The hidden dimensions of biodiversity

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Abstract

Uncovering and describing biodiversity is fundamental to advancing both scientific understanding and public awareness of nature. While many biodiversity facets are visible and even in the spotlight, including those biodiversity features we encounter on a daily basis, much of the world's biodiversity remains hidden. This review addresses the critical questions: What dimensions constitute hidden biodiversity? Why does such a large fraction remain hidden, and what factors contribute to these knowledge gaps? Moreover, why is it important to unveil these hidden facets? To address these questions, we (i) dissect the various dimensions of hidden biodiversity, including the taxonomic, spatio-temporal, genetic, functional, social, and methodological dimensions, and (ii) identify prevalent knowledge gaps. Moreover, we (iii) highlight possible ways forward on how to deal with hidden biodiversity, and (iv) conclude with the proposal of guiding principles to shape future research in this field.

Key words: taxonomic, functional, genetic, social, methodological, spatio-temporal, bias

Contents

I. Introduction

Biodiversity refers to the variety and variability of life on Earth, encompassing genetic, species, community, and ecosystem-level diversity. We have gained an impressive knowledge of taxonomic diversity, yet we have to acknowledge that this amounts to an estimated share of merely 10 % of the total richness (Leibniz Research Network Biodiversity 2024; Larsen *et al.*, 2017; Johnson *et al.*, 2016; Eisenhauer, Bonn & Guerra, 2019) or even significantly less (Overmann, Abt & Sikorski, 2017). New species are constantly being described (with daily updates available at https://tb.plazi.org/GgServer/static/newToday.html or https://lpsn.dsmz.de/), especially in some understudied taxonomic groups, often referred to as "dark taxa" with e.g. about 1,000 new prokaryotic species being discovered per year (Parte *et al.*, 2020; https://lpsn.dsmz.de/statistics/figure/15). Given that the vast majority of biodiversity remains "hidden", an important question arises: how do we define hidden biodiversity, and for whom is it concealed? Here, we define hidden biodiversity as either (i) unknown biodiversity that we have yet to uncover, or (ii) known biodiversity that is underexplored or understudied despite its documented presence (Lindken *et al.*, 2024).

The general perception is that the hiddenness of a given species is often linked to its body size, i.e. smaller organisms such as microbes, insects, and even small mammals may be often overlooked. Yet, there are notable exceptions to this rule, even to the extent that the public's scientific knowledge about a particular small-sized organism might be better studied than many large-bodied ones. For instance, the common ladybug (*Coccinella septempunctata*), the common tick (*Ixodes ricinus*), or even deep-sea tardigrades of the genus *Coronarctus* may be well known to the public, and even better studied than large freshwater organisms, such as the redtail catfish (*Phractocephalus hemiliopterus*), Malaysian giant turtle (*Orlitia borneensis*), or Sunda gharial (*Tomistoma schlegelii*). This pattern emerges because certain traits can elevate a small species' profile: the ladybug, for instance, charms children with its appealing appearance and helps gardeners by preying on aphids; the tick draws attention due to its role in transmitting diseases; and the tardigrade fascinates researchers with its remarkable ability to thrive under extreme conditions. Hence, on the one hand, a taxon's hiddenness is influenced not only by size, but also by its abundance, visibility, habitat, and relevance to humans, where it occurs (e.g. species living below the water surface or in remote areas are more likely to be overlooked), the difficulty of differentiation from other species, its role or service provided to humans, its threat to humans or connection to other features that may contribute to its awareness level. On the other hand, the diversity and variability of abundant and visible species may be equally hidden, because different species of rodents or dipterans may be collectively referred to as "mice" or "flies", respectively.

Each realm is characterised by its distinct habitat types and harbours varying degrees of biodiversity. A simple Web of Science search using the terms "biodiversity + *realm*" reveals that environments such as forests (i.e., "biodiversity + forest*, 87496 publications as of 21.05.2025), grasslands (17206), and coral reefs (6072) have attracted more research attention than less accessible habitats like caves (2478), groundwater (2531) or deep-sea ecosystems (5847). Freshwater ecosystems can be considered isolated while promoting species isolation and the potential for diversification (Grosberg, Vermeij & Wainwright, 2012). Similarly, a taxonomic bias towards certain taxa contributes to knowledge gaps, and thus contribute to hiddenness of biodiversity (Troudet *et al.*, 2017). For instance, vertebrates, particularly mammals and birds, have been extensively studied and are well-represented in public consciousness, while invertebrates and microbial life (insects, fungi, bacteria, and archaea, among others) are often overlooked despite their vast diversity and ecological importance; (Eisenhauer *et al.*, 2019; Eisenhauer & Hines, 2021). In addition, cryptic species, i.e. organisms that are morphologically similar but genetically distinct, are inherently hidden, particularly among microorganisms. For plankton, genetic delimitation has received less attention than morphological classification (Morard *et al.*, 2024; Marrone, Fontaneto & Naselli-Flores, 2022; Van den Wyngaert *et al.*, 2022). The same holds for aquatic plants although many large genera are prone to hybridisation (e.g. Potamogeton: Kaplan & Fehrer, 2013) which challenges their morphological determination (Espinosa Prieto *et al.*, 2023). Li & Wien (2023) even estimate that for every insect species described based on morphology, there are on average 3.1 cryptic species.

Despite remarkable progress in documenting biodiversity at both global (e.g., Dirzo & Raven, 2003) and national (e.g., Wirth *et al.*, 2024) scales, a large fraction of biodiversity remains unknown or hidden. This raises several fundamental questions: What exactly constitutes hidden biodiversity? Why does it remain hidden, and what are the underlying factors contributing to its hiddenness? Moreover, is it critical to understand and address this hidden fraction? Here, we discuss possible ways to uncover the different dimensions of hidden biodiversity, that is, to which extent could hidden biodiversity entities be disentangled from their ecosystem functions, if at all possible? In other words: should all (hidden) biodiversity be uncovered, or should the emphasis lie on critical ecosystem functions that deserve the spotlight and hence targeted resources?

II. What is hidden biodiversity?

Scientific knowledge gaps in biodiversity span multiple dimensions (Fig. 1). These include the primary unknown in taxonomic, functional and genetic biodiversity, which correspond to the so-called shortfalls in biodiversity knowledge (Hortal *et al.*, 2015). In addition, they relate to spatio-temporal, methodological and social dimensions which altogether provide a scaffold to help disentangle the complexity of hidden biodiversity, as discussed in the following sections and supported by examples in Table 1.

