

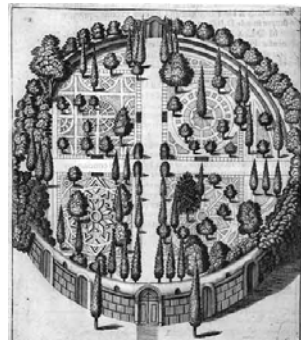


The
**LINNEAN
SOCIETY**
of London



Updating the Linnaean Heritage: Names as tools for thinking about animals and plants

Abstracts



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With the 10th edition of *Systema Naturae*, Linnaeus established what eventually became the start of modern zoological nomenclature. 250 years later, the importance of names in scientific communication still invites fresh discussion on the different aspects of biological nomenclature.

An international panel of 13 renowned scientists will present current perspectives and challenging proposals about names for taxa and names for other important biological objects and concepts.

SCIENTIFIC COMMITTEE

Sandra Knapp, Tim Littlewood, Alessandro Minelli, Vaughan Southgate

LOCAL ORGANISING COMMITTEE

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Abstracts

The Linnaean foundations of zoological and botanical nomenclature

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Polynomial designations were frequently used in pre-linnaean times. The first author who simplified naming by consequent usage of binominal names was Linnaeus: 1753 is regarded as the starting point of plant nomenclature; the equivalent date in zoology is 1758. Different starting points in botany and zoology were followed by an increasing divergence of nomenclatural principles in both kingdoms. The situation was even more complicated by the origin of separate codes for names in bacteria, viruses, etc.

Over decades, principles founded by Linnaeus were perpetuated by tradition. But common usage as such was insufficient for providing uniformity. The number of newly discovered organisms exploded, and the percentage of synonyms and homonyms rapidly increased. Finally, the situation was close to chaos. One of the main reasons for the origin of early international congresses in botany as well as in zoology was to regain a sound basis for understanding. The first congress in botany (Paris 1867) resolved the Candollean rules, the starting point for plant nomenclature. International initiatives in Zoology followed considerably later: the first code regulating animal names came into force in 1905. The botanical rules were modified and adapted from congress to congress, whereas the zoological code is characterized by continuity combined with evolutionary progress.

From 1992 onwards, the president of IUBS tried to start a late international initiative towards the unification of the existing codes. But due to the amount of historical divergence, efforts to replace the schism by one single BioCode were unrealistic: more problems than benefit would be introduced. The approach collapsed. Recently, it was proposed to formulate a so-called PhyloCode.

Compared with attempts to promote more or less radical innovations, adherence to the provisions of the codes in force is the better tool for improving the stability of names.

Registering animal names – problems and strategies

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The stakeholders for a gold-standard registry of animal names are diverse and central to functioning of many biological sciences and to policy for the living world. They include not only taxonomists and ecologists, but also conservationists, medical and veterinary workers, planners, policy makers, lawyers, even customs enforcers. Their requirements include ready access to a system of unambiguous answers to questions on the availability and validity of animal names that can be retrieved both by ordinary people and machines. The ICZN is meeting this need by developing ZooBank, a web-based registry of animal names (see Pyle, this symposium). This will include nomenclatural acts, publications, authors and information on primary type specimens, and serve as a resolver for LSIDs (Life Science Identifiers, a tool for global communication among bioinformatics projects). It will be both a hub and authority for nomenclatural information.

In an ideal world, ZooBank would include full information on all available names for animals. However the logistics of populating the site require strategic approaches. With 16,000 new additions yearly to the 1.25 million described animal species, the numbers of names to be checked for homonymy and primary synonymy is enormous. Informal estimates of the time needed to verify names in consultation with working nomenclature specialists have ranged from 10 to 100 names/person/day. This variation is based on a) different perceptions of what is required to verify a name (this should include consulting the original text where the name was made available through publication); and b) differences in data density in primary or high quality secondary sources (e.g. a few top quality monographs will speed the process for a taxonomic group, whereas a history of controversy and poor taxonomy will retard it). Thus, for full checking, at its fastest the job would take 12,500 person days, or approximately 60 years. The need for reliable names for biodiversity work is urgent, thus the task must be partitioned.

