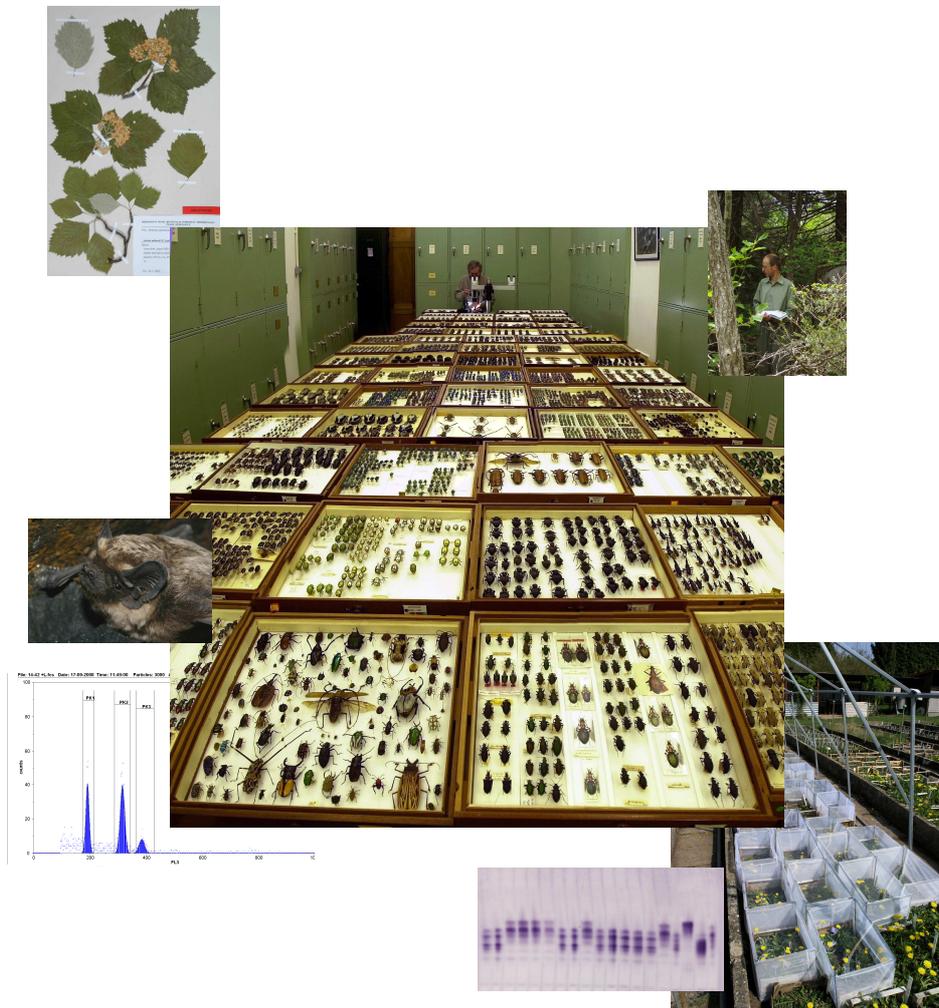


# Strategies in Taxonomy: Research in a Changing World



Report of an electronic conference, May 2009



Ministry of the Environment  
of the Czech Republic

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Cover pictures: Taxonomists at work, holotypus of newly described species, flow cytometry and gel electrophoresis outputs, *Vespertilio murinus*, dandelion's collections

Photographs: Courtesy of the Natural History Museum, T. Černý, P. Tájek, M. Lepší

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# Preface

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Research on biodiversity is essential to help the European Union and EU Member States to implement the Convention on Biological Diversity as well as reach the target of halting the loss of biodiversity in Europe by 2010.

The need for co-ordination between researchers, the policy-makers that need research results and the organisations that fund research is reflected in the aims of the “European Platform for Biodiversity Research Strategy” (EPBRS), a forum of scientists and policy makers representing the EU countries, whose aims are to promote discussion of EU biodiversity research strategies and priorities, to exchange information on national biodiversity activities and to disseminate current best practices and information regarding the scientific understanding of biodiversity conservation.

This is a report of the E-Conference entitled “Strategies in Taxonomy: Research in a Changing World” preceding the EPBRS meeting to be held under the Czech Republic EU presidency in Pruhonice, Czech Republic, from the 19th to the 22nd of May 2009.

# Introduction

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*Yde de Jong, E-Conference Chair*

This EPBRS e-conference on “Strategies for Taxonomy: Research in a Changing World” focused on identifying the key research questions allowing taxonomy to address policy needs in a better way and, vice versa, allowing policy makers to get responses from taxonomists on specific subjects related to the use of taxonomic knowledge.

Taxonomy, as a collectively assembled ‘Body of Knowledge’ formally started with the work of Linnaeus, is the most comprehensive and reliable source of information about biodiversity today. This includes specimen collections, character descriptions, geographic distributions, occurrence details, classification system(s), and links to associated information in literature and other resources. This accumulated ‘Body of Knowledge’ is well structured around the Linnaean system and is our baseline knowledge to monitor changes in biodiversity.

Although there are few doubts that taxonomic information is essential for reliable environmental science, applied users often complain about the inability to get adequate access to taxonomic information to respond to -for instance- the biodiversity crisis. This ‘taxonomic impediment’ is recognised within taxonomy by currently attempting to expand its capacity to explore and accommodate more species and to improve the dissemination and use of taxonomic information on the internet.

Due to these internal and external constraints, pushing taxonomy to advance its working routines and support the applied use of taxonomic information, taxonomy stands, at the moment, at a crossroads. Therefore it is critical for policy makers to make the right decisions for the future of taxonomy, now. This should, for instance, balance not only the emphasis stakeholders, researchers and society often place on new technologies and research tools but also the maintenance of core taxonomic research respecting the often exceptional level of expertise needed to explore and recognise species diversity.

Finding the right connection between taxonomists and policy makers is complicated because of the different intermediate parties (e.g. data centres, agencies and stakeholders) frequently obscuring a profound understanding of the relevance of taxonomy for biodiversity assessments for policy makers, but also hampering a closer commitment of taxonomists to fundamental questions on what information is needed (at what level and at what depth) for policy makers to make the right decisions. I hope this e-conference has contributed to a better understanding among decision makers and taxonomists of the relevant scientific priorities for future strategic policy plans.

# Summary of contributions

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*Fiona Grant and Juliette Young*

## **Week 1**

In his opening statement to the EPBRS e-conference, Yde de Jong set out the main aims of the e-conference namely to focus on identifying key research questions that could improve how taxonomy addresses policy needs and also improve responses that taxonomists should give to policy makers on specific subjects related to the use of taxonomic knowledge.

This week focused on the topic of 'Inventory and identification: What do we have, and how does it fit among its relatives?'. Philippe Bouchet opened discussions by outlining the concept of 'Biodiversity Salvage' as a means to improve taxonomic resources for the future. He argued that taxonomists needed to upscale their fieldwork and sampling dramatically in order to recover as much of the Earth's natural heritage before it disappeared, and to then preserve these species for later identification. In response to Philippe Bouchet, Martin Sharman expressed scepticism over salvaging the 'living dead' in order to examine them at a later date. Ferdinando Boero agreed with Martin Sharman and called for more emphasis to be placed on taxonomy being taught and studied again in universities, not just museums. He emphasized the need to study biodiversity concurrently at both the species and habitat level. Simon Tillier outlined a third aspect of taxonomic production not covered by Philippe Bouchet, namely making undescribed taxic diversity available for ecological analysis and decision making. He argued for the need to urgently start implementing a kind of 'meta-barcoding', which could provide a taxonomic baseline. In turn, this could enable better data for ecological decision making that could complement other new approaches and IT tools allowing for faster and better species descriptions.

Josef Settele considered whether taxonomy could increase its relevance if it adopted a more pragmatic and dynamic approach. In particular he argued for an adaptive taxonomic system that could encompass both the splitting and lumping of species when species status was unclear. He stressed the need for dynamic taxonomy that could allow for the variable conditions present in an ever changing world.

On the topic of collection and observation of data, Walter Berendsohn highlighted the importance of digitizing taxonomic information and outlined the key areas that needed to be improved. In particular he stressed that we needed to investigate the possibility of creating a comprehensive metadata index for European collections which could allow researchers to find specimen holdings relevant to their research. Vishwas Chavan also contributed on this topic, in particular explaining the main aims of GBIF (Global Biodiversity Information Facility), namely to discover up to 5 billion data records and mobilise up to 2 billion primary biodiversity records by the end of 2010. On a similar topic, Mauri Ahlberg suggested NatureGate® Online Services as a reliable source of biodiversity information that could be developed and then used to engage the public, policy makers and decision makers across Europe to promote biodiversity learning, conservation of biodiversity and sustainable use of biodiversity.

The week's discussions concluded on the topic of 'Understanding patterns and change: Where is it, what's happening to it, and where is it going?' Donat Agosti emphasized the need to take a global approach for species conservation and highlighted the need for conservationists and taxonomists to work together to achieve this. He also outlined how e-sciences could be used to help facilitate these potential collaborative efforts. Paulo Borges argued that the reason why conservation efforts were currently restricted to vertebrates and vascular plants was due to incomplete taxonomic descriptions of species-level diversity and the inadequate knowledge of species' distributions. He stressed the usefulness of having the

diversity of all species of a particular region available on the web with distribution maps and images of species for the general public to use and highlighted some initiatives that have already achieved this for specific areas.

## **Week 2**

Discussion continued this week on the topic of 'Inventory and identification: What do we have, and how does it fit among its relatives?' In response to Mauri Ahlberg, Zoheir Sabeur highlighted the need to consider decentralising EU or global databases and instead develop an open standardized interface in order to get access to world databases. He argued that a system of geo-distributed services should be created around the world which would enable a broad range of users to gain access, when and where required. In response to discussions on 'biodiversity salvage', Christos Arvanitidis argued that taxonomy needed to be integrated with phylogeny and molecular taxonomy and as many available tools as possible to allow taxonomic work to be based on a broader scientific basis. In response to Paulo Borges, Nikita Kluge highlighted the need to have a good understanding of systematics in order to develop databases that could become universal and permanent.

Dave Roberts opened discussions on the topic of 'Ecological functions and services: What does it do and what does it do it with?' He outlined the constraints of using the traditional revisionary monograph as a taxonomic tool and highlighted the benefits of a dynamic monograph, as pioneered by CATE, cyberplatforms and scratchpads, as used in the EDIT project. A lot of discussion ensued around this topic. Ferdinando Boero agreed with Dave Roberts about the need to update the old monographs and called for large European projects to be established that would be aimed at revisionary work of fauna and flora. Giuseppe Turrisi agreed with the need for a revision of taxonomic data and argued that revisions of phylogenetic concepts based on modern data and on simultaneous morphological and molecular data also needed to be carried out. Yves Samyn recommended that developers and authors of web-driven monographs needed to consider incorporating capacity building components into their open and dynamic monographs in order to speed up the build-up of taxonomic knowledge and skill, especially in developing countries. Ole Seberg emphasised the need for sophisticated identification keys and image recognition software to be integrated into cyberplatforms and scratchpads. Jan Dick agreed that web-based tools which enabled taxonomists to share information were essential and encouraged data from other fields of science, particularly ecology, to be incorporated into these databases as well.

On a similar topic, Jan Kirschner gave examples of the incorrect or imprecise use of taxonomic data in many summaries and global compilations to highlight the need for long-term work to be carried out on continental or world taxonomic revisions or monographs to enable critical evaluation of data on plant diversity. Chris Yesson described how phylogenetics and ecological niche modelling could combine to provide useful information on threats to species conservation from climate change. He also highlighted the fact that there was still a large deficiency of available data, particularly from the tropics, and emphasised the importance of digitising existing data collections as one way to help fill this data-gap. Hendrik Segers commented on the usefulness of bioinformatics tools at making taxonomic information more readily available to users. He argued that bioinformatics tools did not improve or increase our understanding of biological reality and biodiversity, but only facilitated access to information. Zoheir Sabeur, on the other hand, advocated that these tools' main inputs were to incorporate the missing elements that were required for assessing, monitoring and anticipating the spatial fate of biodiversity at global scales.

Christian Korner and Eva Spehn used mountain systems as an example of linking Geodata with biodiversity information in order to provide novel avenues towards testing evolutionary and ecological theory. They argued that with exact geo-referencing, climatic, topographical and geological data could be linked to organismic data, opening new avenues for research.

Otto Moog, Astrid Schmidt-Kloiber and Ilse Stubauer outlined the need for water quality assessments to include biological monitoring which taxonomists could contribute to by providing the required scientific basis needed to understand the ecological requirements of

species. They also emphasised the importance of re-introducing taxonomy into university curricula to ensure the future of taxonomy was not lost.

Dominique Richard and Doug Evans highlighted the need for taxonomic stability in order to develop biodiversity conservation measures. In response to this, Ferdinando Boero emphasised the importance of linking habitat diversity with species diversity to produce a practicable protocol that could assess changes in species diversity at a habitat level. Similarly, Sandra Luque agreed that in order to restore habitats, knowledge on species composition was essential. She argued that long term data was required to develop appropriate conservation and management options and to plan for changes within climate change scenarios.

### **Week 3**

Discussion continued this week on the topic of 'Ecological functions and services: what does it do and what does it do it with?' Discussions ensued following Jan Kirschner's contribution on 'assessing biodiversity richness' with Petr Petřík arguing that there was a need for a standard approach to mapping and analyzing species richness patterns, especially those based on small areas, and stressing the importance of further training for experts. Roberto Canullo agreed with Jan Kirschner that a full taxonomic revision at a continental scale was essential, but he also emphasized that this was an enormous task that may not be possible. Instead, he emphasized the need for research topics to focus more on species-specific features in order to be of a wider interest than pure taxonomic research topics.

Adam Vanbergen, Ben Woodcock and Rob Griffiths outlined the role of taxonomy in helping to resolve questions based on species' functional ecology. In particular they addressed the need to understand how the relationship between microbial diversity and ecosystem function would continue to operate in a changing environment. In response to this, Ferdinando Boero emphasized the need to link taxonomic knowledge with ecological knowledge at the species and community level, arguing that this improved knowledge would enable better management of ecosystems. Elena Bukvareva highlighted the need for future research to include intra-population and intra-specific diversity when investigating relationships between taxonomic diversity and ecosystem functioning. She also emphasised the need to elaborate on practical methodology, taking into account intra-population and intra-specific diversity along with taxonomic diversity in the course of environmental assessments, identification of conservation priorities and the operation of ecosystems and populations. Similarly, Klaus Henle argued that future taxonomic efforts and funding priorities should accommodate, at the conceptual stage, the needs of conservation biology and policy in addition to the needs of taxonomy.

Following on from last week's discussions Daniel Faith responded to Chris Yesson's contribution on phylogenetics and ecological niche modelling. He emphasized the need for more studies to be carried out to determine whether losses of phylogenetic diversity generally corresponded to the 'good news' or the 'bad news' scenarios with regards to species conservation. Daniel Faith also addressed the topic of 'taxonomy as a basis for ecological research and biodiversity conservation.' He made reference to phylogenetics in his discussion and also outlined the aims of the new DIVERSITAS project, Biogenesis, namely to help bring evolutionary approaches to bear on pressing biodiversity problems. Similarly, Angel Perez-Ruzafa argued that it was necessary for the identification of new species to be linked to their genetic analysis and also to their role in a given ecosystem.

Deng Palomares and Nicolas Bailly opened discussions on the topic of 'Open access to information: How do I find out this information and how do I manage it?' They addressed three main points: current taxonomic databases and their potential use with professional databases; the lack of taxonomic authorities; and ways to increase financial resources to respond to the professional demand for these biodiversity information systems. Mark Costello emphasised the need for sustainable online biodiversity systems and argued that in order to achieve this it was necessary for taxonomy to produce good quality data. Phillip Boegh highlighted the potential benefits associated with implementing direct 'Open Access' of public research. He argued that it was necessary for researchers to adopt a more open management structure, a fairer meritocracy and a far more open networking structure.

Wouter Los outlined the importance using a common infrastructure in order to promote large-scale common research priorities which in turn would promote large-scale funding and data generation. David Remsen discussed the need for an infrastructure that would permit interoperability in order to provide the raw materials needed to define a complete list of scientific names, coupled with the syntactic and semantic information that would enable names to be organised into a framework that had taxonomic integrity. He outlined how the “Global Names Architecture” would enable such a collective discovery and access system.

Further discussion ensued on the topic of integrating taxonomic work. Harvey Tyler-Walters emphasized the need to undertake basic research into the life histories and functional traits of species in order to gain a better understanding of ecosystem structure and function. Nikolay Sobolev emphasized the role that vulnerable species could play in assessing the state of ecosystems. Mark Costello agreed with previous contributions that there was a need for revisionary taxonomy to be funded. He suggested that this could be done thematically, for example invasive species and their relatives; for applied purposes, for example monitoring environmental quality; or to address knowledge gaps such as taxa with many undescribed species. Jean-François Molino emphasized the need to promote and develop ‘citizen science’ in order to improve and increase the amount of information available in databases. Marina Pereira Silva and Isabel Pinto summarised the output from the Portuguese National Review on taxonomy and biodiversity. They highlighted that there was still a lack of human and financial resources available for taxonomic work which was exacerbated by the poor visibility and utilisation of work produced by taxonomists.

# Research priorities

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*Fiona Grant, Juliette Young, Yde de Jong & Allan Watt*

## **1. Assessing species and habitat status: What do we have and how does it fit among its relatives?**

- Develop comprehensive strategies for the discovery, digitisation and mobilisation of primary biodiversity datasets;
- Promote revisionary taxonomic research;
- Further develop master lists of species for each habitat type;
- Further develop meta-barcoding systems to allow more efficient identification of species;
- Develop methods to create comprehensive metadata indexes;
- Develop methods to facilitate further integration between different fields, including taxonomy, phylogeny, and molecular taxonomy in order to provide a broader scientific basis for taxonomic work;
- Further develop inventories of species and habitat distributions, status and trends, and develop methods to link these to biodiversity informatics systems;
- Improve knowledge of species' distribution and abundance through links with other datasets, e.g. remote sensing, climatic data, ecological traits;
- Develop standardised approaches to mapping and analysis of species richness patterns;
- Improve and promote data collection, particularly in biodiversity-rich areas.

