maintenance. Table 1 shows a typical XML metadata file.

Table 1. Sample Metadata file

| |
|---|
| <EFGMetadata MetaDataID=‘Test’> |
| <EFGField> |
| <name>AntennaColor</name> |
| <type>morphological</type> |
| <weight>0</weight> |
| <dataCount>single</dataCount> |
| <dataType>simple data</dataType> |
| <javaType>java.lang.String</javaType> |
| </EFGField> |
| <EFGField> |
| <name>Habitat</name> |
| <type>ecological</type> |
| <weight>0</weight> |
| <dataCount>multiple</dataCount> |
| <dataType>simple data</dataType> |
| <javaType>java.lang.String</javaType> |
| </EFGField> |
| <name>Similar_Species</name> |
| <type>ecological</type> |
| <weight>0</weight> |
| <dataCount>multiple</dataCount> |
| <dataType>taxonomic reference</dataType> |
| <javaType>java.lang.String</javaType> |
| </EFGField> |
| … |
| </EFGMetadata> |

**Sample Data File associated with the above Metadata file** Table 2.

| |
|---|
| <EFGImportDocument MetaDataID='Test'> |
| <CommonPath> |
| <Domain>Eukaryotes</Domain> |
| <Kingdom>Animalia</Kingdom> |
| <Phylum>Arthropoda</Phylum> |
| <Class>Insecta</Class> |
| <Order>Lepidoptera</Order> |
| <Family>Nymphalidae</Family> |
| <Subfamily>Ithomiinae</Subfamily> |
| </CommonPath> |
| |
| <TaxonList> |
| <Taxon> |
| <EFGPath> |
| <Genus>Ithomia</Genus> |
| <Species>heraldica</Species> |
| </EFGPath> |
| <CharacterData> |
| <ForeWingSpot>yes</ForeWingSpot> |
| <AntennaColor>orange</AntennaColor> |
| … |
| </CharacterData> |
| </Taxon> |
| <Taxon> |
| <EFGPath> |
| <Genus>Mechanitis</Genus> |
| <Species>polymnia</Species> |
| </EFGPath> |
| <CharacterData> |
| … |
| </CharacterData> |
| </Taxon> |
| … |
| <Taxon> |
| … |
| </Taxon> |
| </TaxonList> |
| </EFGImportDocument> |

To present to a user with data arising from several heterogeneous sources there are fundamentally two approaches. One may build an integrated database and import each source, or one may build a federated view in response to a particular query that is executed—possibly after rewriting—against all of the data sources. The UMB-EFG architecture supports both, but our current implementation is only of the former. Later we describe some preliminary work in federation in which the UMB-EFG could potentially be one of the data sources, rather than a federating data consumer. However, even in our current implementation, any application anywhere on the Internet could make an IP connection to our Java servlet middleware and make queries in the same way our own HTML forms and Java servlet front-ends now do.

When we import data from an author's database we produce intermediate XML with the character data and such taxonomy as is described in the data source, and we require the author to provide some simple external taxonomy in XML form, namely <CommonPath> element in the example in Table 2. This latter specifies a position in the taxonomic tree at which the group is to be attached, specified as an edge-labeled path in the taxonomic tree, with edges labeled by the taxon level and nodes by the taxon name. The edge labels, i.e. the taxonomic level, are generated automatically—the author need only supply the taxon name. Authors can use simple available tools, such as Microsoft XML Notepad, to provide this CommonPath information. Edge-labeled digraphs have been considered previously for taxonomic data representation (Zhong et al., 1996), (NCGR, 2000). All data in the source must have taxonomy specified relative to the terminal taxon of that path. For example, if the source provides character values for the Ithomid butterflies, each record would provide genus and species. Typical XML generated by the importer is illustrated briefly in Table 2. From XML representation to JavaBeans is a transformation well-supported by currently available Java classes.

In Ithomid butterfly example, the imported data would normally be expected to have a field labeled Genus and one labeled Species and the data will be created in the taxonomic tree by subtrees under the Ithomiinae node, each subtree having edges labeled *Genus* and *Species* and with nodes appropriately named from the values in the imported data. Also, where appropriate, we treat various life forms (e.g. larva, pupa, etc.), and also each sex if the data identifies them as different, as though they were at a taxanomic level below species.

In addition, we have metadata for each character that comprises:

- The character name (e.g. *similarSpecies, 'foreWingSpotPresent')*
- A character type (presently either *morphological* or *ecological*)
- A numeric weight by which the author has ranked the character as to its importance in identifying an organism (See Dallwitz (1999b) for a discussion of this issue.)
- A string describing whether there may be multiple data in the same field
- A data type, presently one of *simple data, image filename, sound filename,* or *taxon reference.* A taxon reference is a reference to another taxon already in, or to be inserted in the database
- A Java data type.

Ultimately, we intend to treat this metadata with an XML Schema (W3C, 2000a) but currently the Java support for XML Schema is not mature. However, at this writing many other XML tools are.

## User interfaces

Our three-tier interface allows us to support a variety of user interfaces. We presently have three in place, requiring increasing levels of biological sophistication.

The first of these is a purely visual interface to the Ithomid butterflies of Costa Rica, designed by one of us (Haber) with extensive field experience in the subject. In this interface the butterflies are first divided into four visually distinctive groups ('Tiger' 'Clearwing', 'Yellow and Black', and 'Translucent Gold'). We display a conventional tree browser, functionally identical to the file system browser found on Windows but instead of folder and file icons, the icons are thumbnail images of actual Ithomids representative of the group. As with a file browser, the user can click to expand one of the icons to another series of 3-4 butterflies representing a more subtle visual distinction within the group. This continues recursively about four deep and usually 3-4 wide. At leaf nodes of this tree, clicking brings a descriptive page for the species identified. There may be several paths to the same species, so internally this UI is represented not by a tree but by a directed graph (digraph). Digraphs are familiar data structures that have found related application in biological keys (Beaman et al., 1999), (Zhong et al., 1996), (NCGR, 2000). Note that key digraphs are not, in general, trees. That is, there may be several paths to the same taxon. We believe that a purely visual interface corresponds closely to the way amateurs use field guides, because we find that amateurs quickly get lost in traditional dichotomous keys and their generalizations. The biggest issue with this or any key is to verify that the identification is in fact correct. As an aid to this, our species description pages also contain links to similar species so that the user may compare their chosen species to ones that the author warns may be confused with it.

The second interface is a tree browser that follows the standard taxonomic tree, similarly to the Tree of Life project (Maddison, 2000). That system moves from web page to web page in the tree traversal, whereas we use the same Java tree browsing classes underlying the visual key. Hence, as for a file system browser, we keep everything on the same screen. The population of our database is presently too small for us to decide whether the attendant required scrolling would be counterproductive in a collection as large as the Tree of Life.

