








## REVIEW

# Going across taxa in functional ecology: Review and perspectives of an emerging field

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## Abstract

1. The emergence of functional ecology has changed the focus of ecological research from investigating patterns of species diversity to understanding how species traits relate to specific ecological processes generating these patterns. Traits, ecological patterns and processes can be shared and driven by species from distantly related taxonomic groups.
2. Crossing the boundaries among distantly related taxonomic groups is still a challenge and a critical knowledge frontier in functional ecology. A cross-taxa approach, merging trait data across distantly related taxonomic groups, could fill this gap. In this context, functionally analogous traits, that is traits that may have distinct ontogenetic origins yet represent similar processes, comprise an important recent advance in functional ecology. However, which taxa and traits (be them analogous or not) have been used in research with multiple taxa, and whether (and how) these data have been combined, still needs to be elucidated.
3. We reviewed articles published in the last 75 years to investigate the use of traits in functional research involving multiple taxa. Our search returned 1006 articles, and a subset of 96 was filtered for data extraction. Studies covered a total of 134 taxa and 491 different traits; they were predominantly observational, and focussed on community ecology and ecosystem monitoring.

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4. Our review showed that current knowledge in this field relies on a limited number of response variables, particularly taxonomic diversity (e.g. species richness and abundance within functional groups). Also, the field relies on a limited number of taxa (e.g. plants, birds and mammals) and trait types (diet, size, habitat and dispersal). Two-thirds of the articles ( $n=72$ ) used functionally analogous traits, and one-third of them ( $n=32$ ) employed a cross-taxa approach.
5. We mapped the limitations of current research in functional ecology involving multiple taxa, presented ecological questions to a functional cross-taxa research and showed directions to pushing the limits of this research field. Our review aimed to encourage researchers in the field of functional ecology to move beyond single taxa and traits, and to integrate more branches and dimensions of the Tree of Life in their research.

**KEYWORDS**

ecosystem functioning, effect traits, functionally analogous traits, multiple-taxa, multitaxa, systematic review, trait-based ecology

## 1 | INTRODUCTION

Looking at nature from the perspective of functional traits has re-invented ecology (Cernansky, 2017), primarily because functional ecology switched the focus of ecological research from species to ecological process (Bellwood et al., 2019; Díaz et al., 2016; Díaz & Cabido, 2001; Enquist et al., 2015; McGill et al., 2006; Violle et al., 2007). Therefore, this research field allowed a deeper understanding, for example, of mechanisms underlying species distribution (Cavender-Bares et al., 2009; Webb et al., 2002) and diversification (Floeter et al., 2018; Siqueira et al., 2020). Functional ecology has also been used to estimate the strength of species interactions within food webs (McFadden et al., 2022), the contribution of individuals and species to community structure (Cianciaruso et al., 2009; Cooke et al., 2019; Díaz et al., 2016; Pimiento et al., 2020; Violle et al., 2007) and the potential biological impacts of extinctions on ecological networks (Bastazini et al., 2022) and communities (Carmona et al., 2021; Cooke et al., 2019; Pimiento et al., 2020; Waechter et al., 2021). Also, trait-based approaches can reveal important information on life history trade-offs (Cooke et al., 2019; Díaz et al., 2016; Junker et al., 2023), ecological functions and critical processes (Lavorel & Garnier, 2002), going beyond population parameters in nature conservation, management and restoration initiatives (Carlucci et al., 2020; Miatta et al., 2021; Mouillot et al., 2013).

The concept of functional diversity was developed in the context of plant ecology, but it is now widely applied to a growing number of taxa, including birds (Tobias et al., 2022), arthropods (Brousseau et al., 2019; Wong et al., 2019), fish (Gomes et al., 2023; Hadj-Hammou et al., 2021), corals (Madin, Anderson, et al., 2016), zooplankton (Martini et al., 2021) and even microorganisms such as bacteria (Ortiz-Álvarez et al., 2018) and viruses (Hurwitz et al., 2015). The expansion of functional ecology

across the Tree of Life offers new perspectives and raises issues. For example, effectively crossing the boundaries among distantly related taxonomic groups (i.e. Class, Phylum; Aubin et al., 2013) remains challenging due to difficulties in finding equivalent traits and functions across groups (Weiss & Ray, 2019). Crossing such taxonomic barrier is crucial for uncovering the general principles that govern species interactions (Schleuning et al., 2023) and abundance distributions across space (Brown, 1984; Brown & Nicoletto, 1991; McGill et al., 2007; Preston, 1948), as well as determining the significance of individuals, species, and traits in ecosystem functioning (Weiss & Ray, 2019). Within this context, the study of multiple taxa in functional trait analysis can complement the traditional approaches that focus on individual taxa, enabling the identification of patterns and general processes that govern various ecosystems (Brandl et al., 2023; Brown et al., 2004; MacLean & Beissinger, 2017; Schmera et al., 2017). For instance, approaches using multiple taxa can enhance predictions of diversity patterns across environmental gradients, such as elevation (Mori et al., 2015), temperature (Brown et al., 2004), productivity (Hawkins et al., 2003) and urbanization (Nagy et al., 2018).

It has long been recognized that ecological communities and their interactions can be effectively characterized by species' universal traits, also known as 'supertraits' (Madin, Hoogenboom, et al., 2016), such as body size or trophic position (Bergmann, 1847; Brandl et al., 2023; Brown & Nicoletto, 1991; Brown et al., 2004; Elton, 1927; Margalef, 1963). Such organismal traits can be translated into common currencies of mass and energy, and have contributed substantially to the understanding of processes happening at higher organizational levels, such as population abundance, species interactions, community species richness and the energy flux within ecosystems (Allen et al., 2005;

Brown et al., 2004; Elton, 1927; Enquist et al., 2015). Although approaches based on single traits can be sufficient for mechanistically predicting ecological processes (Butterfield & Suding, 2013; Lavorel & Garnier, 2002), they fail to explain variation on ecological processes through space and time (Lefcheck et al., 2015) and generally do not consider trait variance in their predictions (Enquist et al., 2015). This unexplained variation could be further explained by alternative, multiple niche axes such as habitat and mobility (Eklöf et al., 2013), colour (Spaniol et al., 2020), phenology (Kraft et al., 2015), stoichiometry (Meunier et al., 2017) and metabolites (Walker et al., 2022). Although organism fitness might depend on the trade-off between traits (e.g. energetic allocation to growth vs. reproduction vs. survival) (Díaz et al., 2016; Junker et al., 2023; Marshall & White, 2019; Schiettekatte et al., 2022; Wüest et al., 2018), ecosystem-level processes such as nutrient cycling and stability may depend on trait complementarity among multiple taxa (Díaz & Cabido, 2001; Schiettekatte et al., 2022). For instance, the same ecological function may be determined by different traits depending on the species; body size in ants and jaw morphology in mammals influence seed predation rates (Kelt et al., 2004); fish and shrimp have different traits, but both perform cleaning mutualism (Quimbayo et al., 2018; see [Box 1](#)). Studying multiple taxa through multiple traits has the potential to help establish a formal link between trait diversity, organismal performance and ecosystem function (Díaz & Cabido, 2001). It is rare to find studies that explore the general principles governing ecological communities, spanning from ants to mammals or taxa encompassing multiple trophic levels, while using multiple traits (or niche dimensions) from these distantly related taxonomic groups. However, recent studies have managed to overcome these difficulties, exemplified by the works of Capdevila et al. (2020), Junker et al. (2023) and Schleuning et al. (2023). Yet, a comprehensive state-of-the-art investigation that involves multiple taxa and traits, and establishes the necessary conceptual foundations, is still lacking.

Most recently, the concept of functionally analogous traits represented an important advance for comparing functional diversity patterns based on multiple traits and taxa (Weiss & Ray, 2019). Functionally analogous traits are commonly characterized by traits with different ontogenetic origins across organisms that perform similar functions. For instance, a pioneer functional study involving multiple taxa combined 'response traits' (see Glossary) such as size (plant height and animal size), dispersal (agent of plant dispersal and animal mobility), among others regarding habitat and habits, which together revealed similar strategies of survival, recovery and dispersal in plants and animals facing disturbances (Moretti & Legg, 2009). Beyond community responses to disturbance, analogous traits have been used to identify life history trade-offs for animals and plants (Anderegg et al., 2018; Capdevila et al., 2020; Junker et al., 2023). However, the main potential of crossing taxonomic barriers (i.e. going across taxa) lies in 'effect traits' (see Glossary), which emphasize 'what' an organism does in the ecosystem, regardless of 'who' and 'how' it does it (Weiss & Ray, 2019).

We define functional cross-taxa research as the ecological research merging morphologically and/or ecologically similar traits, shared across distantly related organisms, with the aim of exploring topics ranging from the ecosystem properties to eco-evolutionary processes underlying trait patterns across coexisting taxa. This is a new and emerging field with vast unexplored research potential that lacks a formal contextualization and framework. Functional cross-taxa research draws inspiration from two main research lines. The first involves searching for correlated responses of different taxa to environmental gradients and stressors, classically addressed using species richness, taxonomic diversity and composition (Gaston, 2000; Heino et al., 2009). The second approach uses one (Brown et al., 2004) to multiple functionally analogous traits (Weiss & Ray, 2019) to uncover mechanistic explanations for how distantly related organisms are influenced by their environment and, more importantly, how they affect and shape their environment (e.g. Barros et al., 2016; Pimiento et al., 2020). The functional cross-taxa approach differs from comparative, multitaxa approach because the former uses similar trait axes across taxa, while the latter uses independent trait axes across taxa. For instance, a functional cross-taxa research can address ecosystem resistance to disturbances by simulating whether a functional diversity metric (often measured in the context of an n-dimensional hypervolume) of all component communities, built by merging functionally analogous traits of distantly related taxa, will decline under disturbances and/or extinction scenarios (Pimiento et al., 2020). In its turn, a multiple-taxa approach can only show the resistance of a specific taxon or a group of taxa with congruent responses to the disturbances. This approach consists of observational, experimental or simulation studies exposing several taxa to disturbances in parallel and, at the end, comparing whether functional diversity correlates across taxa. Furthermore, traits being used are independent across taxa, and may or may not be functionally analogous. Thus, these approaches differ substantially in the potential inferences about ecological patterns and processes mediated by traits.

To provide a state-of-the-art overview of the use of multiple traits and taxa in functional ecology, we conducted a review of articles published in the last 75 years and performed a quantitative analysis of this literature. Our review synthesized the complex relationships among studies, taxa and traits, revealing (i) the predominant ecological subdisciplines (e.g. environmental monitoring, community ecology and conservation) and response variables used in studies, (ii) the core group of taxa that are predominant in functional multitaxa and cross-taxa research, (iii) the potential biases in the studied taxa and ecosystems based on the representativeness of the Tree of Life in this research, (iv) the proportion of studies combining or comparing traits (see Glossary), and the trait types used in each approach and (v) the relationship between the number of traits and the taxonomic distance between studied taxa (as the number of available and definable traits can decrease with greater taxonomic distance between taxa; Weiss & Ray, 2019). Our review also identified limitations in the published research, particularly the paucity of methods for merging distribution and trait data, as well as the difficulties in defining

### BOX 1 Ecological questions to functional cross-taxa research.

1. In deserts, birds, rodents and ants feed on and disperse seeds (Brown et al., 1979). While there is a broad literature on this subject (e.g. Kelt et al., 2004; Saba & Toyos, 2003), it seems that granivory rates are spatially and taxonomically idiosyncratic. Experiments in the Monte Desert of Argentina by Saba and Toyos (2003) showed birds as the major granivore group in this site over seasons—followed by rodents and ants—whereas experiments in the Sonoran Desert of North America by Brown et al. (1975) revealed rodents and ants as the most common granivores rather than birds (see global comparisons in Brown et al., 1979; Saba & Toyos, 2003). The phylogenetic distance between these organisms makes it possible to gather functionally analogous traits in a cross-taxa approach to answer questions such as: Do desert ecosystems function similarly worldwide? Would granivory, calculated across taxa, be constant across deserts? As it is not always feasible to conduct experiments over large spatial scales, by applying a cross-taxa approach we could use traits as proxies of granivory (see tab. 1 in Brown et al., 1979). Granivory might vary with daily (rodents during the night, ants during the day) and yearly activity (either seasonal or not) in function of metabolic constraints, organism size, and dispersal (whereby rodents gather several seeds at once and have limited dispersal, whereas ants and birds gather only one seed at time, but birds have higher dispersal capacity; Brown et al., 1975, 1979). Furthermore, ants are much more numerous than rodents and birds, especially close to ant colonies (Brown et al., 1975) which demands weighting traits by organismal abundance/biomass. Then, after gathering data on functionally analogous traits related to granivory for all taxa and weight them by abundance, we could project traits in a multidimensional trait space (Blonder et al., 2014; see Carvalho & Cardoso, 2020 to deal with categorical variables in hypervolume estimation), make computational experiments removing granivores, and computing changes in the trait space (Blonder et al., 2014; Carvalho & Cardoso, 2020; Mammola & Cardoso, 2020). One could make this experiment per site and region/desert to show whether the hypervolume structure is maintained along the experiment. Also, data from in situ experiments could also be embedded into this framework to improve estimations.
2. In reef ecosystems, cleaning interactions established by fish and shrimp involves a diverse set of traits that goes beyond simple body size (as classically established by Elton, 1927), since traits such as specialization/dedication, colour, and water column position can determine cleaning frequency and interaction strength (Quimbayo et al., 2018). Following interactions can be established by different marine organisms (e.g. fish, invertebrates and marine mammals) with traits (i.e. diet, activity period, mouth position and behaviour) which determine their role within interactions (i.e. nuclear or follower). While large-bodied species with inferior mouths, forming medium groups are mostly nuclear species, small-bodied species inhabiting the bottom are recognized as follower species (Inagaki et al., 2020). Thus, including multiple traits from different taxa can improve estimates of interaction strength between taxa (Eklöf et al., 2013) and reveal species' role within interactions.
3. A functional cross-taxa approach matching species traits and extinction risk can help identify traits that enhance organisms' vulnerability to multiple extinction threats (Cooke et al., 2019; Pimiento et al., 2020; Waechter et al., 2021). This approach may reveal the degree to which ecosystem functions are compromised by redundancy and abundance patterns of different taxa. Such an innovative approach was used to compare functional traits across disparate marine megafauna groups (mammals, fish, sea turtles, sea birds and molluscs) and found, across taxa, a severe loss of function with the loss of species (Pimiento et al., 2020). Similarly, species traits and extinction risk of 15,484 land mammals and birds indicate that the ecological strategies of most species include rapid life-history, small body size, invertivore diets, and generalist use of habitats (Cooke et al., 2019). While land birds and mammals share a limited portion of the trait space (31%), greater extinction risks for both groups concentrate on a similar spectrum of ecological strategies: slow life history, large body size, herbivore diet, and specialized use of habitats. Their projections show that future terrestrial ecosystems will likely consist of small sized, fast-lived, fecund and generalist mammals and birds with a limited range of ecological functions (see also Carmona et al., 2021).
4. Several recent studies have shown life-history trade-offs using a functional cross-taxa approach with multiple traits. Following recent developments and applications of the life-history (Capdevila et al., 2020; Healy et al., 2019) and metabolic theory (Brown et al., 2004, 2018), Junker et al. (2023) found that terrestrial animals (98 taxa from Insecta to Mammalia) could be disposed along a trade-off between investment in reproduction (the classical r- and K-strategies, Pianka, 1970) and the timing and pace of life, both being trait dimensions strictly connected with organism metabolic rates and body size (Brown et al., 2018). Trade-offs between multiple traits might therefore determine organism fitness and performance in the environment (Wüest et al., 2018).
5. By studying taxonomic and functional diversity of moths, long horned beetles, and breeding birds in Indiana, USA, Murray et al. (2017) showed taxon-dependent patterns of functional diversity in silviculture systems. A cross-taxa perspective applied to this study could reveal how much trait and function complementarity and sharing/redundancy is lost with silviculture across groups, highlighting loss of function with habitat modification and simplification.

comparable traits across distantly related taxonomic groups. Finally, we outlined promising directions for pushing the limits of research on functional ecology.

