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update

Taxonomy on the fast track

Biology depends on alpha-taxonomy: high-quality and reliable species delineations, species descriptions and guidance on how to tell species apart. However, taxonomic research can be slow. This problem has been addressed by many recent papers, with numerous options proposed for accelerating the process of inventorying biodiversity. It has long been lamented that taxonomy is underfunded, which is possibly due to its handicap in academic accreditation (low journal impact factors, slow accumulation of citations), but Joppa et al. (2011), in apparent contrast, point out that globally more taxonomists are active today than ever, and that description rates in many taxa are increasing. Awareness is growing among both the producers and consumers of taxonomic knowledge that the discipline, as traditionally practised, is not up to the task of describing global organismic diversity in any reasonable time frame. Formal taxonomy has been practiced for 250 years – yet we know, for example, only an estimated 30% of global arthropod species richness. At current rates, it will take many centuries to even get close to describing and naming all extant species (Hamilton et al. 2010, Maddison et al. 2012).

Thus, the pressing question is how can taxonomy become more efficient without loss of quality? Educating and employing additional armies of specialized taxonomists is probably unrealistic. Skipping proper taxonomy altogether and working on morphospecies is fast, cheap and for some studies justifiable, but it is too error-prone to qualify as a real solution to the problem (Krell 2004). Also, such data cannot be cross-referenced across different studies. Many current ideas tend towards technological solutions, the most discussed of which is DNA barcoding – i.e., defining and identifying species according to a ubiquitous, short DNA sequence (Hebert et al. 2003). This approach is already being widely applied and has some benefits (Valentini et al. 2009, Bik et al. 2012), although it has also been heavily criticised (e.g., Rubinoff et al. 2006).

However, other ways of utilizing new technologies may also be highly relevant. In particular, IT-solutions may be able to replace the often rather ancient and fragmented ways of disseminating taxonomic information. Many studies are still published in journals with limited and slow access (e.g., paper-only), and they offer poor access for speedy community-wide collaboration, feedback and revision. It has been recognized for a while that taxonomy would profit considerably from online solutions (Wheeler 2004, Scoble et al. 2007, Clark et al. 2009). Maddison et al. (2012) summarize current attempts at “e-taxonomy” and discuss how online technology can change the taxonomic workflow towards more collaborative, faster progress and reduced redundancy.

Deans et al. (2012) point out that detailed taxonomic descriptions, an essential part of registering and naming new taxa, do not make full use of the effort because information is not easily collated and compared across larger numbers of species. They suggest that standardization of how taxonomic information is presented combined with advances in text-mining software (e.g., semantic tagging; Penev et al. 2010) may open new avenues to utilize these valuable data in other fields, such as ecological and evolutionary studies (in addition to making it easier for taxonomists to access). Essentially, species descriptions could become the core of a global trait database.

Disciplines such as genetics and astronomy have benefited considerably from embracing sophisticated IT approaches. While it cannot be predicted which of these ideas will prove suitable for taxonomy, it seems clear that times are changing for the discipline.

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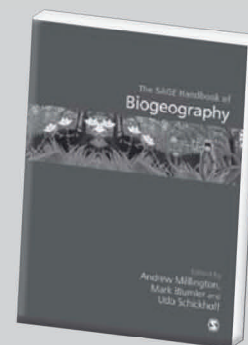
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