Finally, we have a pure html form-based character-value interface. The forms are constructed on-the-fly from the database, and the middleware builds and serves the form to the browser. Each form field offers the user the possible character states. The user can select the maximum number of species they wish to have offered that meet the current character value choices, and if the system finds more, the user is invited to limit the output by further choice from another character. In our present implementation we do not illustrate those choices as do a number of systems, but this is not precluded by our architecture. Without such illustrations, our interface is suitable mainly for users with some training. The use of characters with a finite number of states complicates naturally continuous numeric characters with ranges (Dallwitz, 1999a).

Because our species description pages are made up by the middleware in all cases, it is not difficult for us to produce XML instead of HTML for description pages as we do in the present implementation of our servlet middleware. Doing so has well-known advantages, some of which we have been exploring even though we do not yet output XML. These are discussed in subsequent sections.

## Federating and transforming XML data

Here we describe our preliminary application of XML technologies to some of the issues arising in biodiversity software. Our experience as yet is too small, and the tools too new, for us to offer many engineering insights, so this section is devoted to discussing the capabilities of our prototypes and our current directions. All the applications in this section may be reached from the link 'recent XML work' on our home page http://www.cs.umb.edu/efg. This work is supported by a subcontract from the University of Kansas Biodiversity Research Center under their NSF grant KDI-9873021.

The range and quantity of biodiversity data on the web is large and rapidly growing (UNO, 2000). It is presently difficult to combine data from this large collection of sources for several reasons. First, few such sources publish or support any API to the underlying databases. Therefore, anyone who wishes to interrogate such data programmatically must reverse engineer the arguments passed by the publisher's web interface.

A second impediment to data federation, despite the explosion of XML support, is that the pages that are returned are generally HTML and so contain detailed presentation markup and little, if any, markup of structural or biologically descriptive utility. The Tree of Life project (Maddison, 2000) embeds special markup in support of its own web crawling engine, and this can serve some of the requirement for metadata that can be addressed with XML. We are aware of a number of projects imminent or underway to serve XML, including the Integrated Taxonomic Information System (ITIS, 2000), (ITIS$^{*ca}$, 2000), a joint project of the US Department of Agriculture and the Canadian Ministry of Agriculture. ITIS$^{*ca}$ already has experimental XML service on its site. The Biodiversity Research Center of the University of Kansas has implemented a gateway from Z39.50 servers to XML (Vieglais, 2000), about which we say more below. Indeed, anecdotally we understand that many biodiversity database maintainers and designers intend to serve XML.

XML is widely accepted as a data exchange language and for the specification of metadata and of configuration. We described above some of this use for the UMB-EFG itself. Early public uses of XML as a replacement for HTML for presentation focused on transforming XML to HTML in the browser (supported to date mainly in Microsoft Internet Explorer 5 (MSIE5), and we describe some demonstrations of that below. More importantly, XML can also be used for federating data from heterogeneous data sources (Abiteboul et al., 2000), (Baru et al., 2000). We will next sketch our experiments with these applications of XML to biodiversity software.

XML holds the promise of extremely flexible user interface configuration. Either at the server or in an XML-aware browser, a separate stylesheet is written in XSLT, the transformation language of the XSL stylesheet language (W3C, 2000a). This transforms the XML representation of, say, a descriptive taxon page, into HTML in a manner suited to the browser user or to the policies of the host that is forwarding the XML page (which may well be different from the host holding the original data). For example, among the XML demonstrations linked on the project page (Stevenson and Morris, 2000), we have one in which a number of static species description pages from various sources may be displayed with a number of sometimes widely varying styles (including one that shows the raw XML). When using MSIE5 the user need only push a button in the control panel to instantly change style sheets, the redisplay being handled in the browser itself and not requiring any return to the server for the new view.

Because XSLT is very general, it is possible to make mini-applications simply by transforming to a restricted view. For example, one of our applications accepts a list of (suitably marked) XML species description pages and produces a table of references in each of those pages to other taxa. This application looks like a database operation, but in fact is carried out entirely in whatever is executing the XSLT (in our case, the MSIE5 browser).

Another XSLT application we show is a bilingual display. With a single button click in a control frame, a species page is toggled between a Spanish and an English view. Again all transformations are done by the browser. In this application, text in both languages is kept in a single file (easing maintenance), with a language attribute on each text element. Under control of a simple Java Script program in the control frame, a single variable ('*currentLanguage*') is toggled and a single XSLT function displays an element only if its language attribute matches *currentLanguage*.

Among applications of XML, the promise of support of database federation is the most distant from the conventional applications of XML, but it is also the most challenging and interesting application. There is substantial advantage to standardized DTD's (or better, XML Schemas when they are stable) to combine data from various sources (Baru et al., 1999), (Baru et al., 2000). But recent research suggests that suitable schemas can be inferred from the sources themselves (Ludäscher et al., 1999), (Abiteboul et al., 2000). For the moment we use a fixed DTD and code static XML species description pages to that somewhat spare DTD. Those pages lack complete taxonomy, containing, as is typical, only the genus and species name. We have built a distributed federator based on (a very small part of) that known DTD, and knowledge of the query syntax of *zportal*, an XML/Z39.50 gateway built in The Species Analysis (TSA) project (Vieglais, 2000). Z39.50 is an international data exchange standard in wide use in government agencies and more recently adopted by many museums for their collection data. Because we use the zportal, details of Z39.50 are unimportant here, but they are discussed at the technical pages (on a link named 'Z.X') of the TSA site. In our federator, a JavaScript control panel on the application page looks into the static XML species page to find the scientific name of the species described. This is sent to a mediator on our web server, a Java servlet that understands both the zportal query syntax and the location of taxonomic resources on the web. In this case, these resources comprise a small fixed collection of Z39.50 servers that offer taxonomic authority for specific collections of taxa. The mediating servlet queries each source until it finds the taxonomy for the given species, translates the XML returned by zportal into something user-friendly, and returns a combined page to the browser. (The zportal software returns XML, but based on a DTD whose element tags are simply XML rendering of the underlying numerically coded Z39.50 record tags).