## **2. Assessing species and habitat trends: Where is it, what's happening to it and where is it going?**

- Analyse the impact of environmental processes on biodiversity at different spatial and temporal scales by deploying geo-distributed and 'intelligent' data services to a wide community of experts
- Improve our understanding of how evolutionary history may influence the likelihood of extinction of species in light of global change
- Promote the integration of phylogenetics and niche modelling to determine threats to biodiversity from climate change
- Determine links between phylogenetic diversity losses and scenarios for species conservation and climate change

## **3. Ecosystem functions and services: What does it do and what does it with?**

- Promote research on life histories and functional traits of species
- Better understand the role of biodiversity in ecosystem processes
- Develop methods to link the identification of new species with their genetic information and their ecosystem function
- Better understand the relationship between microbial diversity and ecosystem function and the effects of a changing environment on this relationship
- Assess intra-population and intra-specific diversity when investigating relationships between taxonomic diversity and ecosystem function

## **4. Biodiversity management and access to information: How do I find out this information and how do I manage it?**

- Develop environmental assessment methodologies that take into account intra-population and intra-specific diversity along with taxonomic diversity, in order to

identify conservation priorities

- Link taxonomic knowledge to ecological knowledge at the species level to improve ecosystem management
- Establish an EU-wide taxonomic standard for biodiversity assessments
- Further develop 'open access' to taxonomic data for scientists, policy makers and the public
- Develop interoperability and communication between information systems maintained by different professional biodiversity stakeholders
- Develop tools to cite, archive and track the origin of information accessible via websites

**To develop the necessary research in this area, particular attention should be paid to:**

General:

- Promote taxonomy in university curricula in order to maintain taxonomist base
- Upscale fieldwork and sampling efforts, especially in biodiversity-rich ecosystems and regions
- Develop keys suitable for field use and use by non-professionals, e.g. custom officers
- Conserve collected specimens for future analysis (biodiversity salvage)
- Develop an 'adaptive' taxonomy which encompasses both the splitting and lumping of species when species status is unclear
- Encourage inter-disciplinary research, i.e. taxonomists working with other biological disciplines, such as conservation biology, biogeography, evolutionary biology and ecology
- Ensure funds to maintain taxonomist base
- Promote the use of a common infrastructure to encourage large-scale common research priorities which in turn will facilitate funding and data generation
- Develop a strategy towards publishing monographic work to update the old monographs
- Incorporate capacity building components into dynamic monographs in order to speed up the build-up of taxonomic knowledge and skill
- Integrate interactive identification keys and image recognition software into dynamic cyberplatforms and scratchpads

Databases:

- Ensure that taxonomic databases are globally standardised, linked and permanent and ensure that authorship is made clear.
- Encourage taxonomists to use actively database services
- Digitize and quality control existing data
- Promote training of database experts
- Promote and develop 'citizen science' to help increase the amount of information available in databases
- Develop datasets with non-taxonomists and encourage their use by the broader public

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# Session 1: Inventory and Identification

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## Opening statement

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**Yde de Jong**, Zoological Museum, Amsterdam

This EPBRS e-conference on “Strategies for Taxonomy: Research in a Changing World” focused on identifying the key research questions allowing taxonomy to address policy needs in a better way and, vice versa, allowing policy makers to get responses from taxonomists on specific subjects related to the use of taxonomic knowledge.

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Although there are few doubts that taxonomic information is essential for reliable environmental science, applied users often complain about the inability to get adequate access to taxonomic information to respond to -for instance- the biodiversity crisis. This ‘taxonomic impediment’ is recognised within taxonomy by currently attempting to expand its capacity to explore and accommodate more species and to improve the dissemination and use of taxonomic information on the internet.

Due to these internal and external constraints, pushing taxonomy to advance its working routines and support the applied use of taxonomic information, taxonomy stands, at the moment, at a crossroads. Therefore it is critical for policy makers to make the right decisions for the future of taxonomy, now. This should, for instance, balance not only the emphasis stakeholders, researchers and society often place on new technologies and research tools but also the maintenance of core taxonomic research respecting the often exceptional level of expertise needed to explore and recognise species diversity.

Finding the right connection between taxonomists and policy makers is complicated because of the different intermediate parties (e.g. data centres, agencies and stakeholders) frequently obscuring a profound understanding of the relevance of taxonomy for biodiversity assessments for policy makers, but also hampering a closer commitment of taxonomists to fundamental questions on what information is needed (at what level and at what depth) for policy makers to make the right decisions. I hope this e-conference has contributed to a better understanding among decision makers and taxonomists of the relevant scientific priorities for future strategic policy plans.

## RE: Opening statement

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**Mauri Ahlberg**, University of Helsinki, Finland

In the opening statement to this e-conference Yde de Jong stated that “Taxonomy is the most comprehensive and reliable source of information about biodiversity today.” I agree with this statement and would like to suggest the NatureGate® Online Services approach as a reliable

source of biodiversity information. It is based on the work done by NatureGate® R&D Group and the related NatureGate® Ltd, which the University of Helsinki is a partner.

The first pilots of NatureGate® Online Services are in Finland, but many of the wild flowers described are common all over Europe, some even globally as weeds. Identification tools for birds, butterflies, fishes, trees and shrubs are under construction using the patented method of Eija and Jouko Lehmuskallio<sup>1</sup>.

I suggest that we discuss how we could create regional NatureGate® Online Services for the whole of the EU to engage the public, policy makers, and decision makers to promote a) lifelong biodiversity learning, b) conservation of biodiversity and c) sustainable use of biodiversity.

Educators, citizen scientists, amateurs and the general public (from children to the elderly) are all examples of applied users who complain about their inability to get adequate access to taxonomic information to respond to, for instance, the biodiversity crisis. NatureGate® Online Services provide a free, fast, easy-to-use identification tool for everybody. You do not need to know any name initially, you just look for characteristics of the specimen and click interactively and you receive 1 – 7 candidate species in the end. You can check the beautiful and scientifically accurate photos, and make your tentative decision of the species. Text and necessary links to other sources of information can be added to the descriptions.

NatureGate® Online Services is a prime example of the use of new technologies. It relies on the best available taxonomic expertise to check and validate its photos, videos and texts, to ensure that they are really about the species claimed. On the other hand when we have enough resources to create a server for a community of users of NatureGate® Online Services to upload their photos with geographic data to the server, we would be able to provide plenty of data of common species, their distribution and changes of distribution, for example, caused by Climate Change.

I do not think that it is not enough just to focus only on decision makers. Without educating citizens' decisions, great damage can be done to biodiversity and the sustainable use of biodiversity. Increased public awareness is of the utmost importance for the sustainable use of biodiversity as it is needed to promote the right kinds of decisions in order to have better resources for taxonomic research. At the same time the NatureGate® Online Services approach would create plenty of sustainable paid work opportunities for taxonomists. But we need lots more funding. The possible extra funding for NatureGate® Online Services is a one time investment. After regional NatureGate® Online Services are founded they are planned to create sustainable wealth for the whole region, integrating sustainable development (ecologically, economically and socially). They would be a part of the infrastructure of a greener, more sustainable economy.

## **RE: Opening statement**

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**Zoheir Sabeur**, University of Southampton, UK

Following the recent discussions about biodiversity and the cost to work on it and be up to date with it around the world, I want to bring in my humble input to the discussion here. In particular, I would like to follow on from the latest communication from Mauri Ahlberg, where the idea of creating an EU service providing information on biodiversity for many types of users is proposed. The idea is important and good, however, we need to think about the technical issues one may encounter in its implementation.

In my view, instead of thinking of centralised databases for the EU or indeed for the world, one should perhaps think about decentralising the whole thing altogether in order to

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<sup>1</sup> Reference for Eija and Jouko Lehmuskallio patent:  
<http://www.google.fi/patents?hl=fi&lr=&vid=USPATAPP11574074&id=fwWiAAAAEBAJ&oi=fnd&dq=lehmuskallio+Eija>

exploit the already existing biodiversity databases in the world at low cost. What is needed is the development of open standardized interface for getting access to these world databases. In a way, instead of creating a central system of information, we should create a system of geo-distributed services around the world which will enable all types of users (educators, researchers, operators, regulators, the Public and so on) access to them, when and where they are needed. The European INSPIRE directives will enable us do this as these accommodate the way to resolve issues related to multilingualism, cross border and interoperability between information systems and databases. There is no need to spend millions of euros (pounds or dollars) to reinvent these systems under one centralised system. The task will be almost impossible to achieve with inducing software errors. Instead we should create the service infrastructure which will enable access to existing information databases. Hence it will be important to create perhaps a European catalogue service where biodiversity data services are registered and through which existing biodiversity databases in the EU (and why not elsewhere in the world) can be invoked. Furthermore, we can go beyond that by creating Knowledge Discovery Services where users of all backgrounds can use ordinary language (not necessarily technical for instance) to query discovery services which are specialised in any biodiversity subject in order to obtain specific services (out there) and invoke them to get the answers they want.

The development of Knowledge Discovery Services is in its infancy, simply because it is very hard to create the so called “ontologies” between objects, concepts and processes related to biodiversity and programme them using a web language like OWL. These attempts are happening in pioneering projects in Europe, which have been applied in various environmental science domains and others. Over the years, I have been involved in such work in dealing with environmental risks in atmospheric, marine and land departments (Sabeur et al., 2007) and you can trust me that it is challenging. However, some success has been achieved and we are pushing our knowledge in this direction in order to develop interoperability between information systems. In my view, this is where research investment for making biodiversity information data bases communicate should be focused.

## **Biodiversity salvage: strategically building taxonomic resources in an age of global extinction**

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**Philippe Bouchet**, Muséum National d'Histoire Naturelle, Paris, France

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This contribution outlines the idea of 'biodiversity salvage' as a means to improve taxonomic resources for the future.

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It is being repeated over and over again that we are going to lose one-fourth to one-half of the species on this planet in the next 50-100 years, while at the current pace it is going to take another 250 to 750 years before taxonomists 'complete' the inventory of biodiversity: ca 16,000 new species are described every year and there are an estimated 5-15 million species still to be described and named. Taxonomists are prompt to present these evaluations in support of more taxonomic resources, more funding for taxonomic programmes, better recognition of their discipline, etc. In the present contribution, I would like to argue that taxonomists can/should explore new avenues of strategic thinking in order to make taxonomic resources more palatable to society at large.

One avenue is the notion of 'biodiversity salvage'. Let us face it: biodiversity consists essentially of invertebrates that weigh close to zero when it comes to conservation priorities and conservation action. When he first formulated the concept in 2004, the Australian Robert Mesibov likened 'biodiversity salvage' to 'archaeological salvage'. The aim of archaeological salvage is not to stop development of a new train line or highway or underground car park, but simply to recover some of the archaeological artefacts before they are destroyed by the planned development. In the same vein, the aim of biodiversity salvage is not to stop the new plantation, housing estate, industrial site or ocean outfall, but simply to recover some of the Earth's natural heritage before it disappears. In other words, although it remains desirable to instil as much 'invertebrate thinking' in the conservation world, we must accept that we will save most species only as museum or herbarium specimens, to be studied and described in... 50 or 100 years. But, at least complete specimens - perhaps with complete genomes - will have been salvaged.

For efficient biodiversity salvage, taxonomists must upscale dramatically the way they are conducting field work and sampling, especially in biodiversity-rich ecosystems and regions. We, taxonomists, are still pathetically individualistic when it comes to organizing field work and deploying the massive collecting techniques that are required to do justice to the biodiversity of a tropical forest or coral reef. The quantum of taxonomic 'field work' typically consists of 1-3 people in the field for 2-3 weeks with a budget of 2 to 5,000 €, when thousands of days and people and a budget of several million euros would be necessary. In my experience as an expedition organizer, I have found it relatively easy to attract the attention of corporations and foundations to fund large-scale field work, when the same stakeholders will consider that it is not their business to fund taxonomic research.

To get the attention of decision makers in business and government, taxonomists must go beyond lamenting on the state of their discipline: the notion of large-scale biodiversity salvage has the capacity to create new taxonomic resources in an age of global extinction.

### **RE: Biodiversity salvage**

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**Martin Sharman**, European Commission, Brussels, Belgium

Philippe Bouchet makes an interesting point in saying that in the face of accelerating loss of species, work is needed to salvage as many species as possible as museum or herbarium specimens. The taxonomy can come later.

I find it difficult to know how to approach this idea. Is it not a counsel of despair?

The archaeological analogy is – like all analogies – limited. Any artefact dug from an archaeological site, or any photograph showing the position of objects, brings to light something that was previously lost. Even a single fact or artefact recovered from the site increases our understanding of the past, although 99 artefacts may remain buried - and forever lost - under the advancing road. Salvage, in this case, is a pragmatic matter, and a step forward.

In the case of living things soon to be extinct, it seems odd to talk of salvage. Gathering the living dead, so that we can examine them later, seems more to be an act of mourning.

## **RE: Biodiversity salvage**

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**Ferdinando Boero**, University of Salento, Italy

I enjoyed Philippe Bouchet's contribution on biodiversity salvage, even though I think that there are other things to do to protect biodiversity at species level, besides storing corpses in Museums to study them once the species will be extinct. One needs to protect habitats. It is useless to protect a species if its habitat is not protected. If we do protect habitats, we automatically protect the species that we still have to describe. Habitats are perceived as valuable. Incidentally, the inventory and mapping of marine habitats is far from being complete, whereas, at least in Europe, this has been done for terrestrial ones.

I do not think that we have to convince politicians about the importance of taxonomy, they know it. They know it so well that there are many initiatives to make the inventory of biodiversity and there are many initiatives to sustain taxonomy. The problem is that these initiatives are rarely headed by taxonomists. There have been many initiatives like ENBI, ERMS, GBIF, COML and many others that have attracted lots of funds, but rarely this has fuelled taxonomy. Funds have gone to information and technology initiatives, and now, with barcoding, they will go to PCR experts. The idea is: we know everything already we have just to make it available (with informatics) and easy (with the barcode). This does not stem from the politicians, it stems from the scientific community. Taxonomists are not powerful enough to intercept the money that should go to taxonomy, and somebody else intercepts it in their place.

My impression of the problem is along these lines: Taxonomy cannot remain a museum-only business; it will die if it disappears from universities, where it should be taught. Biodiversity is to be inventoried and studied at a habitat and species level, and the two must go together. If there are initiatives for the study of biodiversity, it should be stated clearly that taxonomy is paramount for this, and the people charged of such initiatives should have proper credentials.

As Martin Sharman rightly stressed, it is strange to think that putting specimens in a museum so at least we will be able to study them when their species will become extinct is a good way forward! Sometimes taxonomists lose contact with the real world and give more importance to their museum than to nature! This is why I complain about the disappearance of taxonomy from universities and marine stations, taxonomy cannot be a museum-only business. We might end up saying that if specimens are safely stored in our little vials, then we are alright.

In the era of biodiversity, the science that studies it is in distress. This is counterintuitive and we must identify the reasons for it. The reasons, in my mind, are that the scientific lobbyists that operate where decisions are taken are not taxonomists, so somebody else takes the money destined for taxonomy, very often to provide services to taxonomy! So, there is a lot of money to serve taxonomy, and there is no money to perform taxonomy (besides in Museums).

I am posing these questions in all forums, I am recalling the PEET strategy, but things are getting worse and worse, at least in Europe. When I started this "battle", about 20 years ago, I was young. Now I am getting old, and I do not see new youngsters behind me. I do not

encourage young people to perform taxonomy, it would be suicide. My best students in taxonomy are in the US.

### **RE: Biodiversity salvage**

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**Simon Tillier**, MNHN, France

I agree with Martin Sharman that Biodiversity Salvage, as explained by Philippe Bouchet, has something of a counsel of despair - even though I would argue that we should still do it if this is the only chance of someday understanding a larger part of our living world, because knowledge is necessarily better than the unavoidable definitive ignorance which will result from doing nothing.

However, Philippe Bouchet's text deals with only two aspects of taxonomic production: access to unknown living organisms through large scale collection campaigns, which have to be implemented rapidly for reasons he gives; and conservation for future analysis of specimens as witnesses or samples of a biodiversity which will not exist any more. The third aspect, not dealt with by Philippe Bouchet, is making this undescribed taxic diversity perceptible for ecological analysis and decision making, i.e. providing rapidly operational taxonomic data.

It is well recognized that we have no chance to delimit and name properly all species-level living populations within a reasonably short time - and that when we have finished, concepts and methods will have changed to such an extent that what we are doing presently will probably have lost most, if not all, of its heuristic value. Nevertheless, I do not believe that for sound decision-making we need to name each and every living species, whereas we do need to know that they are there.

For example, many living invertebrate species have never been cited anywhere since they have been described. Thanks to a conjunction of massive collections and molecular techniques (a mixture of ATBI and metagenomics), we can actually get a good proxy of taxonomic diversity in any given ecosystem without needing to describe and name all species; and through such approaches we can approximate the trophic structure which is correlated with the taxonomic structure of local biodiversity and even compare meaningfully, richness and composition from several locations. However, and as in the case of classical taxonomy, we should always preserve specimens to allow testing and repeating our analysis, in addition to permitting proper description and denomination when needed (for example, for species of particular ecological or economical interest).

In summary, I believe that we should envisage this kind of meta-barcoding approach, and urgently start to implement it, to provide at least a taxonomic baseline which (even if fuzzy) will bring better data for ecological decision-making than a list of a few dozen large species. This should complement new approaches and IT tools allowing faster and better species descriptions, as developed in EDIT (<http://www.e-taxonomy.eu>).

### **RE: Biodiversity salvage**

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**Christos Arvanitidis**, Institute of marine Biology and Genetics, Hellenic Centre for Marine Research, Greece

I agree with the points raised in Philippe Bouchet's and Ferdinando Boero's contributions. Conventional taxonomy is gradually disappearing as a discipline from universities and people prefer to join its sister disciplines: phylogeny and molecular taxonomy. Sooner or later we will arrive at a stage at which young scientists will be capable of providing the whole genome of a species but they will not be able to name it or explain what its morphological characters are. Many may argue that this is why the web information systems on taxonomy have been

developed. However, even the most sophisticated systems which use cutting-edge technology cannot guarantee the quality of the information contained unless a taxonomist does this job.