## 2 | METHODS TO CHARACTERIZE THE RESEARCH

### 2.1 | Literature review

We conducted a systematic literature review of peer-reviewed articles to evaluate the methods and trends in functional/trait-based research across multiple taxa, and examine how species traits have been utilized in this research over time. We set a family level cut-off to define studies as multiple taxa. Generally, organisms within the same genus or family are expected to exhibit similar traits and responses to the environment (Hadly et al., 2009), a trend known as 'ancestral niche conservatism' (the lineages' trend to maintain the ancestral niche; Wiens & Graham, 2005). Above these levels, traits and environmental responses are more varied and tend to exhibit weaker correlation among taxa (Anderegg et al., 2018; Hardy et al., 2012).

The review was conducted in the main collection of studies from the Web of Science (Clarivate Analytics). We followed the PRISMA protocol for reporting procedures of systematic reviews (Liberati et al., 2009; Figure S1.1, Table S1.1). The search was conducted using the keywords: 'ecolog\*' AND 'funct\*' AND 'trait\*', combined with the keywords 'cross-tax\*' OR 'multi-tax\*' OR 'multiple-tax\*' OR 'taxo\*-free' (Figure S1.1).

The literature survey returned 1006 studies published from 1945 to the survey day (2020-06-08). Although we recognize that literature has been published in other languages (e.g. Konno et al., 2020), we focussed on publications written in English because it provides a representative sampling of the studied subject. The title, keywords and abstract of each publication were screened to find whether studies covered multiple taxa, as well as topics in functional ecology. We collected data on 26 descriptors of each article that passed the initial filtering phase (Table S1.2). With these descriptors, we built a data set where each entry consisted of descriptors (columns) per trait, taxon and article (rows).

### 2.2 | Ecological subdisciplines and response variables

We evaluated the predominant subdiscipline and response variables using the information collected from the corpus of the surveyed studies. The predominant subdiscipline of a study was based on a list of possible ecology subdisciplines (Table 1). For each article, we assessed the response variables, whether functional (FRic, functional beta diversity, CWM, Rao'Q) or taxonomic metric (species richness, diversity, beta and, gamma). Articles using the same trait for different groups (e.g. size for both mammals and birds)

**TABLE 1** Main subdisciplines of ecology addressed by functional research using multiple taxa. One study could fit more than one subdiscipline.

Subdiscipline	Number of studies
Community ecology	52
Ecosystem monitoring	49
Conservation	12
Ecosystem functioning	7
Ecosystem services	3
Disturbance effects	2
Ecomorphology	2
Restoration	2
Climate-change ecology	1
Ecological networks	1
Ecophysiology	1
Macroevolution	1
Paleobiology	1
Trade-offs	1

and/or presenting strong arguments that different traits may indicate the same ecological function (e.g. wings for birds and achene for plants) were interpreted as articles that used functionally analogous traits. Articles using abundance (if stated in methods and results) were further analysed to understand whether they used abundance-weighted functional indices (e.g. FEve, FDiv, Rao's Quadratic Entropy, CWM).

### 2.3 | Taxonomic scope & research context

To evaluate the taxonomic groups and ranks being studied, we obtained the total number of articles per taxonomic group and rank (from Family to Domain). The rank was defined as the highest rank encompassing all species within a studied group. We used the nomenclature of the National Center for Biotechnology Information (NCBI). For example, a rank of 'Family' was attributed to a study embracing *Leopardus tigrinus*, *Leopardus guttulus* and *Panthera onca* (Mammalia, Carnivora, Felidae), and a rank of 'Order' was attributed to a study of *Leopardus tigrinus*, *Leopardus guttulus*, *Panthera onca*, and *Cerdocyon thous* (Mammalia, Carnivora). Nonetheless, one study could include several ranks. For instance, Flynn et al. (2009) studied birds (Class), mammals (Class) and plants (Phylum), contributing to three taxonomic groups (birds, mammals and plants) and two ranks (Class and Phylum). We built a network of taxonomic ranks as nodes, and number of articles studying them as weighted links to evaluate to what extent multiple taxonomic ranks were studied together. We measured network nestedness (NODF metric, Almeida-Neto et al., 2008) to identify a potential core of taxonomic ranks in cross-taxa research. The observed NODF was compared with a random NODF produced by 999 runs of the independent-swap null model.

We built a meta-network that links taxa and studies (i.e. a network of study networks linked by shared taxa). We built this meta-network at the taxonomic level of 'Kingdom' (the node in this network) to find connections between disparate branches of the Tree of Life, and measured the degree of each node to explore the number of connections per Kingdom. Then, we measured the centrality degree to evaluate the relative importance of different taxa in the meta-network, and meta-network connectance to determine the proportion of realized interactions relative to the total number of potential interactions among the studied taxa (in the network, nodes are above the Subclass level). We also calculated the modularity of the complete meta-network (Newman, 2006). Modularity measures whether there are different sets of groups studied together more often than others. The observed modularity was compared to a random modularity produced by 100 runs of the 'vaznull' null model with modules computed using the Beckett's method (Beckett, 2016).

We assessed the coverage of our review data across the Tree of Life using the classification of Ruggiero et al. (2015) to all organisms on Earth. We used a tree topology based on the taxonomic classification of studied organisms above the Subclass level (nomenclature of the NCBI), and highlighted the branches of taxa represented in our review. The topology was based on the similarities of taxonomic ranks across taxa (UPGMA clustering algorithm based on Jaccard's distance). Studied taxa were mapped into the topology from the tips to internal nodes of the tree by building an adjacency matrix composed of internal nodes and tips.

## 2.4 | Combining or comparing traits

We classified studies under three different approaches: combined, comparative or both. The combined approach consists of merging distribution data and similar traits across all species taken together from distinct taxonomic groups (e.g. Cooke et al., 2019; Pimiento et al., 2020), while the comparative approach consists of studying taxonomic groups in parallel, using independent trait sets, and comparing them at the end (Aubin et al., 2013; Kellner et al., 2019). The combined approach has been used to identify life history trade-offs across taxa (e.g. Junker et al., 2023) and simulate their functional vulnerabilities (e.g. Cooke et al., 2019; Pimiento et al., 2020). Combining data is also a common procedure in geometric morphometrics methods (also known as 'ecospace analysis' or 'ecospace modelling', e.g. De Esteban-Trivigno, 2011). In turn, the comparative approach is often used in the context of ecological congruence and surrogate taxa (e.g. Heino et al., 2009; Magg et al., 2019). Finally, studies using both approaches are also possible as researchers can be interested in ecological congruence between two different groups (e.g. birds vs. bats), as well as richness within functional groups across taxa (e.g. Renner et al., 2018).

We analysed this classification of combined and comparative approaches in parallel with definitions of trait types to explore the type of trait used in each approach. Given the broad variety of traits in the surveyed research (Table S1.4), we allocated traits

into 12 distinct types based on recent efforts to classify traits (e.g. Hadj-Hammou et al., 2021; Martini et al., 2021): diet, habitat, size, reproduction, dispersal, behaviour, life habit, growth, defence, distribution and interactions (Table S1.4). Finally, we used the number of trait types and the number of taxonomic ranks (the number of different taxonomic ranks within a single study), at the study level, to investigate the shape of the relationship between the number of taxonomic ranks and the number of traits per study. We did so by fitting a Generalized Additive Model with Poisson distribution to the data as  $\ln(y) = \beta_0 + f(x_1) + \epsilon$ . The  $y$  is the response variable (number of trait types) and  $\ln$  (natural logarithm) the link function for a Poisson model,  $\beta_0$  is the model intercept,  $f(x_1)$  is the smoothing function of the descriptor  $x_1$  (the number of taxonomic ranks), and  $\epsilon$  is the error term taken from a Poisson distribution  $\epsilon \sim \text{Poisson}(\lambda)$ , where  $\lambda$  is the mean number of trait types per study. This model allowed us to identify non-linear relationships between variables and a potential trade-off regarding the number of taxonomic ranks and number of traits per study. We ran the same analysis either by keeping or removing the outliers (articles with >15 taxa, e.g. Gwinn et al., 2018), and replacing the number of taxonomic ranks (study taxonomic range) by the mean pairwise phylogenetic distance between taxa (MPD; Webb et al., 2002) for articles with at least two taxa. We also ran two sensitivity analyses to test whether (i) the allocation of traits into groups of trait types affected the results and (ii) the trade-off would be maintained if we removed trait types from the dataset. For the second sensitivity analysis, we used a randomization procedure where we subtracted one trait category from the observed number of types. We repeated this procedure 100 times, and made the subtraction of 10% and 20% of the dataset assembled from the reviewed literature.

Analyses were performed in the R environment v.4.1.2 (R Core Team, 2021) using the following packages: networks: 'igraph' (Csardi & Nepusz, 2006); taxonomic classification: 'taxize' (Chamberlain et al., 2020); Jaccard distance and UPGMA: 'vegan' (Oksanen et al., 2020); topology tree: 'phytools' (Revell, 2012) and 'dae' (Debastiani, 2021); Poisson GAM: 'mgcv' (Wood, 2011).

## 3 | RESULTS FROM THE LITERATURE REVIEW

### 3.1 | Ecological subdisciplines and response variables

The systematic review resulted in a data set with 1336 entries, comprising 134 taxa and 491 traits from 96 different articles (Figure S1; Table S1.3). Most studies were observational with species assemblage data collected at the local/site scale (81%,  $n=78$ ), with the remaining studies comprising experiments ( $n=10$ ) and meta-analyses ( $n=6$ ). Most research focussed on 'community ecology' ( $n=52$ ), 'ecosystem monitoring' ( $n=49$ ) and 'conservation' ( $n=12$ ; Table 1), and largely relied on taxonomic diversity indices (e.g. Shannon, Simpson,

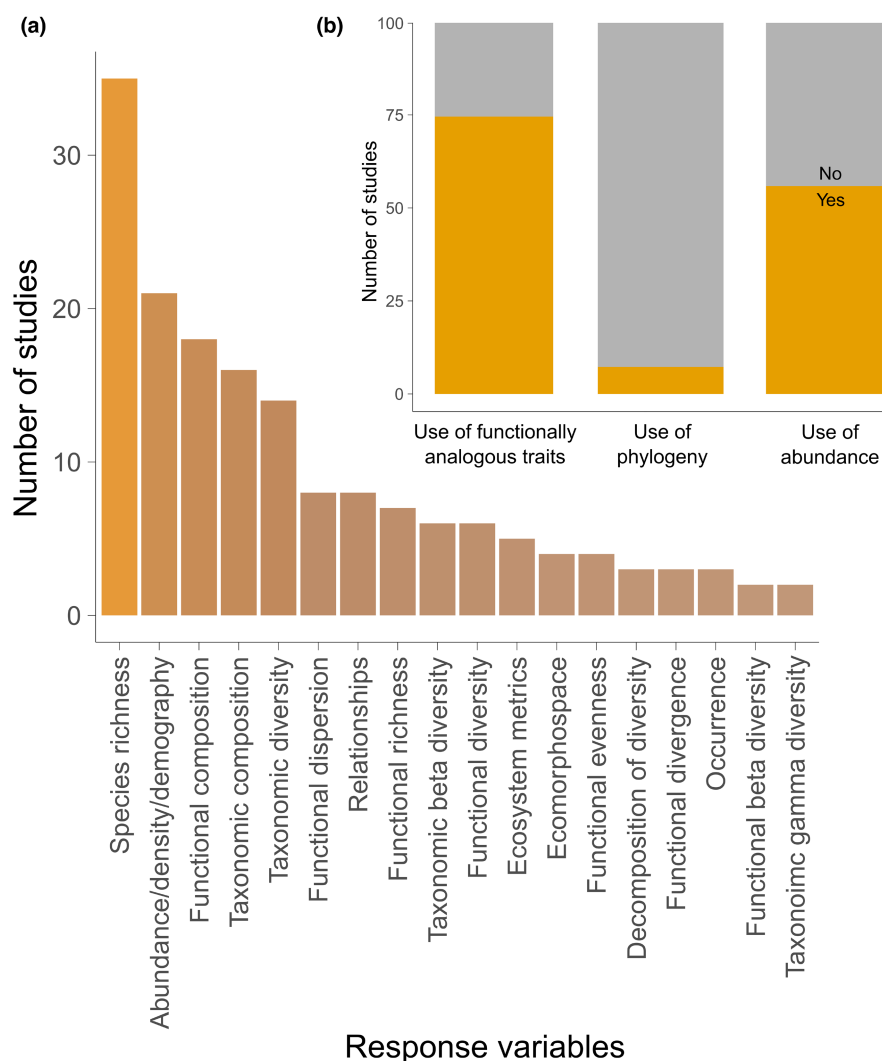
Margalef) to measure diversity within discretely defined functional groups (Figure 1a). The most frequently used functional indices in surveyed articles were Community-Weighted Means (CWM), functional dispersion (including FDis and Rao's Entropy; Figure 1a). Functionally analogous traits were often used in the surveyed research (75% of the reviewed articles, Figure 1b) meaning that authors are striving to represent similar functions across taxa, yet most research only compares data. Phylogenies were rarely used in our review data set (e.g. Thorn et al., 2020; Figure 1b). Nonetheless, the use of abundance was frequent (56% of the studies). While 25% ( $n=24$ ) of the articles used indices that could be weighted by abundance (e.g. FEve, FDis, FDiv), only 15 actually used abundance data, revealing that the effective use of this type of data is still limited in functional (multitaxa or cross-taxa) studies.

