



FORUM

Trait-based paradise – or only feeding the computer with biology?

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Abstract: We briefly discuss the relationship between the biological knowledge and the methodological issues related to trait-based ecological analyses. We provide illustrative examples and argue that the biological novelty of trait-based research is generally less than expected - while new information is mostly coming from data management and methodology.

Till the late sixties, there had been a significant input from engineering, mathematics and physics to ecology. This integration helped researchers to apply some key concepts of cybernetics (Margalef 1968), information theory (Ulanowicz and Puccia 1990) and thermodynamics (Lindeman 1942) to ecological studies. Biological knowledge and adapting novel methodologies developed hand in hand (Odum 1969). From the late sixties, this balance was broken: theory exploded (May 1973, Cohen et al. 1990) and a gap has been emerging between empirical (biology-minded) and theoretical (math-minded) ecologists. Nowadays, the question arises in more and more areas of ecological research: how to put back biology into ecology?

One possible answer to this question is to use trait-based approaches. Trait-based thinking allows describing biological knowledge in such a quantifiable way that databases can store it to build and feed parameterized models. Furthermore, applying harmonized trait-based approaches and developing standard methods may help communication and information-sharing among different expert groups, and also the comparability of different ecosystems. Therefore, the use of traits has become popular in ecology. It is noted, however, that this line of interest goes back, at least, to studies on character structure in vegetation science: here, correlations between characters like leaf shape and coverage (Orlóci et al. 1986) helped to identify important characters by multivariate statistical approaches (Podani 1985).

Traits are now applied widely independently of the level of organization. In the context of ecosystem functioning, traits represent morphological, physiological and phenological characteristics that may impact individual fitness directly or indirectly (Violle et al. 2007). Such traits are

related to growth, reproduction, and survival (Violle et al. 2007), among which many are hard to measure, at least in some groups of organisms. One solution applied is the use of relatively simple morphological traits like body weight or size, which are thought to relate to growth, reproduction and survival directly. Although, by applying morphological traits with very fine details, we might simply return to traditional taxonomy. Unlike merely taxonomic information, species characteristics are quantified, which may enhance our ability to describe mechanisms underlying i.e., the patterns observed in taxonomical compositions quantitatively.

Nevertheless, in many cases, “trait-based” information is not much more than **well-known biological knowledge quantified** and prepared for the computer. Traits like „vertebrate” versus „invertebrate” indicate trivial taxonomic information. Other types like “benthic” versus “pelagic”, while not being related to individual performances directly, do provide relevant ecological information. The combination of “taxonomy traits” and those related to ecological functions (i.e., body size) may enable to advance our understanding relative to taxonomy-based information.

Data on single particular traits are available for more and more ecosystems (like the above-mentioned body size), and there is an increasing number of ecosystems where multiple trait data are compiled (e.g., D’Alelio et al. 2016). Here, for example, traits like “trophic status”, “size”, “individual carbon” and “biomass” articulate a multi-dimensional, trait-based categorization of organisms, which in turn may help to define i.e., functional groups in the ecosystem (Mare Chiara Long-Term Ecological Research site, Gulf of Naples). Functional groups are organisms that share similar adaptive features, i.e. **ecological traits that affect functioning at eco-**

system level in a similar way (shared effect traits), but also those that share similar responses to altered conditions i.e. at the community level (response traits) (Violle et al., 2007). Defining functional groups is an old issue in food web ecology including also the question of how to possibly build on trait-based data (Steneck and Dethier 1994). Traits used widely in the past include body size (Polis 1991) and consumption habits (De Ruiter et al. 1995). Classic trophic groups (like “benthic invertebrates”) may be defined by combinations of several simple traits (here, “benthic” refers to habitat, “invertebrates” refers to taxonomy). In this sense, however, traits have always been used for describing an ecosystem, building and studying system models. One special field of applying trait combinations is the quest for keystones (Power et al. 1996). Here, particular trait combinations may define a single species that is non-redundant and its irreplaceability would make it a single-species functional group (Bond 1994), i.e., a keystone species.

The availability, generalizability and functionality of traits might be highly different; not only among individual species but also among trophic groups. Those measured easily and therefore applied widely (see body size or weight) may require caution. In body size, there can be orders of magnitude difference between life stages in aquatic animals (i.e., zooplankton, fish). In contrast, the size of individual phytoplankton taxa (in the life stage observed) rather show only subtle differences. Size combined with further morphological characteristics is the very basis for its traditional taxonomy. Among taxa, however, phytoplankton size covers several orders of magnitude thus it does reflect reliable functional differences making size a master trait in phytoplankton ecology (Litchman and Klausmeier 2008).

Other traits are clearly useful and describe real functional differences between organisms at all trophic levels. Habitat type is crucial to model interactions and ecological functions (Krause et al. 2003). However, habitat types or templates alone may group species together (co-occurrence data), which may not share other functional traits in a similar way. Moreover, there are some traits with obvious functional importance, which are hard to measure and therefore poorly available. For example, mixotrophic algae affect microbial trophic dynamics and the biological pump, which group is potentially favoured in a changing climate (Mitra et al. 2014). However, we have still limited information about traits characterizing mixotrophy, such as their stoichiometric requirements, or food quality of mixotrophic species for higher trophic levels (Moorthi et al. 2017).

In more general terms, trait-based approaches may help to quantify and better understand the functional roles and similarities among species. It is clearly useful and important to prepare all of this information in a quantitative, easy-to-manage way that can also be treated in a purely mathematical way (Luczkovich et al. 2003). It is also useful to develop and apply standard measures of traits for markedly different taxa. However, while computer scientists or statisticians might be astonished by this new research direction, biologists should not forget to keep in mind eventual limitations of trait-based

approaches and to check whether any novelty is ensured depending on their research question. It is no problem if traditional biological knowledge is translated to statistical variables, but it can be dangerous if biological thinking is simply replaced by data management.

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