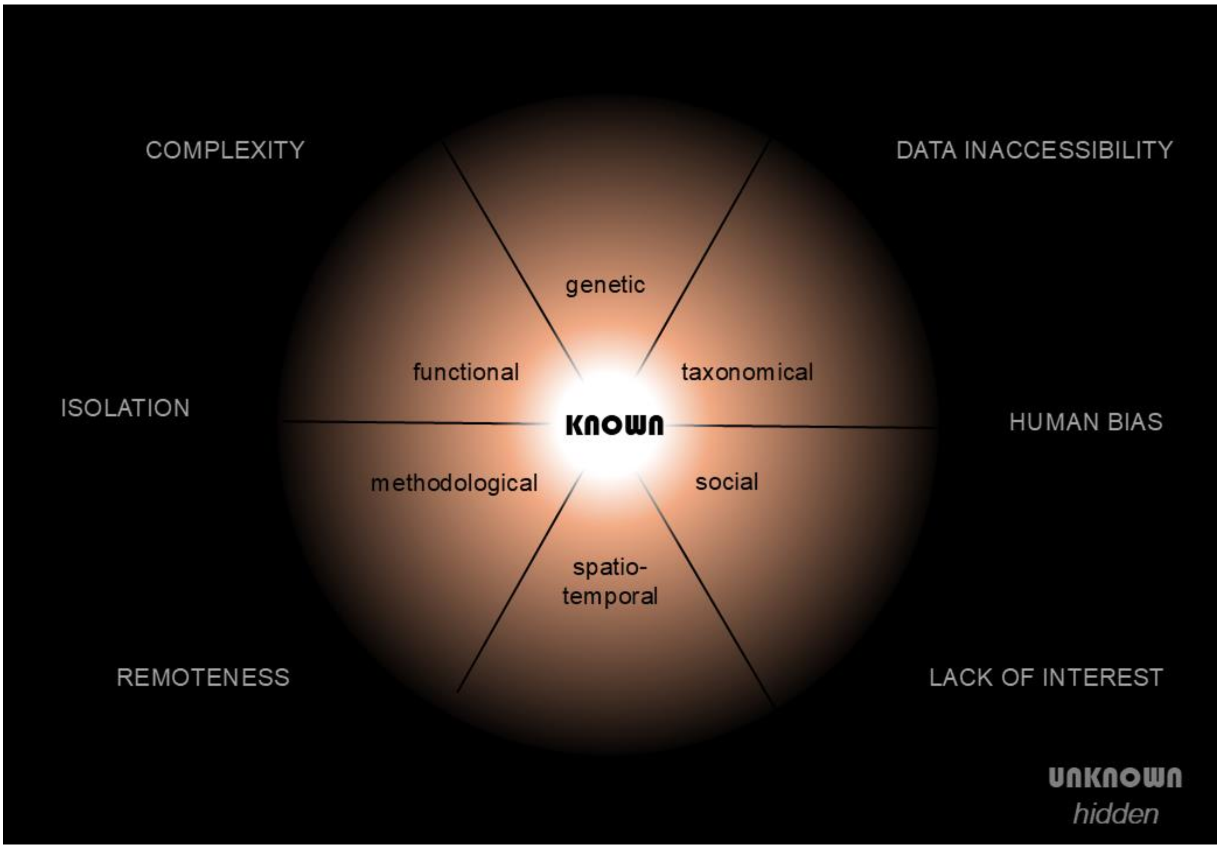

Figure 1 | Scientific knowledge gaps in biodiversity can be related to multiple dimensions. These relate to knowledge gaps in taxonomical, functional and genetic diversity, as well as spatio-temporal, methodological and social aspects. Mapping these dimensions help to disentangle the complexity of hidden biodiversity, which can be also attributed to isolation and remoteness of habitats, data inaccessibility, human bias and a general lack of interest. We provide examples in Table 1.

(a) Taxonomic dimension

The taxonomic dimension is the prevalent one, with 18,000 new species found and described annually (Zamani *et al.*, 2020), highlighting the knowledge gaps characterised by the Linnean shortfall (Hortal *et al.*, 2015). In general, our knowledge of taxonomic diversity is skewed toward larger and charismatic organisms, which tend to be described earlier than smaller organisms (Collen, Purvis & Gittleman, 2004; Jones *et al.*, 2009). Yet the vast diversity of multicellular organisms is allocated to invertebrates that represent 75% of all described species on Earth (Eisenhauer & Hines, 2021). Diversity estimates of *Bacteria and Archaea* range from 10 million species (Louca *et al.*, 2019) to 1.7 billion species (Larsen *et al.*, 2017), with estimates for fungal species ranging between 1 and 11 million (Hyde, 2022) to 160 million species, and an estimated 160 million protist species (Larsen *et al.*, 2017) on land, in marine (Clerissi *et al.*, 2018), and freshwater environments (Metz *et al.*, 2022). A significant knowledge gap exists in insect biodiversity, with an estimated 80% of species diversity still undescribed (Stork, 2018). For example, the number of undescribed species of Hymenoptera and Diptera even in a temperate country like Germany – with a long tradition of taxonomy as a discipline – amounts to a few thousands (Buchner *et al.*, 2025). Little is known about parasite diversity (Carlson *et al.*, 2020). The striking discrepancy between available knowledge and gaps in the taxonomic dimension can be exemplified with one of the largest biodiversity databases, the Global Biodiversity Information Facility portal (GBIF, www.gbif.org): two third of the records pertain to birds, though they represent only 0.2% of the described diversity (Eisenhauer & Hines, 2021; Srivathsan *et al.*, 2023).

(b) Functional dimension

Functional diversity refers to "the value and the range of those species and organismal traits that influence ecosystem functioning" (Tilman, 2001). In recent decades, research on functional diversity has expanded (Naeem, 2002), but the proliferation of definitions and measurement methods (Petchey & Gaston, 2006) has made it challenging to obtain accurate estimates. We lack substantial knowledge on organismic functional diversity in almost every habitat on Earth, a gap coined also as the Raunkiæran shortfall (Hortal *et al.*, 2015). Consequently, multiple levels of functional diversity remain hidden, i.e., regarding individuals, populations, communities, and entire biomes or individual-level traits such as behavioural variation (Grimm *et al.*, 2025). With the rise of OMICS tools, i.e., shotgun metagenomics, transcriptomics, proteomics, and metabolomics, or other high-resolution methodologies such as high-resolution biotelemetry to track behavioural diversity (Nathan *et al.*, 2022), functional diversity can be assessed even in the absence of sufficient species information. However, several studies (Basile, 2022; Petchey & Gaston, 2006; Mouillot *et al.*, 2013) suggested that rare species play a disproportionately important role in functional diversity. Though unknown and rare species can be extremely important for ecosystem functioning including biogeochemical cycles and climate feedback (Jousset *et al.*, 2017), they are often being neglected due to methodological limitations. Thus, it is key to bear the limits of our knowledge in mind when addressing conservation measures aiming to counteract the current loss of functional diversity (Mouillot *et al.*, 2013).

(c) Genetic dimension

Genetic diversity within species has long been overlooked due to the assumption that its effect could be ignored compared to interspecific differences (Violle *et al.*, 2012; Bolnick *et al.*, 2011). However, genetic diversity forms the basis for (rapid) evolution to occur, even on ecologically relevant time scales, resulting in dynamical interactions between ecological and evolutionary processes (Schoener, 2011; Hendry, 2017). The importance of genetic diversity is given by its potential to increase the resilience of populations and communities by enabling adaptive responses to changing environments (Diaz *et al.*, 2013). Moreover, genetic diversity can have ecological effects comparable to those of species diversity and influence primary productivity, population recovery from disturbance, interspecific competition, community structure, and chemodiversity as well as fluxes of energy and nutrients (Des Roches *et al.*, 2018; Hughes *et al.*, 2008).

With the increasing availability of molecular tools and advances in high-throughput sequencing technologies, we are now able to produce high-quality reference genomes of an increasing number of species (Lu *et al.*, 2025) and can reveal the genetic diversity of species populations as well as adaptive processes (Satam *et al.*, 2023; Lu *et al.*, 2025). Yet, until now, a large fraction of the genetic diversity still cannot be interpreted or remains uncovered. Even though DNA sequencing is conducted in high throughput, the entire diversity of microbial populations remains largely unknown, and most genome sequences comprise genes with unknown functions (Vanni *et al.*, 2022; Overmann *et al.*, 2017).

(d) Spatio-temporal dimension

The taxonomic dimension is closely linked to the spatial and temporal dimensions of detecting species, characterised by the Wallacean and Prestonian shortfalls (lack of knowledge in species distributions and abundance, respectively; Hortal *et al.*, 2015). Life on our planet is subject to geophysicochemical boundaries captured as "Nature's envelope" (Patterson, 2022): biodiversity occurs inside the envelope of spatial and temporal scales relevant for life. Species rarity contributes to being hidden, considering either spatially restricted occurrences, regardless of abundance, or low occurrence numbers, regardless of the distribution (Kunin & Gaston, 1993; Crisfield *et al.*, 2024), both of which reduce its detection probability (McCarthy *et al.*, 2012; Royle *et al.*, 2012). The latter is often accompanied by a patchy distribution, particularly evident in soil or benthic flora and fauna, necessitating extensive sampling to achieve accurate detection and counts within a given area and timeframe.