The first task for ZooBank is presentation of a 'Black List' of unavailable names. This would act as a kind of on-line quality control that could be applied across projects, for example, by publishers, to flag up unavailable names. This is somewhat more achievable with the recent digitization of the "Official Lists and Indexes of Names and Works in Zoology" by J.D.D. Smith and which could be implemented through its 2007 version on ZooBank.

The presentation of a 'White List' of all available names is a much more difficult task, comprised of two parts. Prospective registration of new names, as they are published, will require active listing by taxonomists as they describe their 16,000 new species/year in a manner similar to registering GenBank sequences today. This will rely on large scale participant buy-in. Publishers are likely to support this, as the LSID resulting from ZooBank listing will allow greater exposure for their publications. The nomenclatural reliability of bioinformatics initiatives such as the Encyclopedia of Life (EoL) will improve if they support ZooBank and actively link to it for the definitive source for names. We have indications that major taxonomic institutions will encourage good nomenclatural practice, for example by incorporating ZooBank LSID metrics into key performance indicators for taxonomists. This will also increase the reach for linking with type specimen information held in museum databases to wider bioinformatics initiatives. Working taxonomists appear eager to register names, and the incentives will increase with momentum of community use. Although the taxonomic community is strongly behind ZooBank, a straw poll at a large conference on the topic indicated that obligatory registration should wait until the project has sufficient content, exposure and momentum. Ultimately, however, it is envisaged that as electronic (only) publication becomes more common, a mandatory registration system may become necessary. This point will be a central issue in discussions for publication of the fifth edition of the Code of Zoological Nomenclature.

Retrospective registration of past published names is the greatest challenge for populating ZooBank. Initial assembly of published names can come from historical sources such as Sherborn and Neave, and specialized user community sources such as Scratch Pads, FishBase, AntBase, etc. Names will then need to be flagged as to their level of nomenclatural vetting. For example, a Gold flag would indicate the name has been checked to its original published source, a Silver flag indicates it has been checked to a reliable secondary source (e.g. a respected checklist), a Bronze flag indicates it has been dumped from an unvetted source, and a Lead flag would indicate it is under contention (and would not be transferred to other users until the problem is resolved). Groups of names of particular interest could then be targeted to be worked up in toto. For example, groups of CITES concern such as freshwater turtles could be prioritized with targeted funds. It might also be possible, with the completion of the Biodiversity Heritage Library, that 'citizen scientist' initiatives similar to the Herbaria@Home project could be enlisted to populate ZooBank.

Although the ultimate goal is for ZooBank to act as a definitive source of names, it is the nature of historical work and taxonomic research that new information can cast past certainties into doubt. As a result, ZooBank will need to remain updatable, with allowance for external, expert input. We expect that the development of search tools will increase the possibility that conflicts within the ZooBank database, and also with external sources could be flagged up for correction. We anticipate that ZooBank will develop into an indispensable tool, allowing unprecedented access to reliable nomenclatural information for biodiversity workers worldwide.

ZooBank: the official registry of zoological names

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The current scale of global taxonomic studies poses considerable challenges to a registry developed in the age of printing press and card files. Some 15,000 to 20,000 new nominal species are proposed every year in zoology, and together with thousands of other Code-compliant nomenclatural acts these are scattered in a bewildering number of journals, monograph series, books, and CD-based publications.

The ICZN Secretariat and Commissioners in 2005 proposed “ZooBank” - a central, web-based registry of zoological names and nomenclatural acts - as a mechanism for making information about all names and their nomenclatural status more accessible. ZooBank was launched as a functional prototype web site on January 1st, 2008, coinciding with the 250th anniversary of the official start of Zoological Nomenclature. At its launch, the ZooBank registry included all 4,819 names established in the 10th edition of Linnaeus’ “Systema Naturae”, as well as five new fish species names established in an article published concurrently with the launch of ZooBank.

The goal of ZooBank is not to replace existing nomenclatural catalog databases, and it will make no assessment or judgement of the taxonomic content of any piece of published work. ZooBank will function as an archived index of zoological names and nomenclatural acts that affect names, and ultimately contain information regarding the availability or non-availability of all names in zoology. The complete implementation details of the ZooBank registry are currently being discussed, developed, and tested, with involvement from ICZN Commissioners, GBIF, TDWG, catalog and database managers, and the taxonomic community at large.