### 3.2 | The taxonomic scope & research context

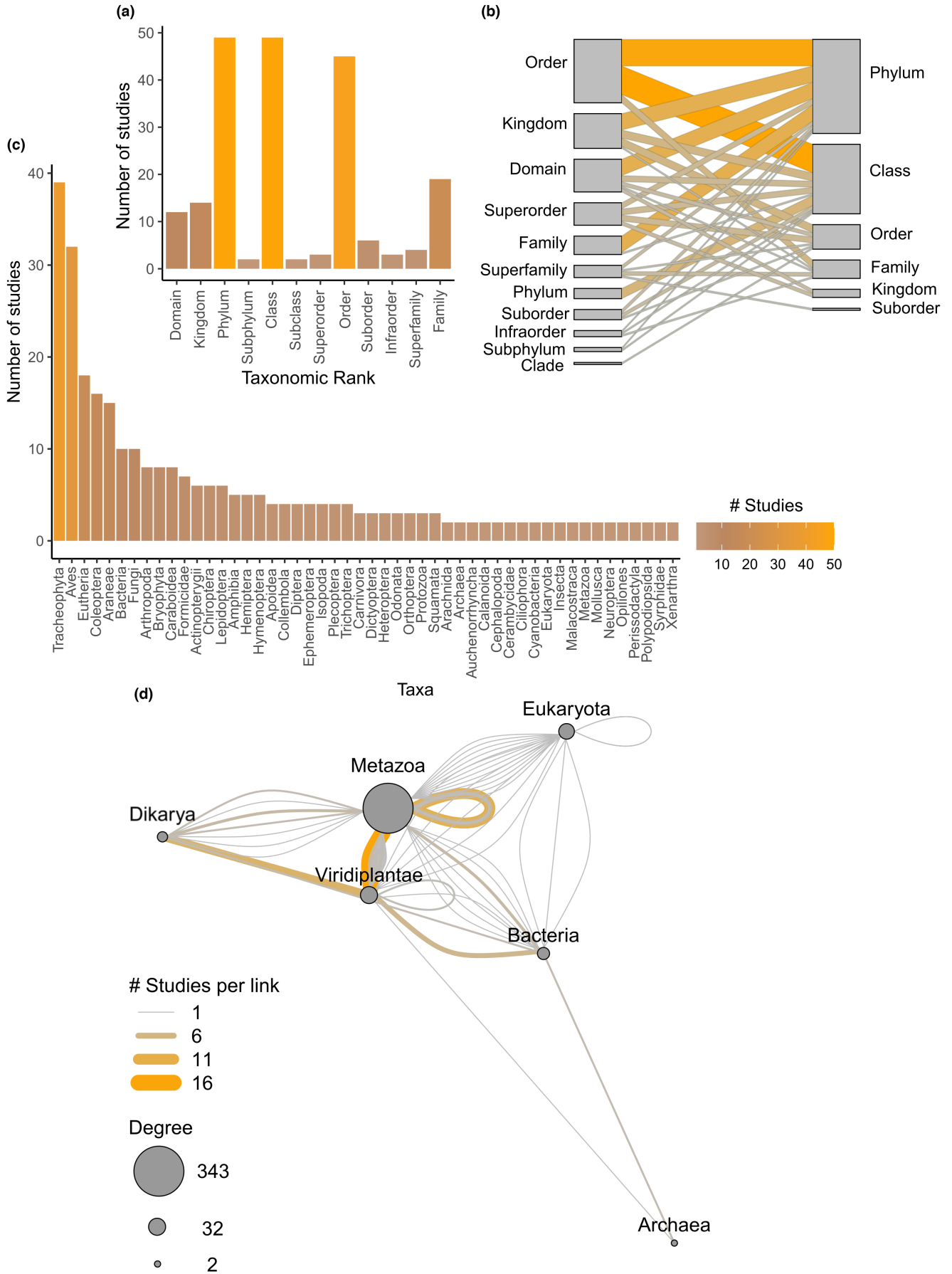
Most taxonomic ranks retrieved from our review were Class, Phylum and Order, with more than 40 studies per rank (Figure 2a). The links between 'Order - Class' and 'Order - Phylum' predominated in our

review (Figure 2b), showing that taxa from these taxonomic levels were frequently studied in conjunction. We detected a nestedness (NODF index) of 31.72 in this network (lower and upper 95% confidence interval: 28.97–33.32), showing that 31.72% of the links of the least connected taxonomic ranks represented a subset of the most connected taxonomic ranks (i.e. the core of taxonomic ranks). Tracheophyta, Aves, Eutheria, Coleoptera, and Araneae were the most frequently cited taxonomic groups in our dataset (Figure 2c). The network at the Kingdom level showed that Metazoa and Viridiplantae were often used together, and that Metazoa was the most connected Kingdom, exhibiting the highest degree value (Figure 2d).

The complete meta-network (Figure S1.2) showed that the most often linked taxa (at the Subclass level or higher ranks, following Ruggiero et al. (2015)) were birds (Aves) and mammals (Mammalia), plants (Streptophytina) and winged insects (Neoptera), winged insects and spiders (Arachnida), and plants and fungi. Given this taxonomic composition, it is clear that most studies were carried out in terrestrial ecosystems, representing 81.25% ( $n=78$ ) of the studies, whereas only 8.3% ( $n=8$ ), 7.3% ( $n=7$ ) and 1.04% ( $n=1$ ) of the articles were conducted in marine, freshwater and estuarine ecosystems,



**FIGURE 1** Number of studies per response variable (a), and proportion of use of functionally analogous traits, phylogenies and abundance data (b) in functional ecology research using multiple taxa. 'Relationships' depict the use of approaches such as species richness-plant functional type (PFT) richness, trait scaling with body mass, and correlation among traits. 'Occurrence' depicts studies that estimated probabilities of site occupancy through hierarchical models, and used these quantities to analyse changes in occupancy across functional groups (FG) or obtain estimates of species richness per FG. 'Taxonomic diversity' depicts diversity indices such as Shannon, Simpson and Margalef.





**FIGURE 2** Barplot showing the identity of studied taxonomic ranks (a), bipartite network depicting the number of articles per pair of taxonomic rank (b), barplot showing the number of studies of each taxonomic group (c) and (d) a meta-network depicting links between pairs of Kingdoms. More than one taxon can be studied in the same article (see b), so that the sum of values in (a) and (c) is greater than the total number of articles. In (d), links represent the connection between taxa from different Kingdoms in our review, and loops refer to links between pairs of taxa within the same Kingdom. The multiple parallel lines represent the different pairwise combinations of taxa that link two Kingdoms (e.g. Streptophytina and Neoptera with 16 studies, and connecting Viridiplantae and Metazoa, or Streptophytina and Fungi with eight studies, and connecting Viridiplantae and Dikaria). Line width represents interaction strength within and between Kingdoms, and circle size denotes the degree metric of each Kingdom (values in the legend; refer to [Figure S1.2](#) for the complete meta-network).

respectively. Only two studies (2.08%) crossed ecosystems (terrestrial, freshwater and marine (MacLean & Beissinger, 2017), terrestrial and marine (Ruthrof et al., 2018)). Meta-network centrality degree and connectance values were 0.27 and 0.25 (i.e. 25% of the potential links are indeed realized), respectively. This meta-network also presented a high modularity regarding taxa linked by the studies ( $Q=0.56$ ), indicating that the number of interactions within each module is 56% larger than what would be expected for a network with the same number of modules (95% Confidence Interval of  $Q$ : 0.34–0.39; [Figure S1.3](#)). There were six modules in this meta-network ([Figure S1.4](#)). Among the largest ones, two comprised terrestrial taxa (Streptophytina, Mammals, Arachnida), and another one comprised aquatic taxa (e.g. Crustacea, Echinodermata) ([Figure S1.4](#)). Nonetheless, we observed missing links in the meta-network (i.e. taxa not connected by studies), such as those between Aves and Acari which have a host–parasite relationship, and Chlorophyta or Cyanobacteria with vertebrates or invertebrates that interact in food webs ([Figure S1.4](#)). Notably, dinoflagellates, cyanobacteria and other microorganisms appeared as an isolated module from other taxonomic groups in our review ([Figures S1.2](#) and [S1.4](#)). About 20% of the tips in the Tree of Life (57 out of 311) were mentioned in the surveyed articles. Most research covered animal rather than plant branches in the Tree of Life, although this can be an artefact of the smaller size of animal clades relative to those of plants, bacteria, fungi, and other microorganisms ([Figure 3](#)).

### 3.3 | Combining or comparing traits

Functional multitaxa research was more frequent than functional cross-taxa research. Most research compared ( $n=52$ ) rather than combined ( $n=32$ ) data across taxa, and a minor portion used both approaches ( $n=12$ ). All approaches mostly used diet (combined: 26%, comparative: 19%, both: 27%) and dispersal traits (combined: 7%, comparative: 9%, both: 14%). The combined approach used size traits more often than the comparative approach (20% vs. 12%; 16% for studies using both approaches), while the comparative approach used habitat traits more often than the combined approach (16% vs. 13%; both: 11%; [Figure 4](#)).

The number of trait types showed a peak at intermediate numbers of taxa (taxonomic range) per study and at intermediate taxonomic distances between taxa (MPD), regardless of outliers ([Figure 5a,b](#)). The relationship was stronger between the number of trait types and the number of taxa, than with MPD. The relationship

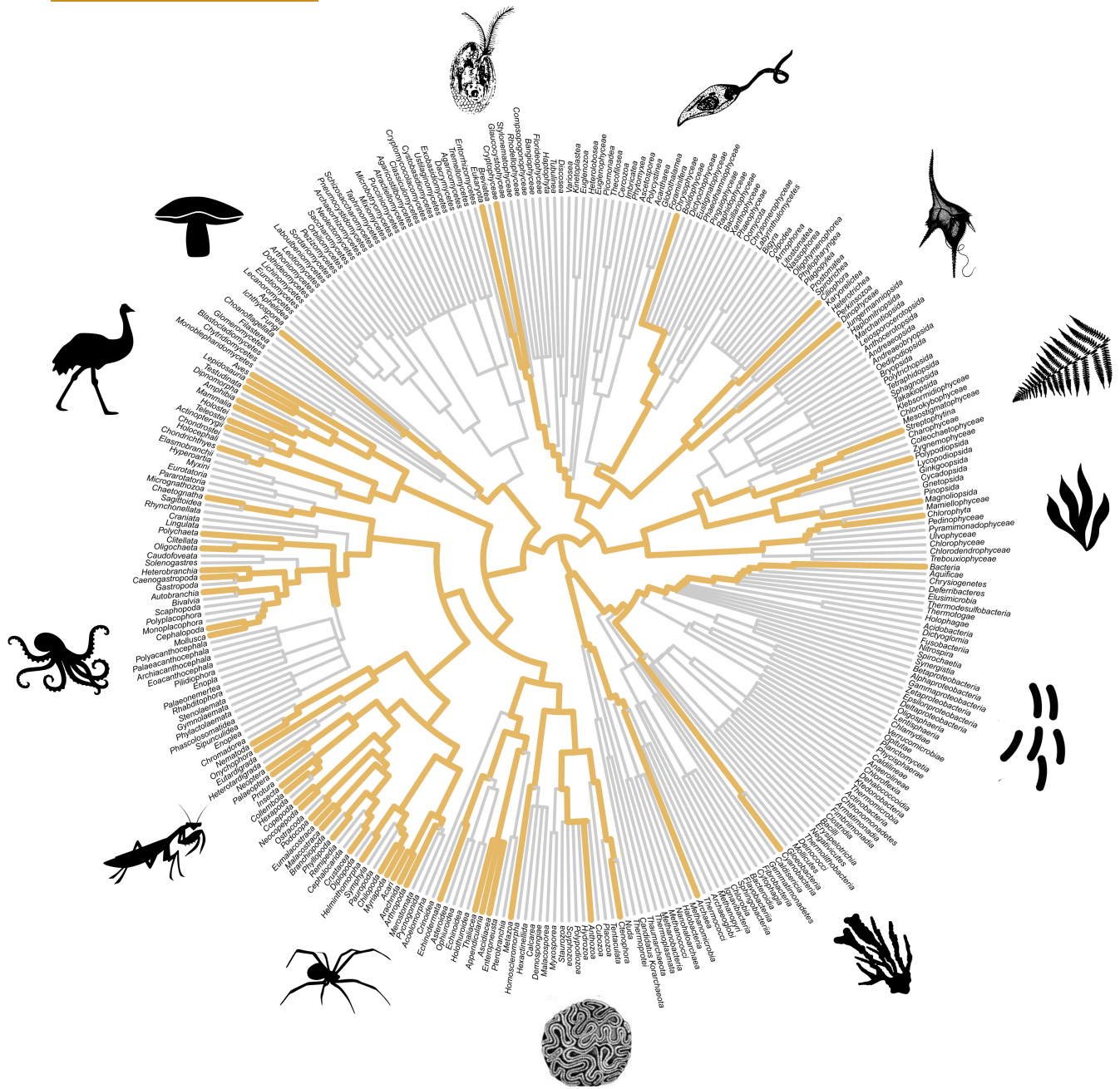
was similar, although weaker, between the number of taxa and the raw number of traits per study (i.e. not allocating traits into groups of trait types); no relationship was detected between the raw number of traits and MPD ([Figure S1.5](#)). These patterns persisted (similar adjusted  $R^2$  statistics) after randomly removing 10% and 20% of the trait types ([Figures S1.6](#) and [S1.7](#)).