The temporal dimension is another aspect to measure the "unknown", and can be split between short-term dynamics such as diel behaviour, i.e. day- or night-time activity, and long-term, such as seasonal changes or multi-year life cycles. Biases in biological research, historically favouring daytime studies, have led to significant data gaps in understanding nocturnal species (Gaston, 2019). For instance, over 80% of mammalian species listed as data-deficient on the International Union for Conservation of Nature (IUCN) are listed as nocturnal (Bennie *et al.*, 2014). Likewise, the majority of insect activity is nocturnal (Wong & Didham, 2024), and the best studied insect groups are — on top of being charismatic — all diurnal, such as butterflies, dragonflies and damselflies, and bees. In a similar vein, certain ecosystem functions such as pollination have mostly been studied during the day, despite nocturnal pollination being almost equally important (Fijen *et al.*, 2023). Consequently, only recently the disruptive impact of artificial light at night on nocturnal pollination and other night related ecosystem services has been brought to attention as a significant concern (Buxton *et al.*, 2022; Cox & Gaston, 2024; Knop *et al.*, 2017; Hölker *et al.*, 2010).

Combined, the spatio-temporal dimension includes species life cycles and migration patterns where a given species may occupy different parts of the spatial and / or temporal continuum during its lifecycle impacting also its detection probabilities. For example, inactive life stages during events such as droughts may not be detected, leading to an underestimation of abundances if species observations are limited to periods of activity. This issue is also evident in species with multi-year life cycles, such as certain insects, where not all stages are active at the same time (Tauber & Tauber, 1981; Heliövaara, Väisänen & Simon, 1994). Aquatic insects with a freshwater larval stage may be challenging to identify or study in their natural environment and remain overlooked, likewise leading to an incomplete understanding of their full life cycles (Dijkstra, Monaghan & Pauls, 2014). Species thus may occupy specific environmental conditions and their niche may shift spatio-temporally, for example when crossing ecosystem boundaries, as in the case of such insects or migratory fish. The gaps in knowledge of species' ecological niches are described as the Hutchinsonian shortfall (Hortal et al. 2015). Reasons contributing to this shortfall are seasonal migration but also long-term adaptation patterns due to climate change, leading to shifting baselines in species distributions, further challenging the analysis of species niches and biotic interactions.

A special case of the temporal dimension is non-native / invasive species, which may remain unnoticed in their newly colonised environment for a long time during their initial lag phase before possible population explosions (Kelly *et al.*, 2021). Similarly, odd multi-year cycles such as El Niño and La Niña affect spatial distributions through temporal climatic contingencies (Ávila-Jiménez, Gutiérrez & Altamiranda-Saavedra, 2024).

(e) Methodological dimension

Given methodological shortcomings and challenges in sampling procedures, entire ecosystems may be considered hidden. Isolated habitats and areas are hard to access, such as caves, high mountain sites, tropical rainforest, deep ocean, and extreme environments in general (Mammola *et al.*, 2019; Basnet *et al.*, 2019; Schultz *et al.*, 2023). Biodiversity in soils and aquatic habitats remains "below the surface" and has a low detection probability. In fact, soils are among the most concealed terrestrial habitats, even though they have long been recognised as exceptionally biodiverse (Anthony, Bender & van der Heijden, 2023). The low accessibility of soil organisms requiring different extraction methods depending on the organism group, high numbers of (cryptic) species and low number of taxonomic experts for some groups of organisms combined lead to a high disparity in estimated *versus* undescribed species in every group of soil meso- and microfauna (Geisen *et al.*, 2019). Likewise, in the marine realm, two-thirds of all species are estimated to be described, and especially the deep-sea encompassing 95% of the ocean's volume can be considered the least explored environment on Earth (Danovaro *et al.*, 2017; Costello & Chaudhary, 2017).

The habitat or ecosystem accessibility relates to sampling and extraction procedures specific to respective organisms (Flocco, Mac Cormack & Smalla, 2019; Hughes *et al.*, 2021). In addition, geographical bias induced by the location of researchers, safety issues in several regions, as well as differences in the implementation of the Nagoya Protocol impede systematic biodiversity assessments in entire geographic regions (Prathapan *et al.*, 2018; Overmann & Scholz, 2017; Heinrich *et al.*, 2020). Many of these aspects contribute to the so-called "biodiversity blindspots" proposed by Ball *et al.* (2025). In addition, sampling biases are often caused by selective perception, collector bias, species body size, as well as species and location attractiveness (Phillips *et al.*, 2017). Size is a human factor explaining the skewed distribution of species knowledge: the smaller an insect body size, the later the year of description (Stork *et al.*, 2015). Similarly, inconsistent sampling protocols, lack of standardisation, and limited technological access can hinder biodiversity detection, for example, molecular methods may miss rare taxa that require deep sequencing. In addition, a lack of data contributes to a limited awareness – an issue across realms and ecosystems, including a lack of open and Findable, Accessible, Interoperable and Reusable data (FAIR; Wilkinson *et al.*, 2016). While most notions of diversity are centred around the presence of certain taxa in a given context, the concept of "dark diversity" (Pärtel, Szava-Kovats & Zobel, 2011) captures information about the absence of such taxa in spatio-temporal contexts for which comparable data and ecological models would suggest that they are present. The combination of species absence and presence data can be further combined into more complete biodiversity measures like the Community Completeness Index (Pärtel, Szava-Kovats & Zobel, 2013).

Finally, some groups of organisms actually have been studied, yet the information gathered about them is not prevalent in the scientific community. This phenomenon can be referred to as "dark knowledge" (Jeschke *et al.*, 2019). This can be due to either highly specialised scientific publications which do not address the larger community, or so-called "forgotten results" given published but neglected research due to inaccessibility e.g. non-English (Amano *et al.*, 2023) or non-digitised publications.

(f) Social dimension

The degree of "hiddenness" also includes social dimensions as it is often related to the cultural background of different human societies, economic practices, and experiences. Many important human-driven environmental changes and their impacts on biodiversity remain surprisingly underexplored (Heger *et al.*, 2019). Moreover, ecological effects of specific facets of global change have been examined, but we lack knowledge on their combined effects and their complexity (e.g., Pendleton *et al.*, 2016; Vos *et al.*, 2023; Orr *et al.*, 2024). This notion results in a large degree of hiddenness for scientists as understanding and projecting ecological complexity such as synergistic, additive, and antagonistic effects of multiple drivers on organisms and ecosystems demands coordinated cross-disciplinary research (Heger *et al.*, 2019).

Human bias is a major driver of imbalanced biodiversity knowledge, as it influences how research is conducted and communicated and thus affects all other dimensions (Mazor *et al.*, 2018; He *et al.*, 2021). A prominent example is the diurnal bias in our society in perceiving nocturnal processes and issues (Kyba *et al.*, 2020). In addition, a lack of knowledge creates lack of the awareness, or knowledge can be unintentionally biased (e.g., introduced species being considered native, Kochalski *et al.*, 2019). These gaps often result from methodological challenges and the undersampling of certain areas, due to a lack of research focus and sufficient fieldwork, which also mirrors temporal and spatial biases in scientific efforts, or challenges in communicating scientific results to the public. Being it a lack of interest, funding, or due to societal, political or regional aspects – such human induced biases unfortunately continue despite better knowledge. Troudet *et al.* (2017) showed that taxonomic biases in biodiversity data have remained broadly the same since the 1950's although the problem has been known since several decades (Bonnet, Shine & Lourdais, 2002).

