SCIRES it
SCIentific RESearch and Information Technology
Ricerca Scientifica e Tecnologie dell'Informazione
Vol 15, Special Issue (2025), 11-22
e-ISSN 2239-4303, DOI 10.2423/i22394303v15Sp11

CASPUR-CIBER Publishing, http://www.sciresit.it

BIODIVERSITY IS NEITHER MATHEMATICS NOR CHEMISTRY

Ferdinando Boero

*University of Salento, University of Naples Federico II, Stazione Zoologica Anton Dohrn, CNR-IAS, Italy.

Abstract

Biology risks losing its core due to a reductionist approach dominated by mathematics and chemistry. To rebalance it, we need to reinvest in natural history and taxonomy, integrate diverse perspectives into holistic frameworks, prioritize scenario-building, and embrace uncertainty. Changing training and publication practices is essential to regain a deeper understanding of life and its diversity.

Keywords

Biodiversity, Ecology, Ecosystems, Biology, Reductionism, Genomics, Taxonomy, Predictive models, Natural history

1. *Introduction*

Biology, due to prevailing research trends, risks losing its core and being dominated by two reductionistic forces—mathematics and chemistry—at the expense of holistic visions towards broader perspectives. Predictive ecological models, genomics, sequencing, metabarcoding have enabled major discoveries, but are increasingly seen as sufficient for understanding biodiversity, evolution, and ecosystem function rather than complementary.

"Physics envy" in ecology and "chemistry envy" in evolutionary biology and biodiversity evaluation, both mediated by machines, contribute to narrowing the scope of inquiry.

Tools like the Digital Twin of the Ocean, Habitat Suitability Models, and Expert Opinions, along with genotypes to detect species, illustrate how biology drifts away from organismal and ecological reality. Data abundance and elegant models generate information, but genuine knowledge often lags.

To rebalance biology's direction, we must reinvest in natural history and taxonomy; integrate molecular, ecological, organismal, and historical perspectives into holistic frameworks; prioritize scenario building over rigid prediction; and embrace uncertainty and contingency as central, not incidental, to the living world.

This shift will enhance our understanding of what life is and how it manifests at the level of genes, species and ecosystems, as the definition of biodiversity calls for. Training and publication practices currently reinforce reductionistic imprinting; changing them is essential.

2. *The knowledge of biodiversity*

Biodiversity is a relatively new name for something humanity has known for a very long time: the variety of living organisms. In the Bible, Adam receives only one job from the Creator: to name animals (Boero, 2010; Valzano & Sartor, 2024). Noah, when instructed to save humans from the deluge, is told to take a pair of each species into the Ark. These stories reflect an early recognition of species diversity. Cave paintings, furthermore, often depict animals, merging observation, symbolic meaning, and nascent scientific interest.

Biodiversity has deep roots from the very early times in our culture: knowing plants and animals was crucial for our survival. This knowledge is not innate in our species and must be built individually, by acquiring a shared culture.

The biblical narratives urge both knowledge of biodiversity (naming species) and its preservation (the Ark). Naming, cataloguing, protecting species are acts aligned with these ancient imperatives. While these ideas hold religious resonance, they also make strong biological and social-ethical sense.

Natural history began with observing, describing, and naming species. Biodiversity exploration started from the surroundings of human settlements and expanded to the whole world with expeditions aimed at specimen collection, to display them in botanical and zoological gardens, and to preserve them in natural history museums.

Ecological and evolutionary biology built upon these taxonomic foundations to reconstruct relationships (phylogenies) and investigate processes like adaptation, competition, selection.

The discovery of DNA ushered in molecular genetics, which dug deeper than morphology and population genetics into the roots of heredity and variation. In parallel, the verbal, descriptive models of natural history were translated into an equational jargon, sparked by Lotka-Volterra's expression of predator-prey fluctuations, (Gatto, 2009).

The Convention on Biological Diversity (1992) formalized what species-based thinking has long implied, expanding its scope: biodiversity includes genetic diversity (within species), species diversity (between species), and ecosystem diversity (among ecosystems).

These investigative strands—pattern description, process explanation, molecular mechanisms—ran in parallel for some time, but a hierarchy of perceived importance emerged: molecular / process-oriented work (from genes to models) rose in prestige, due to their clarity, precision, apparent generality.

This trend led, and is leading, to great advances in the way we approach the study of living matter: modernity replaced tradition, with the feeling that describing nature is not so important, when predictions are at hand. As a result, biology neglected the central core of biodiversity (species) to investigate it either from a genetic or an ecological point of view. The holistic approach of natural history became fragmented by reductionism.

Biodiversity was pulled apart from its center (species and the science that studies them: taxonomy) and torn into two diverging directions, namely that of genomics and sequencing, and that of modeling (Fig. 1).

The detachment from the species approach and the focus on the extremes of the biodiversity conceptual array is the cause of the downgrading of biology to an ancillary science in respect to physics or chemistry, with biologists reduced to technicians that operate machines (Woese, 2004).

As Dyson (2012) observed, science advances in alternating phases: sometimes driven by new ideas, sometimes by new tools—but it stagnates when one dominates without the other.