The federation application described above finesses a number of difficult points that are the subject of our (and others') future work. The problem of resource discovery, e.g. finding taxonomic authority servers, is a deep and interesting one that appears in many similar contexts. So also does query rewriting in case the sources require different query syntax, and record rewriting in case the sources have different record semantics

Finally we mention an interesting issue that is the subject of work we are just starting: circumscription control—the control of the forwarding of sensitive data obtained from trusting sources. Some biodiversity data is sensitive (e.g. the precise location of specimens of endangered species). Consequently this data is often made available only to users who are trusted by the data holder not to abuse it. Unfortunately, most existing biodiversity data is held in databases with granularity of circumscription no finer than the entire database itself. No provision is in place to prevent access to sensitive data on a field-by-field basis or even a record-by-record basis. For example, specimen location data is sensitive only for endangered species, so circumscribing all location data is debilitating to many legitimate users and applications. To address this issue we are designing a *circumscription broker.* This is a set of protocols and software by which a data source can specify its circumscription policies and trust the broker to enforce them, thereby leaving the source able to serve entire records at will. Because the broker is acting on behalf of a database mediator, which is disassembling and reassembling records for the federated view in any case, the task of enforcing the circumscription belongs at the broker/mediator and mediator/query-response interfaces.

## Conclusion

Biodiversity software is best implemented with software tools designed for dealing with data diversity. The engineering details of these tools can be hidden from the biologist who must use or populate the systems built around them. Java and XML technologies prove both suitable for this purpose, and highly synergistic with each other. Using them we have demonstrated an extensible web-based Electronic Field Guide and how to build applications that federate data from distributed sources around the internet.

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# Technological opportunities and challenges in building a global biological information infrastructure

Hannu Saarenmaa [12]

## Abstract

An overview is given how the newest e-business technologies can help to manage biodiversity information. The possibilities have increased dramatically just over the one or two past years. It is important to see the difference between infrastructure, meant to provide shared building blocks, and applications that are there just to solve a specific problem. Many of the new possibilities especially enable the building of infrastructure and are important for global cooperative processes such as CHM and GBIF. Many of them are based on XML that unifies presentation, data and document management. It enables information interchange with both human and computer-readable packages. Using XSL the information can be viewed from various angles. Biodiversity namespaces in XML Schemas should be standardised urgently. Examples of content that should rely on XML from this on include taxon homepages and observation data. Analogously to Internet's DNS, a new addressing system for scientific names of organisms could be designed using stable numeric identifiers. This would be used to overcome the volatility of the Linnéan names, which are not suitable for keys in information interchange. Using such global IDs for both taxa and names, biological information could be addressable from web services worldwide. How these information infrastructure components might be used in the web services of GBIF such as the Catalog of Names of Known Organisms and the SpeciesBank is discussed.

**Keywords**: taxonomy, biodiversity, informatics, DNS, XML, registries, web services.

## The challenge

It is year 2000 and the computer industry has successfully welded off the dreaded Y2K problem that once threatened to shut down the techno-society. It is time to start focussing on the less-known Y3K bug: In the year 3000, there will not be a single species left on the planet if the current rate of extinction is linearly extrapolated. This is based on a best available guesstimates [13] of extinction rate 10^4 per year out of a 10^7 total species. Naturally, the development will not be linear, and the future could be different. The cause of this development is well known: Habitat destruction, which follows from low value of biodiversity, which follows from lack of knowledge about it, and poor access to information.

According to Groombridge (1992) the rate of discovery of new species happens to be of the same magnitude 10^4 per year as the extinction. This rate has remained the same over the past 30-40 years. The slowness of discovery projected against extinction means that one half of the species will not be discovered until they are lost. Again, the development is not going to be linear and it is reasonable to assume that collections already are hiding in them about a similar number (2*10^6) of undiscovered species as there are known organisms.

Regardless of how these projections are going to develop, the facts remain. Serious things are happening and there is poor use of knowledge and difficulty in information access. Meanwhile, taxonomic and biodiversity information is mushrooming on the Internet. Species homepages are spontaneously being created everywhere. Giving a scientific name to a general-purpose search engine returns hundreds of hits that also include serious

[12] hannu.saarenmaa@eea.eu.int; http://www.eionet.eu.int/; http://biodiversity-chm.eea.eu.int/
[13] http://www.iucn.org/info_and_news/press/species2000.html

documentation by competent authors. However, there is almost no coordination, nor standards in this area, and certainly no quality assessment of these content is available. There is only the plain information infrastructure of Internet and variably applied scientific names.

How did it come to this? The main problem is the working habits of taxonomists – taxonomy has not been understood as a separate information science, but has been too closely been coupled with systematics. Outsiders often see taxonomy as an endless sink of resources because its returns are so slow and not shared effectively. Traditions weigh heavy and there has been very little on-line publishing of copies of new taxon descriptions. The Linnéan naming system is volatile and does not support modern information access. In order to cope with the volatility, there is built-in slowness in the Codes (International… 2000) that regulate establishment of new names. There are complex intellectual property rights issues between north and south, requiring repatriation of information ([14]).

Reflecting about the unhappiness with the situation, there has been a proliferation of initiatives and cooperative networks ([15]) and hence plenty of organisational response. However, a technological response has usually been less effective. This diversity, however, signals that some necessary ingredients have been missing from the services of all these networks. I believe what lacks is a better understanding of what constitutes an information infrastructure.

The purpose of this paper is to give an overview to the information infrastructure components that would better allow taxonomists to share and reuse information. Current developments on Internet and e-business have opened a plenty of new possibilities. Indeed, the upcoming Global Biodiversity Information Facility (GBIF) is expected to put the infrastructure components in place for the service of biodiversity informatics.

## What, exactly, is infrastructure?

*If I have seen further than other men, it is because I have stood on the shoulders of giants'* said Isaac Newton of his works, pointing to the history of science all the way back to the ancient Greeks (Turnbull et al. 1959).

The essence of infrastructure is building on each other's work using standardised interfaces. Instead of directly working together, an intermediary shareable service is made available. Scientific publishing is one such service.

There are many kinds of infrastructure, and most people understand it as something purely physical, such as hardware and wiring. However, infrastructure can also be immaterial. Indeed, 'information infrastructure' is everything that supports the flow and processing of information ([16]). It consists of various standards, services, and support actions for representing, addressing, locating, exchanging, and securing information. Building such infrastructure does not necessarily require a mega-projects and new organisations, although they are often viewed as that way ([17]). A simple standardisation process is where to start.

The separatedness of computer software applications and the underlying information infrastructure is seldom fully understood. If you want others to build on it – then you are building infrastructure. These are characterised by the usage of open, standardized interfaces (where to go) and communication protocols (what to say). Examples include IP, Z39.50,

[14] http://www.biodiv.org/doc/meetings/cop/cop-05/information/cop-05-inf-03-en.pdf

[15] An incomplete, alphabetically arranged list of abbreviations to biodiversity information networks and services includes at least the following: ABREN, All Species, BCIS, BIN21, BIODI, BIOSIS, CBD, CHM, CONABIO, DIVERSITAS, ECNC, ETC/NC, EWGRB, GBIF, IABIN, IBIN, ILDIS, INBio, IOPI, IPNI, ITIS, IUCN, MAB/BIS, NBII, Species 2000, TDWG, Tree of Life, WCMC. Individual projects with a begin and an end have not been listed.