## 4 | LIMITATIONS, PERSPECTIVES, AND THE FUTURE OF FUNCTIONAL CROSS-TAXA RESEARCH

We found that community ecology (structure or assembly) and ecosystem monitoring were the main subdisciplines addressed by functional research using multiple taxa. Taxonomic diversity (species richness, abundance) calculated within functional groups was the predominant metric used in our review, and terrestrial groups such as Aves and Mammalia (or birds and mammals), as well as Streptophytina and Fungi (or green plants and fungi) were more frequently combined in comparison to a large number of other groups. Indeed, we identified missing links in the meta-network, which we think can be caused by biological reasons and lack of data. There were a set of key traits such as diet, size, habitat and dispersal, which underlies most functional ecology research with multiple taxa. We detected difficulties in defining comparable traits across distantly related taxonomic groups, as the number of trait types decreased with taxonomic range (i.e. number of taxa per study) and taxonomic distance (i.e. mean pairwise distance, MPD) between studied taxa. Our review also showed that a functional multitaxa approach (data comparisons across taxa, Weiss & Ray, 2019) was more frequent than a functional cross-taxa approach (data combination across taxa). We map these limitations in the next section (4.1), present some ecological questions to functional cross-taxa research ([Box 1](#)), and suggest directions to pushing the limits of functional ecology research (Sections 4.2 and 4.3).

### 4.1 | Limitations of current functional research with multiple taxa

Taxonomic diversity, calculated within functional groups (or functional group richness), predominated relative to other metrics. This is because functional ecology traditionally relies on assigning organisms to functional groups (Ryznar et al., 2021). Criticisms to the



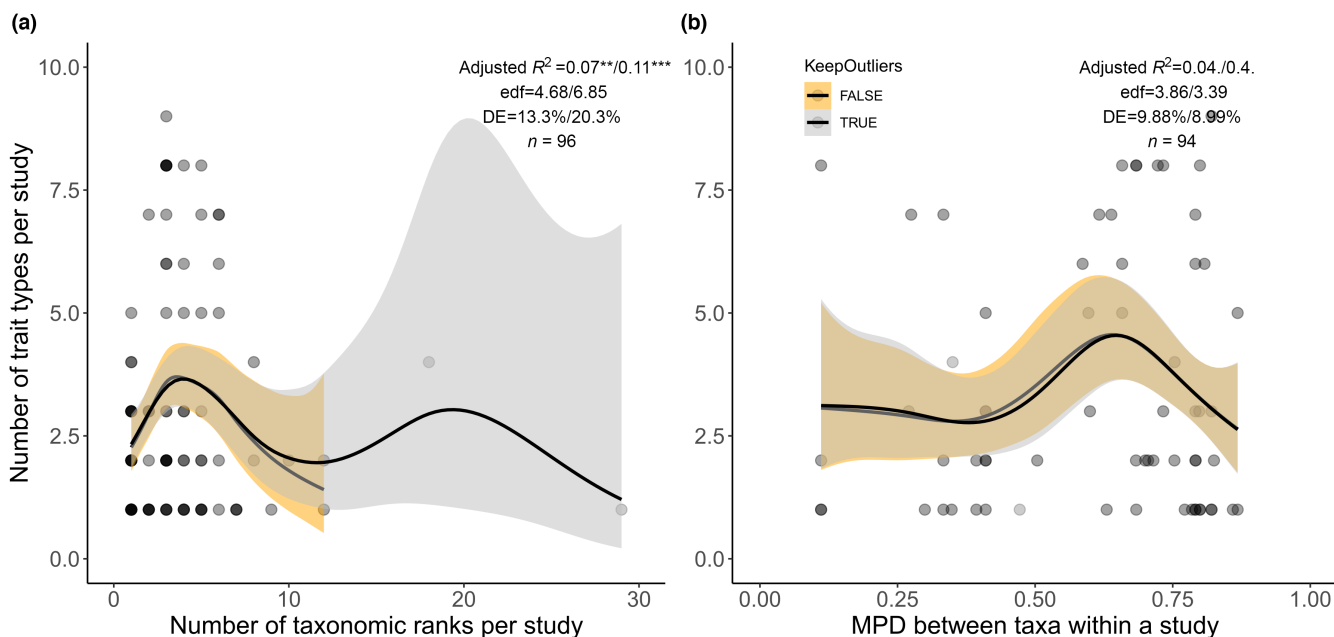
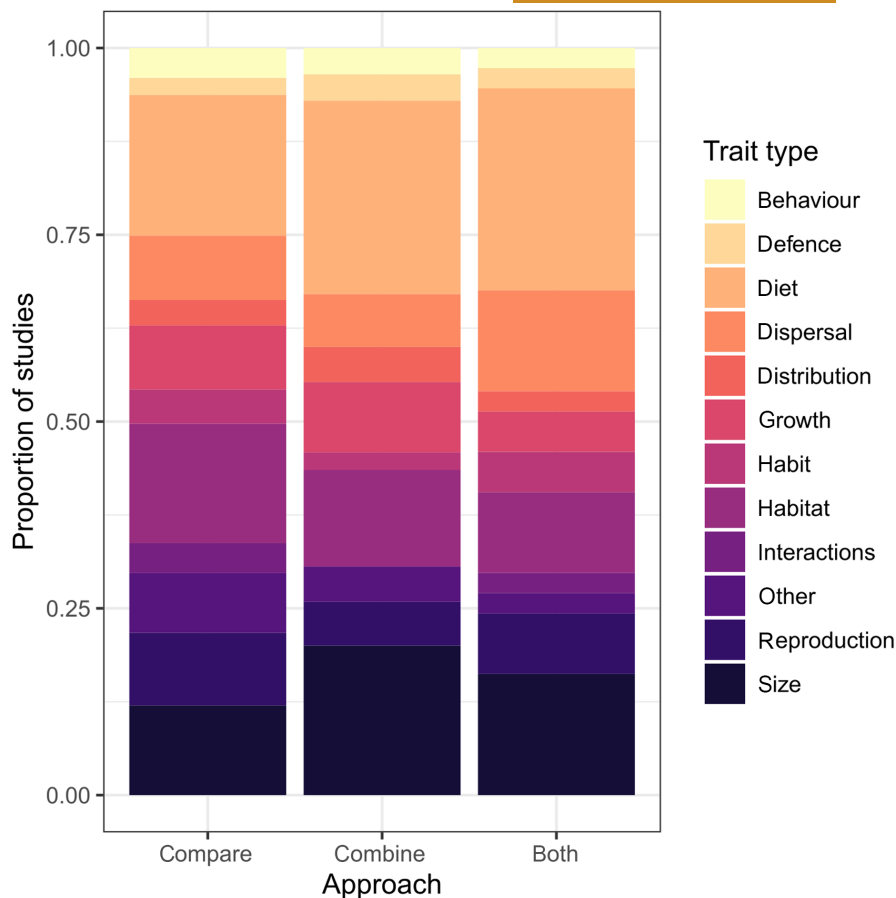
**FIGURE 3** Tree topology of taxa within multiple taxa research in functional ecology (orange branches). The taxonomic tree was based on the taxonomic ranks of studied organisms. Taxonomic nomenclature follows the National Center for Biotechnology Information classification, and is above Subclass level. As some studies have identified varying taxonomic levels for the same organism (e.g. Acari, Arachnida), we have opted to display all taxonomic ranks instead of solely showcasing the higher-level rank as the tree's edges.

functional-group approach fostered the development of metrics that consider the whole range of species' trait values, such as distance-based indices (e.g. Petchey & Gaston, 2006; Webb et al., 2002), Community-Weighted Means (Garnier et al., 2004), convex hulls (Cornwell et al., 2006; Villéger et al., 2008) and  $n$ -dimensional (Hutchinsonian) hypervolumes (Blonder et al., 2014; Mammola & Cardoso, 2020). The growing list of methods and indices to choose from, associated with investment in high-resolution data collection and the broad availability of traits databases, will possibly make the

use of quantitative traits more frequent, as recently seen in the field (e.g. Carmona et al., 2021; Cooke et al., 2019; Junker et al., 2023; Pimiento et al., 2020; Waechter et al., 2021).

Information contained in abundance data is still limited in functional (multitaxa or cross-taxa) studies. Abundance is a fundamental quantity in ecology and evolution (Brown, 1984; Preston, 1948) and is central to functional ecology as the magnitude of ecological functions and interactions changes with abundance (Bernard-Verdier et al., 2012; Enquist et al., 2015; Mouillot et al., 2013). Abundance

**FIGURE 4** Barplot depicting the use of trait types in studies employing different approaches (combined, comparative, or both approaches in the same article). Number of articles per approach: both ( $n=12$ ), combine ( $n=32$ ), and compare ( $n=52$ ). Number of articles per trait category: diet ( $n=65$ ), size ( $n=44$ ), dispersal ( $n=26$ ), habitat ( $n=43$ ), habit ( $n=12$ ), reproduction ( $n=25$ ), defence ( $n=8$ ), growth ( $n=25$ ), distribution ( $n=11$ ), behaviour ( $n=11$ ), interactions ( $n=8$ ), other ( $n=19$ ).



**FIGURE 5** Relationship between the number of different taxonomic ranks and the number of trait types per study (a), and the relationship between the mean pairwise taxonomic distance (MPD) between taxa and the number of trait types per study (b). In (b), MPD was calculated only for articles in which at least two taxa were analysed. Line colours, and parameter values separated by the slash, depict the relationships with or without outliers (number of taxonomic ranks per study >15). The line and confidence intervals were estimated through a Generalized Additive Model (GAM) with a Poisson distribution. GAM parameters: Adjusted- $R^2$  = Adjusted  $R$ -squared statistics, edf—effective degrees of freedom, DE—Deviance Explained,  $n$ —sample size. The shaded area depicts the 95% confidence interval around the non-linear trend. Significance  $p$ -value codes: \*\*\*\*: 0–0.001; \*\*\*: 0.001–0.01; \*\*: 0.01–0.05; !: 0.05–0.1.

comprises a core factor linking traits to ecosystem properties. Differences in relative abundance alter trait frequency at the community level through different individual fitness across gradients (Chacón-Labela et al., 2023). In turn, shifts in the shape of trait frequency distributions with the environment will impact ecosystem-level processes (Chacón-Labela et al., 2023). We foresee that abundance-weighted traits will strengthen the inference on ecological processes, mostly for those processes that depend on taxa having disparate abundance (e.g. rate of seed removal by rodents, birds and ants; Kelt et al., 2004; see Box 1).

We identified missing links in the meta-network, likely caused by two factors: (i) rare or weak interactions among taxa (e.g. algae and mammals), (ii) understudied taxa resulting in lack of data. First, taxa might not coexist or interact in communities of ecosystems, or can explore the environment in different ways, resulting in less frequent/weaker network links. Second, functional ecology reviews show a biased availability of functional traits, which tends to be greater for vertebrate taxa than for other groups such as invertebrates (e.g. Brousseau et al., 2019). Also, the taxonomic composition in our review suggests that most efforts have been concentrated in terrestrial ecosystems, while this approach with multiple traits and taxa is still developing in marine (Green et al., 2022; Martini et al., 2021; Pimiento et al., 2020; Waechter et al., 2021) and freshwater ecosystems (Gomes et al., 2023; Green et al., 2022; Heino et al., 2013; Martini et al., 2021; Schmera et al., 2017; Xu et al., 2019).

Our review shows that diet, habitat, size and dispersal were the trait types most often used in functional ecology research involving multiple taxa. This key set of trait types can be merged in functional cross-taxa research as they are broadly available in databases, apply to multiple taxa, and relate to important ecosystem functions. For instance, mammals, birds and ants can have similarities and a partial overlap in diet and habitat preferences (e.g. eating seeds and living in deserts, Kelt et al., 2004). Also, feeding habits, size and dispersal are frequently used in functional studies of aquatic macroinvertebrates (a broad group that comprises multiple taxa), generally in association with reproductive traits (e.g. number of descendants per reproductive cycle; Schmera et al., 2017). In marine ecosystems, size, diet, space use, gregariousness, and growth rate are widely used to characterize reef fish (Hadj-Hammou et al., 2021; Mouillot et al., 2014). In freshwater ecosystems, the most commonly utilized trait categories for characterizing the function of freshwater fish were feeding and locomotion (Gomes et al., 2023). While the existence of a key set of 'supertraits'—traits responsible for multiple functions—enables much research in functional ecology, this is one of the main weaknesses of the approach as the link between the traits being used and the responses and processes they shape is often weak or indirect (Bellwood et al., 2019; Streit & Bellwood, 2022). Investment in experiments might help us identify traits of one group that modulate ecological interactions, responses, and ecosystem functions of other groups (Schleuning et al., 2023), as well as to find common functional currencies that might apply to many taxa (a point further developed in Section 4.3; Brown et al., 2004; Meunier et al., 2017; Walker et al., 2022). By doing so, functional ecologists can improve

their ability to make direct connections between traits, organism responses, and ecosystem functions (Bellwood et al., 2019; Enquist et al., 2015; Schramski et al., 2015).

The number of trait types used in a single functional ecology study with multiple taxa was influenced by the number of studied taxa and, to a lesser extent, by their taxonomic distance. Although adjusted  $R^2$  statistics were generally low, our models showed a non-linear, hump-shaped relationship between these variables. This suggests there is a trade-off among trait complementarity, trait generality, trait availability and phylogenetic depth/taxonomic range. While single-taxon research implies small phylogenetic distances, low trait complementarity, many well-defined and available traits, only few of these traits are relevant for describing ecosystem functions. Therefore, two factors might explain the low number of trait types used at small numbers of taxa and taxonomic distances. First, this can result from choosing traits that are known and relevant to describe ecological functions of these taxa (e.g. tooth shape to describe herbivory among mammals). Second, phylogenetic constraints on ecological functions (e.g. primary productivity by vascular plants, algae, and cyanobacteria; secondary productivity by herbivores) might explain that pattern. For example, within a trophic level, the number of trait types needed to measure function (e.g. biomass production by plants, feeding rate by herbivores) might remain nearly constant with increases in phylogenetic distance among taxa.

We found a peak in the number of trait types used by the studies at intermediate levels of numbers of taxa and phylogenetic distances. This pattern can arise because researchers are struggling to compare or combine a broad range of ecological responses and functions by increasing trait complementarity and phylogenetic distance among studied taxa (Cadotte et al., 2011, 2017; Díaz & Cabido, 2001). Alternatively, it can arise simply because more traits were needed to compare or combine functions across taxa, as the number of functionally analogous traits decrease at this point. In other words, it may be challenging to find traits that can be combined for taxa belonging to different phyla or kingdoms (Weiss & Ray, 2019).