For some decades the tool-driven tendency prevailed and this way of studying life gained logical primacy over ways that were perceived as old and outdated, especially taxonomy and natural history.

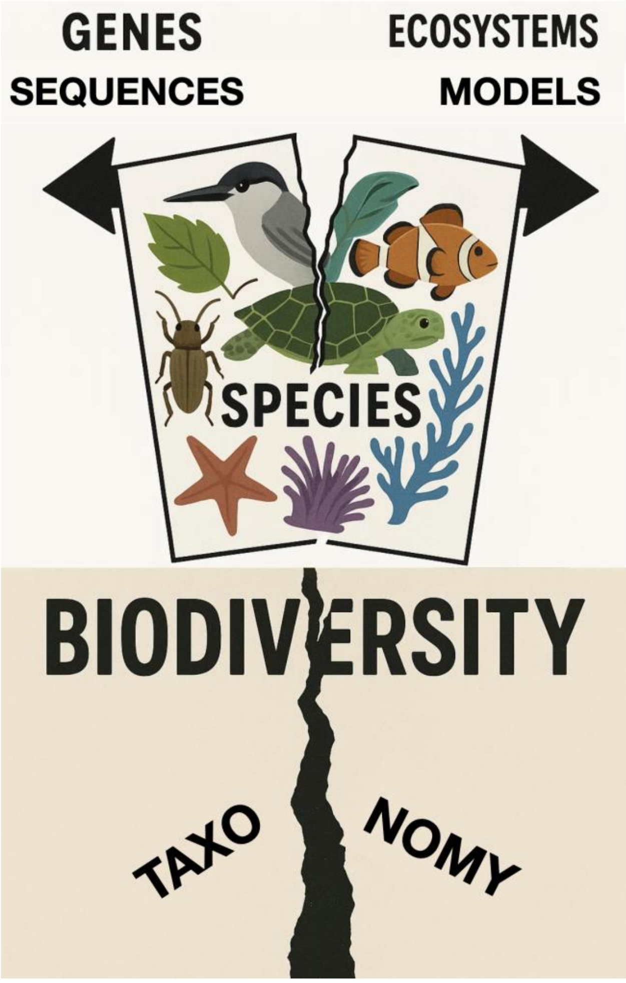

Fig. 1: The Two-Fold Split in Biodiversity Research. Genes and molecular sequences dominate one extreme, ecosystems and mathematical models the other, while species taxonomy and natural history lie torn in the middle. This visual metaphor illustrates how biology's core (species identity, context, ecological interactions) risks being fragmented - reduced to what machines and models can measure, rather than what life truly is.

This tendency still prevails, due to the great advancements it apparently brought, but scientists are starting to question it. The blessing of mathematical and chemical ways of explaining life processes is increasingly perceived as a curse, if pursued in a reductionistic fashion that does not result into a holistic, integrative synthesis.

3. *Physics envy and the Mathematical Curse*

Fascinated by the potential of mathematics in representing ecological interactions, ecologists became affected by physics envy and tried to mathematize their discipline with the aim of making it as scientific (i.e. predictive) as physics (Egler, 1986). Mathematically oriented ecologists and physicists tackled ecological problems with seminal papers that, for instance, mathematically addressed the issue of island biogeography (MacArthur and Wilson, 1963) and showed how simple mathematical models can have very complicated dynamics (May, 1976). Then, both May and Wilson somehow changed their minds. May, in fact, later recognized that models cannot replace data, or infer them from estimates, and asked a central question regarding biodiversity: *How many species are there on Earth?* (May, 1988). Models give the illusion of prediction. But the apparent precision of tight confidence intervals and elegant solutions cannot fully account for rich, complex, under-sampled systems. Removing "the rest" by considering just a few variables (e.g. a prey and its predator) does not do justice to the complexity of living systems.

Mathematical models are aimed at performing predictions, but their precision does not necessarily coincide with accuracy. They should be judged by the consideration they give to the relevant variables that interact with each other and contribute to the behavior of the modeled system. If relevant variables are omitted, the models are irrelevant.

In spite of May's (1988) question on the number of species, taxonomy entered a state of crisis and the knowledge of biodiversity was hindered by the taxonomic impediment (Boero, 2010). The number of papers pretending to deal with biodiversity without considering it seriously, while not knowing species, is steadily increasing (Mammola et al., 2023). This gives an illusion of knowledge and care for biodiversity, with promises that are not maintained: biodiversity exploration is replaced by models, estimates and surrogates (see below).

Mathematics, of course, must be used as a statistical tool to evaluate the outcomes of observations and experiments, but when predictions are invoked, then its power appears evidently flawed: there are no crystal bowls, especially when far too many variables are simply ignored.

After so many false promises of the efficacy of mathematical approaches to biology, biologists started to react. Edward Wilson, a great advocate of the importance of knowing biodiversity, published in the Wall Street Journal an article with a very strong title: *Great Scientist ≠ Good at Math.* Mathematicians reacted to this statement (Wilson and Frenkel, 2013) and some arrived to label Wilson's claim as foolish and offensive.