[16] http://www.whatis.com

[17] .... organizing the information from biological collections would need Museums to develop of standards for data, and database large numbers of records. Providing information in a maximally accessible form could require a distributed database system, probably integrating massive data handling environments with the web. The third aspect, application of that information to meet the needs of society requires integration with analysis and visualization capabilities..'.— *An excerpt from early NBII plans*

LDAP, IMAP, CORBA, SQL, and Posix. However, if you just want to get one job done — then you can build an application, and perhaps hope that others could use it as is. Popular examples include Microsoft Windows and Microsoft Access. Mature, successful, shareable applications often migrate to infrastructure. For instance Microsoft Office is currently found in most personal computers and one can travel with a PowerPoint file and have some confidence that the file can be opened at a remote presentation location.

Infrastructure services are typically built using a layered approach (Figure 1) where services are built on top of each other. Interoperability is achieved when an interface at one level can connect to the next and understands a protocol, which is used to express needs of requesters.

A simple example of infrastructure services is directory service. It is possible to use hierarchically arranged data on people, organisations, and their groupings with the Lightweight Directory Access Protocol (LDAP) on connecting to an appropriate port of a directory server on the Internet. Existence of such an open interface and a related protocol makes it possible for others to build applications that use directory services. These include roles and expertise, security services and accreditation mechanisms can be built on it. Also email applications increasingly build on directory services. Examples include 411.com, Infospace.com, and EIONET ([18]).

What the information infrastructure components would be for biodiversity is discussed in the rest of the article. They are tentatively identified in Figure 2. Special reference is made to the GBIF plans on these areas (OECD… 1999).

## Naming and addressing biodiversity information

Telephone system is one essential community infrastructure. Its usefulness is greatly facilitated by a phonebook linking the names with unique phone numbers that can be called. Similarly, the Internet has a Domain Name System (DNS) (Albitz and Liu 2001) that maps names of computers to IP numbers. They uniquely identify computers' network interfaces, so that data packets can be sent to them. The World Wide Web has Universal Resource Locators that point to files on web servers, so that a web browser can download them.

Names of biological organisms form a comparable phonebook, in fact, a semantic hierarchically arranged network. However, there are no numbers to call, yet.

### *Catalog of Names of Known Organisms*

The GBIF aims at compiling a global Catalog of Names of Known Organisms (CNKO). As Figure 3 illustrates, it would be used to link to all the other data. Therefore, it is clear that it is not just a database application that allows search and lookup of only the names themselves. Such a service has already been achieved for many groups by the federated databases of the Species 2000 ([19]), and there is no need for a duplicating that effort. Instead, the CNKO would have to be a resource discovery mechanism similar to the phonebook, DNS, or those currently being proposed for e-business.

(18) My organisation EIONET provides a directory service at ldap.eionet.eu.int, port 8983, root ou=users,o=eionet,l=Europe.

(19) http://www.sp2000.org/

Figure 1. Three sides of an interoperability pyramid picturing an application, communication, and content harmonization infrastructure. Different layers of services build on each other using standardized interfaces. Examples are given in parentheses

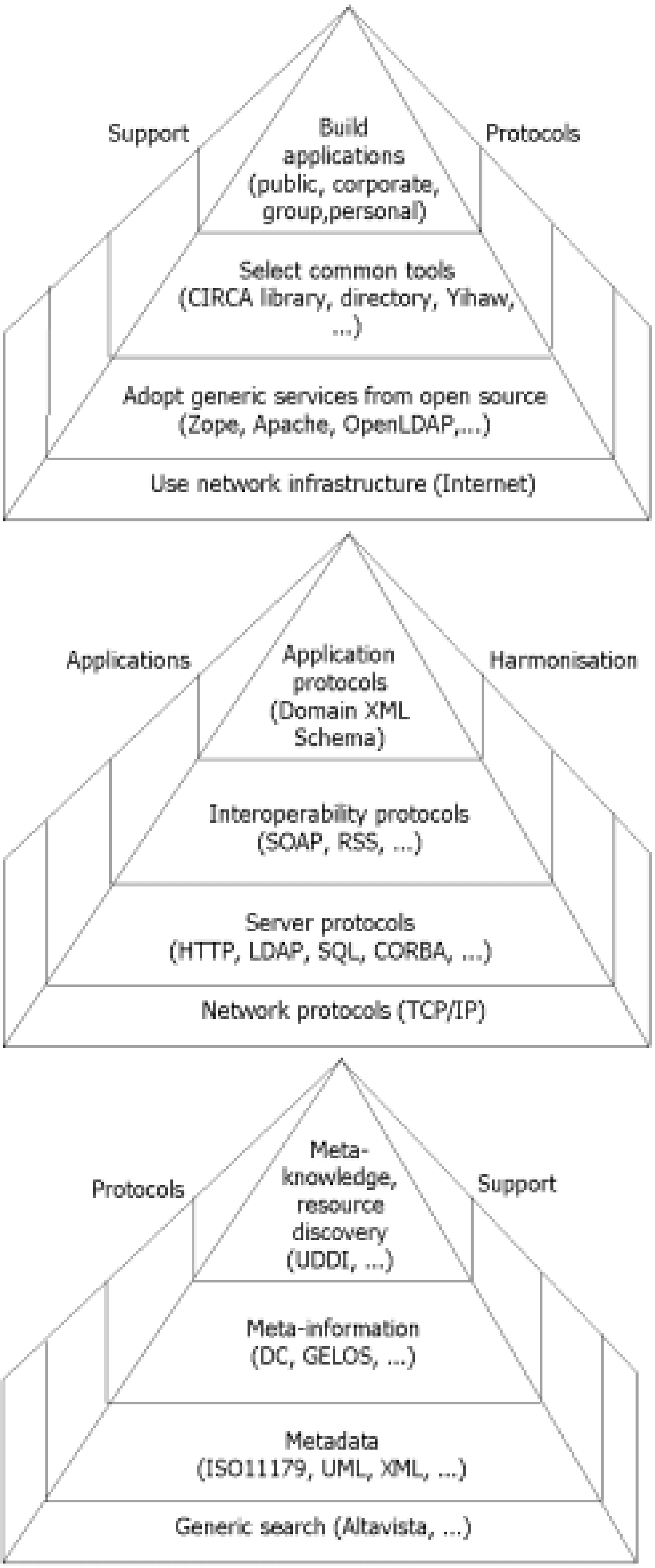

Support
Build applications (public, corporate, group,personal)
Protocols
Select common tools (CIRCA library, directory, Yihaw, ...)
Adopt generic services from open source (Zope, Apache, OpenLDAP,...)
Use network infrastructure (Internet)
Applications
Application protocols (Domain XML Schema)
Harmonisation
Interoperability protocols (SOAP, RSS, ...)
Server protocols (HTTP, LDAP, SQL, CORBA, ...)
Network protocols (TCP/IP)
Protocols
Meta-knowledge, resource discovery (UDDI, ...)
Support
Meta-information (DC, GELOS, ...)
Metadata (ISO11179, UML, XML, ...)
Generic search (Altavista, ...)