Botanical nomenclature – the Linnaean heritage today

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In recent years there has been much discussion on the “Linnaean system”, stigmatised as inappropriate by the adherents of a “phylogenetic nomenclature”. But there is no such thing as a Linnaean System. The principles of hierarchical classification used by Linnaeus are those of Aristotle, further developed by Renaissance naturalists such as Tournefort. The Linnaean system of classification, eminently practical for its time and (for botany) in use well into the 19th Century, is

now completely obsolete. What remains today is Linnaeus's system of binary [species] nomenclature, which is still fully operational. It is indispensable as the all but only link to biological information accumulated during the last 250 years, and when its basic tenets, such as full independence of nomenclature and taxonomy, are well understood, it can be applied to any kind and "philosophy" of organismic classification. The problem is not that Linnaean nomenclature, as codified progressively over the last 1½ centuries, is becoming obsolete, but that it has become increasingly encumbered by the fallout of its long-lasting existence. To maintain it fully functional it must not be set aside or revolutionised but carefully adapted to the challenges and chances of the incipient electronic era. Catchwords that will be discussed in this context are: mandatory registration of new names, protection of vetted lists of names, and at the end of the day, perhaps, unification of biological nomenclature under a single, common set of rules.

Phylogenetic hypotheses and nomina of taxa

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Taxonomic paradigms have changed several times during the history of taxonomy, yet a single nomenclatural system, so-called Linnean, has remained in force all along. It is theory-free regarding taxonomy as it relies on ostensional allocation of nomina to taxa, rather than on intensional definitions of nomina (e.g., "phylogenetic definitions"). Nomina are not descriptions, definitions or theories but simple labels designating taxa. Both for theoretical and practical reasons, this system should be maintained for the allocation and validity of nomina under a phylogenetic taxonomic paradigm. Whereas taxa can be phylogenetically defined by "apognoses" or "cladognoses", nomina remain attached to taxa through onomatophores ("types"), combined in some cases with a Rule of Coordination. Under such a system, the allocation of nomina to taxa is automatic, unambiguous and universal, and nomenclature does not infringe upon taxonomic freedom. However, to avoid misunderstandings and to solve some current problems, the current codes of nomenclature should be improved in several respects. The distinction should be made clear between "taxonomic categories", which have biological definitions, and "nomenclatural ranks", which do not, as they give only a position in a taxonomic hierarchy: if used consistently under a phylogenetic paradigm, they simply express hypotheses of sister-taxa relationships. Taxa referred to a given rank in different groups cannot therefore be considered equivalent by any biological criterion. The nomenclatural rules should cover the whole taxonomic hierarchy, which is currently not the case in zoology. The recent strong increase in the number of higher taxa which results from phylogenetic analyses may quickly lead to chaos and problems in communication if the nomina of these taxa continue to be based on personal tastes and opinions. There is an urgent need for the zoological code to cover these nomina with automatic and stringent rules leaving no place to subjective interpretation. Just like for those currently covered by the code, the status of these nomina should be established in their first publication ("nomenclatural founder effect").

Reference taxa for the phylogenetic nomenclature

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The rise of phylogenetic nomenclature has led to some consideration of the choice of reference taxa for explicit phylogenetic definitions of taxa. One consideration that has been raised is that of the relative phylogenetic stability of candidate reference taxa. It seems reasonable that in a phylogenetic

taxonomy the stability of (the meaning of) names would be promoted by the stability of the underlying phylogenetic hypotheses upon which they are based. This leads to the principle that, all other things being equal, we should prefer candidate reference taxa for which phylogenetic understanding is in some sense most stable. Typically, support for phylogenetic hypotheses is not distributed equally across all relationships implied by a tree, and several methods have been developed to assess the distribution of support that may be relevant for distinguishing between relatively stable and unstable taxa. I consider the concepts of phylogenetic (in)stability, review measures of stability and methods for discovering instability and discuss their proposed and potential use in phylogenetic taxonomy. I hope also to at least partially address the question of to what extent choice of reference taxa is important in phylogenetic taxonomy and to offer some less technical comments on Linnean and phylogenetic taxonomy offered from the perspective of a practicing amphibian taxonomist.