The debate about the effectiveness of mathematics in biological sciences is still burning, with papers like Kauffman and Roli (2023) that end with: "*There really is no 'theory of everything': The diachronic evolution of our or any biosphere is beyond entailing law and beyond any mathematics based on set theory*" (p. 6). This is further argued by Garte, Marshall and Kauffman (2025) with a paper whose title says it all: *The reasonable ineffectiveness of mathematics in the biological sciences.* It is evocative that Stuart Kauffman heavily relied on mathematics in his masterpiece on *The Origins of Order* (Kauffman, 1993), to later recognize the limits of mathematics and the need for more humility in those who pretend to explain life with equations. This conversion is parallel to Robert May's shift from "simple mathematical models" to "how many species are there on Earth?" (May, 1976; 1988): May, Wilson and Kauffman, clearly recognized the limits of "predictive" ecology based on mathematical approaches. Boero et al. (2004, 2015) and Doak et al. (2008), among others, reinforced this request for more "humility" when tackling complex problems with promises of predictions that are inherently impossible.

Such positions are obviously not shared by mathematically oriented scientists, such as the advocates of the Digital Twin of the Ocean (DTO)—a set of models that aims at replicating the features of the ocean so as to allow for predictions about its future states (e.g. Miedtank et al., 2024; Drillet et al., 2025). Since satellites cannot tell what the conditions are below the surface, a world fleet of automated vehicles was released in the ocean, aimed at measuring important physical and biogeochemical variables, from the surface to the deep. This observation network is further supported by sensors carried both by buoys and oceanographic vessels.

The biological features of the ocean (i.e. biodiversity and ecosystems), however, are poorly represented in the DTO, since automated sensors of biodiversity have not been developed yet. This flaw in providing biodiversity data to mathematical models such as the DTO is currently coped with by chemistry in the form of molecular genetics and genomics (see below). Without a decent representation of biodiversity and ecosystems the Twin is just a Dummy: the relevance of physics, chemistry and biogeochemistry becomes evident if their changes affect biodiversity and ecosystems: it is the response of biodiversity and ecosystems that gives a meaning to physical and chemical changes. To cope with the discrepancy between abundant physical and chemical information and scant biodiversity knowledge, it is increasingly proposed that biodiversity data can be generated by using models to impute or simulate the missing bits. For example, Bowler et al. (2025) frame the problem as missing data, and propose weighting, simulation, and imputation to correct for biases in species trend estimates. Furthermore, trait databases use methods like Bayesian hierarchical matrix factorization to "predict" missing trait values (Gorné et al., 2025), thus filling gaps via modeling while admitting that strategy, metadata, context and natural history matter.

The paucity of accurate distribution records for marine biodiversity is often coped with Habitat Suitability Models (HSM). Some of the clearest illustrations of how HSM can both promise insight and pose risk regard *Posidonia oceanica*, the iconic Mediterranean seagrass. A review by Bertelli et al. (2022) shows that most seagrass HSM rely on well-known environmental layers and cross-validation, rather than field surveys or external checks.

If models' predictions are accepted without ground-truthing, we risk treating what are essentially educated guesses as if they reflect real, occupied habitat. This supports the broader point: abundant or wide-ranging data and models are not the same as verified ecological knowledge.

Another surrogate of missing data and knowledge is the growing tendency to substitute or elevate expert opinion in place of empirical field data. When data are scarce, costly, or difficult to obtain, researchers often fall back on asking "experts" to predict species' presence, habitat suitability, or future outcomes. Sometimes assembling such opinions becomes the basis of conservation planning or "accepted truth," even without field verification.

Reviews (Drescher et al., 2019; Dorrough et al., 2024) show that expert knowledge is becoming a significant trend in ecological literature, often with little transparency about how experts are selected or how opinions are combined, and with limited checks against observation.

Efforts to address the severe gaps in biodiversity knowledge, long driven by attempts to model nature mathematically, are now increasingly undertaken using chemical-molecular approaches.

4. *Chemistry Envy and the Molecular Curse*

Maddox's lapidary statement "*Life is chemistry*" (1995) underlines that biology's envy isn't only toward physics, but also toward chemistry. The advent of genomics, in fact, led to the chemical exploration of biodiversity. As mentioned above, May (1988) warned that until we conduct baseline systematic surveys, species estimates must be treated with caution, calling for sustained taxonomic efforts and declaring mistrust for guesses not based on real data. In spite of this warning,

Locey and Lennon (2016) propose the possibility of one trillion microbial species, whereas Mora et al. (2011) estimate ~10 million non-microbial species, most undescribed. Bouchet (2006) estimated marine eukaryotic biodiversity and concluded most species remain formally undescribed.

Instead of field-based taxonomy, as May (1988) advised, biodiversity work increasingly focuses only on genes, as if knowing genes were sufficient to know biodiversity. Chemistry and molecular biology tools (PCR, sequencing, metabarcoding, environmental DNA) are powerful and have revealed enormous novelty.

For instance, the Tara and Malaspina projects uncovered many uncharacterized genes, unknown lineages, and genetic novelty (Sunagawa et al., 2015; de Vargas et al., 2015; Sánchez, 2024). But many such "discoveries" are provisional: the number of species formally named after purely molecular detection remains low (Jones, 2025).