The question now is why this discipline is declining and failing in raising the funds needed for further development? An obvious reason might be that conventional taxonomy has lost much of its prestige and nowadays it is considered as the 'retro' discipline of systematics. On the contrary its younger sister disciplines, phylogenetics and molecular taxonomy, are thriving and have led to major international initiatives such as the Assembling the Tree of Life (ATOL), the GenBank and the Consortium for the Barcoding of Life (CBOL). However, the information that these young disciplines have produced, cannot be compared to the information accumulated over the last 250 years by conventional taxonomy. None of these disciplines can replace conventional taxonomy; they can only supplement it.

However, these young disciplines can offer a new option to conventional taxonomy in order to continue to produce and make available taxonomic information. All taxonomy needs is to be integrated with the younger disciplines and to make use of as many available tools as possible, including web technology, data management, statistics, GIS, etc. This integration would allow us to base our taxonomic work on a broader scientific basis. As Ferdinando Boero stated, although PEET is already history in the US we should think about taking this step in the EU too, even though lagged by 10 years. We should learn from the PEET experience and take a better and broader approach for the sake of the next generation of taxonomists.

## Collection and observation of data: The BioCASE perspective

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**Walter Berendsohn**, Botanical Gardens and Botanic Museum Berlin-Dahlem, Freie Universität Berlin, Germany

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This contribution highlights the importance of digitizing taxonomic information and outlines key areas that need to be improved.

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BioCASE (Biological Collection Access Service for Europe) has evolved from an EU-funded networking project into an initiative of European collection institutions contributing to GBIF (Global Biodiversity Information Facility) and to collection networking through various projects. The metadata for European collections gathered by the BioCASE project have been used by a number of other initiatives; foremost among these is the new Biodiversity Collection Index, which will have a potentially central role in unifying collection resources throughout Europe as well as globally. The BioCASE provider software and protocol for data access today deliver about 16% of all GBIF records. They allow the use of more comprehensive data schemas such as ABCD (Access to Biological Collection Data), which covers the entire rich spectrum of data connected to a specimen or taxon observation. The BioCASE help desk (in the SYNTHESYS project) offers support for data providers connecting their data to the network (this support will be continued in the SYNTHESYS-2 project). BioCASE acts as the GBIF Node for the Consortium of European Taxonomic Facilities (CETAF).

BioCASE and CETAF promote the digitization of natural history collections. A primary goal of these collections is the preservation of the samples that underpin biodiversity research, so that research results become falsifiable and thus truly scientific. Specifically relevant for European collection's is the former colonial role of many European countries – much of the available evidence about the history of global biodiversity is housed in European institutions. It is therefore a specific responsibility of Europe to make this information accessible to countries of origin.

In order to fully exploit the research potential of collections, and to offer access to countries of origin, we must mobilize more data via the GBIF/BioCASE infrastructure. The technology exists and functions well. However, the ongoing digitization efforts of collection institutions lack coordination, and to date only a small percentage of European specimen holdings are digitized in any form. We have concluded that digitizing all specimens is neither an attainable short-time goal nor a reasonable use of resources. On the other hand, we note that for many research purposes, access to un-digitized collection information is simply not possible, because this access is currently done by taxonomic groups, while many researchers require other criteria, most notably geographic location, to make use of historical specimen information. However, this type of metadata (“how many specimens from location X exist in your collection?”) is not readily available, even on the country level. And where it does exist, it is not readily accessible because a unified access mechanism is lacking.

We must investigate the possibility of creating a comprehensive metadata index for European collections, one which allows researchers to discover specimen holdings relevant to their research. These specimens can then be digitized and their data made publicly available. Thus, user demand will be the driver of the detailed digitization of individual specimens. We propose this metadata index to form part of a European Strategy and Action Plan for the Digitization of Natural History Collections.

## Collection and observation of data: The GBIF perspective

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Vishwas Chavan, DIGIT, Copenhagen, Denmark

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This contribution sets out the main aims of GBIF (Global Biodiversity Information Facility) and explains the major steps required in order to achieve these goals.

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GBIF (Global Biodiversity Information Facility) is currently facilitating access to over 171 million primary biodiversity data records of which over 60% are observations and little less than 40% have specimens as the basis of records. However, to fully exploit the research potential of collections and observation data, we need to mobilise an increased quantity of 'fit-for-use' data through the GBIF infrastructure.

While the universe of primary biodiversity data is yet to be ascertained, it is believed that natural history collections worldwide house about 2.5 to 3 billion specimens. Our progress in discovery and mobilisation of primary biodiversity data to date has been at a snail's pace and opportunistic in nature, whereby low hanging fruits are being exploited, where as invisible data is yet to be discovered, digitized and mobilised. This calls for development of comprehensive strategies for discovery, digitization, and mobilisation of these datasets, which are crucial for any kind of analysis, such as predictive studies determining the fate of life on earth and its sustainable use.

GBIF has set the goal of discovery of up to 5 billion data records, and mobilisation of up to 2 billion primary biodiversity records, by the end of 2010. To achieve such ambitious targets GBIF is currently in the process of developing a 'Global Strategy and Action Plan for mobilisation of natural history collections' (GSAP-NHC) data. It will also initiate a similar 'Global Strategy and Action Plan for mobilisation of observation, ecology and multimedia resources data' (GSAP-OEM) later this year. Together these two exercises shall help strategies for the holistic discovery and demand-driven digitization of primary biodiversity data.

The GBIF 'Observational Data Task Group (ODTG)' and the 'Multimedia Resources Task Group (MRTG)' have recently submitted recommendations on how to expedite discovery, digitization and mobilisation of observational and multimedia resources data in biodiversity. While ODTG has suggested the addition of elements in a revised version of the Darwin Core schema, MRTG has drafted a Multimedia Metadata Schema for Biodiversity Resources.

GBIF has realized that a significant quantity of primary biodiversity resides with small providers. However, such players neither have resources nor encouraging reasons to invest their energy in data management, and dissemination. To overcome this impediment, GBIF has recently constituted a 'Data Publishing Framework Task Group' with the aim to recommend the nuts-and-bolts of a 'data publishing regime' which would ensure due credits to all players in a primary scientific data management cycle, and recognize data publishing on a par with scholarly publishing.

## Could taxonomy increase its relevance if practised more pragmatically and dynamically?

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Josef Settele, Helmholtz Centre for Environmental Research – UFZ, Leipzig Halle, Germany

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This contribution considers the benefits of having an ‘adaptive’ taxonomic system which encompasses both the splitting and lumping of species when species status is unclear.

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In the course of conservation and ecology related research activities, we are regularly confronted with taxonomic problems which make our work sometimes quite difficult. In our recently published climatic risk atlas of European butterflies (download at: <http://pensofonline.net/biorisk/index.php/journal>) we had several instances where the taxonomic status of some species was not entirely certain and where discussion on authorship and super-specific levels of systematics are still ongoing. However, waiting for final outcomes of such debates would not be an adequate strategy if one wants to get relevant insights published in time. Thus pragmatic decisions have to be made – which from an ecologist’s point of view (and that’s what I rather am) doesn’t matter as long as one knows which entity one is talking about.

It becomes trickier if the species status is unclear. Here there are good reasons for splitting as well as for lumping – and maybe both should be done depending on the circumstances in which we do our research. ‘Splitting’ might be adequate if one has to refer to somewhat independent units (which might, for example, be of conservation relevance), while ‘lumping’ might be needed in order to show how closely related entities (which sometimes might be regarded as independent subspecies) react as a whole.

An example for the adequacy of the splitting approach might be the ecologically distinct populations of two types of Gentian-feeding Large Blue Butterflies (*Maculinea alcon* and *M. rebeli*), the taxonomists tend to call one species as long as data analysis is based on morphology and genetics alone, but where there are always populations which are ecologically distinct, for example as far as their food plant choice is concerned. From my point of view the subspecies rank might be adequate here –but, if we look at results of Als et al. (2004) we might have to go for a rather large number of subspecies as the specialisation on one food plant might have developed several times independently from each other.

An example for the adequacy of lumping (or of providing good information on species which belong to a group on a super-specific level, for example sister species) is, for example, the ecological modelling of species occurrences and their assessment of potential future ranges under certain scenarios (such as climate change). If two or several closely related species are modelled as separate units, the fit of the model will always be worse than if one would include all the very closely related taxa with an often allopatric distribution.

Why should we not be open for a dynamic taxonomy which fits for the variable conditions in an ever changing world – something like an adaptive taxonomy? As a summary, let me state from Descimon & Mallet (in press; elements taken from there): There is justification for reviving the rather neglected (and misused) rank of subspecies, with the trend to consider only more strongly distinct forms (in morphology, or genetics, but also in ecology) as subspecies, and to lump dubious geographic forms as synonyms. One should always go for a useful compromise between descriptions of geographic variation, the needs of modern taxonomy, and Darwin’s pragmatic use of the term species in evolutionary studies. It is a Sisyphean task to try to give a definitive, irrefutable definition of species, but species will continue to function as useful tools in biology for a long time. With Descimon & Mallet (in press) I’d like to recommend that researchers of the future study gene exchange in the many hierarchical layers of phenotype, genotype and genome (in what Descimon & Mallet call ‘bad’ species of butterflies). Such studies will surely be much more illuminating about the nature of speciation and evolution at the species level than, for example, endless discussions on the ‘essence’ of species. And last but not least – it would be good if ecological and biological characteristics could penetrate the world of taxonomy – as should taxonomic ones into the world of ecology.

# Session 2: Understanding patterns and change

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## Species conservation: Rareness, threats and trends

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**Donat Agosti**, American Museum of National History, New York, USA

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This contribution emphasizes the need to take a global approach for species conservation and highlights the need for conservationists and taxonomists to work together to achieve this. It also outlines how e-sciences can be used to help facilitate potential collaborative efforts.

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Species conservation has a long history; it is biased to the temperate zone and very few, hardly representative taxa, and is very anecdotal. It has been dependent on the work of very devoted pioneers and conservationists that led to the creation of many National Parks, the coinage of the 'biodiversity crisis' and tools like the widely cited Red Lists.

This approach is flawed. There is almost no connection between conservationists and taxonomists. Hardly any of the billions of specimen records sitting in Natural History collections are used in conservation other than through a filter of 'experts' that make guestimate predictions on the status of particular species. There is very little done to create base line survey data that is collected specifically for this purpose, and not just amalgamated from various sources without addressing the critical issue of data quality. Even less is done to create state of the art monitoring programs that would be expected at the base of large scale conservation efforts, such as countdown 2010.

An example of how this might work, albeit in a small landlocked temperate country, is the Swiss BDM-CH monitoring system that includes 2,500 plots that are monitored within 5 year cycles.

The issue behind this not very comfortable situation of species conservation, is that both the conservationists as well as the taxonomists are running a huge highly fragmented global infrastructure, but have failed to formulate an adequate research program to describe and quantify the loss of biodiversity and to re-adjust their institutions accordingly, even with the new tremendous opportunities offered through the internet and e-science. Management, of both conservation organisations as well as natural history museums (as the main driver of taxonomic research), became more competitive, more geared towards edutainment<sup>2</sup> and quasi-commercial institutions.

At the same time, the governments did not set up a biodiversity research agenda similar to what happened in Climate Change and Ozone Depleting Substances, nor did the Science Foundations set up specific, globally coordinated programs keeping up with the globalization of science through the Internet. The scientists themselves continued their very individualistic work as usual. Biodiversity informatics in itself, rapidly developing, is thus barely guided by the relevant scientific questions, such as what the status of global biodiversity and its dynamics are, and is still missing relevant content, such as simple lists of the global species, their distribution, identification, and links to their descriptions.

What is needed is for a truly global approach, addressing the very basic question of species biodiversity: what are the species, how is their abundance changing? These questions

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<sup>2</sup> Edutainment: the act of learning through a medium that both educates and entertains.

are the foundation for successful conservation. Based on this research agenda, set in collaboration with conservation and other fields depending on taxonomic knowledge, a strategy needs to be defined on how to answer the most important questions. This must then define the infrastructure that is needed, especially in a time with very restricted new financial means, as well as where funding will go. Consideration has to be given on how we collaborate, exchange data, distribute and collaborate beyond our fields, and how we optimize and use best new opportunities offered by the e-sciences.

Though most of the e-sciences depend on additional funding, they offer an even greater potential to save funds as well, and at the same time open taxonomy up to external users. This new data will allow us to team up with other areas that recently opened up their extremely rich data sets, such as remote sensing, allowing us to peer at every remote corner of the world. This should stimulate us to be able to pinpoint what species are really living in those places on the ground.

### **Species conservation: Going fast: The ATLANTIS initiative in Macaronesia**

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**Paulo Borges**, University of Azores, Portugal

The known world biodiversity currently includes about 1.9 million described living species and probably an additional ca. 8 million species yet to be described. Among impediments to the study and practice of biodiversity conservation are the so-called ‘Linnaean’ and ‘Wallacean’ shortfalls, i.e. the incomplete taxonomic description of species-level diversity, and the inadequate knowledge of species’ distributions. These two facts are limiting the use of many taxa in monitoring projects, and restricting conservation efforts to vertebrates and vascular plants.

Imagine that all the diversity of species of a particular region could be put available on the web with distribution maps and images of species for the general public! This is now possible for the Azorean islands with the ‘Azorean Biodiversity Portal (ABP)’.

Many initiatives are now extensively gathering taxonomic and distributional data of organisms, for example, the Breeding Bird Survey of North America that was initiated in 1966; the UK Breeding Bird Survey; the Iberian database of the Sacarabaeidae (BANDASCA); the floristic and ecological database of Mediterranean French Flora (BASECO); the database of National Commission of Biodiversity of Mexico (CONABIO); the project Fauna Europaea.

In 1998 the Government of the Canary Islands started an important project on biodiversity, Project BIOTA-Canarias. Software, called ATLANTIS Tierra 2.0, was developed for biodiversity data storage. This software was written in Visual Basic, using a common database environment; it uses the SQL language to develop interrogation queries and has an easy interface with all GIS software. With this database it is possible to store detailed information about the taxonomy and geo-referenced distribution of all species on the surveyed geographical areas of interest. ATLANTIS Tierra 2.0 was inspired on ‘Worldmap distribution analysis software’.

ATLANTIS Tierra 2.0 software was developed mainly with the purpose of managing taxonomic and distributional data in islands. It has several important tools, namely a taxonomic tool and a conservation management analysis tool that allows the calculation of species richness, their rarity or complementarity (displays the minimum number of cells required to ensure that each species in the dataset is represented at least once) in all 500x500m cells of a particular island or, in any special area in one island. The ATLANTIS database was successfully developed in the Canary Islands, Cape Verde and in the Azores, and is still in development in the Madeira archipelago. Data input is complex and implies a validation by taxonomic experts. After a list of species is available with all the synonyms also listed (see Izquierdo et al., 2001, 2004; Borges et al., 2005a, 2008), all available occurrence data stored in the literature, herbaria, animal collections, unpublished datasets was introduced with four levels of quality: 1 – for very precise locations, usually point UTM data; 2 – for

localities not expanding more than 2-3 km<sup>2</sup>; 3 – for imprecise localities; 4 – when only the island occurrence is mentioned (generally in old publications). All geo-referenced data is linked to the year a species was sampled. With this information it is now possible to document species decline.

I argue that with such kind of initiatives taxonomists are providing a service and attracting attention for their good work. With the Azorean Biodiversity Portal, Azorean taxonomists are:

1. Providing resources for colleagues in academia ('Science'), in order to test biogeographical and macro-ecological hypotheses on island systems;
2. Contributing to the conservation management in the Azores in giving detailed information on the distribution of species that is being used by several stakeholders ('Management'). The recent publication of the TOP100 list of management priority species for the European archipelagos of the Macaronesian region (Azores, Madeira and the Canary Islands), taking into account both their protection priority and management feasibility (Martin et al., 2008, subm.) is a good example of the application of the data available on ABP for management purposes;
3. Helping students in their school project and reports ('Education').
4. Attracting the cooperation of many nature photographers ('Communication').

The future of taxonomy implies that taxonomists work with colleagues in other fields (ecology, biogeography, conservation) and make their information available in well organized databases that could be used by managers and other stakeholders.

## **RE: Species conservation**

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**Nikita Kluge**, Saint-Petersburg University, Russia

It is possible to create a beautiful database of your current personal knowledge about animals of Azorean islands, or even of your current personal knowledge about everything (like GBIF), but if you do not understand the principles of systematics these databases can only have a limited use and will never become universal and permanent. It seems that people who spend too much time and money creating such databases do not know where this information comes from.

We have to clearly understand the difference between an author's scientific opinion and a bank of information: the first cannot be universally accepted and permanent, so it should be published as an article or a monograph of limited volume with clear authorship; the second can be universal and permanent, so it can be published as a huge database with an unlimited number of contributors. The databases which have been discussed during this e-conference represent a non-justified mixture of these two approaches. I have elaborated principles which allow taxonomic databases to be built of the second type, and would like to pay your attention to them<sup>3</sup>.

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<sup>3</sup> Database on the systematics of Ephemeroptera: <http://www.insecta.bio.pu.ru/z/Eph-spp/XII-Int-Conf-Eph.htm>;

# Session 3: Ecological functions and services

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## Integrating taxonomic work

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**Dave Roberts**, National History Museum, London, UK

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The traditional mainstay of taxonomy has been the revisionary monograph that synthesised knowledge of a group into a single reference work. This single, authoritative reference is still the best interface for non-taxonomists to current taxonomic understanding of most taxa.

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Time moves on and two factors have conspired against the old monograph. First, the rate of production of new knowledge has meant that the scope became restricted to make the task tractable by one person. Second, those employing taxonomists demanded outputs measured against prevailing modern standards such as the H index, which inevitably favours the most active research fields whose activity level means they cite more papers in total. It has become untenable for an academic to spend years producing a monograph that could easily be outdated in less than a decade. Furthermore, the Internet Explosion of the 1990s meant that today the default place to look for information is on the web (Godfray 2002) and “if you are not online, you’re invisible” (Page, 2009).