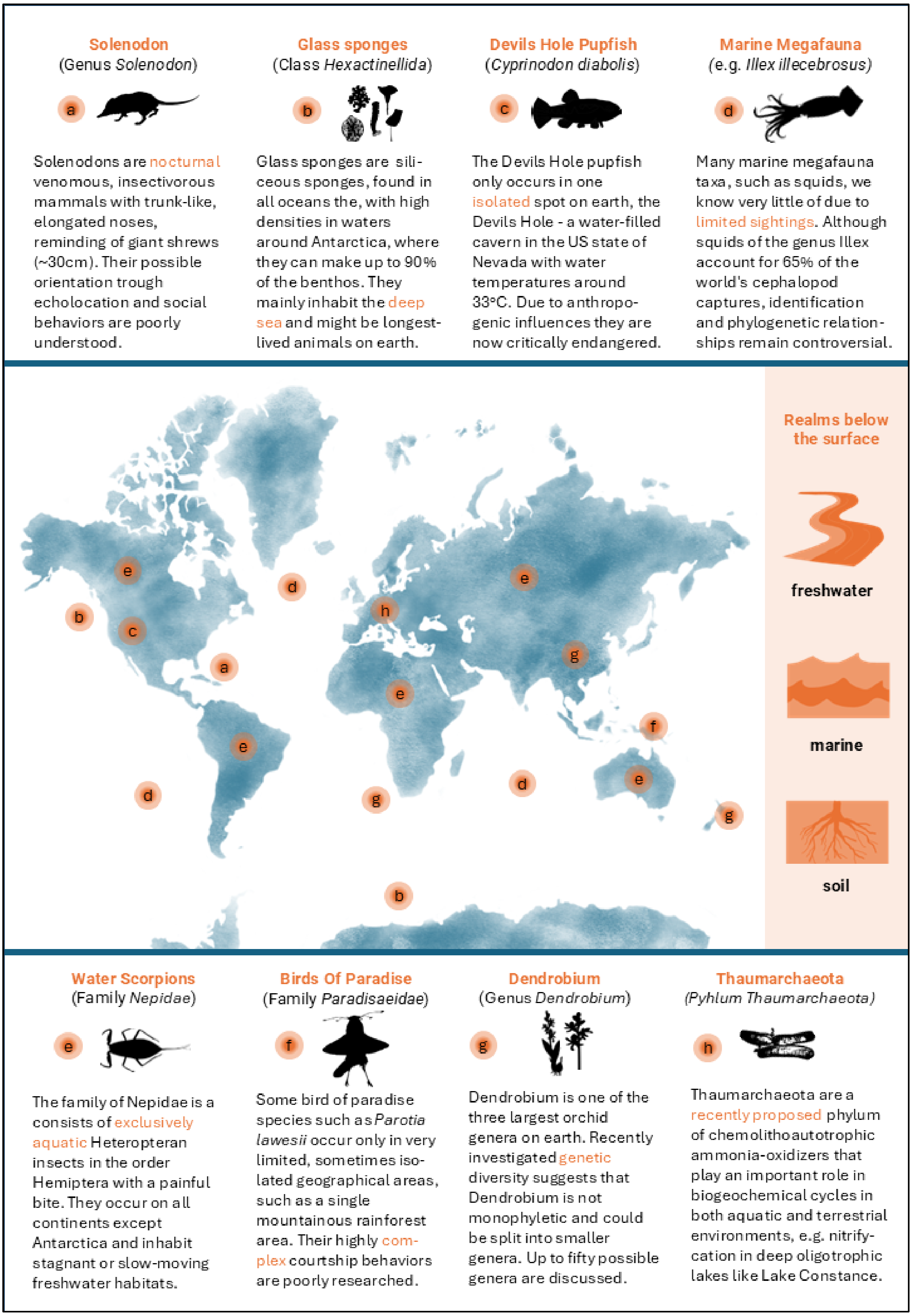

Fig. 2 | Examples of hidden biodiversity across the world, including a) Solenodons, b) Glass sponges, c) Devils Hole Pupfish, d) marine megafauna, e) water scorpions, f) Birds of Paradise, g) *Dendrobium* and h) *Candidatus Thaumarchaeota,* along with their approximate distribution. In addition, different realms that are beneath the surface, such as freshwater, marine and soil environments, can be considered hidden. See Table 1 for more examples and https://hiddenbiodiversity.org/ for an interactive visualisation.

III. Why is hidden biodiversity relevant?

Hidden biodiversity has its intrinsic value, similar to the known biodiversity, however with a major caveat: it is challenging to consider something relevant, or attribute a given process or function to a taxon which is not yet known or described as such. Hidden biodiversity is likely to contribute to many ecosystem functions and services which for humans still remain in the dark, and in this regard, the precautionary paradox is relevant for maintaining ecosystem stability and resilience.

Ecosystem functions may remain hidden but can be considered critical biological entities (Emmett Duffy, Paul Richardson & Canuel, 2003; Lynch *et al.*, 2023; Anthony *et al.*, 2023; Bahram *et al.*, 2018; Hooper *et al.*, 2012; Bell *et al.*, 2005). The biodiversity–ecosystem function (BEF; Schulze & Mooney, 2012) relationship is often explained by niche partitioning, positive interactions, or asynchronous population dynamics of the coexisting species (Barry *et al.*, 2019), which reduce competition, but increase productivity and ecosystem resilience (Tilman, Isbell & Cowles, 2014; Cardinale *et al.*, 2012; Barry *et al.*, 2019). Notably, ecosystem functions can be compromised already by decreases in species abundance opposed to complete species extinctions (Isbell *et al.*, 2017; Spaak *et al.*, 2017). This is relevant, especially in the case of microorganisms which, due to their very large population sizes (Morris *et al.*, 2002; Miller *et al.*, 2005) and their potentially broad or even global geographical distribution (Casamayor *et al.*, 2023), have a low extinction risk, in contrast to many metazoa. The same applies to the vectors of microorganisms: while individual insect species may not be threatened with extinction, their dwindling abundance can silently undermine ecosystem resilience. For example, Mata *et al.* (2015) found knowledge gaps regarding ground and bark-dwelling beetles and insects with an aquatic phase, and revealed hundreds of new insect species delivering ecosystem functions for the metropolitan area. Such knowledge gaps are critical as changes in biodiversity can affect ecosystem functions with considerable delays, where e.g. plant richness can impact belowground processes even after several years (Eisenhauer *et al.*, 2024b; Bongers *et al.*, 2021; Guerrero-Ramírez *et al.*, 2017; Weisser *et al.*, 2017; Reich *et al.*, 2012).

The majority of studies on BEF relationships have so far focused on terrestrial plant communities and their productivity, and the BEF of other communities only recently gained attention. Aquatic fungi take a key role in ecosystems, carbon and nutrient cycling and energy flow, producing essential organic compounds and dynamic food-webs (Vatova *et al.*, 2022). Soil biodiversity is a key regulator in soil ecosystem multifunctionality (Delgado-Baquerizo *et al.*, 2020; Wu *et al.*, 2025; Schuldt *et al.*, 2018; Wagg *et al.*, 2014), and herbivorous insects and microbial decomposers are important promoters of grassland ecosystems (Soliveres *et al.*, 2016). Likewise, many ecosystem services rely biodiversity, such as crop, fish, and timber production, or the regulation of pests and prevention of diseases (Brooks *et al.*, 2016; Isbell *et al.*, 2017; Duffy *et al.*, 2016; Liang *et al.*, 2016; Keesing *et al.*, 2010; Barnes *et al.*, 2020; Lynch *et al.*, 2023). Management of ecological systems might go wrong if hidden biodiversity is ignored. In fisheries management, for instance, many well-intended actions fail because the behavioural diversity and responses of fishes were not taken into account (Pine *et al.*, 2009). Growing evidence shows that biodiversity is generally positively associated with plant, animal, and human health (Banerjee & van der Heijden, 2023; Flandroy *et al.*, 2018; Haahtela, 2019; Rillig *et al.*, 2018), and hidden biodiversity is likely to play an equally important role. On a different note, there are also unknown species that pose considerable health risks to animals and humans. One example is the recently described cyanobacterium *Aetokthonos hydrillicola* (Wilde *et al.*, 2014) that occurs associated with submerged plants and produces potent neurotoxins that can be fatal to herbivores and birds of prey (Breinlinger *et al.*, 2021).