Genetic sequences (i.e. the chemical characterization) of unknown species cannot tell us much about what species are actually out there, and what they do to make ecosystems function.

The pioneer phase of biodiversity exploration led to the publication of monographs on the discovered taxa, with descriptions and figures of all the species found in a given region, often with accounts on their ecology and biology. This "phenotypic" information can be enhanced by molecular approaches that, however, cannot replace the knowledge of phenotypes. Genomic analyses often claim to have found many new species (from a molecular standpoint) but do not lead to monographic accounts on biodiversity.

The illusion of fully understanding what life is by exploring it from a chemical standpoint is not only a curse for biodiversity but also for evolutionary biology. Woese (2004) puts it clearly: "*Biology today is at a crossroads. The molecular paradigm ... is no longer a reliable guide*." He warns that following molecular biology uncritically transforms biology into a technical discipline rather than preserving its capacity for inquiry into life's complexities, as a science should do.

Identifying species by metabarcoding and other molecular techniques has become an almost entirely machine-driven enterprise: machines extract and purify DNA automatically, sequencers generate raw reads, software pipelines clean and filter data, sequence matching tools compare signatures with reference libraries, and phylogenetic inference algorithms reconstruct evolutionary relationships. This chain of technical processes (e.g., Buchner et al., 2021) often gives the appearance of scientific insight, but much of it is dominated by engineering, automation, and computation rather than direct observation, ecological or phenotypic knowledge.

The critique of Woese (2004) to such approaches is burning: "*By the end of the 20th century, however, the molecular vision of biology had in essence been realized; what it could see of the master plan of the living world had been seen, leaving only the details to be filled in. What a stunning example of a biology that operates from an engineering perspective, a biology that has no genuine guiding vision!*" and then: "*Biology today is little more than an engineering discipline*"! Contrary to what Maddox (1995) proposed, Life is not only chemistry (and it is not only physics)!

5. *Information is not knowledge*

The editorial entitled *The Data Deluge* (Anonymous, 2012) warned of a new era where biology and related disciplines are flooded with massive volumes of raw data such as genomic sequences, imaging, environmental sensor readouts, etc. faster than we have tools or theory to digest them. The editorial emphasized that generating data is only one part of the scientific enterprise; equally crucial are curation, accessibility, interpretative frameworks, and instruments to visualize, analyze, and reuse data meaningfully, so as to transform information into knowledge.

That warning resonates sharply with what we see in ecology and biodiversity work, as illustrated by Rivetti et al. (2014), who tapped into existing, large-scale oceanographic data (much of which was almost never fully used to answer biological questions) then linked temperature anomalies with recorded mass mortalities of benthic invertebrates in the Mediterranean, substantiating the impact of physical change on biodiversity.

On a broad scale, Rivetti et al. (2014) revealed the clear and significant differences in strategic planning and coverage between biodiversity data and physical-parameter data: data on species identity, abundances, ecological interactions are collected without standardized strategy, are geographically and taxonomically biased, and lack comparable metadata.

Temperature and physical variables are often collected under long-term strategic monitoring programs with consistent protocols, and stored in open databases, whereas biodiversity observations are largely opportunistic.

This strategic void in biodiversity appreciation weakens the translation from available information to knowledge that is conducive to further understanding. Hochkirch et al. (2021), among others, have documented these gaps and proposed frameworks to fill them. When data are abundant but uncoordinated, the absence of ecological background limits inference, prediction of scenarios, and deeper understanding. Gathering lots of data is good tactics if guided by a strategy that, however, at present seems to be mostly missing.

6. *Surrogates are not enough*

The critical remarks on the prevalent search for surrogates of reality, either as mathematical models or as sequences, delineate a rising concern about such practices. However, the awareness of the combination of the two tendencies, one affecting ecology and the other affecting evolutionary biology, together with species identification, is rare in the scientific community, emerging more in epistemological domains.

The philosophers Brigandt and Love (2023), in fact, warn that "*decomposition of biological systems into lower-level parts and simplifying or ignoring the environmental, developmental, or ecological context*" risks losing sight of higher-level interactions. They emphasize that "*the effect of a molecular entity or mechanism may strongly depend on the context in which it occurs … so that the same pathway can be involved in different functions in different species or in different parts of an individual*." Moreover, the problem of multiple realization is central, since "*the same higher level phenomenon … can be produced by several different molecular mechanisms … many molecular kinds can correspond to one higher level kind*."

In short, Brigandt and Love (2023) help show that molecular/chemical reductionism and mathematical/modeling reductionism aren't separate problems: they reinforce each other, downplaying the biological complexity of natural history, ecology, and phenotypic variation. So far, the critique of ecology's over-mathematization (physics envy) and the critique of evolutionary biology's over-molecularization (chemistry envy) have often been aired separately within different portions of the scientific community. Boero and Mergeay (2023) are an exeption by arguing they represent two sides of the same phenomenon: biology's surrender to mathematics and physics, and chemistry. They also warn that policy and funding often demand predictions, and that too many "naturalists" (i.e., ecologists/evolutionary biologists) feel compelled to deliver them, even when predictions are impossible. Together, these critiques suggest biology has ceded too much, letting machines (computers, sequencing tools, PCR, mathematical abstractions) shape what counts as knowledge. The risk is that biology becomes what instruments can measure, rather than what life in all its complexity truly is.