Anatomical nomenclature and data matrices

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Anatomical nomenclature is in part complicated by disagreements about whether or not structures are homologous (taking it as a given that homologous structures should receive the same name to accurately reflect the identity implied by the homology hypothesis). When the same name is applied to non-homologous structures, ostensive reference to a particular taxon (wing of birds, wing of insects) is generally viewed as sufficient to convey homology at a less inclusive level but non-homology at the broader level. Although morphological terms and homologies are not formally governed by a set of rule as in typification, many of the concepts of typification are in fact employed – a character definition is abstracted from observed variation, and whether or not a taxon possesses the character is an assessment of the degree to which it corresponds to the definition. Morphologists use disparate rules for deciding how a morphological structure should be named when a formerly-endorsed hypothesis of homology is rejected: we have no rule of priority, and variably rely on first usage, common usage, or most recent usage, among other approaches, to justify which of the two (or more) structures will carry the traditional name. Web-based tools like MorphoBank and MorphBank, as well as desktop software like Mesquite, allow morphologists to document character concepts and defend character codings for individual cells in a data matrix by providing digital imagery, annotation and affiliated metadata such as voucher registrations – this promotes transparency and minimises the loss of data / the need to “reinvent the wheel” in future studies. The web-based applications further permit real-time collaboration on a project-by-project basis and make it practical to fix morphological terms by reference to images of particular taxa (again analogous to types in taxonomic nomenclature). The Assembling the Protostome Tree of Life project exemplifies the challenges involved in documenting transparent character concepts for a “supermatrix” that samples an enormous chunk of diversity when homologies are extremely controversial and differences in character formulation in previous matrices are acute.

The linguistic problem in morphology: updating the Linnean heritage

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I will give a brief introduction to the Linguistic Problem in Morphology, which results from the lack of a) a standardized terminology for types of morphological traits and their properties, b) a

standardized and formalized method for describing morphological traits, and c) a rationale for the delimitation of morphological traits. Its impact on the comparability and inter-subjective testability of morphological data is significant. Much of the recent criticism of the role and importance of morphology in modern biological research can be ascribed to this problem. A thorough comparison of the general characteristics of morphological and molecular sequence data reveals fundamental methodological and conceptual shortcomings of morphological data that result from a very high degree of individuality of the average morphological trait.

A problem of morphology, known for a long time and caused by structural variety, is the difficulty with which traditional essentialist definitions, like they are known for chemical kinds, can be employed for defining morphological traits. I will show how it has been addressed in pre-Darwinian times by taxonomists such as Linnaeus. The advent of the theory of evolution, however, had a strong impact on morphological terminology by introducing the idea of homology. With definitions resting on homology assumptions, biologists probably thought they found a solution to the definition problem, since homology provides at least a theoretically clear definition that can deal with structural variety. Unfortunately, this new way of defining morphological terms mixed up the separation of descriptive data and explanatory hypotheses just recently established by Linnaeus and other taxonomists.

By analyzing Linnaeus' concept for taxonomic characters I develop a concept of structure that mediates between the realm of observation (phenomena) and the realm of descriptions (theory and language). I will argue for the necessity of developing a general morphological structure concept that emphasizes purely structural definitions that are taxon-independent and free of homology assumptions. I discuss why only morphological descriptions qualify as morphological data and why images of morphological traits as such and phylogenetic character matrices do not. I conclude with an outlook on how the development of a taxon-independent morphological ontology with purely structural and functional definitions, that is implemented in a morphological data base, has the potential to provide a regional solution to the Linguistic Problem in morphology, which would significantly contribute to improving comparability of morphological data.