None of this means that the monograph is redundant: I would argue that the basic need for a concise source of authoritative taxonomic information (a synopsis) has not changed, but the mechanism for producing and delivering it must change to suit modern circumstances. Such a resource is available not only to taxonomists but to all sectors.

There is no obvious way out of this dilemma, but there are projects producing tools designed to let taxonomists work together on the web and to release their information in stages, rather than waiting for completion of the whole body of work. The result should be, in fact, a dynamic monograph. CATE (Creating a Taxonomic e-Science) was a pioneer in this regard. The EDIT project is pursuing two related approaches to this problem: the Cyberplatform and the Scratchpads. The Cyberplatform is based on a central data model and provides tools to work with the data stored therein (see examples of Palms and Cichorieae). Scratchpads, on the other hand, provide a stable web environment for any group of specialists to address any taxonomic subject area but, most importantly, to work together. The strength of these approaches is that they allow taxonomists to add small pieces of information into a defined framework (Cyberplatform) or into a flexible, needs-driven assembly (Scratchpads).

Whatever the approach, there is a clear need for further work. Specifically:

1. Web services must be reliable, to encourage taxonomists to use services rather than develop local copies that will inevitably drift from the original;
2. Core services are needed from a single point of access, including name servers, synonymy and orthographic variants, specimen locations, etc.;
3. Services must be bi-directional, so that refinements and corrections introduced in one site can propagate to others;
4. The production of consensus ‘views’ needs to be explored, to enable interpretation of detailed taxonomic discussion by non-taxonomists;
5. Taxonomists must come to terms with open science, so tools need to be developed that will apportion credit and measures of that credit need to be used in career development.

## **RE: Integrating taxonomic work**

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**Ferdinando Boero**, University of Salento, Italy

At present, it seems that taxonomic research is heavily financed for two main purposes: make taxonomic information readily available (through the internet) and making taxonomic identification easy (via the barcoding). Taxonomists are involved in these issues only marginally, especially from the point of view of paid work. Taxonomists do know perfectly that we still have to describe the greatest majority of the species inhabiting the planet, and they know also that almost all taxa needs thorough revision. There is a need for big European projects aimed at revisionary work of our fauna and flora and a strategy towards publishing monographic work updating the old monographs. These activities are the core of taxonomic work and are presently ignored at a strategic level, with some noticeable exceptions.

## **RE: Integrating taxonomic work**

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**Giuseppe Fabrizio Turrisi**, Catania, Italy

I agree with Dave Roberts about the importance of making taxonomy an ongoing, open project, at a worldwide scale. But I think it is too premature, even if desirable, to render taxonomy (at its more advanced state) a matter available to all persons, both expert taxonomists and non-taxonomists. It is not only a problem of the circulation of knowledge, but also the correct use of it. I fully agree with Ferdinando Boero, who pointed out that entire groups, sometimes at phylum level, more frequently at family-rank, are in need not only of a whole taxonomic revision, but also of a revision of phylogenetic concepts based on modern data, and preferably on simultaneous morphological and molecular data. This first step, in my opinion, needs to pass through the official board of a peer-reviewed journal, and I am sure that the reference-monographs will be a solid starting point for taxonomists for a long time. The need to make this knowledge more widespread is an old question, but I think also a crucial albeit very delicate one. However, I think that the actual situation, especially when viewed through the eyes of the world web, is well projected towards a worldwide treatment of scientific knowledge that can be shared between professional and non-professional taxonomists. We still have a substantial proportion of biodiversity not known or very poorly known, and the monographic approach to describe biodiversity is, in my opinion, not only highly desirable but also strongly recommended.

Another important question is to consider the possibility of whether non-expert taxonomists or experts in other fields will be able to practically use these taxonomic tools. All taxonomists know how hard it is, in most cases, to build a solid culture on a systematic group, especially if based on a worldwide approach. This takes many years and sometimes a lot of frustration to reach reliable scientific results. I assume that it could be hard or even impossible for non-expert taxonomists, or taxonomists in other fields, to correctly identify taxa, and thus make their results useful and reliable for the scientific community. In my opinion, the actual improvement of taxonomic knowledge (I note with great enthusiasm the big-project of the mega-journal ZOOTAXA) represents a compromise in order to give a solid and authoritative reference guide, based on scientific principles, with the possibility of making knowledge easily and widely accessible through the world web.

## **RE: Integrating taxonomic work**

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**Yves Samyn**, Royal Belgian Institute of Natural Sciences, Brussels, Belgium

Dave Roberts is certainly correct in stating that the 'good old' revisionary monograph is under quite a bit of pressure these days, not in the least because authors are pushed to publish

their qualitative work in several episodes, thus boosting their publication record. This is very unfortunate as the monograph has, ever since the onset of the Linnaean enterprise, always served as the most comprehensive and authoritative source of information for taxonomists. However I concur with Dave Roberts and others that the new-style monographs ('e-monographs') are a very promising alternative to the classical monographs and should be applauded.

However, for novice taxonomists, especially from developing countries, these new style monographs will be as inaccessible (perceived as too technical), compared to the old style ones, if no apt capacity building is done prior to their release. The series *Abc Taxa*, a product from the Belgian National Focal Point to the Global Taxonomy Initiative, has put such capacity building as its core goal. Each volume of the series provides a 'road map' on how to best do the taxonomy of a particular group, and by doing so makes taxonomic information much more widely accessible.

We recommend that developers and authors of web driven monographs will also consider incorporating such capacity building components into their open and dynamic monographs as this will significantly speed-up the build-up of taxonomic knowledge and skill, especially in developing countries where it is most urgently needed.

### **RE: Integrating taxonomic work**

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**Ole Seberg**, Botanical Garden and Museum, Natural History Museum of Denmark

What appears to be needed is, as indicated by Dave Roberts, is a stable, dynamic cyberplatform environment for monographic work and Scratchpads or similar working platforms for collaborating groups of taxonomists. These tools provide access to visual morphological information via photos of type specimens, and the relevant literature.

Sophisticated interactive identification keys and image recognition software are other needs that should be integrated into the previously mentioned tools, as is a strong educational component. Taxonomy is an exciting science and not only an identification service for other scientists and phylogeny is our framework for understanding the evolution of biodiversity, characters, adaptations, not only an tool in modern ecology, etc. If taxonomy is reduced to metagenomics it loses relationships with biodiversity.

Unfortunately most funding agencies (and perhaps even most taxonomists) have not realized that taxonomy is a big science and in essence a 'team sport' with global ramifications. A notable exception is the National Science Foundation's (US) Planetary Biodiversity Inventories (PBI) program, which has the world as its playground not North America, Europe or Australia.

### **RE: Integrating taxonomic work**

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**Jan Dick**, Centre for Ecology and Hydrology, Edinburgh, UK

I would like to support Dave Roberts and other contributors that web-based tools which share information amongst taxonomists is essential in this day and age. I would however encourage the incorporation of data into these databases from other fields of science, notably ecology. Working with taxonomists from the Royal Botanic Garden Edinburgh we are finding a lot of common ground between the needs of the taxonomist and the trait-based functional ecologist. While we appreciate that there are many logistical concerns (Pendry et al., 2007), as an aspiration we believe there is a great deal for both fields of science to gain by integrating databases and sharing knowledge.

## **RE: Integrating taxonomic work**

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**Harvey Tyler-Walters**, MarLIN, Marine Biological Association, Plymouth, UK

I have to agree with Jan Dick that taxonomy needs to be integrated with other information. With current advances in the internet and database driven systems we have many of the tools we need to achieve this goal.

Many of you will know that the Marine Life Information Network (MarLIN) ([www.marlin.ac.uk](http://www.marlin.ac.uk)) has been collating information on the autoecology of numerous species and habitats, and disseminating information on marine species and habitats over the internet. Nevertheless, we recently launched our Biological Traits Information Catalogue (BIOTIC) ([www.marlin.ac.uk/biotic/](http://www.marlin.ac.uk/biotic/)) to provide a free online resource for biological traits information for marine species. So far we have ca 40 traits for ca 200 species but in collaboration with users this will grow. We are actively encouraging researchers to submit information to the catalogue. The traits include information on habitat preferences and life history traits.

We have adopted the World Register of Marine Species (WoRMS) taxonomic list as our standard classification for both the MarLIN and BIOTIC websites. BIOTIC allows users to download biological traits information. In particular, it allows users to upload a species list and download traits, where we have that information. Of course, we want BIOTIC to be user driven as much as possible, so any comments will be gratefully received. As examples of the approach, MarLIN, BIOTIC, AlgaeBASE and FishBASE are clear examples of systems that link taxonomic and ecological information, and there are many others.

Biological traits are increasingly used to look at functional studies of communities, and to investigate issue of 'connectivity' between areas, which is especially important in the current push for Marine Protected Areas. However, the autoecology of many marine species is poorly studied. Life history traits in particular are often lacking for many species of conservation concern. And yet little funding is available to support the kind of basic biology needed to answer questions about how currently threatened species reproduce or disperse, respond to disturbance, or recover after disturbance. If we are to understand ecosystem structure and function, and if we are to be able to make informed decisions regarding 'connectivity' between habitats, then we need to undertake basic research into the life histories and functional traits of many more species than currently receive attention.

## **RE: Integrating taxonomic work**

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**Mark Costello**, University of Auckland, New Zealand

Contributions to this e-conference have noted the need for up to date taxonomic monographs that revise current knowledge (and describe new species) complete with descriptions, keys, source literature, etc.; and that these should be published through online databases that can be built upon as new revisions become necessary. Once in such databases printed copies could be easily produced if desired. Perhaps the greatest inefficiency in taxonomy is the scattered outlets for, and slow nature of, the publication process. Publication through online databases may have advantages over the conventional model in that parts can be published as they are ready (and not wait years for a volume to be finished), peer-review can happen after publication and corrections are made as required, and the source cited similarly to print publications (e.g. as web pages and sub-databases are at: [www.marinespecies.org](http://www.marinespecies.org)). Such monographs open up a taxon for non-experts to study and are thus critical for taxonomy end-users.

The European Commission has funded several successful projects that have built online taxonomic databases but has not had revisionary taxonomy on its list of funding targets; as for example NSF did with its PEET grants. Databases are only as good as their data. The EC now needs to focus on funding the work to contribute top quality content to such databases. This may be done thematically (e.g. pests, parasites, harmful algae or invasive

species and their relatives), for applied purposes (e.g. species of importance for selecting and monitoring nature reserves, or monitoring environmental quality), or to address major gaps in knowledge (e.g. taxa with many undescribed species). In all cases the essential need for a foundation in good (taxonomic) science should be evident. Scientists must impress the EC of this priority in conferences such as this, through related projects (e.g. EDIT), and national delegates to the EC research programme.

As the trend in EU funding is to reduce its financial contribution, then perhaps current salaries of taxonomists can provide the matching funding such that they can supervise newly hired taxonomists to scale-up the efficiency of producing e-monographs. Suddenly institutions would see the benefits of having taxonomists on their staff because they help lever research funding.

## **RE: Integrating taxonomic work**

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**Frank Bisby**, University of Reading, UK

This contribution is to remind ourselves how the varied components mentioned by previous contributors fit together in the wider taxonomic landscape. This landscape is multi-layered, structural and descriptive, regional and global, and fragmented yet united. The author argues that we should focus on strengthening the functioning and connectedness of the layers, but without prejudicing the diversity of separate components.

### 1. Multi-layered activities:

A good way to visualise the multiple layers is to follow the vocabulary of the e-Infrastructures programme – to think of taxonomy itself as an ‘ecosystem’ with multiple layers of services or taxonomic research providers – expeditions, collections, primary publications, names and nomenclature, species, higher taxa, classifications, publications and products, keys and identification aids, checklists, ATBIs, Faunas, Floras, monographs, global species databases (GSDs), CATE units, aggregated species checklists, overarching taxonomic systems. As a simple cut we can divide these into the core taxonomic research, and the provision of external public services, but on closer examination the position is more complex: there are internal research services provided by one research layer to another. There is a ‘food web’, and many components both depend on others and themselves to supply multiple layers above them. It would be wrong and simplistic to say we need one layer and not another – the whole edifice needs strengthening and possibly simplifying. Present provision is patchy in nearly all layers of the ‘ecosystem’ with both good and missing sectors evident. At one of these levels the discussion between Palomares and Costello is very relevant: Species 2000 and WoRMS are developing strategies for filling the gaps for the least well-known groups, but they certainly do represent a problem.

### 2. Structural and Descriptive:

Two different views of taxonomy actually feed one another. One is that the core activity is to disseminate good descriptions, with identification aids, for all species known to taxonomy. Alternatively we focus on providing the taxonomic backbone: getting a current view of which taxa exist, what they are called, and how they fit together in a hierarchy. But in reality the first is not possible without the second, and vice-versa.

### 3. Regional and Global

Nowhere is the interplay of regional and global taxonomies more interesting than in Europe. We have responsibility to deal adequately with our native biota as do all continents (see contribution from Dominique Richard and Doug Evans). However, beyond this we have both the normal needs to use a global taxonomy, as do other continents, and special responsibilities for global taxonomies. This is because of our global collections (see contribution from Walter Berendsohn), and because it appears that the world’s largest body of

monographic expertise is also here in Europe – an assertion based on the findings of EDIT, and the CoL. One schema to play with is the idea that if only we had monographic experts producing global taxonomies for all groups, then this would permit both closing gaps at the European level (for use in PESI), and at the global level (for use in Sp2000 CoL). If you are uncertain why we also need global taxonomies even here in Europe, then look in your salad, aquarium, refrigerator, garden and street: every day we encounter species from around the world. Also our museums are dominated by specimens from around the world that need to be catalogued.

#### 4. Fragmented yet united

We also need to encourage diversity in taxonomic projects, and the compartments through which outputs are delivered. This will widen participation, and provide a level of evolution and selection. So we may join Wouter Los in craving a one-stop-shopping portal such as LifeWatch. But in the middle layers of the ecosystem that will support LifeWatch, the federation of knowledge should come from a thriving community of providers, in many cases via an intermediate layer of aggregators and synthesisers. Zoheir Sabeur is right to promote distributed systems with multiple sources unified by agreed protocols, rather than a single centralised system. Examples of aggregators are BioCASE (with its array of specimen and observation providers), Species 2000 and its new 4D4Life project (with its array of GSDs providing checklists for the CoL), and Biodiversity Heritage Library – Europe (with its array of library providers across Europe). Also each of these intermediate aggregators can itself serve a variety of user programmes at the upper levels. For instance, CoL ‘feeds’ the taxonomic backbone to GBIF, Encyclopaedia of Life, SeaLifeBase and the Global Taxonomy Initiative.

## Pitfalls awaiting users of plant taxonomic data when assessing biodiversity at the species level

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Jan Kirschner, Institute of Botany, Academy of Sciences, Czech Republic

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This contribution emphasizes the need for a re-examination of basic taxonomic data at a European scale.

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Basic taxonomic data have a few peculiar features complicating their direct applicability and/or generalization as an index system for organismic biodiversity. They are:

- Time Span: Old and new records and publications of plant names are equally relevant. Absence or non-representative inclusion of old data in modern databases cause the same gap as an absence of modern data.
- Geographic Range: Equal relevance of data published from (or in) any part of the world and in any language. A low impact factor or difficult accessibility of a publication is not a criterion for further exploitation of basic data.
- Cultural Differences: Level of exploration, language differences or long-term isolation under regimes imposing travel restrictions may lead to 'local taxonomies'. Local or "amateur" taxonomies also result from a gradual decrease of taxonomic expertise in developed countries.
- 'Democratic Character' of the data: No qualification is required, no sophisticated laboratories needed, nothing but a few words of Latin diagnosis and a permanently deposited herbarium specimen references - that is all that was required for anybody to publish a new name of a plant taxon.

Conclusion: Basic taxonomic data are not available for further generalization without re-examination. This can be documented by a strikingly high proportion of incorrect or imprecise data in summaries or global compilations (examples at global scale):

- Estimates of the global number of species of vascular plants vary between 220,000 and 420,000 (current 'compromise' around 350,000) (Scotland and Wortley, 2003; Govaerts, 2001)
- The proportion of wrong data in the 1997 IUCN Global Red List of Threatened Plants is 55 to 85%, as could be shown by a comparison with recent monographic treatments (Kirschner and Kaplan, 2003)
- Global phylogenetic tree of cyanobacteria (blue-green algae) was based on 40% of wrongly identified strains (J. Komárek, pers.comm.)
- Re-examination of published older chromosome numbers in *Myosotis* (Boraginaceae) shows only 25% of correct records, i.e. correct counts on correctly identified material (25% of wrong identifications and wrong chromosome counts, 25% of correct name but wrong number and 25% of wrong name but correct number) (Merxmuller and Grau, 1963)
- Plant DNA C-values Database includes about 40% of wrong data (i.e. data assigned to the wrong taxon name) (J. Suda, pers. comm.)
- Conservative estimates of incorrectly attributed data in GenBank amount to 20% (Nilsson et al., 2006; Vilgalys, 2003)

Research in this field cannot avoid long term work towards continental or world taxonomic revisions or monographs critically evaluating the data on plant diversity.

Among programmes involving taxonomic monographs as one of the major objectives are Planetary Biodiversity Inventories (NSF, USA) at the continental scale and Species Plantarum - Flora of the World programme for global revisions of plant families. At the European level, no similar programme for plants has been funded. The existing efforts are seriously under-funded and restricted to providing a coherent checklist, which cannot replace a profound taxonomic revision. Any programme of this type also involves practical taxonomy training. Let us develop a funding tool for Continental Biodiversity Revisions, a programme aiming at taxonomic revisions of families or genera in the whole of Europe.

## **RE: Assessing biodiversity at the species level**

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**Hendrik Segers**, Royal Belgian Institute for Natural Sciences, Belgium

Several posts during this e-conference have drawn attention to bioinformatics tools that come, or may come, to the aid of making taxonomic information more readily available to users. There is no doubt that these tools are useful, and are effective in achieving their stated goals. Both producers and users of taxonomy welcome them and it is only right that they attract attention from policy makers or providers of research funding. Hence, a substantial amount of resources have been invested in bioinformatics developments and this has resulted in the production of a plethora of undeniably useful tools.