Figure 2. **An example of a biological interoperability pyramid**

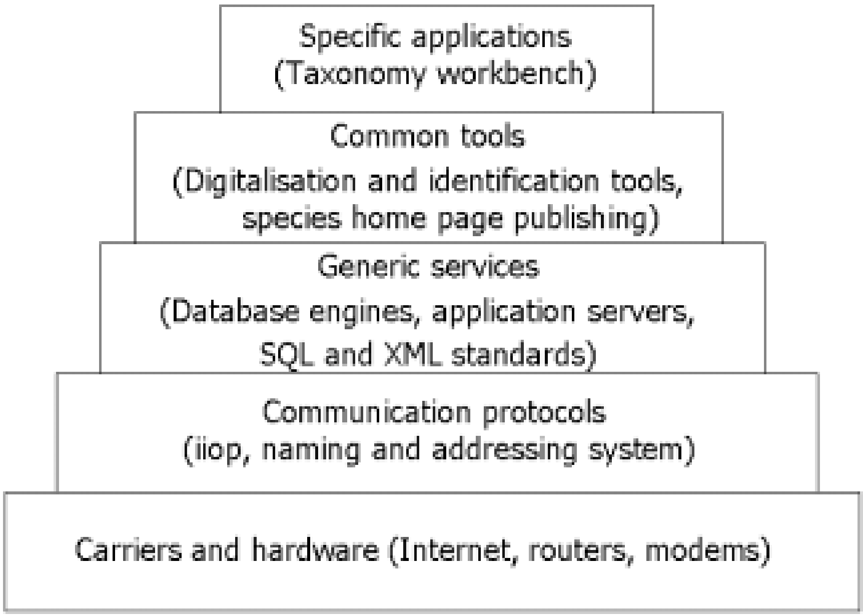
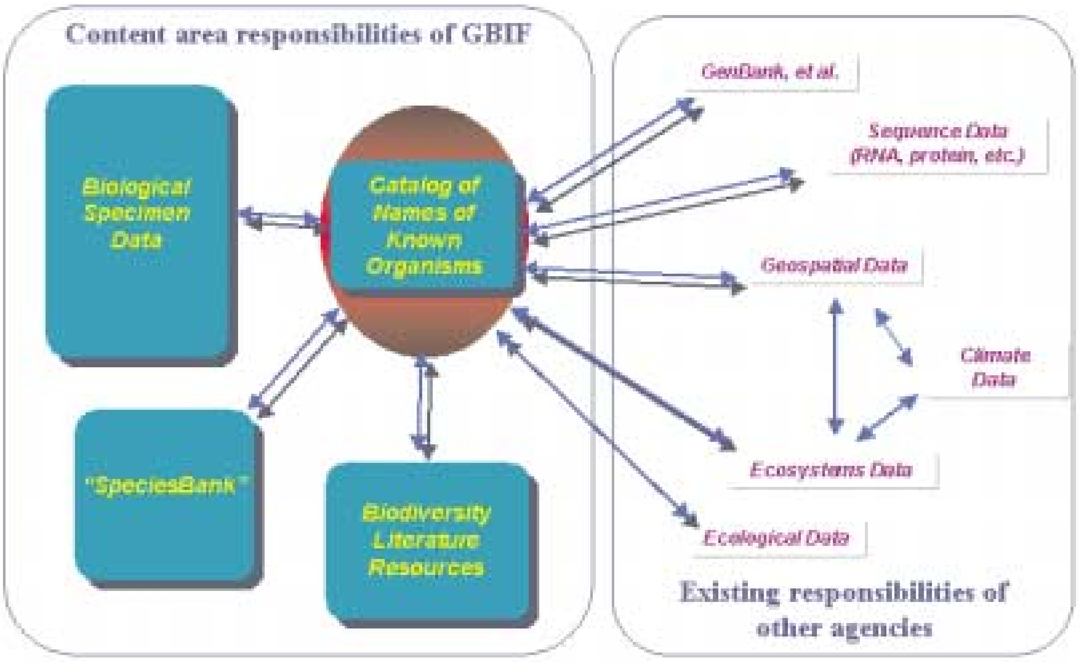

Specific applications
(Taxonomy workbench)
Common tools
(Digitalisation and identification tools, species home page publishing)
Generic services
(Database engines, application servers, SQL and XML standards)
Communication protocols
(iiop, naming and addressing system)
Carriers and hardware (Internet, routers, modems)

Figure 3. **The GBIF would enable synergism among existing investments that is not possible at present. The Catalog of Names of Known Organisms is the key linking component in GBIF information architecture**


Content area responsibilities of GBIF
Biological Specimen Data
Catalog of Names of Known Organisms
"SpeciesBank"
Biodiversity Literature Resources
GenBank, et al.
Sequence Data (RNA, protein, etc.)
Geospatial Data
Climate Data
Ecosystems Data
Ecological Data
Existing responsibilities of other agencies

If the name is used as linking mechanism it must have other qualities than just describe a placement of an organism in a certain genus or higher taxon, species and subspecies. It must be short, unique, stable, and universally accepted.

Unfortunately the Linnéan name system does not fulfil these requirements alone. The names are not short, they change their form, they are not always associated with the same taxa, and are even used variably in the different parts of the world. Association with taxa will always remain subject to change, which should not be seen as a problem, but as progress and a result of taxonomic research. However, the other problems could probably be overcome by adoption of new globally unique identifiers for both names and taxa, such as the taxonomic serial numbers used and maintained by ITIS ([20]) and the taxon codes once created by the Nordic Code Centre ([21]).

Creating unique identifiers for names is straightforward. However, linking them to taxa is not. The only solid anchor to taxa is the name-bearing type specimen in some collection. This means that also these type specimens must bear globally unique identifiers (and be digitalised, see section 5 below). Then a linkage must be made between the type specimen identifier and the identifiers of names that have been used to describe it. It is this link, which can be called a taxon identifier that can be reused to point to other information.

Stability of names is beyond this discussion, but a few side notes could perhaps be allowed here. Much could be achieved if the concept of genus would be discontinued. Moving over to Phylocode (Cantino et al. 1999), which essentially means adoption of only single-word names would eliminate changes in the form of names and also reduce the frequency of other name changes dramatically. However, as common names in many languages will still have to be supported, there is no avoidance of synonyms of some kind. Hence, synonymy should be fully supported by any addressing system.
These requirements resemble a lot those of the Internet's DNS. So it is worthwhile to consider how far the analogy would go.

