

COMMENTARY

Linnaeus in the information age

As we celebrate the visionary genius of Carl Linnaeus, it is time to analyse how professional taxonomy interfaces with the rest of biology and beyond. Where next for Linnaeus's heirs, asks H. C. J. Godfray?

It is one of the triumphs of contemporary science that we have a means of naming and referring to all described organisms on Earth, as well as their fossil ancestors. It was Carl Linnaeus who realized that, to understand anything in science, things have to have a name that is recognized and is universal — a lesson that has not been forgotten by the creators of today's gene and protein databases. The year in which we celebrate Linnaeus's achievements is an opportune time to think about how modern taxonomy relates to the rest of biology, and how this relationship may evolve.



In Linnaeus's time, the natural world seemed static and relatively untouched by humans. This is no longer true, and a greater appreciation of our planet's changing biodiversity is increasing the demand for taxonomic information and expertise. Simultaneously, the nature of biology is changing, so that tasks that were once the unique preserve of the taxonomist can now be done by most biologists. In confronting these realities, taxonomists need to think about where to prioritize their efforts, and how to make the best use of limited resources.

Do it yourself

Most biologists use taxonomic information in one way or another, from the dedicated molecular biologist who is content that 'the fly' is understood to mean *Drosophila melanogaster*, to the community ecologist who has to identify hundreds of species at a study site. Taxonomy provides opinions on species boundaries, and on the phylogenetic relationship between species. It provides a stable naming system that in today's jargon is a portal to a huge, if not always easy to access, store of information about a species. Advocates of increased investment in taxonomy highlight all these potential benefits, but often forget that many of the traditional user communities of taxonomy can now investigate these questions themselves.

Consider the role of taxonomy in deciding what is a species. Arguments for the importance of taxonomy frequently note how accurate species identification is essential for, say, combating a particular human pathogen, or



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for discovering the appropriate biological control agent for an agricultural pest. In the past, these critical decisions could be made only by taxonomists, and typically involved careful morphological study and comparison of preserved specimens. Today, molecular markers are increasingly used to study population differentiation, and most biologists can do this. Indeed, for any taxonomic issue with medical or economic consequences, it is inconceivable that molecular techniques would not be applied. Similarly, biologists who might have previously looked to taxonomists to provide a phylogeny of a group are finding it increasingly easy to do it themselves as sequencing becomes cheaper and more widely available.

Biodiversity scientists, those interested both in fundamental and applied questions,

frequently need to identify large numbers of species. To do this, they need either the products of taxonomy — field guides, monographs and floras — or the taxonomists themselves. Excellent identification resources exist for some groups in some geographic regions, but often these are absent, especially in the tropical biodiversity hotspots that need most protection and research. Ten years ago the only solution to this would have been more investment in traditional taxonomy. Today there is an alternative: molecular identification methods, DNA barcodes or related technologies that would allow the high-throughput allocation of specimens to different sequence clusters. DNA barcodes could develop completely independently of Linnaean taxonomy, although this is definitely not the intention of its leading proponents.



Ecologists in the field rely increasingly on molecular methods to 'do' taxonomy themselves.

So there is a threat that the usefulness of taxonomy may seem to diminish as new techniques become available. Taxonomy itself would remain intrinsically interesting, but the rise of alternative technologies could dangerously undermine arguments for increased investment in the subject. To counter this, I believe that taxonomists need to do the following: first, ask difficult questions about the efficiency and value for money of taxonomy as it is currently conducted; second, consider the needs of their user communities and prioritize some 'big science' projects to meet them; third, integrate their current practices with new molecular techniques, as many already do; and fourth, improve the ease with which taxonomic information can be accessed by non-taxonomists, and emphasize how taxonomy provides a portal to the totality of information available about different species.