However, these tools only facilitate access to information; they do not improve or increase our understanding of biological reality and biodiversity. Furthermore, at present they only provide access to a very restricted subset of the existing information, namely, information that is available in digital format and, for economic reasons, the most favoured, flagship taxa (the nice, cuddly and cute), and in many cases even plainly and painfully incorrect data, as illustrated by Jan Kirschner. It is unrealistic to believe that effective, science-based sustainable management and protection of biodiversity can be based on this selection of information. Even more crucial is the point that our knowledge on the taxonomy of organisms (the taxonomic “body of knowledge”) is largely insufficient in many instances, as so nicely illustrated in Josef Settele’s recent posting, even for taxa as ‘cute’ as butterflies.

With the new tools and methodologies that are becoming available for taxonomic research, we now have the ability to produce data content with an unprecedented accuracy, objectivity and speed. It is these such efforts, and digitisation and quality control of existing information, that are needed most to improve the information content and, consequently, relevance to society, of taxonomy.

## **RE: Assessing biodiversity at the species level**

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**Zoheir Sabeur**, University of Southampton, UK

I disagree with the somewhat sceptic viewpoints raised in Hendrik Seger’s contribution, about bioinformatics tools as tools for “facilitating access to information” only. These tools main inputs are to incorporate the missing discovery elements that are required for assessing, monitoring and anticipating the spatial fate of biodiversity at global scales that are desperately needed by biodiversity experts. The future is about the deployment of services which enable the fusion of information and processed inference rules between biodiversity data from different sources (reliable or non-reliable data), automatically. Under these services, the prediction of biodiversity trends both in spatial and temporal scales should also be provided. I believe this can only be welcomed by biodiversity experts.

Furthermore, I cannot see how one can monitor and predict the trends of biodiversity without proceeding with the analysis of natural environmental processes and their impact on fauna and flora at global and temporal scales. This can only be achieved if we deploy geo-distributed and ‘intelligent’ biodiversity data services to a wide community of experts. Some of these services should also be made available to regulators, educators and the public as stated in my previous communication.

## **How far can we trust the distribution databases?**

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**Petr Petřík**, Institute of Botany, Academy of Sciences, Czech Republic

We have explored potential biases due to recording effort in species richness (number of vascular plant species) recorded in taxonomy-based mapping projects (Petřík et al., under

review). Although the sampling effect can be neglected if operated on a broad scale, on a finer-scale a significant amount of the variation in plant species richness can be ascribed to recording effort. Hence, this indicates the need for a standard approach to mapping and analyzing species richness patterns, especially those based on small areas, and further training for the experts.

As today's knowledge becomes increasingly based on meta-analyses and on large scale datasets (Kier et al. 2005; Orme et al., 2005; Pysek et al., 2007), keeping potential sources of bias in mind is of high practical importance. The non-critical use of recording data may be misleading as the data are influenced by many unpredictable factors, such as those mentioned by Jan Kirschner, and misuse of biodiversity statistics (Palmer et al., 2008). We may avoid potential biases by using a standard method such as grid-mapping (Elith et al., 2006; Royle et al., 2007).

In our study, we have reviewed 80 regional and national grid mapping projects on the vascular plant flora of Central Europe. The measure of recording effort used was the duration and extent of the mapping project, resolution of the mapping grid and the number of botanists involved. Furthermore, several environmental and geographic factors associated with the variance in species richness were used as co-variables. The effects of individual factors on species richness were compared by using multiple regression analysis and hierarchical partitioning.

Multiple regression analysis indicated a significant role of duration of study, and hierarchical partitioning revealed significant effects of the duration, number of botanists and used resolution. Generally, 8% of the variation in the total number of species recorded was attributed to the duration of mapping, 9% to the used resolution, and 7% to the number of botanists involved in mapping. However, this bias is scale dependent, i.e. more important on a fine scale.

Conclusion: The potential biases due to recording effort or the effect of using different taxonomic concepts must be taken into account when sharing large data sets and modelling species distribution; (Loiselle et al., 2008). This is particularly important in regional studies or large data sets incorporating data at different spatial scales (e.g., [www.alarmproject.net](http://www.alarmproject.net)). Such standards are already applied at the landscape scale (Bunce et al., 2008), re-interpretation of published data, and quality assessment of species databases (Hortal et al., 2006; Rich and Karran, 2006). However, suitable standards for monitoring purposes at the habitat scale do not exist (but see Dengler, 2009).

Applying standard approaches in the mapping of species (particularly on a fine scale) is still an important factor and cannot be eliminated from the models based on taxonomic data. It is crucial to clearly state the methods and standards that are to be used for recording species when starting EU FP projects (e.g., a correction for the amount of time spent recording) and education of experts mapping the species.

## **RE: Assessing biodiversity at the species level**

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**Roberto Canullo**, Dep. of Environmental Sciences, Camerino University, Italy

From the point of view of EU trans-national monitoring programmes involving biodiversity issues, Kirschner's 4-groups of constraints to applicability of present taxonomic data at a continental level have dramatic consequences with regards to taxonomical reliability in suggesting biodiversity trends and tendencies.

ICP-Forests' Expert Panel on Biodiversity and Ground vegetation, adopted a unified coded species list (Vascular and Cryptogams) and a related updating procedure, in order to have a common reference ('a coherent checklist') and enhance the QA of the Forest Plant Diversity monitoring projects. The problem is that the original reference system (a reduced version of the Flora Europaea) is a static taxonomic reference, and it is necessary to implement the coded list when there is increased project participation (Cyprus, Turkey, Canary Islands...).

I fully agree that ‘a profound taxonomic revision’ at a continental scale is necessary, but it is also necessary to understand how it is possible to guarantee a long-term activity in this sense (or continuously), and how this can also produce a ‘stable authority’ for the effective needs of ‘coherent checklists’. Exploring the direction of Globally Unique Identifier systems or other such tools (barcodes) and even the use of molecular-based tools doesn’t overcome the needs of a revision of the continental flora as a whole, but such a big project can hardly be founded. I suggest to eventually increase research topics from ‘pure’ taxonomy to species-specific features, which can serve to implement current topics that seem to be of ‘wider’ interest.

Morphological traits, growth characters, organ dimensions, etc. are of interest to life history definitions, that are often linked to niche and assembly rules studies, as stated by a number of old projects producing local or regional databases<sup>4</sup>.

The absolute need of a taxonomic authority for biodiversity assessments EU-wide is also a very important link. But any taxonomic revision is a dynamic process, and must answer the question about the level of stability which is needed. Open-web sources can be produced to offer real-time updates avoiding bias on richness assessments due to ‘changing entities’ and synonyms, and ‘cultural differences’. But it also becomes a matter of data quality! The effect of ‘pseudo-turnover’ (observer’s effect) is well known (Allegrini et al., 2009).

### **Using the presence of vulnerable species for biodiversity assessments**

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**Nikolay Sobolev**, Institute of Geography of Russian Academy of Sciences and Biodiversity Conservation Centre, Russian Federation

We consider ecosystem services to be the main benefit of biodiversity conservation, so we must aim our biodiversity conservation activities at ensuring good ecosystem functioning and adapt biodiversity assessments to this task. Evolutionary co-adapted species provide their community with good and stable functioning including the ability to self-regulate and self-restore. So, when assessing biodiversity within the habitat we must begin not by calculating the total number of species that occur there but by dividing them into native and alien species. The partial overlap of potential ecological niches occupied by species with similar ecological requirements within a community ensures ecosystem stability, but also fluctuations of species abundance. So we need to assess the state of the biodiversity separately for each functional assemblage of species within a considered habitat.

When assessing the state of ecosystems as a whole, we use data on vulnerable native species. Usually, a species becomes rare because of its high vulnerability to changes in environmental conditions within its habitat. So, we can use such species as indicators of suitable conditions for itself and also for the species with similar environmental requirements but less vulnerability. A permanent presence of vulnerable species belonging to many different parts of the same ecosystem indicates the low level of deviation of environmental conditions from natural ones within the habitat as a whole. There is a need for a more precise taxonomic study of species with large ecological amplitude. It is also necessary for official priority lists to contain the full Latin species names including the author name and the description date.

The use of data on vulnerable native species for habitat assessments may be an effective tool to join species diversity and habitat diversity approaches in practice. For example, the Emerald Network implementation in Russia faces the problem of variability in status of many species in Western, Central, and Eastern Europe: some priority species after

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<sup>4</sup> [www.ecoflora.co.uk/index.php](http://www.ecoflora.co.uk/index.php), [www.ufz.de/biolflor/index.jsp](http://www.ufz.de/biolflor/index.jsp), [www.biochange.ie/alien-plants/search.php](http://www.biochange.ie/alien-plants/search.php), <http://clopla.butbn.cas.cz/>, [www.leda-traitbase.org/LEDAportal/](http://www.leda-traitbase.org/LEDAportal/), For Biodiversity in Forest Monitoring programmes, see: [www.icp-forests.org/EPbiodiv.htm](http://www.icp-forests.org/EPbiodiv.htm) including a LIFE+ project

the Bern Convention are neither rare, nor endangered in Russia, and on the contrary, some species red-listed in Russia are not protected under the Convention. On the other hand, the Areas of Special Conservation Interest should contribute substantially to the objectives of the Convention. So, in order to reach the objectives of the Convention in Russia, we must recommend including into the Emerald Network the areas being not only formally fitting one or several ASCI general conditions but also in the best environmental state among similar areas in the region.

During the pilot assessment of Protected Areas in Moscow Oblast we have selected such areas by two mandatory criteria:

1. The presence of pan-European priority species;
2. Simultaneous permanent presence of several regionally rare (red-listed) species having different environmental requirements within the geographically determined natural conditions of the Central Russian plain.

Thus we revealed at least 18 natural sites that we consider as candidates for entering into the Emerald Network.

## **Mountains: a laboratory for understanding basic questions of evolution using taxonomy oriented electronic data bases**

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**Christian Körner and Eva Spehn**, Institute of Botany, University of Basel, Switzerland

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This contribution uses mountain systems as an example of linking Geodata with biodiversity information in order to provide novel avenues towards testing evolutionary and ecological theory.

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Geo-referenced archive databases on mountain organisms are very promising tools for achieving a better understanding of mountain biodiversity and predicting its changes. The Global Mountain Biodiversity Assessment (GMBA), a cross-cutting network of DIVERSITAS, in cooperation with the Global Biodiversity Information Facility (GBIF, [www.gbif.org](http://www.gbif.org)), encourages a global effort to mine biodiversity databases on mountain organisms, on a thematic webportal, which will be available in late 2009.

The wide range of climatic conditions and topographies across the world's mountains offers an unparalleled opportunity for developing and testing biodiversity theory. Mountains are islands of varying size, and thus present a good opportunity to ask questions about genesis of mountain biota, the impact of competition from other biota on speciation rates, and adaptive evolution. Where arid climates have developed at lower elevations, alpine areas can act as "conservation areas for phylogenetic lineage" for lowland lineages (see Hershkovitz et al., 2006). Mountains have acted (and will act) as refuges for species survival during extreme climatic events, including ancient phylogenetic lineages. Rapid rates of speciation have been documented in recent phylogenetic studies for genera in high-elevation areas (eg Hughes and Eastwood, 2006). Rapid evolution is also a factor for predictions related to climate change. The origin and assembly of mountain biota have to be understood in a historical context. To determine patterns of species richness, ecology and climate are important, but they should be linked to evolutionary and biogeographical processes (e.g. speciation, dispersal and extinction) for a deeper understanding and better predictions of biodiversity change with global change (Wiens and Donoghue, 2004).

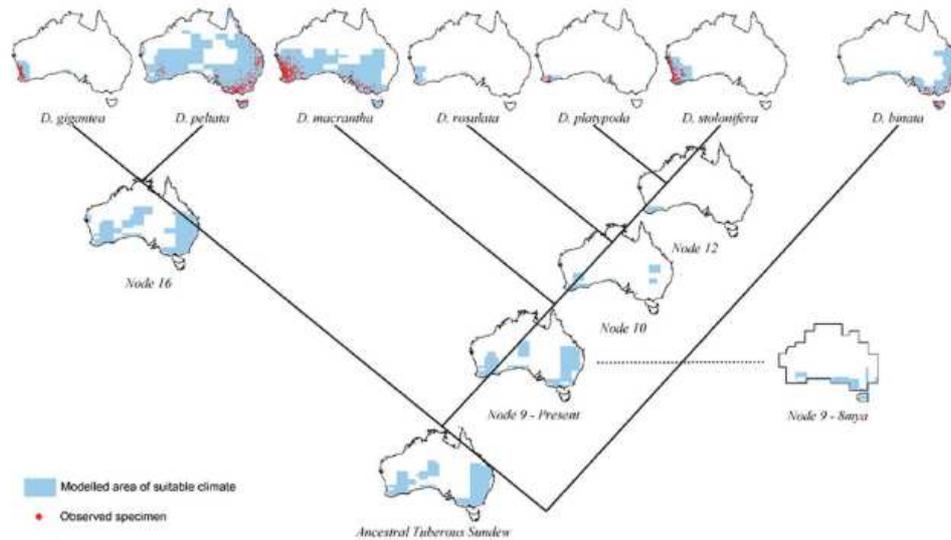
When taxonomic information is fed into electronic databases, it is crucial to keep the multipurpose scientific use in mind. Well designed and documented data in phylogenetic and phylogeographic databases, combined with regional species lists, and additional information such as classification of species by elevation (e.g. selection of alpine species), geographic distribution and species range limits, have immense value to answer questions like: where did taxa of a given mountain area arise, and how were taxa assembled over time? How many of the extant species resulted from the radiation of lineages that evolved within the area as opposed to the radiation of lineages that were introduced from other areas or even continents or other ecosystems? How important has long-distance dispersal been for the assembly of mountain biota, and how and when did evolutionary lineages migrate from one mountain area to others? What are the main sources of long-distance dispersal events? Has the capacity of long-distance dispersal itself been a factor in the rapid radiation of alpine lineages? With novel database tools, a new area of science is emerging with taxonomy, biogeography, evolutionary research and ecology becoming partners. The central issue to make this become a reality is precise geo-referencing. With exact geo-referencing, climatic, topographical and geological data can be linked to organismic data, opening totally new avenues of research (Körner et al., 2007).

In summary, mountains may be seen as 'experiments by nature' and the results of this globally 'highly replicated experiment' can be explored by e-mining of openly accessible, interconnected electronic databases for scientific biodiversity research, which by far exceeds the original intent of archiving for mainly taxonomic purposes. Exact geo-referencing is the key for such novel use of archived data. Examples of e-mining such mountain biodiversity databases are shown in a synthesis volume of two GMBA workshops (Spehn & Körner, 2009).



used to predict threats from climatic change when insufficient data is available (Yesson & Culham, 2006b).

**Figure 2.** Ancestral reconstructions of bioclimatic niches for tuberous sundews. Full extent of bioclimatic range marked blue. Red dots show locality data used to construct models. All models are projected into present day climate, additionally node 9 is projected into a palaeoclimate scenario for 8Ma, at which time this lineage was extant according to the molecular dating analysis. Southern Australia is shown to be climatically suitable for this ancestral lineage (Yesson & Culham, 2006a)



The data required for niche modelling, such as digitised herbarium records, is increasingly rapidly due to the efforts of organisations such as the Global Biodiversity Information Facility (<http://www.gbif.org>). However, there is still a long way to go before the majority of collections are digitised and the data is publicly available. We are still data deficient, particularly for the tropics (Yesson et al, 2007, see table 1).

The digitisation of existing collections is one way to fill this data-gap.

**Table 1.** Digitised plant specimens from the 10 largest herbaria via the GBIF data portal.

Herbarium	Institution Specimens	Specimens online	
		GBIF 2005	GBIF 2009*
Muse`um National d'Histoire Naturelle, Paris France	7,500,000	448,437	4,069,707
Royal Botanic Gardens, Kew UK	7,000,000	0	144,337
New York Botanical Garden USA	7,000,000	91,037	257,094
Conservatoire et Jardin botaniques, Gene`ve, Switzerland	6,000,000	202,855	n/a
V. L. Komarov Botanical Institute, St. Petersburg Russia	5,770,000	0	0
Missouri Botanical Garden USA	5,522,000	1,966,000	3,729,548
Natural History Museum, London UK	5,200,000	232,418	n/a
Harvard University, Massachusetts USA	5,005,000	0	389,814
Swedish Museum of Natural History, Stockholm Sweden	4,400,000	617,047	822,795
Smithsonian Institution, Washington DC USA	4,340,000	0	0

Adapted from Yesson et al. (2007)

\*2009 figures from [www.gbif.org](http://www.gbif.org) accessed March 2009

Phylogenetics and niche modelling can combine to provide useful information on threats from climate change, but only if the data is available to complete such studies.

## **RE: Phylogenetics and ecological niche modelling**

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**Daniel Faith**, The Australian Museum, Australia

Chris Yesson's contribution nicely covers the dual role for phylogenetics in assessments of climate change impacts:

1. Phylogeny, through measures such as PD (phylogenetic diversity), provides a measure of impacts on evolutionary history or 'feature diversity' – so addressing what Schipper calls “a more relevant currency of diversity...”
2. Phylogeny can help overcome lack of data for some species, because closely related species are likely to have similar climatic niches

With reference to point number 1, I wish to highlight a research challenge posed by Chris Yesson's early work on this issue. In lectures, I often use the Yesson and Culham (2006) phyloclimatic study of Cyclamens to raise the question: “Will the impacts of climate change on PD be large or small?”

Yesson and Culham found that those Cyclamen taxa likely to survive potential climate change impacts were phylogenetically 'dispersed' – spread out over the phylogenetic tree. This pattern (see appendix 1) implied that the potential loss of PD, and evolutionary potential, was smaller than might be expected based on simple species-counting. Yesson and Culham concluded: “while many individual species are at high risk, each major lineage is seen to contain at least one species with a reasonable chance of survival. This pattern lowers the overall risk to phylogenetic diversity”

As can be seen in appendix 1, I contrasted their pattern – where secure species (shown in red) were phylogenetically dispersed, and there was a small loss of PD for a given amount species loss - with the alternative, where the secure species are phylogenetically clumped, and so there is a large loss of PD for the given species loss.