In most ecosystems, small organisms constitute a major fraction of the hidden biodiversity not only by the number of species but also by their sheer biomass. Microorganisms constitute the second most dominant biomass fraction in soils after plant roots (Bar-On, Phillips & Milo, 2018) and can amount to > 1 ton of biomass carbon per hectare (Fierer, 2017), being equally dominant and important also in marine sediments (Hoshino *et al.*, 2020). The fact that hidden biodiversity is most prominent among small organisms has important implications for its functional relevance, since the mass-specific metabolic activity of organisms is increasing with decreasing size. This is exemplified by biomass-specific respiration rates, which are up to five orders of magnitude higher for bacteria than for multicellular organisms ranging from copepods to elephants (up to 100,000 versus 1-100 mmol O_2 kg^{-1} h^{-1}). As a consequence, the composition of microbial communities is a major driver of carbon sequestration, nutrient cycling, or greenhouse gas emissions, and is relevant for key ecosystem services like pathogen control and pollutant degradation (Azam & Malfatti, 2007; Täumer *et al.*, 2021; Bardgett & van der Putten, 2014; Deubel & Merbach, 2005; Harms, Schlosser & Wick, 2011; Kandeler, Stemmer & Gerzabek, 2005; Falkowski, Fenchel & Delong, 2008; Delgado-Baquerizo *et al.*, 2020; Abs, Chase & Allison, 2022). For example, the metabolic activity of bottom sediment bacteria contributes to the transformations and mineralisation of organic matter, and in certain conditions to the release of regenerated nutrients to near-bottom waters (Lewicka-Rataj *et al.*, 2024).

The persisting knowledge gaps of hidden biodiversity, particularly those of functional biodiversity, not only have high relevance for the understanding of these ecosystem functions and services, or aggravate the uncertainties in predicting the consequences of biodiversity change (Burian *et al.*, 2024; Dornelas *et al.*, 2023), but also impede the development of mitigation strategies for the preservation of key ecosystem functions during environmental change (Pereira *et al.*, 2024; Oliver *et al.*, 2015; Hong *et al.*, 2022; Averill *et al.*, 2022). In general, ecosystem functions provided by biodiversity play a key role in, e.g., climate change mitigation and adaptation (Cavicchioli *et al.*, 2019; Aben *et al.*, 2022; He *et al.*, 2010; Weiskopf *et al.*, 2024; Shin *et al.*, 2022; Oliveira, Moore & Dong, 2022; Jansson, 2023), and this can be expanded likewise to hidden biodiversity (Table 1).

Beyond ecosystem functions, hidden biodiversity is likely to offer new and innovative solutions for biotechnology, agriculture, and human or veterinary medicine. For instance, genome sequences of understudied microbial lineages have been found to contain novel biosynthetic gene clusters or metabolic pathways (e.g., Cuadrat *et al.*, 2018; Overmann *et al.*, 2017). Given that bacterial phyla without any cultured representatives contain the highest fraction, up to 85% of unknown genes, dark taxa appear particularly promising targets for future biodiscovery. In a large, comparative metabolomic study across four bacterial phyla, thousands of mostly unknown different metabolites were detected, of which only 12% occurred in all four phyla while up to 107 unique metabolic features were observed in just a single bacterial strain, including an entire novel compound family (Fiorini *et al.*, 2022). More broadly, hidden biodiversity is likely to have manifold so-called Nature Contributions to People (NCPs; IPBES, 2019; Díaz *et al.*, 2018). For instance, (Gascon *et al.*, 2015) review many ecosystem services provided by species, including several of unexpected value to humans.

Taken together, hidden biodiversity has, beside its intrinsic value, far-reaching impacts on ecosystem functions and services as well as management of aquatic ecosystems. There are some fundamental issues to solve, e.g., if a global policy goal is to protect all biodiversity, how do current policies do when a major portion of biodiversity remains hidden? Our insufficient understanding of hidden biodiversity severely impedes our ability to comprehensively (i) elucidate the biological basis (taxa, phenotypic traits, genes, and gene regulation) of specific ecosystem functions (Overmann *et al.*, 2017; Zoccarato *et al.*, 2022), (ii) identify drivers and feedback mechanisms of ecosystem functions during environmental change (Eisenhauer & Hines, 2021; Eisenhauer *et al.*, 2024a), (iii) assess biological interactions, functional similarity and ecosystem resilience (Bishop *et al.*, 2022; Kost *et al.*, 2023; Rousk, Brookes & Bååth, 2009; Philippot *et al.*, 2013), (iv) develop appropriate, state-of-the-art monitoring and management approaches (Mammola *et al.*, 2020; Guerra *et al.*, 2021; Singleton *et al.*, 2024), (v) comprehensively assess the effects of conservation measures (Waldron *et al.*, 2020), and (vi) exploit the full potential of biodiversity for future applications in sustainable agriculture, fisheries, bioeconomic development and ecosystem restoration, or human and veterinary medicine (He *et al.*, 2024; Overmann *et al.*, 2017; Krause *et al.*, 2022; Humphries & Winemiller, 2009).

IV. How to proceed?

Given the challenges in the different dimensions of hidden biodiversity, the question arises: what could be done regarding this so-called known unknown? Targeted research to uncover hidden biodiversity may be perceived as a tension zone in comprehensive *versus* purpose-driven biodiversity research, with the latter reflecting the importance to accumulate *sufficient* knowledge. However, what should be considered sufficient? One approach could be to focus on the major NCPs and develop incentives for society to invest into biodiversity research and protection linked to these NCPs. This approach is, however, at the risk of being circular, since we would focus on aspects that are already known. We also have to ask ourselves: how much has the “uncovering of hidden biodiversity” in the past decades contributed to, e.g., biodiversity protection, restoration, and the understanding of NCPs? While valuable examples of beneficial impacts exist (see Table 1), the detrimental anthropogenic impacts on biodiversity outweigh these positive examples, as shown e.g., by the negative trend in population abundance of monitored vertebrates globally (He *et al.*, 2019; WWF, 2024). While this does not mean that interest-driven efforts to uncover hidden biodiversity should be neglected, we have to be mindful of our limited resources regarding time, labour and funding. In addition, raising awareness for hidden biodiversity is essential, and we aim to support this by collating examples from the larger community using our newly-developed interface at https://hiddenbiodiversity.org/. [Note to reviewers: this is a first prototype and more functionalities will be added, and we are happy to implement possible suggestions].

We call for a balance between addressing interest-driven and purpose-driven biodiversity research. However, the emerging questions are evident: how do we prioritise the efforts? Which are the critical ecosystem functions? Which realms, ecosystems, and habitat types should ‘deserve’ being on the fast-track? The circularity of hidden biodiversity where insufficient knowledge might impede the establishment of an appropriate restoration baseline, raises the question: what is the ultimately desired *versus* realistic status of biodiversity? We discuss important trends and opportunities in biodiversity research and methodological developments across the dimensions, concluding in seven principles for future research on biodiversity sustainability.