More than a name

Some readers will dislike the utilitarianism of these arguments. Taxonomy is rightfully a proud science and does not need to justify its existence as a service provider. But it lives in the real science-funding world, and frequently suffers from it. Too often, taxonomists are pressurized by their bosses to reinvent themselves as ecologists, evolutionists or even computer scientists to chase research funding. Biology, and especially biodiversity science, need more taxonomists doing more real taxonomy. This will be easier to achieve if the field does today what Linnaeus did: provide its end users with products that are so good they clamour for more.

Linnaeus's brilliance was that he initiated the solution to the first bioinformatics crisis: how to organize knowledge about the increasingly large number of species that were being discovered during the age of exploration. His solution was appropriate to the days of paper publication and surface post, but what would his approach have been today? I believe he

would have been a 'techie', exploiting the Internet and other modern means of sharing and coordinating data. No one denies that the web will be increasingly crucial for taxonomy, but what is much less clear is the degree to which taxonomy should transfer wholly to the web, and how this will change the hallowed rules of nomenclature enshrined in the International Codes. I think that a move to a universally accessible, web-only taxonomy is essential for the future health of the subject. But I also understand the caution felt by critics of these ideas.

Whether taxonomy does or does not move *in toto* to the web, I believe it is critical for the subject to emphasize its role as a curator of information about taxa, in addition to names and specimens. There are some excellent projects starting to do this, for example *FishBase*, which collates all types of information on its eponymous taxon. Here you can learn about a fish species' morphology, reproductive biology and ecology; the environments it can tolerate and its population dynamics; whether you can eat it and whether it can eat you. More projects like this are needed, along with moves to integrate basic taxonomy with new initiatives such as DNA barcoding.

The web also has a role in making taxonomy more economically efficient. It can be used to collate the literature and specimen information required to do taxonomy, as well as disseminate its outputs. But why stop there? The type specimen plays a critical part in taxonomy, for example settling disputes over species identification. But type specimens are often very old and have deteriorated in some way. The more they are consulted the greater the risks of further damage, and access to types is sensibly restricted. Most types also lack associated sequence data. Perhaps we need a way to create a new form of

type specimen (call it a cybertype) to be displayed on the web using the very best current imaging methods — often far superior to normal examination — and for which appropriate sequence data are available. Plant taxonomists can already designate a new specimen (an epitype) to help interpret an ambiguous original type, and I think it would be helpful to extend this practice to animals and specifically adapt the concept for web and molecular taxonomy.

Access for non-professionals

As scientists, we are rightly encouraged to engage more with the public. Taxonomy is one of the few subjects (astronomy is another) where non-professionals can make genuinely important contributions, and the sheer scale of Earth's biodiversity makes this engagement essential. Difficulties in accessing taxonomic information act as a brake on research and reduce its quality. Moving as much taxonomy to the web as possible will enfranchise a huge amateur community and greatly aid professionals in developing countries, where most biodiversity hotspots are.

By its nature, taxonomy is a broad subject that finds difficulty in prioritizing research and investment. Big taxonomic projects have sometimes been too big and all-embracing — for example, proposals to catalogue all the species on Earth — and have failed to progress. Other projects are exceptionally valuable for taxonomists (for example, lists of names and synonyms) but are of less relevance to taxonomy's user communities. The field could usefully work with the broader biological community to define and prioritize a series of big taxonomic projects that are achievable over the next decade or so, much like the physics and astronomy communities do.

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My personal wish list, biased towards terrestrial eukaryotes and living rather than fossil organisms, would include a web-based global flora, a complete phylogeny of the living vertebrates, and a comprehensive web-based taxonomic and

identification resource (morphology plus DNA barcodes) for the world's macrolepidoptera. I chose macrolepidoptera (butterflies and large moths) because I think that this is the only large, ubiquitous invertebrate group that is relatively easy for non-specialists to identify, and so would be invaluable as a biodiversity-monitoring tool. Others would pick a different set, and it will undoubtedly be hard for taxonomists and other biologists to reach a consensus. But such a list, backed by the community and firmly linked to end-user demand, would be a wonderful lever for bringing new resources into the field. ■

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