Further increasing taxonomic range and phylogenetic distances implies high trait complementarity, and few generic but broadly applicable and available traits. In other words, the higher the number of taxa and taxonomic distances between them (i.e. greater taxonomic range; top right region in Figure 5a), the lower the trait resolution and the number of traits that taxa would share. In a functional cross-taxa approach, larger phylogenetic distances might hamper trait acquisition (in methodological and analytical terms) and, potentially, the inference on ecosystem processes because organisms can respond differently to or affect differently the ecosystem (i.e., no functional overlap/complete complementarity) (Brousseau et al., 2019; Weiss & Ray, 2019). Also, a functional cross-taxa approach might be more feasible at broad scales of analysis (hundreds of meters to kilometres), as organisms tend to converge their response to broadscale gradients such as temperature and energy (Brown et al., 2004). Nonetheless, the taxonomic coverage of a functional cross-taxa approach might be limited at local scales by (i) differential dispersion, use of habitats, and sensitivity to microhabitats by large and

small organisms, (ii) issues of sampling multiple taxa with common or complementary protocols that capture ecological patterns and processes at comparable scales. Of course, this trade-off is complex and summarizes the challenge of cross-taxa approaches, resulting in a paucity of functional cross-taxa studies in ecological literature. Future studies may consider the state of the art presented here to further advance this line of research in functional ecology.

## 4.2 | Overcoming taxonomic boundaries in functional ecology

A functional multitaxa approach (data *comparisons* across taxa, Weiss & Ray, 2019) was more frequent than a functional cross-taxa approach (data *combination* across taxa). In fact, efforts to apply a cross-taxa perspective in functional ecology are rather recent (Cooke et al., 2019; Junker et al., 2023; Pimiento et al., 2020; Waechter et al., 2021), and the predominance of comparative studies could result from the longer use of ecological congruence/surrogate frameworks in ecological monitoring research (Aubin et al., 2013; Gaston, 2000; Heino et al., 2009) and the unavailability of functionally analogous traits for several taxa (Weiss & Ray, 2019). While comparing diversity among multiple taxa and finding surrogate taxa has been at the core of ecosystem monitoring (e.g. Heino et al., 2009; Magg et al., 2019), we advocate that using a functional cross-taxa approach (i.e. explicitly merging distribution and trait data across organisms) will open new avenues for research, improving our ability to understand the drivers of ecosystem structure and change. Crossing taxonomic boundaries may improve understanding of ecosystem functioning and its vulnerabilities across the tips of the Tree of Life, which is possible thanks to the burgeoning interest in functional ecology (Brousseau et al., 2019; Cadotte et al., 2011), and the proliferation of published trait databases for a wide range of taxa (e.g. Brousseau et al., 2019; Kattge et al., 2020; Madin, Anderson, et al., 2016; Quimbayo et al., 2021; Tobias et al., 2022; Wong et al., 2019).

A recent challenge to functional ecologists has been to identify emergent properties of whole communities and ecosystems. The range of ecosystem functions addressed in any study seems to depend on trait complementarity among component taxa, whereas ecosystem resistance and resilience might rely, at least in part, on the number of taxa performing the same function (Cadotte et al., 2011; Díaz & Cabido, 2001). Thus, complementary functions performed by organisms within an ecosystem, and also the functions shared among them, may be better described if community assessments include more phylogenetically distant taxa. For instance, under experimental settings, both ecosystem multifunctionality and single functions (litter and biomass production, habitat structure complexity, and decomposition) scale positively with MPD among taxa in a community (Cadotte et al., 2017). This requires ecosystem properties to be assessed from the perspective of their whole components rather than a sample of taxa based on methodological convenience (Margalef, 1963), or from a set of taxa with representative functions in the ecosystem (e.g. primary producers, predators, facilitating and pioneer species; Aubin

et al., 2013; Flynn et al., 2009; Moretti & Legg, 2009). Taxonomic coverage enables crossing geographical barriers when inferring, for instance, common rules of assembly (Lessard et al., 2012) and organism response to climate change (MacLean & Beissinger, 2017; Pinsky et al., 2022) across regions and realms.

Studies scattered throughout the literature show how to integrate distribution and trait data to quantify ecosystem resistance and resilience at regional scales (Waechter et al., 2021) and global scales (Cooke et al., 2019; Newbold et al., 2020; Pimiento et al., 2020; see Box 1). These studies show that addressing ecosystem resistance to disturbances will benefit from a cross-taxa approach, from which it is possible to know whether distantly related taxa can perform similar and vulnerable functions, as those of threatened taxa (Pimiento et al., 2020; Waechter et al., 2021). By merging trait data across taxa, including 15,484 species of land mammals and birds, an unprecedented loss of ecological functions has been detected and connected to human impacts (Cooke et al., 2019). In another initiative, 25,166 land vertebrate and invertebrate species were allocated to broad functional groups to show that large endotherms, small ectotherms, carnivores and fungivores were negatively influenced by human activities (Newbold et al., 2020). Measuring ecological functions across multiple taxa can help us understand whether functional redundancy could be really interpreted as a 'life insurance' for ecosystem functioning in a changing world. Recent studies have also revealed that organisms can be arranged along life-history trait gradients (Cooke et al., 2019; Díaz et al., 2016; Junker et al., 2023), suggesting that it will soon be possible to depict spatial patterns of trait distribution (and vulnerability) across taxa. A functional cross-taxa approach matching species traits and extinction risk can better identify traits that enhance organisms' vulnerability to multiple threats (Cooke et al., 2019; Pimiento et al., 2020; Waechter et al., 2021). This approach may also reveal vulnerable ecosystem functions that rely on different taxa, their vulnerability, redundancy, and patterns of abundance. In the Atlantic Ocean, a functional cross-taxa study looking at the ecosystem functions of reef vertebrates showed that the loss of mesopredators has a greater impact on the functional structure of reef vertebrate assemblages compared to the loss of species performing other ecosystem functions (Waechter et al., 2021; see also Box 1).

## 4.3 | Finding common currencies for functional cross-taxa research

We might need common 'functional' currencies for functional ecology—traits that can be combined across most of the Tree of Life. While such common currency could be functionally analogous traits, other approaches could be complementary. For instance, energy and matter can be used as common universal currencies to unite all life forms, from Archaea to blue whale (Brandl et al., 2023; Brown et al., 2004, 2018; Capdevila et al., 2020; Enquist et al., 2015; Healy et al., 2019; Junker et al., 2023; Margalef, 1963). Terrestrial organisms (98 taxa from Insecta to

Mammalia) can be arranged along a common currency, the 'animal economics spectrum', that represents a trade-off in life history strategies of species (Junker et al., 2023; see Box 1). Such trade-offs seem to be consistent across both terrestrial and aquatic organisms, despite the fundamental differences in life-history strategies between them (Capdevila et al., 2020). Stoichiometry (Meunier et al., 2017) and metabolome (Walker et al., 2022) are other promising common currencies and approaches that might reveal important trade-offs in life-history traits. Stoichiometry describes trade-offs between environmental availability/element fluxes and organisms' nutrient uptake (Meunier et al., 2017), which are fundamental parameters describing organism fitness, performance and function (Arnold, 1983; Violle et al., 2007). The metabolome, in turn, informs on the diversity of metabolites synthesized when organisms interact with each other or face environmental harshness, potentially providing a more mechanistic understanding of how fitness, performance and function change with environment than the usual morphological traits (Walker et al., 2022). Therefore, the use of functionally analogous traits coined through a metabolic/energetic perspective (as also highlighted by Meunier et al., 2017) might provide the taxonomic breadth and the power of generalization that functional ecologists desire. However, positive or neutral species interactions, which are crucial to understand evolutionary outcomes in a long-term conservation perspective (Goldberg & Friedman, 2021), may be underestimated or neglected by metabolic-based approaches, and should be complemented by additional traits (e.g. symbiont dependency, known facilitation, complexity building).

Conservation and sustainable resource-use may also benefit from advances in functional cross-taxa research. Functional cross-taxa studies can reveal patterns of functional loss (Newbold et al., 2020), and help map functional hotspots in the geographic space by identifying areas that maintain functional rarity and distinctiveness across taxa (Loiseau et al., 2020; Waechter et al., 2021). By incorporating the abundance or biomass of organisms in functional cross-taxa research, one could measure the resistance and vulnerability of ecosystem functions that are maintained by multiple coexisting taxa with varied densities and life-history traits. This field can offer a unique perspective into the conservation and prioritization of ecosystem services, as these might be offered by taxa across disparate branches of the Tree of Life, or even by a single taxon, with differences in local abundance/ density patterns. Recent research about the potential of seafood resources (comprising various animal taxa) to nourish global nations showed that increasing diversity of harvested species might enable higher nutrient supply (Golden et al., 2021) and that, among fish, nutrient composition was highly variable across trophic groups (Robinson et al., 2022). Furthermore, the impacts of climate-driven regime shifts on ecosystems, from coral to algae-dominated reefs, might alter fish nutrient supply as this depends on functional diversity through potential compensatory mechanisms among species (Robinson et al., 2022; see also Heilpern

et al. (2021) for a single-taxon example in the Amazon). Changes in nutrient supply remain to be accessed across a broader range of taxa (e.g. fish, molluscs, crustaceans and mammals), which will soon be possible with the growing availability of nutritional content data for multiple taxa (e.g. FAO INFOODS).

Research crossing taxonomic barriers is a knowledge frontier in ecology (Capdevila et al., 2020; Junker et al., 2023; Weiss & Ray, 2019). To be treated as such, we invite the community of functional ecologists to explicitly declare their research as 'cross-taxa'. We saw that several cross-taxa contributions were published during and after the period embracing our literature search (e.g. Capdevila et al., 2020; Cooke et al., 2019; Newbold et al., 2020; Pimiento et al., 2020). However, these studies were not tracked in our systematic review because they did not declare themselves as 'cross-taxa' (or used searched terms) in article title, abstract or keywords, or because a formal framework for functional cross-taxa research was missing. This might largely stem from the lack of consensus on the 'cross-taxa' term in functional ecology. It is fundamental that functional cross-taxa research declares itself as belonging to this line of investigation. This would help this research area gain theoretical and empirical support, becoming increasingly useful for application in studies of ecosystem functioning, conservation, management, and restoration.

## 5 | CONCLUDING REMARKS

Our review aimed to encourage researchers in the field of functional ecology to move beyond single taxa and traits and integrate more branches and dimensions of the Tree of Life in their research. Functional ecology has moved fast to become a geographically and taxonomically comprehensive field of investigation. We conducted a systematic review of articles comprising multiple taxa published in the last 75 years, highlighting the predominance of a multi-taxa over a cross-taxa approach in the published research. We identified limitations to the use of a functional cross-taxa approach, its strengths and weaknesses. In doing so, we outlined questions that can be addressed using this approach in a bid to stimulate this field. We advocate that the term 'cross-taxa' should be used for research crossing significant taxonomic boundaries with integrative rather than comparative approaches. Although we provided a screening of applied solutions using available metrics, considerable advances will come from developing common ground of trait measurements beyond those that are already available. Linking easily measured traits (e.g. biochemical universal properties of organisms) to scalable metrics could allow the inclusion of any organism in the Tree of Life along a continuum using integrative approaches, as already done in single trait approaches (Brown et al., 2004) and recently extended to multiple trait approaches (Brandl et al., 2023; Enquist et al., 2015; Schiettekatte et al., 2022). Significant advances in functional cross-taxa research will come from working on the development of common metrics and traits to be applied across taxa.

## GLOSSARY

**Distantly related organisms:** The organisms used in a single study whose phylogenetic relatedness is above the family level.

**Effect traits:** Traits that impact ecosystem processes (e.g. primary productivity, litter decomposition) or affect other trophic levels, as in the case of predator–prey interactions or mutualistic relationships. These traits are considered ‘functional’ as they explain or predict organisms’ possible roles in overall ecosystem functioning (Lavorel & Garnier, 2002). An example of an effect trait is the content of nitrogen in the leaves, which will impact ecosystem productivity.

**Functional cross-taxa research:** Ecological research merging morphologically and/or ecologically similar traits, shared across distantly related organisms. This field enables exploring topics ranging from ecosystem properties to eco-evolutionary processes underlying trait patterns across co-existing taxa. Traits can be response or effect traits (Lavorel & Garnier, 2002).

**Functional hypervolume:** A quantitative multivariate representation of the main axes of trait variation across taxa based on the seminal ideas of Hutchinson (1957)—that is, the n-dimensional hypervolume that permeates the niche concept.

**Functional multitaxa research:** Research in functional ecology comparing, but not merging data, across multiple taxa.

**Functional redundancy:** A pattern where many species share similar functional traits, and therefore respond similarly to the environment and perform similar functional roles.

**Functionally analogous traits:** Functional traits with different ontogenetic origins across organisms that perform similar functions (Weiss & Ray, 2019). These could be response traits such as the wings of birds and the winged achenes of plants (representing dispersal ability), and effect traits such as jaw morphology of rodents and body size of ants (representing rates of seed predation).

**Resilience:** Emergent property of ecosystems depicting their ability to recover structure and function after disturbances.

**Resistance:** Emergent property of ecosystems depicting their ability to maintain structure and function under disturbances. Along with resilience, resistance is one of the dimensions of ecosystem stability, and both parameters are generally correlated with species richness and functional diversity at the community scale.

**Response traits:** Traits that control species distributions and responses to the environment. Response traits are functional when they affect an organism’s survival, growth and reproductive success (Lavorel & Garnier, 2002). Examples of response traits are leaf thickness and area, which respond to moisture and light gradients.

**Traits:** Measurable morphological, behavioural, and physiological attributes of individuals and species that determine their fitness (growth, reproduction and survival), performance and function (Arnold, 1983; Violle et al., 2007).

## AUTHOR CONTRIBUTIONS

André L. Luza, Guilherme O. Longo and Mariana G. Bender conceived this study. André L. Luza executed the literature survey, organized the framework for filtering, extracting and analysing data from the surveyed articles, and reviewed the collected data, wrote the first draft together with Mariana G. Bender and Guilherme O. Longo. André L. Luza, Cesar A. M. M. Cordeiro, Diego R. Barneche, Fernanda C. Silva, Juan P. Quimbayo, Vinicius J. Giglio, Thiago C. Mendes, Luiza Waechter, Vitor A. P. Picolotto, Mariana G. Bender and Guilherme O. Longo fully screened the selected articles, and collected information from them. All authors had a critical contribution to improve it through writing and suggestions of analyses. All authors also approved the final version to be published.