(a) Taxonomic dimension

Neglecting the taxonomic diversity of organisms with low charismatic appeal leads to a distorted view, where neglect increases with diversity and decreases with body size. For instance, Srivathsan *et al.* (2023) found that insect families contributing more to global insect communities are those that been most neglected. This neglect, which cascades into the lack of research efforts, could be addressed by identifying and tackling the diversity of hidden taxa with scalable techniques. One such important tool to detect everyday yet important taxa is Next-Generation Sequencing (NGS) barcoding. This allows cost-effective high-throughput generation of short specimen-specific barcodes and yields new barcodes, including some that are potentially new to science. The method can be implemented by a wide range of laboratories, accelerating, e.g., invertebrate species discovery and yielding relative abundance information (Wang *et al.*, 2018). Nowadays, decreasing processing costs enable sequencing genomes at scale and in projects such as the Darwin Tree of Life for the British fauna (https://www.darwintreeoflife.org/), the Psyche Project for European Lepidoptera (https://www.projectpsyche.org/) or the Ten Thousand Plant Genome Project (Cheng *et al.*, 2018). Similarly, employing machine-learning such as deep clustering has the potential to support taxonomic identification, as shown by Milošević *et al.* (2025) for Chironomids.

The cost-effective method of identifying taxonomy by DNA leads to a rapid increase of taxonomic databases, yet also the errors in taxonomic labelling bear huge challenges. Grenié *et al.* (2023) reviewed this topic and developed a Shiny app in an attempt to solve the puzzle (https://mgrenie.shinyapps.io/taxharmonizexplorer/). They (i) identify the correct treatment of taxon names as a prerequisite for robust biodiversity research, (ii) suggest the taxonomic name harmonisation by employing a thorough search for the most suitable (i.e. most reliable and up-to-date) databases and existing related tools and (iii) propose a typology of widely used taxonomic databases and extensively reviewed R packages, along with the documentation of the harmonisation workflow (software versions, functions, parameters and database versions). To facilitate such efforts, database managers and tool developers need to make their resources discoverable for all researchers globally and describe them with all necessary meta-data. Such joint efforts between taxonomists and ecologists could therefore strengthen efforts across research communities and disciplines for obtaining robust information.

Finally, any new species descriptions and findings must find their way into public knowledge, but also into backbone taxonomies of national and global databases for taxonomic search queries. The Freshwater Animal Diversity Assessment (FADA) project (http://fada.biodiversity.be/) mobilises experts and collates information on freshwater biodiversity and taxonomy globally. These efforts are the prerequisite to query for freshwater taxa and to address the spatio-temporal dimension of hidden biodiversity.

(b) Functional dimension

Addressing the functional dimension provides a complementary perspective to shed light on, e.g., the community composition and structure given species traits and contributions to ecosystem functioning, and to identify keystone species which drive community composition and function irrespective of their abundance. Accordingly, their loss can cause significant shifts in the structure and function of communities (Banerjee, Schlaeppi & van der Heijden, 2018; He *et al.*, 2024). A promising avenue to identify keystone species are co-occurrence and network analyses which allow identifying those hub species that are highly interconnected to other community members. Such network analyses would benefit from moving from exploratory correlation analyses to testing hypothesised interactions among taxa. However, the identified keystones need to be also verified, e.g., through experimental removal from / addition to their communities (Röttjers & Faust, 2019; Weiss *et al.*, 2023) which might be feasible for animal and plant communities, but challenging for complex microbiomes. As an alternative approach, microbial keystones may be identified as species that are capable of key or bottleneck reactions in community-wide metabolic networks (Roume *et al.*, 2015). The caveat is however the urgent requirement regarding data to uncover their spatio-temporal dimension. Moreover, investments in so far overlooked traits that are likely of fundamental importance for ecology and evolution and largely overlooked, such as studying the behavioural variation in organisms, is recommended. Novel tracking technologies can be a stepping stone in the right direction (Nathan *et al.*, 2022).

(c) Genetic dimension

Time-series and spatial surveys are important to uncover some of the hidden genetics, i.e. the role that contemporary evolution plays in species survival and acclimation to environmental stressors, and how this acclimation affects future generations (Brennan & Logares, 2023). Large scale, complex genetic and environmental assessments can be customised by focusing and adding detailed parameters pertinent to specific niches or tackling particular questions. For instance, in microbiology the assessment of plant rhizosphere communities can be used to design pest biocontrol or enhanced crop yield strategies (e.g., Syed Ab Rahman *et al.*, 2018). The identification of microorganisms furnishing crops with resistance to environmental stressors is of particular importance in the context of climate change (Scheben, Yuan & Edwards, 2016) or the identification of key microbial organisms bound to the occurrence of a disease (e.g., Milliken *et al.*, 2021). The genetic diversity in wild relatives can be used to protect the yields by improving the disease and stress resistance in crops and domestic animals (Andersson & Purugganan, 2022; Zhu *et al.*, 2000). The same applies to sustainable aquaculture which depends on genetically diverse wild stocks (Yáñez, Newman & Houston, 2015). However, the resources for both terrestrial and aquaculture crops are at threat given the incentives for farmers to abandon traditional crops (Bellon *et al.*, 2017) and by declines in wild populations (FAO, 2019). Furthermore, the use of non-native improved strains in aquaculture can impact the genetic composition and diversity of wild populations (Sanda, Metcalfe & Mable, 2024). Likewise, efforts towards securing sustainable seafood production benefit from improved and innovative genetic monitoring schemes to obtain data on the health state of aquatic ecosystems, and to adjust management decisions accordingly (Bernatchez *et al.*, 2017). For the sustainability of domestic cultures and the conservation of wild species resources, NGS is a highly useful technology (Bohan *et al.*, 2017).

(d) Spatio-temporal dimension

It is vital to perform regular and standardised monitoring to detect the spatio-temporal dynamics in biodiversity. High-resolution long-term records of biodiversity help to detect the variation in biodiversity which otherwise remains hidden due to a missing baseline to compare. Examples for long-term biodiversity records include marine prokaryotes and protists (Yeh & Fuhrman, 2022), fish catches (Froese *et al.*, 2012), harmful marine algal blooms (Wells *et al.*, 2015), marine zooplankton data (Chiba *et al.*, 2018), freshwater invertebrates (Haase *et al.*, 2023; Gillmann *et al.*, 2024), as well as terrestrial and soil organisms (Fischer *et al.*, 2010). Efforts can build on numerous important ongoing monitoring efforts and networks such as The Group on Earth Observations Biodiversity Observation Network (GEO BON) and thematic BONS (e.g., SoilBON, FWBON), the European Reference Genome Atlas (ERGA), the Long Term Ecological Research Network (LTER), the Global Lake Ecological Observatory Network (GLEON), or the World Register of Marine Species (WoRMS). Likewise, species observation databases such as GBIF, speciesLink, or VertNet, FishNet2, Atlas of Living Australia (Belbin *et al.*, 2021), observation.org, eBird, iNaturalist (Della Rocca *et al.*, 2024), Edaphobase (Burkhardt *et al.*, 2014) provide the basis for addressing the spatio-temporal dimension. Yet the key issue is that the data collection is not happening where it is most needed: the tropics (Meier, Lawniczak & Srivathsan, 2025).