Clearly, PD assessments are de-coupled to some degree from traditional species-level assessments. The challenge is to produce more studies to determine whether PD losses generally correspond to the 'good news' or the 'bad news' scenarios.

In these assessments, we also may go beyond using 'all-or-nothing' impacts on species, and use estimated probabilities of extinction, through 'probabilistic PD' methods.

## **Role of taxonomy in river water quality assessments and sustainable water management**

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**Otto Moog**, Astrid Schmidt-Kloiber, and Ilse Stubauer, BOKU Vienna, Austria

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The authors strongly endorse the need to strengthen and re-establish taxonomy in university curricula and to find funds to enable a sufficient number of employed taxonomists. If the current situation continues, bio-monitoring (and thus the sustainable use and conservation of nature) will drop back to its infancy.

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Water of good quality is finite resource! Therefore water issues create major problems that humanity must solve for its survival. Accurate water management decisions cannot be made at the green table. Sustainable management needs to be based on a first-class scientific background, namely on knowledge of the quantity and quality of a water body to be managed. Chemical monitoring is a customary practice in quite a few states. Nevertheless, in recent years there has been a strong focus towards the establishment of biological monitoring of water quality or the ecological status of water bodies respectively.

The different nature and the large variety of pressures and impacts on surface and groundwater bodies cannot be documented sufficiently by physical-chemical monitoring only. There is a common agreement among 'water people' that due to the manifold uses of water only a biological investigation provides the opportunity for an integrated view of a water bodies' status and quality. Especially in coherence with the implementation of the EU Water Framework Directive, a focus of European research activities concerning aquatic ecology was put on the development of assessment methods for European freshwater ecosystems. Several European research projects have been completed or are still running, in particular all projects are based on or incorporate elements of taxonomy<sup>5</sup>.

Among the methodologies used for ecological river status assessments different levels of taxonomic resolution are applied (species, genus, families and higher systematic units). The scientific community increasingly agrees that species level indicators are inevitable and that assessment techniques based on generic or higher taxonomic levels result in a loss of precision (De Pauw & Vanhooren, 1983; Hilsenhoff, 1987; Resh & Unzicker, 1975; Furse et al., 1984; Hilsenhoff, 1982; Rosenberg et al., 1986, Cranston, 1990; Stubauer & Moog, 2000; Schmidt-Kloiber & Nijboer, 2004).

Most biological monitoring techniques are dependent on the correct identification of the organisms collected. Better taxonomy can be expected to produce more accurate results and clearly increase the precision of site classifications, with a better ability to detect subtle changes in water quality (Lenat & Barbour, 1994). A number of studies make it clear that for a sound and integrative ecological assessment the higher taxonomic levels increase the possibility of misevaluating the ecological quality of an investigated water body (Furse et al., 1984; Hawkins & Norris, 2000; Lenat & Resh, 2001; King & Richardson, 2002).

The given situation clearly points out the fundamental need of applied working limnologists, hydro-biologists and aquatic ecologists for a vital taxonomic community. There is a need for taxonomists who provide the scientific basis by describing species (especially of poorly known groups), providing user-friendly keys and identification courses, custody voucher collections, supply species inventories and zoogeographic information (occurrence and distribution of species) and by linking the research of taxonomy and ecology to understand the ecological demands of species. In contrast to the demands of applied aquatic ecology the number of active taxonomists who provide the basics for applied work seems to be shrinking, probably due to a declining offer of academic taxonomy lessons and a change in scientific objectives/trends.

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<sup>5</sup> Examples: <http://www.aqem.de>, <http://www.eu-star.at>, <http://www.freshwaterecology.info>, <http://aquaeco.ups-tlse.fr>, [www.eurolimpacs.ucl.ac.uk](http://www.eurolimpacs.ucl.ac.uk), <http://fame.boku.ac.at>, [www.assess-hkh.at](http://www.assess-hkh.at), <http://www.mountain-lakes.org/emerge>, <http://www.wiser.eu>

## Taxonomy and Ecosystem Function

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Adam Vanbergen, Ben Woodcock and Rob Griffiths, NERC Centre for Ecology & Hydrology, UK.

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This contribution outlines the role that taxonomy plays in helping to resolve questions based on species functional ecology.

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To convey any information about an organism requires a name. This has become a cornerstone of ecology since the hierarchical classification produced by Linnaeus in 1735 and developed during the 19th century by notable taxonomic authors such as Halliday, Meigen, and Fallén. This effort to catalogue the myriad of species led to, and became superseded by, questions regarding the process of driving and maintaining the adaptation and origin of species. This culminated in Wallace and Darwin's theory that species were not immutable but evolved through natural selection. Moreover, the modern successor of 19<sup>th</sup> century taxonomy – systematics - uses molecular tools and cladistic approaches to provide insight into phylogenetic relationships among species. Taxonomy has, therefore, gone from being an end in itself, to a tool used to demonstrate the evolutionary relationships that underpin the diversity of life.

Simply recognizing distinct varieties (e.g. the so called 'Recognisable Taxonomic Unit' approach), while useful for estimating species richness, does not convey ecological information associated with identification of individual species under the Linnaean system. There is increasing awareness that it is not just species richness *per se* but functional redundancy in the traits across all species which plays a role in ecosystem processes, such as pollination, biocontrol and nutrient cycling. This link between a name and published knowledge regarding a species functional ecology is therefore becoming increasingly important.

Considerable challenges, however, remain for ecology and the origin and identity of species remains central to resolving those questions, hence modern systematics has an important part to play. Below we detail some first thoughts on research priorities:

### **1. Much remains to be understood about the role of biodiversity in ecosystem processes.**

For example, is it diversity or dominance of particular species that influence biogeochemical processes? Are there functional keystone species? To what extent is functional redundancy or complementarity in communities important in ecosystem stability and resilience? How does the link between biodiversity and biogeochemical cycles feedback to the climate system, and hence mitigate or inflate climate change? What are the relative roles of taxonomic versus functional trait diversity in determining ecosystem function?

These questions are important to better understand ecosystem function in order to better manage our environment. In all cases the identity of species either needs to be established, or contribute to a better understanding of how its functional role (e.g. predator, nitrogen-fixer, decomposer etc) affects ecosystem processes. Thus systematics is central to that research effort.

### **2. We need to improve our understanding of how evolutionary history may influence the likelihood of extinction in the face of global change.**

The ability of species to adapt or go extinct in response to changing climate may well be constrained by evolutionary origin. Phylogenetic analyses can enable prediction of which species are likely to go extinct because closely related species are likely to be sensitive to the same ecophysiological parameters, and consequently should respond similarly to anthropogenic disturbance. If those species vulnerable to extinction from climate change happen to also be important for ecosystem function, then systematics has a role in explaining how climate change can affect stability of ecosystem function via changes in biodiversity.

Hyper-diverse ecosystems, like soil, are where conventional Linnaean taxonomic approaches are often constrained either because of limited human resources or because the biodiversity itself is cryptic. Crucially these hyper-diverse systems are those that are important in the health of the environment. For example, the questions posed under points 1

& 2 are especially pertinent for soil microbial communities which regulate many key ecosystem processes of relevance to climate change, yet are poorly understood from both a taxonomic and functional perspective.

While progress has been made with genetic techniques to catalogue both taxonomic and functional diversity in microbial communities we now need to understand how the relationship between microbial diversity and ecosystem function will continue to operate in a changing environment. Does the observed genetic diversity of microbial assemblages correlate with phenotypic or functional diversity? Given the supposed functional redundancy within diverse microbial communities, coupled with the rapid evolvability of microbial taxa, how are microbial functions likely to be affected by climate change, if at all? Molecular systematics coupled with experiments is needed to answer these questions on ecosystem function and stability in the microbial realm.

## **RE: Taxonomy and Ecosystem Function**

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**Ferdinando Boero, University of Salento, Italy**

We always say that high biodiversity is good, and that it allows for better ecosystem functioning. There is a problem, though, in how to measure ecosystem functioning. The bulk of marine ecosystem functioning, for instance, is based on microbes (both as primary producers and decomposers) and is usually measured through their performances. This means that more complex organisms might look irrelevant for that function. Furthermore, in highly diverse ecosystems, the bulk of biodiversity is made up of rare or inconspicuous species. Ecological theory described this under the insurance model: it is true that these species do nothing relevant (from our way of measuring things) but they might spring into action if something goes wrong (the insurance).

With global warming, warm water species expand their distribution ranges, and make ecosystems function under the new conditions, integrating the resident set of species. But this is perceived as bad: the aliens are invading us. This is also the case when even residents become abundant, eventually substituting the formerly abundant ones, leading to a different state of ecosystems.

We like stability. So we expect that nothing changes. The insurance hypothesis is not linked to structure but to function, and we like it, in principle. But when the insurance enters into action, we do not like it because conditions are different from what we expect (stability). This simple example shows how ecological theory is seldom used to cope with real situations. Our view of ecosystems and biodiversity, however, should not be based on emotion, but on science. As for marine species, besides ignoring a great deal of them since we have not described all of them, we ignore the role of a lot of the known ones. We ignore their life cycles and their trophic position.

We need knowledge to manage the world around us. The best way of improving our knowledge is through science, but there is some sort of mismatch between knowledge and its application. Last week almost all contributors agreed that we must revise our knowledge of biodiversity, updating the old monographs. This week it is time to state that taxonomic knowledge must be linked to ecological knowledge at the level of species (what each species does, throughout its life cycle) and of communities (what do these species do together). Taxonomic knowledge is necessary (and cannot be replaced by information through databases) but is not sufficient (and must be supported by ecological knowledge). Then, once we have acquired this knowledge, we can improve our management of ecosystems.

## **Taxonomic and intra-specific diversity: the two-faced Janus of biodiversity**

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**Elena Bukvareva, A. N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow**

This contribution proposes to consider taxonomic diversity in ecological communities as a 'second face' of the integral conception of biodiversity. The 'other face' is intra-specific diversity. Combined consideration of diversity at these two levels shows that most effective ecosystem functioning corresponds to optimum values of diversity but not maximum or minimum values.

The question about interconnection between diversity and ecosystem functioning is a key point of practical application of taxonomy in the field of nature protection. The integral functioning of an ecosystem which is essential for human life consists of contributions of all species of this ecosystem.

The contributions of individual species depend on their internal diversity - phenotypic and genetic diversity, intra-population structure (for example social and family) population structure (metapopulation). This intra-specific diversity determines width of specific ecological niche and stability of specific ecological functions in fluctuating environments.

The integral ecosystem functioning consists of specific functions and depends on the structure of biocenosis (the number and relative abundance of species, interconnections between species) – that is it depends on both intra-specific and species (taxonomic) diversity.

We have showed that ecosystem functioning may be maximized if diversity is optimum (short English summary: <http://biosystems.narod.ru/ECCEM-Short.htm>). The results of our investigation bring us to the following conclusions:

1. Natural (minimally disturbed) ecosystems and ecological communities have intra-specific and species (taxonomic) diversity near optimum values (as far as it is possible in consideration of the history of the given ecosystem). This optimum diversity ensures maximum effectiveness of ecosystem functioning.
2. Intra-specific and species (taxonomic) diversity are inseparable linked with each other in the course of ecosystem functioning.
3. Optimum values of diversity depend on the amount of resources ('richness' or 'fertility' of environment, not 'productivity') and environmental instability, and reaction of populations and communities on destabilization is opposite: the optimum values of intra-population diversity increase in more unstable environments while the optimum values of species diversity decrease.
4. The opposite reaction of these levels on environmental destabilization allows us to make an assumption about their different role in a fluctuating environment: intra-population diversity is the basis for adaptation to environmental instability, while species diversity enables the community to use resources to the maximum and effectively.
5. Taxonomic diversity per se cannot be considered as the main criterion of environmental value of localities. Some ecosystems (for example, peat bogs of northern ecosystems) play a critical role in environmental regulation though have low taxonomic diversity.

Therefore, it is necessary for future research to:

- include intra-population and intra-specific diversity in the scope of investigations of interrelation between taxonomic diversity and ecosystem functioning;
- elaborate on practical methodology, taking into account intra-population and intra-specific diversity along with taxonomic diversity in the course of environmental assessments, identification of conservation priorities, and the operation of ecosystems and populations.

## Needs for improved taxonomic tools for policy support and applied biodiversity research

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**Klaus Henle**, Department of Conservation Biology, Helmholtz Centre for Environmental Research, Germany

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I argue that future taxonomic efforts, and funding priorities, should accommodate, at the conceptual stage, the needs of conservation biology and policy in addition to the needs of taxonomy. This contribution outlines the role that taxonomy plays in helping to resolve questions based on species functional ecology.

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It is difficult to get a decent overview of species level biodiversity, even for the better known and smaller taxonomic groups, such as most of the vertebrates. Being able to identify species correctly and have a basic knowledge about their distributions and status is a fundamental prerequisite for sound science in many fields of biology, including conservation biology, but also in many other human endeavours, including the use of biodiversity and the implementation of policies.

Biodiversity expertise and advances in the description and identification of species is widely scattered. Apart from a few popular taxonomic groups this knowledge was available only for specialists, until recently. The inability to get adequate access to taxonomic information is a major impediment to solving the biodiversity crisis, for applied biodiversity research, and for the implementation of policies for the sustainable use of biodiversity, such as CITES. Taxonomy has made major progress recently in attempting to compile this huge body of knowledge and to disseminate it through the web. GBIF has played a pivotal role in this endeavor. There are now several webpages available that compile species lists, provide taxonomic background information and references, present information on the distribution and status of species and display photographs.

While this endeavour is highly laudable and certainly needs to be continued, there are some conceptual deficits in the currently available tools. With few exceptions the web-based information systems were designed and written by taxonomists for taxonomists. And the same applies for many published compilations. While it is understandable, and the information is of great value for scientists working on taxonomic issues, it is of more limited use for field biologists and people working in the implementation of policies - even for comparably well-known forms, such as amphibians and reptiles, and a conservation biologist like me, who is mainly doing ecological research but having done some limited taxonomic work as well.

As a concrete example: within the EuMon project we analyzed gaps in the Natura 2000 network based on the official database of 2007. 44 of the 905 ANNEX II 'species' were not listed for any designated Natura 2000 sites. While evaluating these gaps it turned out that some of these missing taxa are probably due to taxonomic

problems but it is not easy and will take considerable time even to find out how many of the gaps are true gaps and how many are discrepancies in names or taxonomic status used. Thus, even for such high profile EU policies such as the Habitats Directive, web-based taxonomic tools are insufficient to easily resolve such important issues as: how many real gaps do we have in the Natura 2000 network?

Important information that I am often searching for in vain - or for which I have to compile the knowledge myself from many different sources - are:

1. Species lists broken down to regions at different scales (at least national, and sub-national scales, and in the EU) or tools with which users could construct such lists.
2. Adequate documentation of the distribution instead of rough distribution maps without documentation of references used for their compilation.
3. Keys that are designed for field use and for use by custom officers (a few exist, e.g. for the skins of crocodiles, but links to them are usually not available on taxonomic information websites); note, that what the conservation biology community at large needs are not keys designed by taxonomists for use by taxonomists with museum specimens but keys that can be used in the field and for custom purposes!

4. Reliable photographic documentation that is checked by specialists or against reference collections etc. I fear the easy access of many photographs stimulates unreliable species identification in many non-taxonomic fields (it is not rare that photos that belong to different species are labelled under the same name). How could the taxonomic community develop quality standards for this problem?
5. Links to other relevant databases, such as on ecological traits of species and species monitoring.

## **Taxonomy, biodiversity and its conservation: How to manage it in a sustainable way?**

**Dominique Richard and Doug Evans**, European Topic Centre on Biological Diversity, Paris, France

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Conservation measures need taxonomic stability or at least the ability to track changes.

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Implementing species and habitat conservation measures first implies that the species of concern are well defined and recognised: unresolved basic species taxonomy means that action at the species level cannot efficiently address those taxa most in need of conservation. Protection or restoration of habitats requires knowledge on their species composition.

The importance of taxonomy is particularly evident for instruments which have defined lists including entities which are of priority for conservation action, such as selected species and habitats. This is the case for several national or regional instruments such as nature reserves, the French “Arrêté de biotope”, or the Spanish “Micro-reserves” (Valencia region).

This is also the case for the EC Birds and Habitats Directives and for the Bern Convention which sets provision for the implementation of networks of sites, based on lists of species (Annex I of the Birds Directive, Annex II of the habitats directive, Resolution no. 6 of the Bern Convention) and habitats (Annex I of the Habitats Directive, Resolution no. 4 of the Bern Convention) requiring specific conservation measures. One of the main issues, when dealing with European instruments is that related assessments have to be made on a European scale, beyond national approaches.

Several main issues are at stake:

- Instability of taxonomic references leads to discrepancies in legal texts, which, in principle aims at a converging approach.
- For instance, although the Habitats directive (1992) was a direct implementation, at Community level, of the Bern Convention (1979), there were several cases where species were listed under different names in the two legal texts. This may undermine the credibility of legal conservation measures and open the way to opponents to such measures.
- Differences in taxonomic references used by countries create problems in comparing species and habitat status across Europe and adds to the complexity in the evolution of legal texts (for instance, adaptation of the annexes of the Habitat Directive due to the enlargement process).
- Most critical is the absence of an operational updated “Flora of Europe”, which can be used for analyses, assessments and comparisons at a European scale. Flora Europae is not accepted as accurate by many botanists in central Europe and the Med-Checklist is only partly complete. It is not clear how far the EuroMed plantbase is yet to being operational. This is a major case for improvement in the near future.
- Complementary to agreed-upon reference taxonomic lists, the need to have spatial and temporal information on species is critical for any kind of conservation related assessment. For instance, an atlas of species distribution per grid unit (such as Atlas Flora Europea, Atlas of Butterflies, etc...) provide a very useful reference for any kind of assessment on species rarity, endemicity, limit of distribution range, index of species homogeneity, index of species richness, species climatic envelopes, overlaying species distribution with different pressure maps (nitrogen deposition, fragmentation by infrastructures etc...).