7. Where to go from here

Both mathematical and molecular approaches bring tremendous value and must continue to be refined. However, many treat them not just as necessary, but as sufficient per se for understanding the living world, as claimed by Cooper (2024) who raised a case against simplistic genetic explanations of evolution.

The reduction of biology to "simpler" physics and chemistry resonates with a cognitive bias described as attribute substitution by Kahneman and Frederick (2002): when faced with a difficult, multifaceted question, humans (including scientific communities) tend to substitute a simpler, more tractable question and treat its answer as if it addressed the original one. Hence, biology is reduced to physics and chemistry! Boero and Mergeay (2023) observe exactly this: many modelling efforts and molecular extrapolations are claimed to have broad predictive power, yet many eco-evolutionary phenomena defy predictability due to history, contingency, scale, and non-linearity. Mathematical models dominate ecology; molecular approaches are often taken as the gold standard in evolutionary biology and biodiversity assessment. Meanwhile, neglecting natural history and taxonomy has produced oversimplifications.

Physics and mathematics are at the base of the hyerarchy of complexity of the natural sciences, followed by Chemistry which, in biology, comprises both biochemistry and molecular biology.

Cell biology considers a higher level of organization, the cell being the basic building block of living matter. Organismal biology considers both the form and function of living beings, with anatomy and the physiology. Developmental biology studies the life cycles of organisms, from simple to more complex stages.

Ecology studies the interactions among organisms. Evolutionary biology studies speciation and natural selection, and biodiversity is its product.

Ecology and evolution, together, form natural history (Fig.2).

Ecology, on the one hand, relies much on mathematical models and tries to be predictive. Whereas, on the other hand, chemistry is widely used to understand the form and function of living beings at all levels of organization.

Both approaches, the mathematical and the chemical ones, have heavily contributed to the understanding of biological facts. Their success, however, has led to the dismissal of observation, the main scientific method of natural history. The reductionist understanding must be upgraded to a synthesis that is still missing.

The knowledge gaps on species and their interactions call for a revival of natural history, taxonomy, and ecological field work, as convincingly argued by Boudouresque et al. (2020). Investigations with these aims can make much better use of molecular techniques, but knowledge must build upwards: from chemistry (sequencing etc.), through taxonomy (what species exist), to ecology (what they do *in situ*).

Models and sequences should follow, not lead; they must be rooted in empirical reality, sensitive to ecological nuance and historical contingency.