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## CONFLICT OF INTEREST STATEMENT

Diego R. Barneche is an associate editor of functional ecology, but took no part in the peer review and decision-making processes for this paper.


## DATA AVAILABILITY STATEMENT

All data and codes supporting this research are available on GitHub: ([https://github.com/Sinbiose-Reefs/wg\\_syn](https://github.com/Sinbiose-Reefs/wg_syn)) and Zenodo: <https://doi.org/10.5281/zenodo.8355903> (Luza et al., 2023).

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## REFERENCES

- Allen, A. P., Gillooly, J. F., & Brown, J. H. (2005). Linking the global carbon cycle to individual metabolism. *Functional Ecology*, *19*, 202–213. <https://doi.org/10.1111/j.1365-2435.2005.00952.x>
- Almeida-Neto, M., Guimarães, P., Guimarães, P. R., Jr., Loyola, R. D., & Ulrich, W. (2008). A consistent metric for nestedness analysis in ecological systems: Reconciling concept and measurement. *Oikos*, *117*, 1227–1239. <https://doi.org/10.1111/j.0030-1299.2008.16644.x>
- Anderegg, L. D. L., Berner, L. T., Badgley, G., Sethi, M. L., Law, B. E., & HilleRisLambers, J. (2018). Within-species patterns challenge our understanding of the leaf economics spectrum. *Ecology Letters*, *21*, 734–744. <https://doi.org/10.1111/ele.12945>
- Arnold, S. J. (1983). Morphology, performance and fitness. *American Zoologist*, *23*(2), 347–361. <https://doi.org/10.1093/icb/23.2.347>
- Aubin, I., Venier, L., Pearce, J., & Moretti, M. (2013). Can a trait-based multi-taxa approach improve our assessment of forest management impact on biodiversity? *Biodiversity and Conservation*, *22*, 2957–2975. <https://doi.org/10.1007/s10531-013-0565-6>
- Barros, C., Thuiller, W., Georges, D., Boulangeat, I., & Münkemüller, T. (2016). N-dimensional hypervolumes to study stability of complex ecosystems. *Ecology Letters*, *19*, 729–742. <https://doi.org/10.1111/ele.12617>
- Bastazini, V. A. G., Debastiani, V., Cappelatti, L., Guimarães, P., & Pillar, V. D. (2022). The role of evolutionary modes for trait-based cascades in mutualistic networks. *Ecological Modelling*, *470*, 109983. <https://doi.org/10.1016/j.ecolmodel.2022.109983>
- Beckett, S. J. (2016). Improved community detection in weighted bipartite networks. *Royal Society Open Science*, *3*, 140536.
- Bellwood, D. R., Streit, R. P., Brandl, S. J., & Tebbett, S. B. (2019). The meaning of the term ‘function’ in ecology: A coral reef perspective. *Functional Ecology*, *33*, 948–961. <https://doi.org/10.1111/1365-2435.13265>
- Bergmann, C. (1847). Über die Verhältnisse der Wärmeökonomie der Thiere zu ihrer Grösse. *Göttinger Studien*, *3*(1), 595–708.
- Bernard-Verdier, M., Navas, M.-L., Vellend, M., Violle, C., Fayolle, A., & Garnier, E. (2012). Community assembly along a soil depth gradient: Contrasting patterns of plant trait convergence and divergence in a Mediterranean rangeland. *Journal of Ecology*, *100*, 1422–1433. <https://doi.org/10.1111/1365-2745.12003>
- Blonder, B., Lamanna, C., Violle, C., & Enquist, B. J. (2014). The n-dimensional hypervolume. *Global Ecology and Biogeography*, *23*, 595–609. <https://doi.org/10.1111/geb.12146>
- Brandl, S. J., Lefcheck, J. S., Bates, A. E., Rasher, D. B., & Norin, T. (2023). Can metabolic traits explain animal community assembly and functioning? *Biological Reviews*, *98*, 1–18. <https://doi.org/10.1111/brv.12892>
- Brousseau, P.-M., Gravel, D., & Handa, I. T. (2019). On the development of a predictive functional trait approach for studying terrestrial arthropods. *Journal of Animal Ecology*, *87*, 1209–1220. <https://doi.org/10.1111/1365-2656.12834>
- Brown, J. H. (1984). On the relationship between abundance and distribution of species. *The American Naturalist*, *124*, 255–279.
- Brown, J. H., Gillooly, J. F., Allen, A. P., Savage, V. M., & West, G. B. (2004). Toward a metabolic theory of ecology. *Ecology*, *85*, 1771–1789. <https://doi.org/10.1890/03-9000>
- Brown, J. H., Grover, J. J., Davidson, D. W., & Lieberman, G. A. (1975). A preliminary study of seed predation in desert and montane habitats. *Ecology*, *56*(4), 987–992. <https://doi.org/10.2307/1936310>
- Brown, J. H., Hall, C. A. S., & Sibly, R. M. (2018). Equal fitness paradigm explained by a trade-off between generation time and energy production rate. *Nature Ecology & Evolution*, *2*, 262–268. <https://doi.org/10.1038/s41559-017-0430-1>
- Brown, J. H., & Nicoletto, P. F. (1991). Spatial scaling of species composition: Body masses of north american land mammals. *The American Naturalist*, *138*(6), 1478–1512.
- Brown, J. H., Reichman, O. J., & Davidson, D. W. (1979). Granivory in desert ecosystems. *Annual Review of Ecology and Systematics*, *10*, 201–227. <https://doi.org/10.1146/annurev.es.10.110179.001221>
- Butterfield, B. J., & Suding, K. N. (2013). Single-trait functional indices outperform multi-trait indices in linking environmental gradients and ecosystem services in a complex landscape. *Journal of Ecology*, *101*, 9–17. <https://doi.org/10.1111/1365-2745.12013>
- Cadotte, M. W., Carscadden, K. A., & Mirotchnick, N. (2011). Beyond species: Functional diversity and the maintenance of ecological processes and services. *Journal of Applied Ecology*, *48*, 1079–1087. <https://doi.org/10.1111/j.1365-2664.2011.02048.x>
- Cadotte, M. W., Livingstone, S. W., Yasui, S.-L. E., Dinnage, R., Li, J.-T., Marushia, R., Santangelo, J., & Shu, W. (2017). Explaining ecosystem multifunction with evolutionary models. *Ecology*, *98*, 3175–3187. <https://doi.org/10.1002/ecy.2045>
- Capdevila, P., Beger, M., Blomberg, S. P., Hereu, B., Linares, C., & Salguero-Gómez, R. (2020). Longevity, body dimension and reproductive mode drive differences in aquatic versus terrestrial life-history strategies. *Functional Ecology*, *34*, 1613–1625. <https://doi.org/10.1111/1365-2435.13604>
- Carlucci, M. B., Brancalion, P. H. S., Rodrigues, R. R., Loyola, R., & Cianciaruso, M. V. (2020). Functional traits and ecosystem services in ecological restoration. *Restoration Ecology*, *28*, 1372–1383. <https://doi.org/10.1111/rec.13279>
- Carmona, C. P., Tammé, R., Pärtel, M., de Bello, F., Brosse, S., Capdevila, P., González-M, R., González-Suárez, M., Salguero-Gómez, R., Vázquez-Valderrama, M., & Toussaint, A. (2021). Erosion of global functional diversity across the tree of life. *Science Advances*, *7*(13), eabf2675. <https://doi.org/10.1126/sciadv.abf2675>
- Carvalho, J. C., & Cardoso, P. (2020). Decomposing the causes for niche differentiation between species using hypervolumes. *Frontiers in Ecology and Evolution*, *8*, 243. <https://doi.org/10.3389/fevo.2020.00243>
- Cavender-Bares, J., Kozak, K. H., Fine, P. V., & Kembel, S. W. (2009). The merging of community ecology and phylogenetic biology. *Ecology Letters*, *12*(7), 693–715. <https://doi.org/10.1111/j.1461-0248.2009.01314.x>
- Cernansky, R. (2017). Biodiversity moves beyond counting species. *Nature*, *546*, 22–24. <https://doi.org/10.1038/546022a>
- Chacón-Labela, J., Hinojo-Hinojo, C., Bohner, T., Castorena, M., Violle, C., Vandvik, V., & Enquist, B. J. (2023). How to improve scaling from traits to ecosystem processes. *Trends in Ecology & Evolution*, *38*, 228–237. <https://doi.org/10.1016/j.tree.2022.10.007>
- Chamberlain, S., Zoecs, E., Foster, Z., Arendsee, Z., Boettiger, C., Ram, K., Bartomeus, I., Baumgartner, J., O'Donnell, J., Oksanen, J., Tzovaras, B. G., Marchand, P., Tran, V., Salmon, M., Li, G., & Grenié, M. (2020). *taxize: Taxonomic information from around the web*. R package version 0.9.98. <https://github.com/ropensci/taxize>
- Cianciaruso, M. V., Batalha, M. A., Gaston, K. J., & Petchey, O. L. (2009). Including intraspecific variability in functional diversity. *Ecology*, *90*(1), 81–89. <https://doi.org/10.1890/07-1864.1>