### *Addressing*

A scientific name is unique within a kingdom. So, something like http://sylvestris.pinus.plantae.bio/ should in principle work ([22]). What would it return? ([23]). Given to a web browser, it would first be translated by the DNS to a unique IP number, such as 130.226.11.38. Then the **one server** listening the default port of the Hypertext Transfer Protocol in that interface number would return its default content, that will be called the taxon home page (THP) in this paper. The THP would probably be an XML formatted rich homepage of the content that can be associated with that name. More about use of XML for THPs below.

The DNS routinely works with synonyms, so entering silvestris instead of sylvestris would be possible to map to the same IP number. Scots.pine is not a problem, either.

However, as there probably are dozens of equally qualified scientific laboratories that can put up authoritative content under this name, it would lead to interesting discussions at the pinus.plantae.bio root name server authority for whom to assign sylvestris. One possibility is to assign it to the institution that holds the holotype specimen, but as these may not always be capable of providing such a service, this could not be the rule. Wherever the THP is assigned, some sort of registration and broadcasting mechanism from the there on to all other sites providing related content should be devised.

One possibility is to build on the upcoming IPv6 that allows 16-byte IP numbers instead of the four of the currently used IPv4. IPv6 also comes with a broadcasting system, so that the query, which in the above scenario would go to one server only, could for instance go to all the 255 servers under 130.226.11.38.* (we don't show the 11 heading bytes here). IPv6 has so much address space that hundreds of IP numbers can be assigned for each m$^2$ of Earth's surface. It should be possible to allocate a set of 255 numbers for each known taxon. However, as an Internet Service Provider actually owns its set of numbers and handles the routing to them, using a fixed set of numbers is not straightforward, and would require elaborate reverse proxy schemes at a central location.

[20] http://www.itis.usda.gov/
[21] http://www.nrm.se/ncc/
[22] Of course, a top level domain .bio does not yet exist.
[23] Entering *Pinus sylvestris* to AltaVista search returns 6251 hits today. Several of these are serious, elaborate home pages to the species.

To summarise, the DNS offers interesting possibilities for linking biodiversity information. It maps changing computer names to stable IP numbers easily. However it requires additional layers of standardisation in order to support resource discovery beyond a single THP.

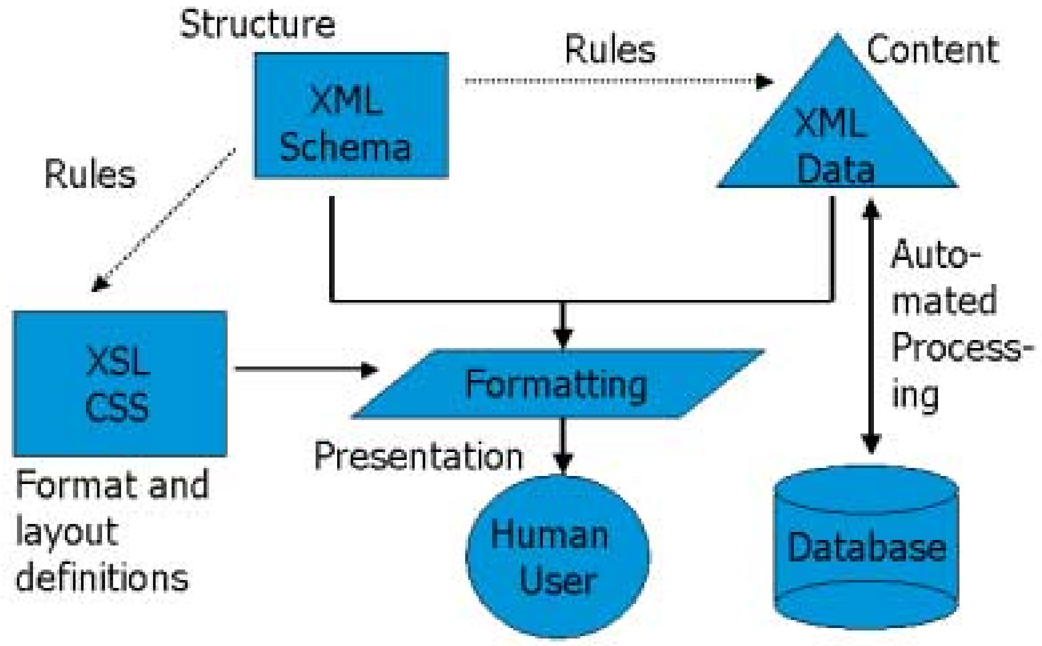
## Representation of biodiversity content

Biodiversity information covers many levels of aggregation, such as molecular, genetic, species, population, habitat, site, and ecosystem. The two first ones have had their representation issues solved by the bioinformatics research community. Ecosystem modelling has thrived also for decades in ecological research. The biggest unresolved question is on how to represent species-level knowledge.

Earlier we identified taxon home pages (THP) as a main form of such content. These should not be understood as simple web pages in HTML, but as semantically well-organised pieces of knowledge. They need to be viewable by humans as simple or elaborate web pages, depending on the user needs. They also need to be understandable by machines for automated processing.

This can all be achieved by using the eXtended Markup Language (XML) for representing species-level biodiversity information. The XML idea is to separate content from presentation so that it can be semantically understood by machines and processed automatically (Figure 4). There are many excellent books on XML (e.g., Harold 1999) so we skip general overview to it and only discuss the basics of representing taxonomic information in XML. This is a hot issue in biodiversity informatics research currently.

Figure 4. **The structure of XML data is defined in XML Schema and is separate from its formatting information on XSL**



On regular web pages, the content and formatting are hard-wired. Tags such as <I>Pinus sylvestris</I> around the italicised Latin name of a species contain no hint of what has been placed inside these tags. On XML, the same could be tagged <NAME>Pinus sylvestris</NAME>. However, now there is a need to say that all <NAME> tags should be formatted using <I> when viewing on regular web browsers. This is achieved by the eXtended Stylesheet Language (XSL). When viewing an XML file, new web browsers can choose among several XSL files so that different views can be generated to the same content. However, as this requires the browser to actually understand XML, this step of XML Transformation is often processed by the server and plan HTML returned.

XML format makes it possible to analyse and process web page content automatically. XML files are therefore very popular in data exchange and are in fact replacing all other formats. However, a new problem emerges when XML files have to be understood by computers. They have to be built according to some rules so that some logical entities are formed. Otherwise the content could be misinterpreted. These rules are expressed in XML Schema language.

Table 1 illustrates how a THP would look like in HTML and XML. Table 2 shows an XML Schema that can be used to define how THPs should be formed. Of course, most THPs in XML would be formed automatically from content in databases. End user support for creation of these XML files should probably be provided by a specialised client application.