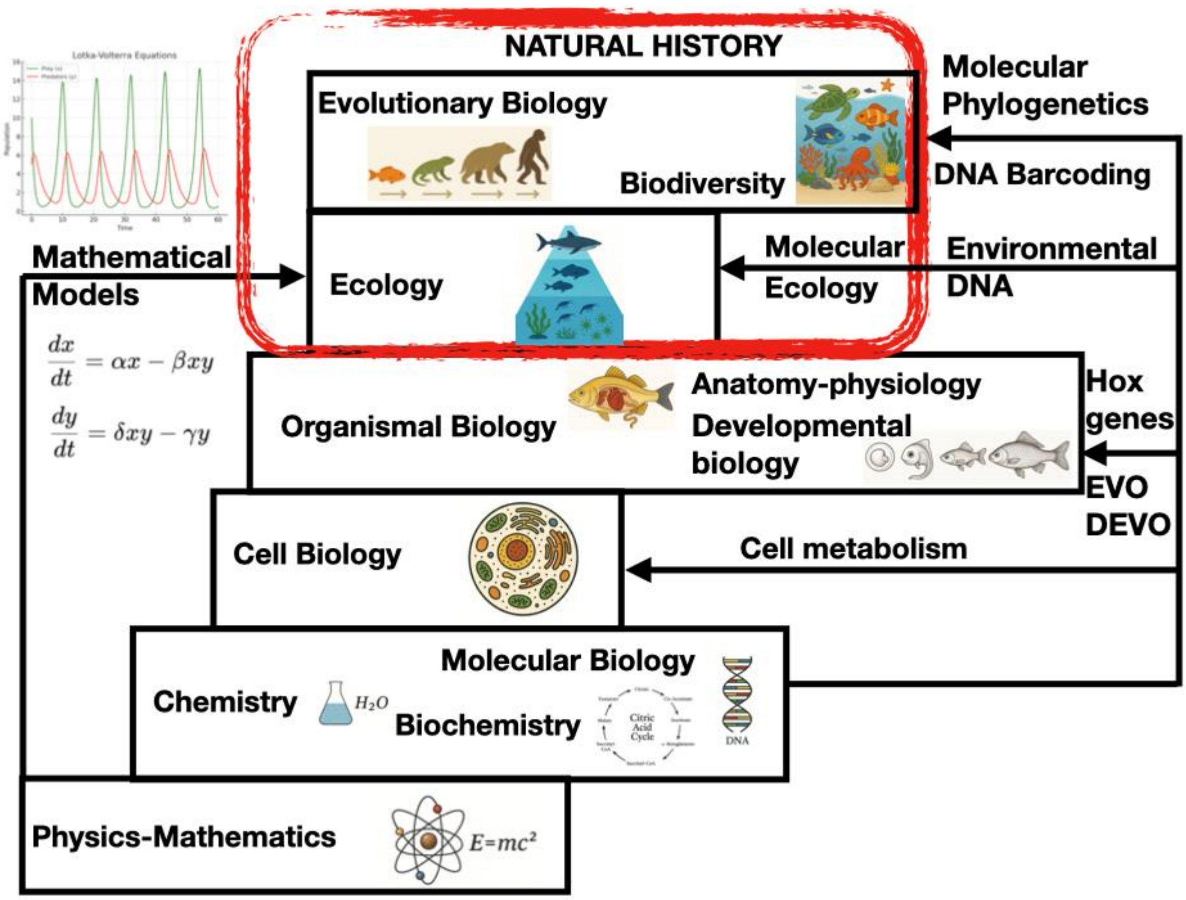

Fig. 2: The hierarchy of complexity of the natural sciences

To revert the tendency privileging reductionism against integration, the priorities are clear: favor scenarios over rigid predictions in complex systems, recognize and transparently communicate uncertainty, broaden attention to neglected taxa (microbes, fungi, invertebrates) and under-explored regions (deep sea, tropics), with a timely exploration of biodiversity, integrating molecular, organismal, ecological, and historical data; let molecular data and mathematical models be part of the picture, not its definition. A possible roadmap in this direction is sketched in Boero (2024).

This change in perspective, however, requires a shift in how scientists are trained and in the career opportunities offered to them. PhD theses tend to embed a reductionistic imprinting reminiscent of Lorenz's ethological notion of sensitive periods. Journals of high rank tend to favor 'robust' molecular or mathematical work, teaching researchers to stay strictly within those boundaries. Boero (2015) argues that, before tenure, deviation from the mainstream is risky, and only afterward one may try new directions, but often by then it's 'too late': once the reductionistic imprinting has been internalized, the transition to more integrative science becomes arduous. Hill et al. (2025) show that researchers who pivot far from their prior work experience suffer significantly reduced impact, fewer publication successes, and hindered career progression. It's a Catch-22: to innovate you must change, but if you change you risk being shut out. At present, biological training programs do not have holistic and integrative objectives, focusing on hyperspecialization. Top-down policies should encourage such a transition.

The European Union, for instance, explicitly mentions holistic approaches in its calls for projects. The route towards change, however, is delineated, as The European Marine Board (2024) recommends to "*train a new generation of marine taxonomists and systematicians in Europe through the reinforcement of dynamic collaborative networks, the mainstreaming of taxonomy training schools, and reintegration of this fundamental knowledge into university curricula to ensure this expertise is not lost*".

Such concepts have been repeated over and over again, one for all by Ricklefs (2012) whose summary ends with "*The diversity, abundances, and distributions of species represent the unfolding of many processes over a historically and geographically contingent landscape, for which experimental methods of scientific inquiry are poorly suited. To interpret patterns of diversity, we must continue to depend on inductive reasoning inspired by the data of natural history*". In spite of the validity of these arguments, the scientific community still resists to their strength. Instead of being shortcuts towards biological understanding, technological approaches with no biological insight are just short-circuits.

Acknowledgements

Virginia Valzano invited me to produce this essay. No direct support was available, but I profited earlier from funding from various DGs of the European Commission, the National Science Foundation of the USA via the Partnership for Enhancing Expertise in Taxonomy, several Italian Ministries. Participation to the activities of the Mediterranean Commission (CIESM), the European Network of Excellence on Marine Biodiversity and Ecosystem Functioning, the European Marine Board, and the European Academies Science Advisory Council has been conducive to developing what is proposed here.

This little essay is dedicated to the memory of Walter J. Gehring (1939–2014). He mastered molecular genetics, but he remained deeply attentive to organisms and their natural history; his work and his zoology textbook exemplify the awarness that biology must be integrative. I do not claim that he voiced the precise arguments presented here, but his career — moving fluidly between genes and animals — embodies the conviction that biological understanding requires connection across levels.

References

Anonymous. (2012). The data deluge. *Nature Cell Biology*, *14*, 775. https://doi.org/10.1038/ncb2558

Bertelli, C. M., Stokes, H. J., Bull, J. C., & Unsworth, R. K. F. (2022). The use of habitat suitability modelling for seagrass: A review. *Frontiers in Marine Science, 9*, 997831. https://doi.org/10.3389/fmars.2022.997831

Boero, F. (2010). The study of species in the era of biodiversity: A tale of stupidity. *Diversity, 2*(1), 115–126. https://doi.org/10.3390/d2010115

Boero, F. (2015). Scientists can be free, but only once they are tenured. *Ethics in Science and Environmental Politics, 15*(1), 63–69. https://doi.org/10.3354/esep00164

Boero, F. (2024). A roadmap to knowledge-based maritime spatial planning. *Advances in Marine Biology, 131*. https://doi.org/10.1016/bs.amb.2024.07.003