Morphological nomenclature for a continuum of forms

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In various vascular plants (and perhaps also some groups of animals) the structural categories for the description of forms are less distinct than often supposed. Thus, there are morphological misfits not fitting exactly into one or the other category. In these cases it becomes very difficult or even impossible to accept names for organs and appendages as long as we stick to a concept of total ("all-or-nothing") homology. At least in plants and animals that appear to be "morphological misfits" we have to go beyond either-or thinking. We need a comparative approach and a suitable language that better fits the continuum of forms around us. Thus, it may be favourable to accept an as-well-as approach allowing the concept of partial homology. A fuzzy way to use scientific concepts coincides with what was called "injunction" by the German biologist Bernhard Hassenstein. Forerunners of the continuum approach (also called dynamic or fuzzy morphology) are Agnes Arber and Rolf Sattler. Both have been aware that in flowering plants (their special field of interest) the examples of, e.g., root-shoot indistinction or leaf-stem indistinction belong to heterogeneous continua with intermediate forms being rarer than the more typical ones. The present talk will focus on aquatic flowering plants such as the river-weeds (Podostemaceae) which are adapted to tropical waterfalls. These dicots are related to Clusiaceae sensu lato with *Hypericum* (St.

Johnswort, Erba di San Giovanni) as sister group. The “roots” of river-weeds are completely flattened and green. Their flowers may arise from endogenous sites of “roots”, “stems” and even from “leaves”. Additional examples will show that several plants are used to having identity crises. There is some hope: comparative developmental genetics may yield other types of information that help assess homologies. The results of evo-devo research will shape a scientific language that allows to better deal with (heterogeneous) continua of forms in plants (and perhaps animals).

Morphological nomenclature, between patterns and processes

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Development biology and evolutionary biology are both science of change through time. Formulating and testing hypotheses within these two disciplines, or at their interface (the so called evolutionary developmental biology, or evo-devo) needs sound names. Names are essential for organism features, that are both (anatomical) patterns and (physiological) processes and their changes across ontogeny and generations, two processes that produce developmental and evolutionary patterns, respectively. Thus, although the question of names is not a distinctive element of this area of biology, it is nonetheless deeply entangled in scientific investigation and communication.

The words we use for describing biological systems and their transformations risk continuously to perform as ‘conceptual traps’, i.e. conceptions that limit our ability to ask (and hopefully answer) sensible questions. There are many examples in descriptive morphology (‘segment’, ‘tagma’, ‘body axis’), in development (‘embryo’, ‘larva’, ‘adult’), and in evolution (‘heterochrony’, ‘novelty’, ‘adaptation’). Continuous vigilance is thus in order.

The main focus of this contribution is on segmentation and its evolution, both as morphological pattern and developmental process, as a paradigmatic case.

A segmental pattern may be defined as the serial occurrence of homologous structures along one axis, this being the main body axis or the axis of an appendage. When this pattern is referred to the whole body axis, rather than to a specific set of repetitive structures along that axis, the idea of a body or a limb ‘comprised of’ a certain number of ‘modules’ (trunk segments, or appendage articles) will result. However, logical and practical difficulties arise when different serial structures of the same axis show discordant serial arrangement. Similar occurrences are traditionally referred to as cases of ‘segmental mismatch’, something that with a “body module” concept of segment is clearly an oxymoron.

Similar descriptive systems, based on the depiction of a ‘general rule’ followed by a list of ‘exceptions’, are very common. This is logically unsatisfactory and leads to an ineffectual proliferation of morphological nomenclature. An alternative strategy might be: a) recognizing and accepting the non-resolvable approximate nature of morphological nomenclature; b) simplifying nomenclature accordingly; c) always keeping in mind the distinction between the (simple) level of description and the (complex and multifaceted) reality, asking, before usage, what a given name is for.

The structure of taxonomic information: the 'FishBase-Catalog of Fishes' collaborative experience

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By 2007, there are more than 30,000 species described for recent fishes, understood here as the paraphyletic group of Craniata:non-Tetrapoda (a group usually named Pisces for convenience), including for the recent forms Myxiniiformes among Hyperotreti; Petromyzontiformes among Hyperoartia; Elasmobranchii and Holocephali among Chondrichthyes; Actinopterygii, Coelacanthimorpha and Dipnomorpha among Osteichthyes (and among Sarcopterygii for the two latter). Tetrapoda are included in Osteichthyes and Sarcopterygii to make the two groups monophyletic.