A simplified taxon home page in HTML (left) and XML (right) Table 1.

| | |
|---|---|
| <HTML><br> <HEAD><br> <TITLE>Homepage for<br> Cosmotriche lobulina</TITLE><br> </HEAD><br> <BODY><br> <H2>Name</H2><br> <I>Cosmotriche lobulina</I>,<br> syn. <I> Selenephera lunigera</I>.<br> <H2>Distribution</H2><br> Palearctic.<br> <H2>Host</H2><br> <A href=http://www.examplesite.org/<br> ?ID=27.111.1.0>Pinus</A>.<br> </BODY><br></HTML> | <?XML version '1.0'><br><TAXON ID='122.120.10.1'><br> <NAMES><br> <VALID>Cosmotriche lobulina</VALID><br> <SYNONYM>Selenephera<br> lunigera</SYNONYM><br> </NAMES><br> <DISTRIBUTION>Palearctic<br> </DISTRIBUTION><br> <HOST><br> <ID>27.111.1.0</ID><br> <NAME>Pinus</NAME><br> </HOST><br></TAXON> |

An XML Schema that defines the XML taxon home page in Table 1 Table 2.

```
<?XML version '1.0'>
<elementType id='TAXON'/>
 <DESCRIPTION>A taxonomic unit, a homogenous group
 of organisms.
 </DESCRIPTION>
 <element type='#ID'occurs='REQUIRED'/>
 <element type='#NAMES'occurs='ZEROORMORE'>
 <element type='#VALID'occurs='REQUIRED'/>
 <element type='#SYNONYM'occurs='ZEROORMORE'/> </ELEMENT>
 <element type='#DIAGNOSTIC'occurs='ZEROORMORE'/>
 <element type='#DISTRIBUTION'occurs='ZEROORMORE'/>
 <element type='#LIFECYCLE'occurs='ZEROORMORE'/>
 <element type='#HOST'occurs='ZEROORMORE'>
 <element type='#ID'occurs='REQUIRED'/>
 <element type='#NAME'occurs='ZEROORMORE'/> </ELEMENT>
 <element type='#PROTECTION'occurs='ZEROORMORE'/>
 <element type='#REFERENCES'occurs='ZEROORMORE'/>
</elementType>
```

Most industrial and commercial sectors are now working on standardisation of their XML Schemas. The schemas can be registered on dedicated services such as OASIS [24] so that anyone interested in information interchange can download and use them. Recommendations already exist [25] for simple time and space representation, and XML records can be downloaded at least from ITIS today, but it is still a challenge for the biodiversity informatics community to agree on its own standards in this area. Such

[24] http://www.oasis-open.org/
[25] http://www.dublincore.org/documents/

comprehensive standards are called namespaces, and they can be referred to from the XML file. So it should not be necessary for every project to define its own XML Schema before being able to interchange data.

## Digitalisation

Biodiversity content is not just HTML and XML. There are many multimedia aspects that are important. Below we cover some of them. Going 'from atoms to bits' as conceived by Negroponte (1995), which in essence means tuning the physical object into its digital representation, brings numerous benefits. This can be done via imaging or by generating character-based descriptions of the objects for digital identification.

### *Imaging*

Digital imaging has recently become surprisingly easy and affordable. Today's garden-variety digital cameras produce 3 megapixel images that are large enough to fill the screen of even largest monitors. This resolution is enough to document almost anything that can be shown in 2 dimensions. Such an image can be downloaded even with a regular modem. Collapse of the costs of mass storage (disk drives and writable CD-R) has also made archiving such content inexpensive.

There are many benefits in digitalisation. Loans of material become faster and risk free, if the specimens or their details are digitised by their keepers, and the results are made available over the web. Imaging also acts as backup of the specimens in case that they are accidentally destroyed or lost. Also the original colours will be saved for future. Repatriation of information to the originating country becomes feasible. In fact it should no longer matter where the specimens are physically stored. They could even be stored in fumigated vaults only accessible to a robot…

Images do not necessarily have to be true representations of individual specimens. It is possible to form arbitrary non-existing species by 'morphing', i.e., overlaying many images with each other. Such an image could represent an intermediate step in an identification process. Possibilities for automatic pattern recognition and automated diagnosis have not been studied much.

The remaining difficulties in widespread digital imaging are mainly organisational. How to set up a system such that remote material requests are processed and the digital content is made available in a demand-driven fashion. There simply is so much material to be digitised that a supply-driven approach will not work. Another related matter is creation of the appropriate storage procedures. Even though mass storage is cheap, making backups and keeping material in order is still a chore.

### *Digital identification*

Traditionally identification of organisms has been done through literature, expert advise, and by comparing specimens with those already identified in collections. All these can be done, and also augmented with modern web services.

We have already covered how THPs could be made. Electronic field guides ([26]) consisting of collections of THPs can complement in an important way the printed media. They can include interactive features such as executable keys and links to new information that would have been released after a print date. Applied entomology, in particular is building heavily on home pages of economically important organisms and diagnostic expert systems that can reason over their content (Väkevä et al. 1996).

DELTA is a character description language that has been adopted by the international Taxonomic Databases Working Group TDWG ([27]) as a standard for data exchange. DELTA-

[26] http://www.cs.umb.edu/efg
[27] http://www.tdwg.org/

formatted data can be used to produce natural-language descriptions, interactive or conventional keys, cladistic or phenetic classifications, and information-retrieval systems (Dallwitz 1980, Dallwitz et al. 1993, 2001).

Remote human expert advise over the web is nowadays routinely available from several web services ([28]). It is only matter of time that similar specialised services appear for biology. Even today, without any special service a question posted on newsgroups such as sci.bio.entomology will not remain unanswered. However, the results do not accumulate and the practice is not common.

### *Electronic publishing*

Making the original taxon descriptions available on the Internet is of course very much desirable. Only using a digital format is not possible for a publication to be recognised. However, a workable combination of printed and electronic should now be possible, as the 4th edition of the International Code of Zoological Nomenclature (1999) states: *'A work not printed on paper (e.g., on a read-only laser disk) issued after 1999 in numerous identical and durable copies may be regarded as published if supplemented by identical copies deposited in at least 5 named and publicly accessible libraries.'* So, the paper copy is only needed for the record and archive anymore.

Descriptions have already appeared as preprints on Internet. Two new species of the plant genus Tetranema were documented on the InBio web site in 1996 before the printed publication appeared (Grayum and Hammel 1996). An enhanced electronic copy of the paper is still available.

Issues that remain to be solved in electronic publishing are mainly related to copyright. Will the traditional publisher, if employed, allow an electronic copy? Standards should be established how to represent a taxon description in XML. A registry of such descriptions is needed so that they can be searched and found.