Boero, F., Belmonte, G., Bussotti, S., Fanelli, G., Fraschetti, S., Giangrande, A., Gravili, C., Guidetti, P., Pati, A., Piraino, S., Rubino, F., Saracino, O., Schmich, J., Terlizzi, A., & Geraci, S. (2004). From biodiversity and ecosystem functioning to the roots of ecological complexity. *Ecological Complexity, 2*, 101–109. https://doi.org/10.1016/j.ecocom.2004.01.003

Boero, F., Kraberg, A. C., Krause, G., & Wiltshire, K. H. (2015). Time is an affliction: why ecology cannot be as predictive as physics and why it needs time series. *Journal of Sea Research, 101*, 12–18. https://doi.org/10.1016/j.seares.2014.07.008

Boero, F., & Mergeay, J. (2023). Darwin's feathers: Eco-evolutionary biology, predictions and policy. *Advances in Marine Biology, 95*, 91–111. https://doi.org/10.1016/bs.amb.2023.08.004

Bouchet, P. (2006). The magnitude of marine biodiversity. In C. M. Duarte (Ed.), *The Exploration of Marine Biodiversity: Scientific and Technological Challenges* (pp. 33–64). Fundación BBVA.

Boudouresque, C. F., Médail, F., Ponel, P., Astruch, P., Barcelo, A., Blanfune, A., Changeux, T., Chevaldonné, P., Cheylan, G., Le Diréach, L., Martin, G., Moussay, C., Peirache, M., Perret-Boudouresque, M., Ruitton, S., Taupier-Letage, I., & Thibaut, T. (2020). Species-based or ecosystem-based approaches to conservation practices: Lessons from the Port-Cros National Park (South-East France, Mediterranean Sea). *Vie et Milieu / Life & Environment, 70*(3–4), 89–112.

Bowler, D. E., Boyd, R. J., Callaghan, C. T., Robinson, R. A., Isaac, N. J. B., & Pocock, M. J. O. (2025). Treating gaps and biases in biodiversity data as a missing data problem. *Biological Reviews, 100*(1), 50–67. https://doi.org/10.1111/brv.13127

Brigandt, I., & Love, A. (2023). Reductionism in biology. In E. N. Zalta & U. Nodelman (Eds.), *The Stanford Encyclopedia of Philosophy (Summer 2023 Edition)*. Retrieved from https://plato.stanford.edu/archives/sum2023/entries/reduction-biology/

Buchner, D., Macher, T.-H., Beermann, A. J., Werner, M.-T., & Leese, F. (2021). Standardized high-throughput biomonitoring using DNA metabarcoding: strategies for the adoption of automated liquid handlers. *Environmental Science & Ecotechnology, 8*, 100122. https://doi.org/10.1016/j.ese.2021.100122

Convention on Biological Diversity. (1992). *Convention on Biological Diversity (Rio de Janeiro, 5 June 1992)*. United Nations Treaty Series, 1760, 79.

Cooper, K. L. (2024). The case against simplistic genetic explanations of evolution. *Development, 151*(20), dev203077. https://doi.org/10.1016/j.dev.2024.203077 de Vargas, C., Audic, S., Henry, N., Decelle, J., Mahé, F., Logares, R., Lara, E., Berney, C., Le Bescot, N., Probert, I., Carmichael, M., Poulain, J., Romac, S., Colin, S., Aury, J.-M., Bittner, L., Chaffron, S., Dunthorn, M., Engelen, S., Flegontova, O., Guidi, L., Jaillon, O., Not, F., Ogata, H., Pesant, S., Speich, S., … Bowler, C. (2015). Eukaryotic plankton diversity in the sunlit ocean. *Science, 348*(6237), 1261605. https://doi.org/10.1126/science.1261359

Doak, D. F., Estes, J. A., Halpern, B. S., Jacob, U., Lindberg, D. R., Lovvorn, J., Monson, D. H., Tinker, M. T., Williams, T. M., Wootton, J. T., Carroll, I., Emmerson, M., Micheli, F., & Novak, M. (2008). Understanding and predicting ecological dynamics: Are major surprises inevitable? *Ecology, 89*(4), 952–961. https://doi.org/10.1890/07-0965.1

Dorrough, J., Travers, S. K., Val, J., Scott, M. L., Moutou, C. J., & Oliver, I. (2024). Evaluating models of expert judgment to inform assessment of ecosystem viability and collapse. *Conservation Biology, 39*(2), e14370. https://doi.org/10.1111/cobi.14370

Drescher, M., Edwards, R. C., & Wiersma, Y. (2019). A systematic review of transparency in the methods of expert knowledge use. *Journal of Applied Ecology, 56*(2), 436–449. https://doi.org/10.1111/1365-2664.13275

Drillet, Y., Fablet, R., Federico, I., Le Sommer, J., Mészáros, L., Seracini, M., She, J., Staneva, J., Trotta, G., Castillo, M., Melo, C., Brajard, J., Garcia, T., & Malicet, M. (2025). EDITO-Model Lab: towards the next generation of ocean numerical models. *One Ocean Science Congress 2025*, OOS2025-587. https://doi.org/10.5194/oos2025-587