A collaboration between the ETC/BD and the PESI project is foreseen for a cross validation of the last version of species lists of the Nature Directives annexes against the pan-European checklists of Fauna Europaea, ERMS and E+M PlantBase.

## **Taxonomy to understand ecological change**

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**Ferdinando Boero**, University of Salento, Italy

We need to compile master lists of species for each type of habitat, once a habitat is sampled we can have two species lists: the species that have been found and the species that have not been found (those present in the master list that have not been recorded). Only taxonomists can produce these master lists, reconstructing them by analysing the available information on each species, contained in the taxonomic literature and, also, in ecological literature.

Matching master lists with new lists will mean that we are able to trace when a species has been recorded for the last time. If a species is unrecorded for, let's say, 50 or more years, there are two possibilities: it is understudied or it is either extinct or in distress. Having these lists of species that are not found for decades will give us real "red lists" that might call for proper investigation on each case of putative extinction.

This would radically change our perception of biodiversity. The joining of habitat diversity and species diversity, thus, is a practicable protocol to assess change of species diversity at habitat level, encompassing two main definitions of biodiversity. The species diversity of a habitat, furthermore, gives us an indication of its state in terms of hosted biodiversity.

## **RE: Taxonomy, biodiversity and its conservation**

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**Sandra Luque**, Cemagref, France

Protection or restoration of habitats requires knowledge of their species composition. Regrettably, as pointed out by Dominique Richard and Doug Evans, we lack harmonisation and spatial and temporal coherence in existing data. In that sense despite the many international mechanisms set up under the framework of the CBD 2010 not much has been achieved. Furthermore, the 'Paris Declaration for biodiversity' (Paris Conference, January 2005), set up a compromise to reinforce the links between the North and the South in order to work towards an improved protection of biodiversity through cooperation on harmonised data. However, currently nothing concrete has been accomplished with regards to data bases. The political instability of the South and the lack of funding, at the regional level mean that the North should assume a responsibility on serious programs that can secure the continuity of long term observation sites and data bases at species level.

We all agreed that National and international support on monitoring and restoration activities is needed. Subsequently, long term data are needed to be able to develop appropriate conservation and management options and plan for changes within climate change scenarios. Free and open access to biodiversity data is today a reality ([www.gbif.org](http://www.gbif.org)), but much work needs to be done to fulfil the data portal with good data quality and reliable data sources for countries where this is most needed. Strong mechanisms still need to be developed to reach North-South cooperation in tandem with international academic programs in conservation.

Just to provide one example of the alarming situation, the Chilean flora is estimated to consist of about 5.1 thousand species, more than 180 families and one thousand genera. More than 50% (2630) of the species are thought to be endemic (Marticorena, 1990). Within Chile more than 60% of the total flora and the endemic species are concentrated into an area that focuses on Central Chile from ca 29.0o S to 43.5o S. Central Chile has been identified as one of the world's 25 biodiversity hotspots, namely areas that contain at least 1,500 endemic species of vascular plants (>0.5% of the world's total) and have lost at least 70% of the original habitat (Myers et al. 2000). In a recent review of the world's hotspots, the Central Chile area was expanded and re-designated as the 'Chilean Winter Rainfall - Valdivian Forests Biodiversity Hotspot'. The native vegetation of this area is estimated to have declined from almost 400 thousand km<sup>2</sup> to less than 120 thousand km<sup>2</sup> (Myers et al., 2000).

Despite all the progress achieved and the many existing international organisations, integrative research is lacking, innovative questions are evasive or difficult to get funded. Global cooperation is urgently needed.

## Taxonomy as a basis for ecological research and biodiversity conservation

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**Daniel Faith**, The Australian Museum, Australia

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This contribution will address a designated topic ‘Taxonomy as a basis for ecological research and biodiversity conservation’. I will refer to phylogenetics as well, noting that the aim of the new DIVERSITAS program, Biogenesis, is to help bring evolutionary approaches to bear on pressing biodiversity problems.

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Many of the most-pressing biodiversity issues lie at the interface of systematics, conservation, and ecology. Examples include important research topics such as the role of dispersal corridors, or the compositional changes in communities as a consequence of climate change. Naturally, single species studies provide well-known links between taxonomy and ecology – for example, in research investigating how management and conservation priorities are influenced by species designations. But I think that key research challenges arise from the need for biodiversity conservation to address overall biodiversity (e.g. all species). True biodiversity conservation must address not just the known but also the still-unknown variation (in Australia, only about 175,000 species of perhaps 680,000 are described and named). Of course, our knowledge-gap is even worse because decision-makers also need information about species’ geographic distributions.

Conservation planning approaches this knowledge gap by using surrogates – e.g., one set of taxa stands in as a proxy for all the rest. Research so far suggests that individual taxon groups do not do very well as surrogates. This limitation highlights the need for more taxonomic work, and for research on new surrogate strategies.

One possible way to boost surrogacy is to make better use of ecological principles. We can infer ordinations assuming unimodal response of species to gradients. If the ordination space and gradients, derived using one set of species, are relevant to the distribution of many other species, then selecting reserves to fill gaps in the environmental space may improve representation of overall biodiversity. Research is needed to further develop such approaches.

Another possible way to boost surrogacy is to make better use of phylogeny. Recent work illustrates how phylogenetic patterns for different taxa may reflect shared history among areas – so that localities that are special for observed species also may be special for many other taxa. Research is needed to evaluate this hypothesis.

DNA Barcoding and related approaches may contribute to conservation planning using estimated phylogeny and a phylogenetic approach, “PD”, with or without species designations. Recent work (e.g., Faith, 2008) suggests that we gain surrogates power by using PD and phylogeny. This approach contrasts with a conventional view that sees DNA barcoding as providing rapid assessment through conventional species-level indices applied to operational taxonomic units.

A possible advantage of the PD framework is that most indices that are conventionally calculated for species can instead be calculated using phylogeny. For example, we can estimate the PD-endemism of regions (the unique evolutionary history represented by the region). Such phylogenetic ecology may give different answers compared to species-ecology. How do we reconcile these?

I’ve highlighted surrogates strategies using phylogeny, and using gradients, but these two strategies can be combined. Microbial ecologists have pioneered “phylogenetic beta diversity” (Lozupone et al. 2007). PD-dissimilarities among localities are calculated using phylogenetic tree branches, and then ordinations reveal key gradients that may inform us about functional variation and ecosystem services. Future research can extend these new phylo-ecology approaches to biodiversity conservation research.

In order to address overall biodiversity, we need more taxonomic knowledge. At the same time, research linking taxonomy, phylogeny, and ecology must help us to use current knowledge to estimate patterns for overall biodiversity.

## **RE: Taxonomy as a basis for ecological research and biodiversity conservation**

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**Angel Perez-Ruzafa**, University of Murcia, Spain

One of the more important things needed to understand the real role of taxonomy and its links with ecological and biogeographic processes is to know the links between a relatively fixed concept of species (both at human scale and at phylogenetic scale) with the genetic variability and the plasticity of phenotypic expression depending on local conditions that can change both, spatially and temporally.

In my opinion, identification of new species must be linked to their genetic analysis and the record of their role (at least data on abundance and distribution) in a given ecosystem. It would be important that taxonomic field surveys respond to a previously well-defined quantitative sampling design that permits cumulative information on this basic knowledge, and vice versa, ecological studies (and other biological studies) should warrant the correct identification of species.

However, to get expertise in a taxonomic group requires years of work. A European strategy (the same could be applied to other areas or at global scale) would be to maintain a stable network of taxonomists and taxonomic-geneticists working in the context of other biological projects in which the taxonomic status of the species should be adequately identified. A coordinated database could be maintained to include the biodiversity records (including genetic identification) and basic ecological or biological information recorded in the context of these projects. Such databases would make large projects able to analyze spatial variability in species phenotypic, genotypic and ecological characteristics and, after some years, temporal trends and changes in biodiversity at local and large geographical scales. The power of the system could be reinforced if a set of observatories on biodiversity could be established (most of them using actual institutions) with a minimum common program of surveys using the same protocols and taking advantage of the network of taxonomists. This structure could sound utopian, but probably is mainly a matter of coordination of actual specialists and institutions under an EU level coordination and economically is probably easier to maintain than the actual structure due to the synergy of very diverse projects.

In this context, the Spanish Ministry of Science and Innovation is promoting a series of Singular Scientific and Technological Infrastructures, one of them named (OOCMUR-Coastal Oceanographic Observatory of Murcia), which will be placed in Murcia (Spain) close to the Cape of Palos in the South-Western Mediterranean. OOCMUR will be devoted to the study of the ecological and oceanographic processes linked to biodiversity changes produced by climate change, introduction-colonization of allochthonous species and other human impacts, with special focus in coastal lagoons and open coastal areas. It will also include genetic analyses of species and populations, an open data-base and the recording and study of oceanographic processes and parameters affecting biodiversity and that determine the connectivity between populations at different spatio-temporal scales.

The idea is that such infrastructures will be open to all international researchers interested in developing research, analyzing genetic samples, or performing comparative studies at different spatio-temporal scales (from short term comparisons to long term dynamics). The project is still under construction, and any suggestion on the topics, services, facilities and infrastructures that you consider important to take into account or you would like to have available for future (particular or collaborative) projects are welcome.

# Session 4: Open access to information

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## Taxonomy and Biodiversity Information Systems: The FishBase and SeaLifeBase Experience

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**Deng Palomares**, Fisheries Centre, University of British Columbia, Vancouver, Canada and  
**Nicolas Bailly**, The World Fish Centre, Philippines Office, Los Baños, Laguna, Philippines

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This contribution opens discussion on three points: current taxonomic databases and their potential use with professional databases; the lack of taxonomic authorities; and ways to increase financial resources to respond to the professional demand for these biodiversity information systems.

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The efficient use of all biodiversity information for natural resource management (exploitation and conservation) relies on the good communication/interoperability between information systems maintained by various professional biodiversity stakeholders. Taxonomy and its nomenclature permit this communication. Therefore, stakeholders look for exhaustive and stable taxonomic backbones. In the aquatic domain, FishBase, and now SeaLifeBase, are often used as this taxonomic backbone (although it was not their primary aim).

Stakeholders from governmental and non-governmental agencies request data from FishBase/SeaLifeBase, such as: fishery managers, conservationists and Marine Protected Area managers, aquarium trade operators, public aquarium managers, school professors, customs and associated veterinary (and phytosanitary) services, legal workers, environmental agencies, researchers, etc. Many requests include information other than classification and names. However, statuses of species and names remain important features of these requests.

For these taxonomy users, the proliferation of online Biodiversity Information Systems (BIS) tends to create confusion on which of these databases is most appropriate to use for taxonomy. Even the Catalogue of Life (CoL) with 1.160 million valid species names and 764,000 synonyms from 66 Global Species Databases (GSDs) has gaps, tentatively filled by regional databases (RSDs), which may lead to contradictory statuses for same species and names.

### 1. Automatic and real-time updates among existing BIS, and with professional databases

For fishes, the accepted taxonomic authority is the Catalogue of Fishes (CofF); FishBase adds many string-names (new combinations and misspellings) providing a complementary online resource. However, due to unsynchronized updating schedules, the two databases can be contradictory.

From a professional perspective, which one should we use? Can updates between FishBase and CofF be improved in terms of valid species and names content equivalence? Can they propose tools to biodiversity stakeholders to automate updates in their own information systems?

### 2. Lack of taxonomic authorities: synergy and collaboration with taxonomists

This problem is even larger for SeaLifeBase where unlike for fishes, no taxonomic authority exists for marine metazoans. SeaLifeBase relies on partial taxonomic lists from CoL (including ITIS) and the World Registry of Marine Species (WoRMS). Thus SeaLifeBase avoided reinventing the taxonomic and nomenclatural wheels. However, neither CoL nor WoRMS can provide the world list of marine species. To go forward, SeaLifeBase actively encodes taxonomic data, most often upon request from professionals, by fixing short-term do-able targets and making full use of published taxonomic literature.

How can we improve integration of several current initiatives to avoid duplication of work, and eventually concurrent taxonomies delivered to non-taxonomists<sup>6</sup>? How can we involve taxonomists and help them organise collaborative work to fill the gaps?

### 3. Increasing financial resources by responding to professional demand

Several stakeholders requested annual subscription to web services for regular update downloads. Most often, such web services are very specific and require programming time, though usually no more than two days.

Can BIS/GSDs/RSDs custodians improve responsiveness to professional users' requests? Would professional users pay a reasonable fee to access these services? Regular income under the form of an annual subscription fee for customized updating web services could be part of the business plan that the biodiversity informatics domain is still looking for.

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<sup>6</sup> We acknowledge the fact that taxonomies are not fixed once and for all. We are talking here about names that should be disseminated for uses by non-specialists.

## **Do not let ‘Open Access’ stand alone in the EU as barriers will kill it**

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**Phillip Boegh**, University of Copenhagen, Denmark

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This contribution highlights the potential benefits associated with implementing direct ‘Open Access’ of public research.

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Unless the EU politicians agree to direct Open Access<sup>7</sup> of public research (as they do in the USA), then we will need to rely on our abilities to overcome these massive barriers ourselves. This is possible and perhaps we can and do it even better due to this ‘Open Sourcing’<sup>8</sup> process, as we may gain the side benefits of:

- motivating openness,
- involving management,
- strengthening the science and
- including networking throughout our struggle to get acknowledgement for providing Open Access resources.

The reason that this is not likely is that we can implement Open Access in Europe without major changes occurring. Therefore, we also need to prepare an open-minded university environment.

At present, Open Access may intervene with the merit of most researchers because only closed, peer reviewed papers are of repute due to university traditions in the EU. In fairness, this has been the case in many branches, even though scientific open journals and databases are coming up. Nevertheless, the traditional structure is an unfair barrier for Open Access: Merit for maintaining online scientific databases is not ranked alongside maintaining physical collections in, for example, university museums. Library structures held up decisions to change to Open Access – a shift that would include more stakeholders and provide more common knowledge. If scientists insist on publishing under Open Access it may even influence their research economy. However, if we ensure decent quality control of the Open Access resources, there should be no way back to acknowledging Open Access. Prior to the quality control, we could implement a package with tools to strengthen the science including better reviews and certification of all experts involved<sup>9</sup>.

The opposing arguments that I hear against an Open Sourcing process are divided into two camps – although a few even choose both: ‘My department is already perfectly open’ or ‘You advocate for unrealistic openness’. If you find your scientific branch is open, you’ll be astonished by the comprehensive levels of openness in the Open Source theories or by practical experience of different open source environments. If you find the openness unrealistic, you have not noticed that even related areas have proved that extensive openness is highly beneficial. Please keep in mind, we do not need to accept the whole Open Source Society pathway to make Open Access a reality, but we need to pick components from all three areas:

- A more open management structure
- A fairer meritocracy
- A far more open networking structure.

I’d like to recommend Open Sourcing: At least ‘Open Decision making’, and ‘Open Review’ to supplement the gate-keepers review, and the development of open but ‘meritocratic’ networks to overcome the barriers of Open Access.

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<sup>7</sup> Open Access of the scientific resources is Literature, database collections & physical collections.

<sup>8</sup> Open Source community and theories behind: <http://www.sci-mate.org/item.php?id=21> (A review of the Open Source terms)

<sup>9</sup> Taxonomic certifications: <http://www.wikigenes.org/e/art/e/32.html>  
(An example of certifications in various levels)

## **Sustainability of online taxonomic information systems**

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**Mark Costello**, University of Auckland, New Zealand

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This contribution emphasises that in order for online biodiversity information systems to be sustainable it is necessary for taxonomy to play a key role in order to produce good quality data and for this data to clearly show authorship, ensuring credibility.

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The need for rapid access to taxonomic information has never been greater because of the pace of harvesting natural resources, habitat loss, and species extinction's is unprecedented. Taxonomy is the key part of the quality control system for biodiversity data, and the credibility of the information is based on its authors. Thus the best information will clearly show who its authors are and indicate their professional status (e.g. peer-selected, institutional affiliation). A global community effort is essential to produce and manage information on biodiversity because of the amount of information that is known and yet to be discovered is vast. How can this information be quality-assured and maintained in the way some print media are?

The first place most people look for information now is the internet, almost all scientific journals are available online (some only so), and more scientists are publishing content on websites every year (see table 1). A criticism of websites was that they are not archived but this is now happening (e.g. [www.archives.org](http://www.archives.org)). However, databases that serve data through search-portals are not archived like web pages and so must be maintained by their hosts, and/or mirrored at other locations (like GenBank is). In contrast many print publications are scarce and often unavailable to people without funds to purchase or borrow them. In the future, all publications will need to be available through the internet. The conventional publication models of non-peer reviewed, peer-reviewed, and scientifically edited or unedited, have transferred to the internet. However, there remains work to be done to clarify how to cite, archive, and track the origin of information accessible via websites; and the scientific community must formally recognise the value of such publications in their assessment of their peers for employment and promotion.

Online resources have the advantage over print media in that they can be quickly updated, and grow organically with unstructured contributions from one to many authors. They should grow in quality and quantity over time. However, resources created by one person, or hosted on commercial or institutional websites, are less likely to be sustained over time than those for which the scientific community takes a collective responsibility. Thus, the Global Biodiversity Information Facility (GBIF) is financially supported by many countries, and these countries and a range of scientific organisations support the delivery and development of its content. A group of institutions and international organisations take responsibility for the maintenance and development of FishBase, the longest established online species database. A third approach is for individual scientists to form a scientific society that takes responsibility for finding authors and editors of an online publication. The members of the Society for the Management of Electronic Biodiversity Data ([www.smebd.eu](http://www.smebd.eu)), a legally incorporated not-for-profit scientific society that is a member of GBIF, are the people who contributed to the databases it takes responsibility for; such as the European and World Registers of Marine Species, Fauna Europaea, and Euro+Med PlantBase. SMEBD (Society for the Management of Electronic Biodiversity Data) sources additional and replacement editors to manage the content of its databases, and appoints institutions to host the database. This is comparable to a society that appoints a publisher for its scientific journals, and whose members are authors, editors and peer-reviewers of the journal content. Society members take responsibility for obtaining funding to maintain and develop the resources. There are a significant number of excellent online resources created by individual scientists, and more being created by research projects. These initiatives should plan to ensure the long-term sustainability of their resources.