## Registering and locating of biodiversity content

Above we have discussed how biodiversity content could be identified, represented, and turned into bits. The most important issue, though, is coming up with an infrastructure that motivates the users to contribute their pieces of content into the common pool. It is exciting to put digital images up on the web and create flashy taxon home pages, but if these are not contributing to a common, shared pool of knowledge, they remain just nice demonstrations. Value of such content is low.

The key here is to create a global registry of biodiversity content. It is rather surprising that such a key infrastructure component has received only little attention until lately. Examples how it might work and change how information is shared can be seen in other areas, for instance on GenBank, Napster ([29]), or any business-to-business (B2B) service that connects content providers together into a value chain.

### *SpeciesBank*

The GBIF plans (OECD… 1999, Figure 3) identify a 'SpeciesBank'. Not much has been yet written how it might work, but the following excerpts from the GBIF plans list the requirements.

- Link to any accessible existing database that holds information about species.

[28] http://www.allexperts.com/ ; http://www.experts-exchange.com/; http://www.sciam.com/askexpert/; http://experts.yahoo.com/

[29] http://www.napster.com/. When discussing Napster as a model technical solution, one should not be distracted by the unresolved IPO issues that affect that particular service. The biodiversity community has its IPO issues solved by the CHM and GBIF processes.

- Facilitate searching of Internet resources by non-specialists.
- Assist taxonomists to avoid re-naming already-described species.
- Enable rapid dissemination of information on newly discovered species.
- Speed up repatriation of information about species native to developing world.
- Increase the rate at which new species are described.
- Enhance accessibility of species information to users.

Above all, the SpeciesBank should be a central registry of distributed content, and facilitate new species discovery and description. By registry, we mean a place where meta-information of remotely held biodiversity content is stored and can be searched. This meta-information can be centralised so that many aspects of the content, such as names of taxa, locations, collections, observers, dates, etc. are held there. Alternatively it could only hold a minimum set, and the queries are forwarded to the original content providers. Probably a rich central meta-information set is better for users and robustness of the system, although it may not always be as up to date as a distributed one. Anyway, the provided meta-information fields must be soon identified. Appropriate standards such as Dublin Core ([30]) and RDF ([31]) should be built on.

An important question is how the remote content providers actually register their content such as THPs at the SpeciesBank. A manual entry using web forms is the simplest choice. However, if the content were provided in a form of rich THPs in XML, just sending an URL in an email would be sufficient.

A more sophisticated approach would be to design a special SpeciesBank protocol. A remote content provider would use a SpeciesBank tool to properly format the THP in XML and publish it on a local web server. The tool would then announce the new content to a central registry. This is how, for instance, the Napster registry of music works using its own client and protocol.

Another approach to discover distributed content is through portal web services. It should be attractive to maintain a central biodiversity portal using meta-information of the SpeciesBank. This could allow regular users to personalise the content the way they like and create an interface 'MySpeciesBank' that only shows the interesting content. Personalisation can be achieved in many ways, but one popular standard is Rich Site Summary RSS ([32]). That is an XML format for providing channels of information that can then be tiled up on the customised 'My' page.

In addition to providing access to distributed content, it could be harvested and archived into a repository. Certainly many sites with valuable content will go down for a variety of reasons. Unless explicitly forbidden by their custodians, cached copy of such content could still be made available. This concerns especially taxon descriptions and type specimen images. However, a fully central solution similar to GenBank is probably not desirable for species level biodiversity.

The link between CNKO and SpeciesBank is particularly intriguing. The CNKO forms a semantic net that is hierarchically arranged for taxonomy, but there can be many cross-links for other relations such as host-parasite. Such meta-information, if made available in SpeciesBank is very valuable when dynamically creating portals and other web services.

### *Resource discovery and database access*

Any biodiversity web service that covers more than just basic content will need to provide its contents dynamically from a database. There are many ways to make such a connection, but the most popular ones employ a language such as Perl, PHP, Python, Java and ASP, and database connector, like JDBC. More sophisticated approaches employ an application server such as Enhydra or Zope.

[30] http://www.dublincore.org/
[31] http://www.w3.org/RDF/
[32] http://my.netscape.com/publish/formats/rss-spec-0.91.html

The problem with database access is that databases cannot be directly searched using general-purpose search engines. Therefore their content must be made queriable by remote programs, or at least described somehow.

Not long time ago, the obvious answer to the access problem would have been 'query using distributed objects'. The database would have to be guarded by a group of agents that receive remote requests on protocols such as CORBA or COM+ from other objects somewhere on remote sites. Sophisticated agent formalisms are available for such communication (Saarenmaa 1999). Another approach is to use the Z39.50 protocol, as the Species Analyst ([33]). In order to make two databases able to interchange data such way, their data models would have to be harmonised with each other. Plenty of effort has gone into standardisation of taxonomic databases, especially in botany.

XML has changed the picture dramatically. No standardisation of data models necessary if only an XML data interchange format can be agreed on. Any taxonomic and biodiversity data model easily translates to XML Schema.

Moreover, there are other standards and protocols available from the e-business world that could be useful for resource discovery and remote access. Most of them build on XML, including ebXML ([34]); Universal Description, Discovery and Integration UDDI ([35]); Advertisement and Discovery of Services ADS ([36]); Web Services Description Language WSDL ([37]); and more. Particularly interesting is Simple Object Access Protocol SOAP ([38]), which can be used to invoke queries to remote databases after they have been discovered with some of the above-mentioned services. The relevance of all these new solutions should be studied urgently.

## Conclusion

Above we have covered how biodiversity information could be addressed, represented, digitalised and registered. None of these services will alone scale up beyond demonstration, but when pieced together into a standardised and shared biodiversity information infrastructure, breakthrough is possible.

To summarise the priorities, also suggesting an order of importance, the following things should be achieved in near future: 1) XML namespaces for taxonomic and other biodiversity information should be standardised. 2) Central registries of this distributed content should be started. 3) Electronic publishing (online copies) of new organism descriptions should be facilitated. 4) Digitalisation of types should become the practice and museums should stop borrowing materials in any other way. 5) A distributed biodiversity addressing system, including .bio Internet top-level domain will have to be studied further.

When the above has been achieved, I believe biodiversity informatics will emerge as a new important science and will help taxonomy to gain ground again. Entomologists who are responsible of the largest chunk of biodiversity information have a key role here.

(33) http://habanero.nhm.ukans.edu/TSA/
(34) http://www.ebxml.org
(35) http://www.uddi.org/
(36) http://d23xapp2.cn.ibm.com/developerWorks/web/ws-ads/index_eng.shtml
(37) http://www.w3.org/TR/wsdl
(38) http://www.w3.org/TR/SOAP/

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