- Cooke, R. S. C., Eigenbrod, F., & Bates, A. E. (2019). Projected losses of global mammal and bird ecological strategies. *Nature Communications*, 10, 2279. <https://doi.org/10.1038/s41467-019-10284-z>
- Cornwell, W. K., Schilck, L. D., & Ackerly, D. D. (2006). A trait-based test for habitat filtering: Convex hull volume. *Ecology*, 87(6), 1465–1471. [https://doi.org/10.1890/0012-9658\(2006\)87\[1465:ATTFH\]2.0.CO;2](https://doi.org/10.1890/0012-9658(2006)87[1465:ATTFH]2.0.CO;2)
- Csardi, G., & Nepusz, T. (2006). The igraph software package for complex network research. *InterJournal, Complex Systems*, 1695, 1–9. <https://cran.r-project.org/web/packages/igraph/citation.html>
- De Esteban-Trivigno, S. (2011). Ecomorphology of extinct xenarthrans: With analysis of the mandible using geometric morphometrics methods. *Ameghiniana*, 48(3), 381–398. <https://www.ameghiniana.org.ar/index.php/ameghiniana/article/view/269>
- Debastiani, V. J. (2021). *dae: Data analysis for ecology and evolution*. R package version 0.1.7.
- Díaz, S., & Cabido, M. (2001). Vive la difference: Plant functional diversity matters to ecosystem processes. *Trends in Ecology & Evolution*, 16, 646–655. [https://doi.org/10.1016/S0169-5347\(01\)02283-2](https://doi.org/10.1016/S0169-5347(01)02283-2)
- Díaz, S., Kattge, J., Cornelissen, J., Wright, I. J., Lavorel, S., Dray, S., Reu, B., Kleyer, M., Wirth, C., Prentice, I. C., Garnier, E., Bönisch, G., Westoby, M., Poorter, H., Reich, P. B., Moles, A. T., Dickie, J., Gillison, A. N., Zanne, A. E., ... Gorné, L. D. (2016). The global spectrum of plant form and function. *Nature*, 529, 167–171. <https://doi.org/10.1038/nature16489>
- Eklöf, A., Jacob, U., Kopp, J., Bosch, J., Castro-Urgal, R., Chacoff, N. P., Dalsgaard, B., de Sassi, C., Galetti, M., Guimarães, P. R., Lomáscolo, S. B., González, A. M. M., Pizo, M. A., Rader, R., Rodrigo, A., Tylianakis, J. M., Vázquez, D. P., & Allesina, S. (2013). The dimensionality of ecological networks. *Ecology Letters*, 16, 577–583. <https://doi.org/10.1111/ele.12081>
- Elton, C. (1927). *Animal ecology*. The University of Chicago Press. ISBN 0-226-20639-4.
- Enquist, B. J., Norberg, J., Bonser, S. P., Violle, C., Webb, C. T., Henderson, A., Sloat, L. L., & Savage, V. M. (2015). Scaling from traits to ecosystems: Developing a general trait driver theory via integrating trait-based and metabolic scaling theories. In S. Pawar, G. Woodward, & A. I. Dell (Eds.), *Trait-based ecology—From structure to function* (pp. 249–318). Academic Press.
- Floeter, S. R., Bender, M. G., Siqueira, A. C., & Cowman, P. F. (2018). Phylogenetic perspectives on reef fish functional traits. *Biological Reviews*, 93, 131–151. <https://doi.org/10.1111/brv.12336>
- Flynn, D. F. B., Gogol-Prokurat, M., Nogeire, T., Molinari, N., Richers, B. T., Lin, B. B., Simpson, N., Mayfield, M. M., & DeClerck, F. (2009). Loss of functional diversity under land use intensification across multiple taxa. *Ecology Letters*, 12, 22–33. <https://doi.org/10.1111/j.1461-0248.2008.01255.x>
- Garnier, E., Cortez, J., Billès, G., Navas, M.-L., Roumet, C., Debussche, M., Laurent, G., Blanchard, A., Aubry, D., Bellmann, A., Neill, C., & Toussaint, J.-P. (2004). Plant functional markers capture ecosystem properties during secondary succession. *Ecology*, 85, 2630–2637. <https://doi.org/10.1890/03-0799>
- Gaston, K. (2000). Global patterns in biodiversity. *Nature*, 405, 220–227. <https://doi.org/10.1038/35012228>
- Goldberg, Y., & Friedman, J. (2021). Positive interactions within and between populations decrease the likelihood of evolutionary rescue. *PLoS Computational Biology*, 17(2), e1008732. <https://doi.org/10.1371/journal.pcbi.1008732>
- Golden, C. D., Koehn, J. Z., Shepon, A., Passarelli, S., Free, C. M., Viana, D. F., Matthey, H., Eurich, J. G., Gephart, J. A., Fluet-Chouinard, E., Nyboer, E. A., Lynch, A. J., Kjelleve, M., Bromage, S., Charlebois, P., Barange, M., Vannuccini, S., Cao, L., Kleisner, K. M., ... Thilsted, S. (2021). Aquatic foods to nourish nations. *Nature*, 598, 315–320. <https://doi.org/10.1038/s41586-021-03917-1>
- Gomes, L. C., Dias, R. M., Ruaro, R., & Benedito, R. (2023). Functional diversity: A review on freshwater fish research. *Neotropical Ichthyology*, 21(2), 1–16. <https://doi.org/10.1590/1982-0224-2023-0022>
- Green, S. J., Brookson, C. B., Hardy, N. A., & Crowder, L. B. (2022). Trait-based approaches to global change ecology: Moving from description to prediction. *Proceeding of the Royal Society B: Biological Sciences*, 289, 20220071. <https://doi.org/10.1098/rspb.2022.0071>
- Gwinn, D. C., Middleton, J. A., Beesley, L., Close, P., Quinton, B., Storer, T., & Davies, P. M. (2018). Hierarchical multi-taxa models inform riparian vs. hydrologic restoration of urban streams in a permeable landscape. *Ecological Applications*, 28, 385–397. <https://doi.org/10.1002/eap.1654>
- Hadj-Hammou, J., Mouillot, D., & Graham, N. A. J. (2021). Response and effect traits of coral reef fish. *Frontiers in Marine Science*, 8, 640619. <https://doi.org/10.3389/fmars.2021.640619/full>
- Hadly, E. A., Spaeth, P. A., & Li, C. (2009). Niche conservatism above the species level. *Proceedings of the National Academy of Sciences of the United States of America*, 106(2), 19707–19714. <https://doi.org/10.1073/pnas.0901648106>
- Hardy, O. J., Couteron, P., Munoz, F., Ramesh, B. R., & Pélissier, R. (2012). Phylogenetic turnover in tropical tree communities: Impact of environmental filtering, biogeography and mesoclimatic niche conservatism. *Global Ecology and Biogeography*, 21, 1007–1016. <https://doi.org/10.1111/j.1466-8238.2011.00742.x>
- Hawkins, B. A., Field, R., Cornell, H. V., Currie, D. J., Guégan, J., Kaufman, D. M., Kerr, J. T., Mittelbach, G. G., Oberdorff, T., O'Brien, E. M., Porter, E. E., & Turner, J. R. G. (2003). Energy, water, and broad-scale geographic patterns of species richness. *Ecology*, 84, 3105–3117. <https://doi.org/10.1890/03-8006>
- Healy, K., Ezard, T. H. G., Jones, O. R., Salguero-Gómez, R., & Buckley, Y. M. (2019). Animal life history is shaped by the pace of life and the distribution of age-specific mortality and reproduction. *Nature Ecology & Evolution*, 3, 1217–1224. <https://doi.org/10.1038/s41559-019-0938-7>
- Heilpern, S. A., Defries, R., Fiorella, K., Flecker, A., Sethi, S. A., Uriarte, M., & Naeem, S. (2021). Declining diversity of wild-caught species puts dietary nutrient supplies at risk. *Science*, 7(22), eabf9967. <https://doi.org/10.1126/sciadv.abf9967>
- Heino, J., Schmera, D., & Erös, T. (2013). A macroecological perspective of trait patterns in stream communities. *Freshwater Biology*, 58, 1539–1555. <https://doi.org/10.1111/fwb.12164>
- Heino, J., Tolonen, K. T., Kotanen, J., & Paasivirta, L. (2009). Indicator groups and congruence of assemblage similarity, species richness and environmental relationships in littoral macroinvertebrates. *Biodiversity and Conservation*, 18, 3085–3098. <https://doi.org/10.1007/s10531-009-9626-2>
- Hurwitz, B., Brum, J., & Sullivan, M. (2015). Depth-stratified functional and taxonomic niche specialization in the 'core' and 'flexible' Pacific Ocean Virome. *The ISME Journal*, 9, 472–484. <https://doi.org/10.1038/ismej.2014.143>
- Hutchinson, G. (1957). Concluding remarks. *Cold Spring Harbor Symposia on Quantitative Biology*, 22, 415–427.
- Inagaki, K. Y., Mendes, T. C., Quimbayo, J. P., Cantor, M., & Sazima, I. (2020). The structure of fish follower-feeding associations at three oceanic islands in southwestern Atlantic. *Environmental Biology of Fishes*, 103, 1–11. <https://doi.org/10.1007/s10641-019-00924-0>
- Junker, R. R., Albrecht, J., Becker, M., Keuth, R., Farwig, N., & Schleuning, M. (2023). Towards an animal economics spectrum for ecosystem research. *Functional Ecology*, 37, 57–72. <https://doi.org/10.1111/1365-2435.14051>
- Kattge, J., Bönisch, G., Díaz, S., Lavorel, S., Prentice, I. C., Leadley, P., Tautenhahn, S., Werner, G. D. A., Aakala, T., Abedi, M., Acosta, A. T. R., Adamidis, G. C., Adamson, K., Aiba, M., Albert, C. H., Alcántara, J. M., Alcázar, C. C., Aleixo, I., Ali, H., ... Wirth, C. (2020). TRY plant trait database—Enhanced coverage and open access. *Global Change Biology*, 26, 119–188. <https://doi.org/10.1111/gcb.14904>
- Kellner, K. F., Duchamp, J. E., & Swihart, R. K. (2019). Niche breadth and vertebrate sensitivity to habitat modification: Signals from multiple

- taxa across replicated landscapes. *Biodiversity and Conservation*, 28, 2647–2667. <https://doi.org/10.1007/s10531-019-01785-w>
- Kelt, D. A., Meserve, P. L., & Gutiérrez, J. R. (2004). Seed removal by small mammals, birds and ants in semi-arid Chile, and comparison with other systems. *Journal of Biogeography*, 31(6), 931–942. <https://doi.org/10.1111/j.1365-2699.2004.01045.x>
- Konno, K., Akaska, M., Koshida, C., Katayama, N., Osada, N., Spake, R., & Amano, T. (2020). Ignoring non-English-language studies may bias ecological meta-analyses. *Ecology and Evolution*, 10(13), 6373–6384. <https://doi.org/10.1002/ece3.6368>
- Kraft, N. J. B., Godoy, O., & Levine, J. M. (2015). Plant functional traits and the multidimensional nature of species coexistence. *Proceedings of the National Academy of Sciences of the United States of America*, 112(3), 797–802. <https://doi.org/10.1073/pnas.1413650112>
- Lavorel, S., & Garnier, E. (2002). Predicting changes in community composition and ecosystem functioning from plant traits: Revisiting the holy grail. *Functional Ecology*, 16, 545–556. <https://doi.org/10.1046/j.1365-2435.2002.00664.x>
- Lefcheck, J., Bastazini, V., & Griffin, J. (2015). Choosing and using multiple traits in functional diversity research. *Environmental Conservation*, 42(2), 104–107. <https://doi.org/10.1017/S0376892914000307>
- Lessard, J.-P., Belmaker, J., Myers, J. A., Chase, J. M., & Rahbek, C. (2012). Inferring local ecological processes amid species pool influences. *Trends in Ecology & Evolution*, 27(11), 600–607. <https://doi.org/10.1016/j.tree.2012.07.006>
- Liberati, A., Altman, D. G., Tetzlaff, J., Mulrow, C., Gøtzsche, P. C., Ioannidis, J. P. A., Clarke, M., Devereaux, P. J., Kleijnen, J., & Moher, D. (2009). The PRISMA statement for reporting systematic reviews and meta-analyses of studies that evaluate health care interventions: Explanation and elaboration. *PLoS Medicine*, 6(7), e1000100. <https://doi.org/10.1371/journal.pmed.1000100>
- Loiseau, N., Mouquet, N., Casajus, N., Grenié, M., Guéguen, M., Maitner, B., Mouillot, D., Ostling, A., Renaud, J., Tucker, C., Velez, L., Thuiller, W., & Violle, C. (2020). Global distribution and conservation status of ecologically rare mammal and bird species. *Nature Communications*, 11, 5071. <https://doi.org/10.1038/s41467-020-18779-w>
- Luza, A. L., Barneche, D. R., Cordeiro, C. A. M. M., Dambros, C. S., Ferreira, C. E. L., Floeter, S. R., Giglio, V. J., Luiz, O. J., Mendes, T. C., Picolotto, V. A. P., Quimbayo, J. P., Silva, F. C., Longo, G. O., & Bender, M. G. (2023). Data from: Going across taxa in functional ecology: Review and perspectives of an emerging field (v1.0.0). *Zenodo* <https://doi.org/10.5281/zenodo.8355903>
- MacLean, S. A., & Beissinger, S. R. (2017). Species' traits as predictors of range shifts under contemporary climate change: A review and meta-analysis. *Global Change Biology*, 23, 4094–4105. <https://doi.org/10.1111/gcb.13736>
- Madin, J. S., Anderson, K., Andreason, M., Bridge, T. C. L., Cairns, S., Connolly, S. R., Darling, E. S., Diaz, M., Falster, D., Franklin, E. C., Gates, R. D., Hoogenboom, M. O., Huang, D., Keith, S. A., Kosnik, M., Kuo, C.-Y., Lough, J. M., Lovelock, C. E., Luiz, O., ... Baird, A. H. (2016). The coral trait database, a curated database of trait information for coral species from the global oceans. *Scientific Data*, 3, 160012. <https://doi.org/10.1038/sdata.2016.17>
- Madin, J. S., Hoogenboom, M. O., Connolly, S. R., Darling, E. S., Falster, D. S., Huang, D., Keith, S. A., Mizerek, T., Pandolfi, J. M., Putnam, H. M., & Baird, A. H. (2016). A trait-based approach to advance coral reef science. *Trends in Ecology & Evolution*, 31(6), 419–428.
- Magg, N., Ballenthien, E., & Braunisch, V. (2019). Faunal surrogates for forest species conservation: A systematic niche-based approach. *Ecological Indicators*, 102, 65–75. <https://doi.org/10.1016/j.ecoli.2019.01.084>
- Mammola, S., & Cardoso, P. (2020). Functional diversity metrics using kernel density n-dimensional hypervolumes. *Methods in Ecology and Evolution*, 11, 986–995. <https://doi.org/10.1111/2041-210X.13424>
- Margalef, R. (1963). On certain unifying principles in ecology. *The American Naturalist*, 97(897), 357–374. <http://www.jstor.org/stable/2459227>
- Marshall, D. J., & White, C. R. (2019). Have we outgrown the existing models of growth? *Trends in Ecology & Evolution*, 34(2), 102–111. <https://doi.org/10.1016/j.tree.2018.10.005>
- Martini, S., Larras, F., Boyé, A., Faure, E., Aberle, N., Archambault, P., Bacouillard, L., Beisner, B. E., Bittner, L., Castella, E., Danger, M., Gauthier, O., Karp-Boss, L., Lombard, F., Maps, F., Stemmann, L., Thiébaud, E., Usseglio-Polatera, P., Vogt, M., ... Ayata, S.-D. (2021). Functional trait-based approaches as a common framework for aquatic ecologists. *Limnology and Oceanography*, 66, 965–994. <https://doi.org/10.1002/lno.11655>
- McFadden, I. R., Fritz, S. A., Zimmermann, N. E., Pellissier, L., Kissling, W. D., Tobias, J. A., Schleuning, M., & Graham, C. H. (2022). Global plant-frugivore trait matching is shaped by climate and biogeographic history. *Ecology Letters*, 25, 686–696. <https://doi.org/10.1111/ele.13890>
- McGill, B. J., Enquist, B. J., Weiher, E., & Westoby, M. (2006). Rebuilding community ecology from functional traits. *Trends in Ecology & Evolution*, 21(4), 178–185. <https://doi.org/10.1016/j.tree.2006.02.002>
- McGill, B. J., Etienne, R. S., Gray, J. S., Alonso, D., Anderson, M. J., Benecha, H. K., Dornelas, M., Enquist, B. J., Green, J. L., He, F., Hurlbert, A. H., Magurran, A. E., Marquet, P. A., Maurer, B. A., Ostling, A., Soykan, C. U., Ugland, K. I., & White, E. P. (2007). Species abundance distributions: Moving beyond single prediction theories to integration within an ecological framework. *Ecology Letters*, 10, 995–1015. <https://doi.org/10.1111/j.1461-0248.2007.01094.x>
- Meunier, C. L., Boersma, M., El-Sabaawi, R., Halvorson, H. M., Herstoff, E. M., Van de Waal, D. B., Vogt, R. J., & Litchman, E. (2017). From elements to function: Toward unifying ecological stoichiometry and trait-based ecology. *Frontiers in Environmental Science*, 5, Article 18. <https://doi.org/10.3389/fenvs.2017.00018>
- Miatta, M., Bates, A. E., & Snelgrove, P. V. R. (2021). Incorporating biological traits into conservation strategies. *Annual Review of Marine Science*, 13, 421–443. <https://doi.org/10.1146/annurev-marine-032320-094121>
- Moretti, M., & Legg, C. (2009). Combining plant and animal traits to assess community functional responses to disturbance. *Ecography*, 32(2), 299–309. <https://doi.org/10.1111/j.1600-0587.2008.05524.x>
- Mori, A. S., Shiono, T., Haraguchi, T. F., Ota, A. T., Koide, D., Ohgue, T., Kitagawa, R., Maeshiro, R., Aung, T. T., Nakamori, T., Hagiwara, Y., Matsuoka, S., Ikeda, A., Hishi, T., Hobara, S., Mizumachi, E., Frisch, A., Thor, G., Fujii, S., ... Gustafsson, L. (2015). Functional redundancy of multiple forest taxa along an elevational gradient: Predicting the consequences of non-random species loss. *Journal of Biogeography*, 42, 1383–1396. <https://doi.org/10.1111/jbi.12514>
- Mouillot, D., Graham, N. A. J., Villéger, S., Mason, N. W. H., & Bellwood, D. R. (2013). A functional approach reveals community responses to disturbances. *Trends in Ecology & Evolution*, 28(3), 167–177. <https://doi.org/10.1016/j.tree.2012.10.004>
- Mouillot, D., Villéger, S., Parravicini, V., Kulbicki, M., Arias-González, J. E., Bender, M., Chabanet, P., Floeter, S. R., Friedlander, A., Vigliola, L., & Bellwood, D. R. (2014). Functional over-redundancy and high functional vulnerability in global fish faunas on tropical reefs. *Proceedings of the National Academy of Sciences of the United States of America*, 111(38), 13757–13762. <https://doi.org/10.1073/pnas.1317625111>
- Murray, B. D., Holland, J. D., Summerville, K. S., Dunning, J. B., Jr., Saunders, M. R., & Jenkins, M. A. (2017). Functional diversity response to hardwood forest management varies across taxa and spatial scales. *Ecological Applications*, 27, 1064–1081. <https://doi.org/10.1002/eap.1532>