More than 59,000 taxon names have been recorded so far, in majority published as new descriptions averaging almost 2 names per valid species. Quite a few are re-descriptions, which was a usual practice in the first part of the 19th century, and some are new replacement names. Only about 300 subspecies are considered as valid nowadays. All these names are recorded in the Catalog of Fishes (CoF: Eschmeyer and coll., 1990, 1998 and online): this is the nomenclator for fishes (with type information).

In addition, about 32,000 new combinations and spelling variants are recorded so far from the whole ichthyological literature (not only from the taxonomic literature). These names are recorded in FishBase (FB: Froese and Pauly and coll., 1995 to 2000, 2004, and online).

CoF and FB have different goals but complementary roles. FB aims at gathering information on many topics (mainly for natural resources management) on all fishes of the world. As in all Biodiversity Information Systems (BIS), a strong, relatively stable and reliable taxonomic backbone is necessary, which is mainly provided by CoF that has strictly taxonomic and nomenclatural purposes: as a general rule, FB follows the statuses gathered by CoF, especially which species names are valid, but there are difficulties to follow strictly this rule as we will show.

The presentation will detail database structure, data management, and collaboration. Examples will be given on the 416 fish names published in Linnaeus 1758 of which 337 are still considered as valid taxa.

Both CoF and FB adopted simple database structures to link valid names, synonyms, and name variants: one table manages the names that are linked through a taxon identifier; one table manages the classification linked to name table by a higher taxon identifier; in addition, there is a genus table but that can be skipped for the most frequent uses of species names. This structure is perfect to search any synonym linked to the valid current accepted name. It works well to display all the variant names used for a species (although in the case of CoF, these names are recorded under a memo field format). Both CoF and FB have adopted simple classification schemes (classes, orders, suborders for CoF, families, subfamilies and genus), managed in only one table. In some cases and when necessary, FB refers also to the Fishes of the World (FoW: Nelson, 1976, 1984, 1994, 2006) which uses much more intermediate categories.

Nevertheless, the structures have serious limitations when complete ordered synonymy lists have to be provided for taxonomic research purposes (hence the creation of the Annotated Check-Lists

documents by Eschmeyer). And in the case of FishBase, if changes of names as new combinations are easy to manage, splitting or lumping species are tedious and time-consuming for all information other than names. It is suggested that the adoption of the TDWG TCS standard for names and taxa, the use of Global Unique Identifiers (GUID) such as TDWG LSID and the onymology analysis by Dubois (2000) should solve many difficulties, although they are all quite demanding to implement both in terms of database structure and data encoding. These considerations have to be balanced with the philosophy of the two databases to keep them simple.

Up to now, CoF publishes a version twice a year, and FB tries to update only once a year due to the time necessary to catch up all additions and changes. This has created confusion among users and we currently work to improve this collaboration. Issues will be presented as general examples for name management of other groups.

Although well in advance compared to many other groups, there is still much to do to propose updated and harmonized list of valid species at the same time through information systems that have different goals. Some considerations will be discussed and proposals suggested for rooting species information more deeply in sound taxonomic practices compared to the web communication-oriented (and sometimes constraining) practices.

**The structure of taxonomic information:
the ‘Checklist of the animal species of Italy’ experience**

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The ‘Checklist of Italian Fauna’ lists all the animal species reported from Italy and univocally identifies them with codes. With its publication in 1995, Italy was the first European country to complete the list of its fauna, from protozoans to mammals. The ‘Checklist’ consists today of a hierarchical database, with data organized in a tree-like scheme which strictly corresponds to the formal taxonomic classifications. The creation of a hierarchical database requires the use of numerical codes of at least three-digit numbers, which are attributed to each Linnean taxon. This simple tree-structured list allows taxa to be sorted both in alphabetical and in current taxonomical order. The hierarchical ‘Checklist’ represents a sound operational tool for species distribution mapping and conservation planning, allowing a simple but detailed analysis of taxonomic distinctness of local and regional faunas in Italy. The Italian ‘Checklist’ inspired both ‘Fauna Europaea’ and the ‘European Register of Marine Species’; an integration process of pan-European and national checklists is the main objective of some European projects, like EDIT and PESI. Unfortunately, designing these large databases, data were itemized to such a degree that part of traditionally coded taxonomic information was lost, and consequently the value of checklists for conservation biology was lowered as well.