**Table 1. Examples of some scholarly online resources (with an aquatic bias)**

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AlgaeBase	A database on the names, key literature and images of seaweeds and other algae	<a href="http://www.algaebase.org/">www.algaebase.org/</a>
Aquamaps	Maps the probable distribution range of species using editable environmental data (e.g. from OBIS) that may be expert validated	<a href="http://www.aquamaps.org">www.aquamaps.org</a>
Dictionaries	WordNet, Wordweb	<a href="http://wordnet.princeton.edu">http://wordnet.princeton.edu</a> <a href="http://wordweb.info/free">http://wordweb.info/free</a>
Encyclopedia of Life	Gathers information from other online resources to produce information pages on species (including from Species 2000 Catalogue of Life, marinespecies.org)	<a href="http://www.eol.org">www.eol.org</a>
FishBase	The best developed and oldest online species information system, with a wide range of applications for fisheries research and management	<a href="http://www.fishbase.org">www.fishbase.org</a>
Global Biodiversity Information Facility	Data on distribution of species in all environments	<a href="http://www.gbif.net">www.gbif.net</a> <a href="http://data.gbif.org">http://data.gbif.org</a> <a href="http://www.gbif.org">www.gbif.org</a>
Google Scholar	Searches scholarly resources, such as scientific journals, reports and websites	<a href="http://scholar.google.com">http://scholar.google.com</a>
iSpecies	The first ‘mashup’ page for species. It automatically searches a pre-determined range of internet resources for information on any species, including molecular, images, literature, etc. Very simple interface.	<a href="http://www.ispecies.org">www.ispecies.org</a>
Marinespecies.org	An expert edited collection of databases on marine species aiming to have some information on all marine species by 2009. Minimum information is the correct name and classification. Some pages contain extensive information on distribution, ecology, biology and literature. Several Global Species Databases within the system include freshwater and terrestrial species.	<a href="http://www.marinespecies.org">www.marinespecies.org</a>
MarLIN	The Marine Life Information Network for Britain and Ireland contains expert approved information on marine species and their habitats, aimed at public and scientists, including a large glossary.	<a href="http://www.marlin.ac.uk/">www.marlin.ac.uk/</a>
NABIS	Expert prepared maps of the distribution range of economically important (e.g. commercially fished, invasive) marine species around New Zealand	<a href="http://www.nabis.govt.nz">www.nabis.govt.nz</a>
OBIS-SEAMAP	An award winning portal “Spatial Ecological Analysis of Megavertebrate Populations” to databases on the distribution of marine mammals, birds and turtles	<a href="http://seamap.env.duke.edu/">http://seamap.env.duke.edu/</a>
Ocean Biogeographic Information System	Allows discovery, exploration and mapping of data on the distribution of marine species plus tools to predict their environmental range. Includes over 500 interoperable datasets and 100,000 species. All this data and more on marine species is available through GBIF.	<a href="http://www.iobis.org">www.iobis.org</a>
Plazi	Taxonomic information used to describe species re-compiled from excerpts of publications	<a href="http://www.plazi.org">www.plazi.org</a>
uBio	A more complex librarian-designed system “Universal Biological Indexer and Organiser” that searches pre-determined electronic resources for information on any species. Unlike iSpecies, it uses ‘taxonomic intelligence’ to find related species names. It will be superseded by EoL.	<a href="http://www.ubio.org">www.ubio.org</a>

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## How will large-scale research infrastructures benefit our science?

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**Wouter Los**, University of Amsterdam, The Netherlands

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This contribution outlines the importance of researchers using a common infrastructure in order to promote large-scale common research priorities which in turn promotes large-scale funding and data generation.

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Biodiversity made much progress with the reductionist approach by studying isolated separate components of the biological system. However, this reductionist approach fails to capture the wider picture of the full complexity of biological systems. It is very often not possible to understand a biological system by extrapolating from the known behaviour of single units which constitute the system. In such situations it is inevitable to apply a different methodological approach by analyzing the correlation properties of (ensembles of) system units with statistical and modelling methods. Intensive computation of available large data-sets related to these units would assist in detecting patterns of strong correlations with evidence for 'collective system organizations', which in turn can be further analyzed to retrieve the processes behind such patterns. This is what some like to call 'systems biology'.

However, the current practice to follow this scientific approach is not easy. Although GBIF now offers >170 million (species level) records, you will always miss the data you are looking for. And you still have to go to other facilities for different data categories (e.g., genetics of ecosystems), providing that such facilities exist. It is even more cumbersome to select the appropriate analytical modelling software, and to have the selected data sets compatible with the input format of a software package. Finally you may find yourself in the situation that the required computational capacity to run your analysis or model is too high. You would not be happy with the implication to simplify your preferred workflow of data and software.

Progress in biodiversity research would greatly benefit from a one-shop portal where you can access all required resources, and where the compatibility of very large databases (from collections, observations and sensors) together with advanced analytical and modelling software is offered with a compatibility report. You would be really happy if such a portal also allows you to create your preferred work flows with access to powerful computational capacity, and if you could share these capabilities with your colleagues in a personalized virtual laboratory. Well, this is exactly what the LifeWatch project wants to implement ([www.lifewatch.eu](http://www.lifewatch.eu)).

It is important to show that biodiversity researchers want to scale up their research efforts and that they together opt for a common infrastructure. A common infrastructure also promotes large-scale common research priorities. And this in turn is an attractor for large-scale funding; also for data generation with respect to large-scale digitization, observation technologies and sensor development.

Recommendations on research priorities and associated funding will only attract enough attention when the research community demonstrates its common strategic agenda, including the construction of the LifeWatch research infrastructure. The EU countries are getting increasingly excited about the LifeWatch research infrastructure, but the challenge now is to agree on the related grand research questions in a common strategic agenda.

## **Biodiversity informatics: The Global Names Architecture**

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**David Remsen**, Global Biodiversity Information Facility, Denmark

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This contribution highlights the need for an infrastructure that permits interoperability between those who mobilize and serve content tied to scientific names with those who can provide information about those scientific names. The author outlines how the Global Names Architecture will enable such a collective discovery and access system.

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Biodiversity informatics focuses on mobilizing, accessing, and synthesizing information about individual species, their temporal and spatial relationships with other species, and with human and natural environments. All historic and contemporary information about a species is tied to a scientific name. Biodiversity, however, lacks a complete list of scientific names of organisms and an effective mechanism for assessing the scope and quality of names actually employed as tags that tie a particular piece of information or data to our understanding of taxa. This is especially problematic because names of species are neither stable nor unique and a single species may be known by more than one name while the same name may not only refer to more than one taxon, it may refer to different definitions of the same nominal taxon. These factors all significantly impact on the means to find, access, and effectively synthesize biodiversity data.

Effectively addressing these challenges requires the means to discover, access, and utilize information about names that exist in a distributed array of nomenclatural and taxonomic databases. It requires the means to identify gaps and overlaps in taxonomic and nomenclatural coverage between these systems and the full array of names that exist in the vast corpus of literature, specimens, observations, reports, images, gene sequences, and other data or information objects that collectively form the knowledge-base of all information for all species.

This requires an infrastructure that permits interoperability between those who mobilize and serve content tied to scientific names with those who can provide information about those scientific names. The former provides the raw materials that define the complete list of scientific names. The latter provides the syntactic and semantic information that enable names to be organized into a framework that has taxonomic integrity. There is currently no collective mechanism for coordinating and collating the activities between these two domains in order to evaluate the degree of completeness and overlap both within and among them. The most basic requirement of this infrastructure is a common discovery and access architecture that allows those who provide information about names to be visible to those who curate content containing them.

The Global Names Architecture is an effort to enable such a collective discovery and access system. It seeks to promote a common method for registering and discovering sources of taxonomic information, a common means to exchange these data, a common, single reference point proceeding from the nominal taxa, and a collective indexing mechanism for collating the totality of names treated within authoritative taxonomic and nomenclatural senses, with the full scope of names tied to all information about all taxa.

The intent of the Global Names Architecture is to be able to collectively identify and redirect those who need taxonomic information to those who can provide it. It seeks to identify methods that reduce latency in accessing these data, incentives for those who provide them, and a path toward creating a complete list of scientific names that are comprehensively integrated into a consistent, comprehensive, and stable taxonomic framework that can be directly utilized as a global informatics service for providing access to information about species. In Europe the EC FP7 PESI project takes care of the European contribution to the Global Names Architecture developments (supported by EDIT and Life Watch).

## Taxonomy and citizen science

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**Jean-François Molino**, IRD, France

Taxonomists face a great challenge: pursuing the long-term task of describing all living species, while trying to respond to the increasing public demand for accurate and up to date Biodiversity Information Systems. For at least some groups (e.g. plants, birds, butterflies), one of the possible means to reconcile these apparently contradictory tasks is to promote and develop what is called 'Citizen Science'.

Citizen science ([http://en.wikipedia.org/wiki/Citizen\\_science](http://en.wikipedia.org/wiki/Citizen_science)) is a powerful means to enrich databases with information on species location, life stages, ecology and images, thus providing huge amounts of data for taxonomic work. At this point of the debate, taxonomists usually object that they would not use such data sets unless they have been carefully checked and validated by recognized authorities (i.e. themselves), and that this time-consuming validation would probably not be worthwhile.

I argue that:

a) All data sets and databases contain a proportion of irrelevant, false or inaccurate data, which is often very difficult to estimate. Even databases provided by taxonomic institutions, such as Museums, are all but free from such defects. For instance, on some distribution maps of land plant species provided by these institutions through the GBIF, it happens that a record falls on the open sea. As such errors are probably only the tip of the iceberg; it is tempting to question altogether the validity of all these GBIF distribution maps. It would certainly be a mistake. Actually, the accuracy of these maps only partly rely on the proportion of erroneous records. They are more dependent on the size of the data set. A species distribution map drawn from a large data set is usually fairly accurate, since most erroneously located records still fall within its actual distribution area. As a matter of fact, citizen science has proven very effective for knowledge accumulation, for instance on bird and butterfly migrations, mating and nesting dates, etc.

b) Data validation a posteriori is not the only means to improve data set accuracy. Non-taxonomist participants can provide good quality data if they have access to proper tools for species identification. Thus citizen science works best when taxonomists invest in education and diffusion of their results, notably through the development of easy access and audience identification tools.

On these grounds, Agropolis Fondation ([www.agropolis-fondation.fr/uk/abouts.html](http://www.agropolis-fondation.fr/uk/abouts.html)) has recently chosen the Pl@ntNet initiative as its first flagship programme. Pl@ntNet is a web-oriented scientific, informative and educational network and software platform dedicated to the collaborative gathering, sharing and use of large, multi-disciplinary data sets on tropical and Mediterranean plants. It will be implemented over a period of four years and will include, among others, new easy-access tools dedicated to automated plant identification<sup>10</sup>, to establish potential distribution maps of useful or key plant species and plant communities, and to the search and exploitation of internal as well as external knowledge banks on plant use and production.

The Pl@ntNet programme will certainly benefit from, and contribute to European initiatives on Taxonomy.

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<sup>10</sup> [http://umramap.cirad.fr/amap2/logiciels\\_amap/index.php?page=idao](http://umramap.cirad.fr/amap2/logiciels_amap/index.php?page=idao), and [www-rocq.inria.fr/cgi-bin/imedia/circario.cgi/bio\\_diversity?select\\_db=1](http://www-rocq.inria.fr/cgi-bin/imedia/circario.cgi/bio_diversity?select_db=1)

## Recommendations for taxonomy from a Portuguese perspective

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**Marina Pereira Silva and Isabel Sousa Pinto**, CIMAR, Portugal

It is recognized by all that global biodiversity is being lost at an unprecedented rate as a result of human activities, and decisions must be taken now to stop this loss. In order to decide what to do to stop and reverse biodiversity loss we must have the necessary knowledge. Taxonomy provides the species-level information required to better define the biological diversity baseline and assess biodiversity loss, necessary for effective decision-making about conservation and sustainable use.

To decide where to establish protected areas decision makers need to know what is being protected. To identify and combat harmful invasive species regulators need to distinguish them from native species. Developing countries can only ensure that they reap the benefits of the use of their biological diversity, if they know the biological diversity that is being used.

In Portugal some taxonomy-based tools are used for biodiversity assessments and policy making, e.g. MACOI database, Portuguese Seaweed Web site, P-MarMAT, Portuguese Marine Macroalgae Assessment Tool, Lichen-diversity based tools, ATLANTIS Tierra database. Some very recent checklists of Portuguese species were identified, including algae, fungi, fauna and flora of the Azores Islands, some red lists, as the Red Book of terrestrial vertebrates from Portugal, or bryophytes from the Iberian Peninsula. Lists of invasive species were also identified, showing some recent activity in the study of Portuguese flora and fauna.

Portugal is partner in several international projects, not only as a user of the data but as a data provider, namely in the GBIF. According with the results of an inquiry carried out during the summer of 2006 in connection with the establishment of the Portuguese node of GBIF, there are approximately 2,4 million specimens, in 94 collections recorded. Most of them (67%) of the flora domain and only 10% of the records are digitalized in databases (see table 1).

In the Biodiversity collections index online we can find 22 biological collections from Portugal, mainly herbariums and entomology (insects and spiders). From the report presented under the CBD and GTI Portugal did not have an assessment of taxonomic needs and capacities at the National level. Most of the problems are due to a lack of human and financial resources and with the poor visibility and utilisation of the work produced by taxonomists.

**Table 1.** Number of biological collections and specimens recorded from national institutions, digitalised data and percentage of digitalised data, as a result of the Biocase inquiry carried out during the Summer of 2006

	N° collections	N° specimens	Digitised data	% digitised data
Animal	28	762051	61489	8,00%
Flora	52	1628091	162161	10,00%
Microbial	14	19250	9151	48,00%
Total	94	2409392	232521	10,00%

[http://biomonitor.ist.utl.pt/gbif/media/outros/PlanoAccaoGBIF\\_PT.pdf](http://biomonitor.ist.utl.pt/gbif/media/outros/PlanoAccaoGBIF_PT.pdf)

In summary, to overcome the existing problems and to improve the taxonomic expertise in Portugal and its use to help stop the loss of biodiversity it is necessary to:

- Invest more in training and education of new taxonomists.
- Invest more in preparation of checklists and data bases, and update existing ones
- Increase the digitalisation of the national biological collections.
- Increase and improve the dissemination of work carried out by the depositaries of the

- existing national biological collections
- Use taxonomist's knowledge and work to support regional planning and conservation of habitats and species.
  - Recognise the importance of taxonomy in the production of knowledge needed for prevention and control of invasions and introduction of indigenous/exotic species.

## Recommendations for taxonomy from a Ukrainian perspective

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**Viktor Gasso**, Dnipropetrovs'k National University, Ukraine

From a Ukrainian perspective I can say that taxonomic research and practice has some impediments:

1. Lack of taxonomic experts is a medium-term goal. Low financing entails the unwillingness of young scientists to be taxonomists
2. 'Demand determines supply!' Ukraine and, I presume, many other countries in the world need legislation that rigidly fixes obligatory taxonomic studies in Environmental (and/or Ecological) Impact Assessments. If the economy doesn't require 'taxonomy' no state budget will provide the required funds
3. Taking into account the general needs of taxonomy, 'open access to information' is extremely important.
4. I entirely agree with Klaus Henle that nature conservation should be the ultimate goal. Ukraine and other East European countries, such as Belarus or Russian Federation, have substantial areas for possible conservation, but they are unexplored from the viewpoint of taxonomic study.

Ukrainian science has considerable achievements in taxonomy. Valuable traditions were laid more than a century ago. Taxonomy is still essential for the set-up of the Red Data Book of Ukraine and the organisation of new reserved territories. Red-list species are widely used as key reasons for the management of nature conservation, ecological network realization and nature reservations. Despite this there isn't a national species checklist in Ukraine; we have checklists of all classes of vertebrates, but only some data on invertebrates (e.g. Gastropoda, Carabidae). Efforts at local levels spill over into regional checklists (the Carpathians, Crimea and Dnipropetrovs'k region).

A challenging event was the organisation of the Research Taxonomy Centre of Ukraine (<http://izan.kiev.ua/rtcu/>) in 2008. It was in response to the GTI devoted against information gaps in national taxonomic study. Unfortunately the lack of financing hampered the progress of the Centre's development.

National taxonomy-based monitoring is illustrated by an Annals of Nature. This is an annual data collection for the assessment of the state and trends of nature reserves. A recent overview of biodiversity monitoring programmes in Ukraine (Kostiushyn et al, 2008) described 95 relevant programmes and most of them involved taxonomists. To understand ecological functions and services some taxonomic research is usually used for Environmental Impact Assessments and nature protection management.

Despite the lack of necessary equipment and financing there are several research projects integrated with morphological and molecular taxonomy. Most of them are conducted in cooperation with European scientists.

Biological invasion is considered as a dangerous threat to the native biological diversity of Ukraine. Unfortunately that consideration wasn't put into any special programme of research for the prevention of invasions. Participation in the ALARM project allows intensification of this research.

Status and trends of key functional groups are under investigation, such as soil detritophages. For the last 15 years taxonomic research of that group in Ukraine developed into 34 new species of collembolan, 5 species of proturan and 15 new species of free-living nematodes.

Ukrainian experts have worked in South and Central America, South-East Asia and China to contribute to international biodiversity initiatives: GTI, Fauna Europea, Collembola Checklist ([www.collembola.org](http://www.collembola.org)). In general, the extent of the Ukrainian contribution may be characterized as inadequate, as the abilities of the Ukrainian experts was not used to their full potential. State of the art biodiversity informatics in Ukraine is unsatisfactory. Though relevant work is being carried out (e.g. e-version of the Red Data Book of Ukraine), the progress is insignificant. Some databases of systematic collections are under design as well as digitization of the zoological museum's collections and herbaria.

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