- Nagy, D. D., Magura, T., Horváth, R., Debnár, Z., & Tóthmérész, B. (2018). Arthropod assemblages and functional responses along an urbanization gradient: A trait-based multi-taxa approach. *Urban Forestry & Urban Greening*, 30, 157–168. <https://doi.org/10.1016/j.ufug.2018.01.002>
- Newbold, T., Bentley, L. F., Hill, S. L. L., Edgar, M. J., Horton, M., Su, G., Şekerçioğlu, Ç. H., Collen, B., & Purvis, A. (2020). Global effects of land use on biodiversity differ among functional groups. *Functional Ecology*, 34, 684–693. <https://doi.org/10.1111/1365-2435.13500>
- Newman, M. E. J. (2006). Modularity and community structure in networks. *Proceedings of the National Academy of Sciences of the United States of America*, 103(23), 8577–8582. <https://doi.org/10.1073/pnas.0601602103>
- Oksanen, J., Blanchet, F. G., Friendly, M., Kindt, R., Legendre, P., McGlenn, D., Minchin, P. R., O'Hara, R. B., Simpson, G. L., Solymos, P., Stevens, M. H. H., Szoecs, E., & Wagner, H. (2020). *vegan: Community ecology package*. R package version 2.5-7. <https://CRAN.R-project.org/package=vegan>
- Ortiz-Álvarez, R., Fierer, N., de Los Ríos, A., Casamayor, E. O., & Barberán, A. (2018). Consistent changes in the taxonomic structure and functional attributes of bacterial communities during primary succession. *The ISME Journal*, 12(7), 1658–1667. <https://doi.org/10.1038/s41396-018-0076-2>
- Petchey, O. L., & Gaston, K. J. (2006). Functional diversity: Back to basics and looking forward. *Ecology Letters*, 9, 741–758. <https://doi.org/10.1111/j.1461-0248.2006.00924.x>
- Pianka, E. R. (1970). On r-and K-selection. *The American Naturalist*, 104, 592–597. <https://doi.org/10.1086/282697>
- Pimiento, C., Leprieur, F., Lefcheck, J. S., Albouy, C., Rasher, D. B., Davis, M., Svenning, J.-C., & Griffin, J. N. (2020). Functional diversity of marine megafauna in the Anthropocene. *Science Advances*, 6, eaay7650. <https://doi.org/10.1126/sciadv.aay7650>
- Pinsky, M. L., Comte, L., & Sax, D. F. (2022). Unifying climate change biology across realms and taxa. *Trends in Ecology & Evolution*, 37(8), 672–682. <https://doi.org/10.1016/j.tree.2022.04.011>
- Preston, F. W. (1948). The commonness, and rarity, of species. *Ecology*, 29, 254–283. <https://doi.org/10.2307/1930989>
- Quimbayo, J. P., Schlickmann, O. R. C., Floeter, S. R., & Sazima, I. (2018). Cleaning interactions at the southern limit of tropical reef fishes in the Western Atlantic. *Environmental Biology of Fishes*, 101, 1195–1204. <https://doi.org/10.1007/s10641-018-0768-5>
- Quimbayo, J. P., Silva, F. C., Mendes, T. C., Ferrari, D. S., Danielski, S. L., Bender, M. G., Parravicini, V., Kulbicki, M., & Floeter, S. R. (2021). Life-history traits, geographical range, and conservation aspects of reef fishes from the Atlantic and Eastern Pacific. *Ecology*, 102(5), e03298. <https://doi.org/10.1002/ecy.3298>
- R Core Team. (2021). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing. <https://www.R-project.org/>
- Renner, S. C., Suarez-Rubio, M., Kaiser, S., Nieschulze, J., Kalko, E. K. V., Tschapka, M., & Jung, K. (2018). Divergent response to forest structure of two mobile vertebrate groups. *Forest Ecology and Management*, 415–416, 129–138. <https://doi.org/10.1016/j.foreco.2018.02.028>
- Revell, L. J. (2012). phytools: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution*, 3, 217–223. <https://doi.org/10.1111/j.2041-210X.2011.00169.x>
- Robinson, J. P. W., Maire, E., Bodin, N., Hempson, T. N., Graham, N. A. J., Wilson, S. K., MacNeil, M. A., & Hicks, C. C. (2022). Climate-induced increases in micronutrient availability for coral reef fisheries. *One Earth*, 5(1), 98–108. <https://doi.org/10.1016/j.oneear.2021.12.005>. PMID: 35128392; PMCID: PMC8791602.
- Ruggiero, M. A., Gordon, D. P., Orrell, T. M., Bailly, N., Bourgoin, T., Brusca, R. C., Cavalier-Smith, T., Guiry, M. D., & Kirk, P. M. (2015). A higher level classification of all living organisms. *PLoS ONE*, 10(4), e0119248. <https://doi.org/10.1371/journal.pone.0119248>
- Ruthrof, K. X., Breshears, D. D., Fontaine, J. B., Froend, R. H., Matusick, G., Kala, J., Miller, B. P., Mitchell, P. J., Wilson, S. K., van Keulen, M., Enright, N. J., Law, D. J., Wernberg, T., & Hardy, G. E. S. J. (2018). Subcontinental heat wave triggers terrestrial and marine, multi-taxa responses. *Scientific Reports*, 8, 13094. <https://doi.org/10.1038/s41598-018-31236-5>
- Ryznar, E. R., Fong, P., & Fong, C. R. (2021). When form does not predict function: Empirical evidence violates functional form hypotheses for marine macroalgae. *Journal of Ecology*, 109, 833–846. <https://doi.org/10.1111/1365-2745.13509>
- Saba, S. L., & Toyos, A. (2003). Seed removal by birds, rodents and ants in the austral portion of the Monte Desert, Argentina. *Journal of Arid Environments*, 53, 115–124. <https://doi.org/10.1006/jare.2002.1029>
- Schiettekatte, N. M., Brandl, S. J., Casey, J. M., Graham, N. A., Barneche, D. R., Burkepille, D. E., Allgeier, J. E., Arias-González, J. E., Edgar, G. J., Ferreira, C. E., Floeter, S. R., Friedlander, A. M., Green, A. L., Kulbicki, M., Letourneur, Y., Luiz, O. J., Mercière, A., Morat, F., Munsterman, K. S., ... Parravicini, V. (2022). Biological trade-offs underpin coral reef ecosystem functioning. *Nature Ecology & Evolution*, 6(6), 701–708. <https://doi.org/10.1038/s41559-022-01710-5>
- Schleuning, M., García, D., & Tobias, J. A. (2023). Animal functional traits: Towards a trait-based ecology for whole ecosystems. *Functional Ecology*, 37, 4–12. <https://doi.org/10.1111/1365-2435.14246>
- Schmera, D., Heino, J., Podani, J., Éros, T., & Dolédec, S. (2017). Functional diversity: A review of methodology and current knowledge in freshwater macroinvertebrate research. *Hydrobiologia*, 787, 27–44. <https://doi.org/10.1007/s10750-016-2974-5>
- Schramski, J. R., Dell, A. I., Grady, J. M., Sibly, R. M., & Brown, J. H. (2015). Metabolic theory predicts whole-ecosystem properties. *Proceedings of the National Academy of Sciences of the United States of America*, 112, 2617–2622. <https://doi.org/10.1073/pnas.1423502112>
- Siqueira, A. C., Morais, R. A., Bellwood, D. R., & Cowman, P. F. (2020). Trophic innovations fuel reef fish diversification. *Nature Communications*, 11, 2669. <https://doi.org/10.1038/s41467-020-16498-w>
- Spaniol, R. L., Mendonça, M. D. S., Hartz, S. M., Iserhard, C. A., & Stevens, M. (2020). Discolouring the Amazon rainforest: How deforestation is affecting butterfly coloration. *Biodiversity and Conservation*, 29, 2821–2838. <https://doi.org/10.1007/s10531-020-01999-3>
- Streit, R. P., & Bellwood, D. R. (2022). To harness traits for ecology, let's abandon 'functionality'. *Trends in Ecology & Evolution*, 38, 402–411. <https://doi.org/10.1016/j.tree.2022.11.009>
- Thorn, S., Chao, A., Bernhardt-Römermann, M., Chen, Y. H., Georgiev, K. B., Heibl, C., Müller, J., Schäfer, H., & Bässler, C. (2020). Rare species, functional groups, and evolutionary lineages drive successional trajectories in disturbed forests. *Ecology*, 101(3), e02949. <https://doi.org/10.1002/ecy.2949>
- Tobias, J. A., Sheard, C., Pigot, A. L., Devenish, A. J. M., Yang, J., Sayol, F., Neate-Clegg, M. H. C., Alioravainen, N., Weeks, T. L., Barber, R. A., Walkden, P. A., MacGregor, H. E. A., Jones, S. E. I., Vincent, C., Phillips, A. G., Marples, N. M., Montaña-Centellas, F. A., Leandro-Silva, V., Claramunt, S., ... Schleuning, M. (2022). AVONET: Morphological, ecological and geographical data for all birds. *Ecology Letters*, 25, 581–597. <https://doi.org/10.1111/ele.13898>
- Villéger, S., Mason, N. W. H., & Mouillot, D. (2008). New multidimensional functional diversity indices for a multifaceted framework in functional ecology. *Ecology*, 89, 2290–2301. <https://doi.org/10.1890/07-1206.1>
- Violle, C., Navas, M.-L., Vile, D., Kazakou, E., Fortunel, C., Hummel, I., & Garnier, E. (2007). Let the concept of trait be functional! *Oikos*, 116, 882–892. <https://doi.org/10.1111/j.0030-1299.2007.15559.x>
- Waechter, L. S., Luiz, O. J., Leprieur, F., & Bender, M. G. (2021). Functional biogeography of marine vertebrates in Atlantic Ocean reefs.

*Diversity and Distributions*, 24, 1–14. <https://doi.org/10.1111/ddi.13430>

- Walker, T. W. N., Alexander, J. M., Allard, P.-M., Baines, O., Baldy, V., Bardgett, R. D., Capdevila, P., Coley, P. D., David, B., Defosse, E., Endara, M.-J., Ernst, M., Fernandez, C., Forrister, D., Gargallo-Garriga, A., Jassey, V. E. J., Marr, S., Neumann, S., Pellissier, L., ... Salguero-Gómez, R. (2022). Functional traits 2.0: The power of the metabolome for ecology. *Journal of Ecology*, 110, 4–20. <https://doi.org/10.1111/1365-2745.13826>
- Webb, C. O., Ackerly, D. D., McPeck, M. A., & Donoghue, M. J. (2002). Phylogenies and community ecology. *Annual Review of Ecology and Systematics*, 33(1), 475–505. <https://doi.org/10.1146/annurev.ecolsys.33.010802.150448>
- Weiss, K. C. B., & Ray, C. A. (2019). Unifying functional trait approaches to understand the assemblage of ecological communities: Synthesizing taxonomic divides. *Ecography*, 42, 2012–2020. <https://doi.org/10.1111/ecog.04387>
- Wiens, J. J., & Graham, C. H. (2005). Niche conservatism: Integrating evolution, ecology, and conservation biology. *Annual Review of Ecology, Evolution, and Systematics*, 36(1), 519–539. <https://doi.org/10.1146/annurev.ecolsys.36.102803.095431>
- Wong, M. K. L., Guénard, B., & Lewis, O. T. (2019). Trait-based ecology of terrestrial arthropods. *Biological Reviews of the Cambridge Philosophical Society*, 94(3), 999–1022. <https://doi.org/10.1111/brv.12488>. Epub 2018 Dec 13. PMID: 30548743; PMCID: PMC6849530.
- Wood, S. N. (2011). Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. *Journal of the Royal Statistical Society (B)*, 73(1), 3–36. <https://doi.org/10.1111/j.1467-9868.2010.00749.x>
- Wüest, R. O., Münkemüller, T., Lavergne, S., Pollock, L. J., & Thuiller, W. (2018). Integrating correlation between traits improves spatial predictions of plant functional composition. *Oikos*, 127, 472–481. <https://doi.org/10.1111/oik.04420>
- Xu, J., García Molinos, J., Su, G., Su, G., Matsuzaki, S.-I. S., Akasaka, M., Zhang, H., & Heino, J. (2019). Cross-taxon congruence of multiple diversity facets of freshwater assemblages is determined by large-scale processes across China. *Freshwater Biology*, 64, 1492–1503. <https://doi.org/10.1111/fwb.13322>

## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

**Table S1.1.** Questionnaire applied in the initial filtering phase (Figure. S1.1). We describe the inclusion and exclusion criterion for each question.

**Table S1.2.** Complete set of descriptors collected in the surveyed articles.

**Table S1.3.** Full list of references ( $n=96$ ) assessed in this review.

**Table S1.4.** List of terms included in the 12 trait types used in this study. All these terms were mentioned by the authors that screened the articles (see the section of authors' contribution).

**Figure S1.1.** PRISMA workflow showing the number of articles included and excluded along the systematic review process. The literature survey was conducted on Web of Science, on 08-06-2020.

**Figure S1.2.** Connection between pairs of taxa among studies. The interaction strength (links) represents the number of articles (shown in the legend) per pair of taxa.

**Figure S1.3.** Deviations of the observed modularity (vertical dashed line) relative to random modularity (density) produced by 100 runs of the “vaznull” null model.

**Figure S1.4.** Modules in the meta-network of taxa grouped by their studies. The empty spaces show prohibited links between taxa, or the lack of studies according to the reviewed research. The colors indicate the number of studies per taxa combination.

**Figure S1.5.** The relationship between the number of different taxonomic ranks and the number of traits per study (A), and the relationship between the mean pairwise taxonomic distance (MPD) between taxa and the number of traits per study (B).

**Figure S1.6.** Trade-off between the number of trait types and the number of taxonomic ranks per study (left) and the mean pairwise phylogenetic distance (MPD) between taxa (right) in the surveyed research.

**Figure S1.7.** Trade-off between the number of trait types and the number of taxonomic ranks per study (left) and the mean pairwise phylogenetic distance (MPD) between taxa (right) in the surveyed research.

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