Strengthening scientific networks is essential to enhance monitoring and data exchange, to avoid redundancies and instead to create synergies, including especially economically weaker states and those at risk of warfare (Hanson *et al.*, 2009). Credits should be given to how and by whom data is collected, and to support the diversity of researchers and bridge the Global North-South divide (Nakamura *et al.*, 2023) and to emphasise biodiversity hotspots (Wentzel *et al.*, 2023). Bowler *et al.* (2025) discuss weighting techniques to potentially reduce both the bias and variance of parameter estimates to overcome those gaps in biodiversity monitoring data. However, reducing such bias critically depends on knowledge and the availability of data. Addressing the primary cause requires accounting for the distance between researchers and the study area, supporting local research funding and participation in data-sharing networks (Meyer *et al.*, 2015). Furthermore, new tools are essential to overcome barriers in sampling and monitoring of species that are remote or occur in times when we are unable to detect their behaviour. For instance, nocturnal ecology has recently benefited by new and improved technologies that allow organisms to be tracked at night under natural conditions (Gaston, 2019; Nathan *et al.*, 2022; Degen *et al.*, 2024). Aquatic research can use Unmanned Aerial-Aquatic Vehicles capable of performing underwater sampling (Farinha *et al.*, 2022). Remote sensing is increasingly used for both day and night time observations and to research about hidden biodiversity functions (Wang *et al.*, 2024; Fu *et al.*, 2024). Spaceborne and airborne sensors provide information that incorporate wavelengths unperceivable for the human eye. Moreover, modelling techniques enable research on functional diversity changes over different spatial and temporal scales (Rocchini *et al.*, 2022).

(e) Methodological dimension

Missing access to biodiversity data is a major obstacle to adaptive management in the conservation and management of natural resources. Stephenson & Stengel (2020) have identified a preliminary list of important data resources, yet many are difficult to find, access or not easy to use. Enhancing global biomonitoring strategies should leverage existing initiatives and programs while identifying and addressing gaps. For example, eDNA sampling could be integrated into existing environmental monitoring stations to enhance data collection and analysis (Thomas *et al.*, 2018). Often, it is not biodiversity which is hidden but the data describing it (Kühl *et al.*, 2020). Efforts should address the scattered monitoring data across administrators, the appropriate format, ensuring that data is centralised, accessible, and that data is consistently updated. Examples of initiatives that could benefit from such integration include intergovernmental, national, and regional environmental monitoring programs that track changes in biodiversity and environmental health. In an attempt to develop a robust conceptual framework for monitoring, Dalton *et al.* (2023) recommend seven key conceptual questions related to the broad application and development of effective biodiversity monitoring programs: “why monitor”, “which indicators” should be included, “where” and “when” monitoring will occur, “who” will be involved, and “how many” resources are required. The seventh question of “how” to conduct protocols is the result of the conceptual requirements and is considered in the implementation phase.

Combining biomonitoring with environmental, geographical, and other datasets should further be emphasised to model trade-off scenarios in the conservation policy arena. For example, the assessment of ecosystem corridors, areas of connectivity, migration routes, and other transnational scenarios is of high relevance for the design and implementation of area-based conservation measures, such as for example the “30 by 30” biodiversity strategy (European Commission 2024) or the implementation of 25,000 km free-flowing rivers in Europe (Stoffers *et al.*, 2024) to address the various hidden biodiversity dimensions below the surface.

Further, combining data across science, society, and policy will be necessary. As the catastrophic event in the Oder River in 2022 highlighted, compounded human impacts, like pollution, habitat alteration, and climate change, destabilised an entire freshwater ecosystem (Köhler *et al.*, 2024). By integrating datasets from genetic information to environmental and anthropogenic stressors predictive models should be developed, supporting the assessment of ecosystem vulnerabilities and resilience, informing conservation strategies and policy actions, for example limiting pollutants and preventing disruptive engineering projects (IGB, 2020).

Shared open-access databases can allow robust analyses on a wide range of questions on the causes and trends of large-scale biodiversity change (Kühl *et al.*, 2020; Güntsch *et al.*, 2024). This can be achieved in integrating stakeholders within unified networks, which need to value the diversity of stakeholder motivations, responsibilities, expertise, and knowledge pathways and the variety of existing biodiversity recording schemes. Thus, high coordinating efforts to integrate stakeholder groups and provide shared institutional values, rules, and norms have to be considered.

(f) Social dimension

Inviting and including "the society" will support, on the one hand, uncovering hidden biodiversity by reducing the limitations in time and space (i.e., person power) in biodiversity research and monitoring efforts on a large scale (Fraisl *et al.*, 2022; Belletti *et al.*, 2020; Premke *et al.*, 2022; Gąsiorek *et al.*, 2024). The combination of classical methods with citizen science can significantly increase insights and generate new data (Zulian, Miller & Ferraz, 2021; Kimmig *et al.*, 2025; Table 1). In addition, citizen science enhances the stewardship for the value of biodiversity and its protection (Peter, Diekötter & Kremer, 2019; Merenlender *et al.*, 2016), and can thus broaden institutionalised science's horizon and foster innovation in sociological and political areas of science (Austen *et al.*, 2024). On the other hand, citizen science data also offers challenges, which can blur the view on hidden biodiversity itself since participants can introduce variation, bias, and errors into the newly collected datasets given e.g. personal preference of sampling location and time. Involving the society in biodiversity monitoring requires developing software, tutorials, and guidebooks, workshops but also software and data storage solutions for citizen scientists, which are as essential as more quantitative training for ecologists to align with the more complex and sophisticated analytical approaches increasingly used for big data in ecology (Johnston, Matechou & Dennis, 2023). Thus, to maximise the potential for scientific innovation through citizen science, trained scientists should be involved to strengthen data quality assurance, adapt standardised protocols and ensure adequate resources (Kosmala *et al.*, 2016; Austen *et al.*, 2024). Only through large interdisciplinary networks can the whole suite of biodiversity be uncovered because biases and preferences for specific taxa exists within academia and academic silos are prevalent (e.g., terrestrial vs. aquatic or marine vs. freshwater).

Societies across the globe have to be invited to biodiversity research given that, e.g., indigenous cultures provide biodiversity monitoring in everyday life, and nature-centric indigenous languages exist around the world. These languages are a great source of biodiversity knowledge, describing organisms and their functions onomatopoetically (Zimmer, 2024). The challenge is, however, that the languages often do not exist in any written form or are suppressed. So-called "Talking Dictionaries" have been created since 2005 (https://talkingdictionary.swarthmore.edu/) to avoid losing the knowledge from these languages. However, as it is a race against time to capture knowledge about species that will soon no longer be found described in languages that soon may be extinct, it is of utmost importance to meet indigenous cultures at eye level and to share knowledge with each other (Ogar, Pecl & Mustonen, 2020). This also requires addressing the problems of colonialism in biodiversity research, and perspectives from other knowledge traditions should be brought to the fore using methods that allow multiple voices and perspectives to be heard and assessed for relevance (Austen *et al.*, 2024; Ogar *et al.*, 2020).

V. Conclusions

We conclude with seven suggestions and guiding principles aimed at scientists and their networks designed to strengthen sustainability research by uncovering hidden aspects of biodiversity:

1. Promote data that are Findable, Accessible, Interoperable, and Reusable (FAIR) as a prerequisite for uncovering hidden biodiversity and expanding our collective knowledge.
2. Establish regular and standardised biodiversity monitoring, including sampling at night, in remote locations, and of highly diverse or small-bodied taxa.
3. Employ a wide range of tools and technologies, including DNA techniques in a standardised way, especially to explore taxa with high diversity and small body size to remote sensing for large-scale assessments.
4. Use key biological entities and abiotic parameters as proxies to model and monitor biodiversity patterns and changes under different scenarios.
5. Focus on microbial species that act as metabolic bottlenecks or keystone players in ecosystem processes and community-wide networks.
6. Involve society to support monitoring efforts on a large scale, especially addressing indigenous cultures that can provide their knowledge about organisms and their functions.
7. Strengthen cross-border biodiversity research and conservation by combining datasets and modelling, and by informing governance across jurisdictional boundaries.

We strongly advocate for research that reveals the diversity of species and biological dimensions that have been hidden so far. By integrating knowledge on the state and dynamics of biodiversity in a human-dominated world, biodiversity research can better align with conservation goals, which maximises benefits to people and nature, and addressing the complexity of social-ecological systems (Kareiva & Marvier, 2012; Urban *et al.*, 2021; Guerra *et al.*, 2022).

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VII. Author contributions

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VIII. Tables

Table 1 Examples for the different dimensions of hidden biodiversity (Fig. 1), what specifically is hidden, why can be considered hidden, and why is it considered relevant and its relevance.

[Note to reviewers: this table could possibly be an online-only table.]

Dimension	What is hidden?	Why is it hidden?	Why is it relevant?	Reference
Taxonomic	Most of arthropod biodiversity is unknown to science.	Taxonomic neglect, with little signs of increasing activities in recent years	Taxonomic families that dominate insect diversity are often 'hidden taxa' particularly from the megadiverse orders Hymenoptera and Diptera; neglect of dark taxa could severely affect our perception of how life on Earth is organized.	Srivathsan *et al.* (2023); Forbes *et al.* (2018); Karlsson *et al.* (2020)
Spatial	Studies about the genus Eurythenes, the largest scavenging deep-sea amphipods (max. 154 mm), have revealed a cryptic species complex	Lives in the remote hadal zone	Eurythenes plasticus sp. nov., recovered between the depths 6010 and 6949 m in the Mariana Trench (Northwest Pacific Ocean) in 2014 presented plastic fiber in its guts, probably from anthropogenic pollution	Weston *et al.* (2020); Gerringer *et al.* (2017)
Spatial	Deep-sea: A third of the species and 25% DNA	Lack of accessibility	Underestimated taxa offer the potential of a biological carbon pump by binding atmospheric carbon dioxide to the sea floor	Cordier *et al.* (2022)
Spatial	Blooms of benthic toxic cyanobacteria: relative proportion of toxic and non-toxic strains	Lack of appropriate monitoring approaches	Health risks, global increase in associated animal poisonings	Wood *et al.* (2020)
Spatial	Ground water biodiversity	Little number of efforts to assess subsurface ecosystems so far even in research	Unknown impact on quality drinking water in many regions of the world, incl. ESS such as purification of human chemical inputs.	Zhong *et al.* (2023)
Temporal	Night-time activity by particular species	Lack of human resources at night time	Knowledge about the ecological functions of nighttime organisms and how the evolution of day- and nighttime ecological functions differ, provides a better, more holistic ecological understanding	Gaston (2019); Buxton *et al.* (2022); Fijen *et al.* (2023)

Temporal	Long-term time series, e.g. in aquatic ecosystems	Changing methods, discontinuous funding and staff availability	A large fraction of biodiversity can be hidden in the rare biosphere, but that may change at different time points of sampling throughout seasons or several years. Shifts only visible/explainable if time series are sufficiently long with comparable methods	Pilotto *et al.* (2020); Outhwaite *et al.* (2020); Haase *et al.* (2023)
Spatio-temporal	Evolution of diversity in insect species that have a larval freshwater stage	100,000 species from 12 orders spend one or more life stages in freshwater. Little is known about how this remarkable diversity arose.	Insights in aquatic insect diversity may be highly suitable to study ecological diversification.	Dijkstra *et al.* (2014)
Spatio-temporal	The freshwater pearl mussel (*Margaritifera margaritifera*) larval and juvenile stages	has an obligate parasitic phase, where its larvae (glochidia) develop on specific host fish, like brown trout and Atlantic salmon, relying on their dispersal, before transitioning to juveniles. Juveniles then bury themselves in the hyporheic zone, remaining hidden for years before emerging as long-lived adults, with lifespans exceeding 100 years.	The mussel's survival depends on hydrodynamic conditions without significant sediment movement, and disturbances at any life stage can disrupt the population	Geist (2010); Baldan *et al.* (2021); Barouillet *et al.* (2024)
Functional	Plant resilience to habitat loss and fragmentation	Missing research mainly in tropical areas where landscape fragmentation has high impact	A better understanding of the effects of habitat loss and fragmentation on functional diversity will improve predictions of the resilience and resistance of fragmented systems under global change	Zambrano *et al.* (2019)
Functional	Benthic communities are poorly described	Although the littoral and profundal habitats are full of ecosystem service providers intensive studies about the communities is missing.	The vast majority of fish species feed on profundal or littoral resources	Vadeboncoeur, McIntyre & Vander Zanden (2011)
Functional	The mechanisms and magnitude of interactions mediated by tube-dwelling invertebrates such as chironomid larvae organisms are still poorly understood	The large effects stand in contrast to the conventional limnological paradigm emphasizing predominantly pelagic food webs.	Based on existing research and models, tube-dwelling invertebrates play a central role in controlling water column nutrient pools, hence water quality and trophic state. Furthermore, they influence the thresholds that determine shifts between alternate clear and turbid states of shallow lakes.	Hölker *et al.* (2015)
Genetic	Genetic diversity of wild plants for resilience against abiotic extremes and subsequent conditions.	Domestication provide genetic bottlenecks as cultivation involves only limited diversification, subsequent conscious or unconscious selection by farmers leads to a further narrowing of the gene pool.	The conservation of a diversity of crops and livestock reproductive material in gene banks constitute only "snap-shots" of the genetic diversity present at the time of collection. Knowledge about the diversity of wild plants is important to ensure long term viability of breeds and varieties.	Bellon *et al.* (2017)

Genetic	Genetic status of many farmed aquaculture species.	Lack of financial instruments, training and policies.	To monitor farmed types used for aquaculture and their wild counterparts for risk assessment when introducing non-native species and when managing native species including developed farmed types.	Sonesson *et al.* (2023)
Genetic	Genetic diversity can increase the resilience in ecosystems.	Experimentally increasing the genotypic diversity of the cosmopolitan seagrass *Zostera marina* has been shown to enhance ecosystem resilience.	A low genotypic diversity within a lake population of the pondweed *Stuckenia pectinata* was assumed to be the reason for slow recovery of macrophytes from eutrophication.	Reusch *et al.* (2005); Hilt *et al.* (2013)
Social	Underestimated extent of existence of the Vinaceous-breasted Parrot (*Amazona vinacea*) with conservative methods for wildlife management.	Conservative estimates used for the IUCN Red List underestimated the occurrence of the endangered bird, suggesting current range estimates being inadequate for planning purposes.	The increasing availability of citizen-science datasets offers a great opportunity to improve species distribution maps. eBird, WikiAves and Xeno-canto jointly produced 1.45 times more parrot detections, from samples that covered 45 times more municipalities, than the researcher-led counts.	Zulian *et al.* (2021)
Social	Knowledge about organisms and their functions	Missing connection to indigenous cultures	A lot of knowledge about biodiversity and functions is available in indigenous languages. Loss of languages and species leads to the extinction of knowledge.	Zimmer (2024)
Methodological	Insect biodiversity on a Global scale, especially in areas with low funding for biodiversity monitoring.	Access to cost -effective and non-invasive methods for global monitoring. Biodiversity hotspots are often not well equipped in funding and the killing of specimens is prohibited in many protected areas.	Smartphone-macro lens-based setup can enable low cost monitoring of insects. The method can enable researchers of all social backgrounds to contribute to insect monitoring, even in low income states and protected areas.	Riyaz & Ignacimuthu (2023)
Methodological	Habitat-specific eDNA assessments. For example, ponds which are highly diverse, yet understudied systems.	Combined knowledge and expertise to review applications and challenges that must be addressed for the future and consistency of habitat-specific eDNA monitoring .	Robust, comparable, and ecologically meaningful data to enable effective conservation and management	Harper *et al.* (2020)

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