Dyson, F. J. (2012). Is science mostly driven by ideas or by tools? *Science, 338*(6113), 1426–1427. https://doi.org/10.1126/science.1232773

Egler, F. E. (1986). Physics envy in ecology. *Bulletin of the Ecological Society of America, 67*, 233–235. https://doi.org/10.2307/20166525

European Marine Board. (2024). *Navigating the Future VI: Placing the Ocean within the wider Earth system* (Position Paper 28). https://doi.org/10.5281/zenodo.13329469

Garte, S., Marshall, P., & Kauffman, S. (2025). The reasonable ineffectiveness of mathematics in the biological sciences. *Entropy, 27*(3), 280. https://doi.org/10.3390/e27030280

Gatto, M. (2009). On Volterra and D'Ancona's footsteps: The temporal and spatial complexity of ecological interactions and networks. *Italian Journal of Zoology, 76*(1), 3–15. https://doi.org/10.1080/11250000802364657

Gorné, L. D., Aguirre-Gutiérrez, J., Coelho, F. C., Swenson, N. G., Kraft, N. J. B., Marimon, B. S., Baker, T. R., de Lima, R. A. F., Vilanova, E., Álvarez-Dávila, E., Mendoza, A. M., Llampazo, G. R. F., dos Santos, R. M., Boenisch, G., Araujo-Murakami, A., Torres, G. F. R., Ramírez-Angulo, H., dos Santos Prestes, N. C., Morandi, P. S., Ribeiro, S. C., Cruz, W. J., Disney, M, Di Fiore, A, Marimon-Junior, B. H, Feldpausch, T. R, Malhi, Y, Phillips, O, Galbraith, D, & Díaz, S. (2025). Use and misuse of trait imputation in ecology: The problem of using out-of-context imputed values. *Ecography (early view)*. https://doi.org/10.1111/ecog.07520

Hill, R., Yin, Y., Stein, C., Wang, X., Wang, D., & Jones, B. F. (2025). The pivot penalty in research. *Nature, 642*(8069), 999–1006. https://doi.org/10.1038/s41586-025-09048-1

Hochkirch, A., Samways, M. J., Gerlach, J., Böhm, M., Williams, P., Cardoso, P., Cumberlidge, N., Stephenson, P. J., Seddon, M. B., Clausnitzer, V., Borges, P. A. V., Mueller, G. M., Pearce-Kelly, P., Raimondo, D. C., Danielczak, A., & Dijkstra, K. D. B. (2021). A strategy for the next decade to address data deficiency in neglected biodiversity. *Conservation Biology, 35*(2), 502–509. https://doi.org/10.1111/cobi.13589

Jones, B. (2025). The search for Earth's most mysterious creatures is turning up extraordinary results. *Vox*. Retrieved from https://www.vox.com/down-to-earth/459398/animals-species-unknown-dark-taxa

Kahneman, D., & Frederick, S. (2002). Representativeness revisited: Attribute substitution in intuitive judgment. In T. Gilovich, D. Griffin, & D. Kahneman (Eds.), *Heuristics and Biases: The Psychology of Intuitive Judgment* (pp. 49-81). Cambridge University Press. https://doi.org/10.1017/CBO9780511808098.004

Kauffman, S. A. (1993). *The Origins of Order: Self-Organization and Selection in Evolution*. Oxford University Press. Retrieved from https://academic.oup.com/book/53153

Kauffman, S. A., & Roli, A. (2023). A third transition in science? *Interface Focus, 13*, 20220063. https://doi.org/10.1098/rsfs.2022.0063

Locey, K. J., & Lennon, J. T. (2016). Scaling laws predict global microbial diversity. *Proceedings of the National Academy of Sciences, 113*(21), 5870–5875. https://doi.org/10.1073/pnas.1521291113

MacArthur, R. H., & Wilson, E. O. (1963). An equilibrium theory of insular zoogeography. *Evolution, 17*(4), 373–387. https://doi.org/10.1111/j.1558-5646.1963.tb03295.x

Maddox, J. (1995). On the widespread distrust for science. *Nature, 378*, 435–438. https://doi.org/10.1038/378435a0

Mammola, S., Fukushima, C. S., Biondo, G., Bongiorni, L., Cianferoni, F., Domenici, P., Fruciano, C., Lo Giudice, A., Macias-Hernández, N., Malumbres-Olarte, J., Milicic, M., Morganti, M., Mori, E., Munévar, A., Pollegioni, P., Rosati, I., Tenan, S., Urbano-Tenorio, F., Fontaneto, D., & Cardoso, P. (2023). How much biodiversity is concealed in the word 'biodiversity'? *Current Biology, 33*(2), R59–R60. https://doi.org/10.1016/j.cub.2022.12.003

May, R. M. (1976). Simple mathematical models with very complicated dynamics. *Nature, 261*, 459–467. https://doi.org/10.1038/261459a0

May, R. M. (1988). How many species are there on Earth? *Science, 241*(4872), 1441–1449. https://doi.org/10.1126/science.241.4872.1441

Miedtank, A., Schneider, J., Manss, C., & Zielinski, O. (2024). Marine digital twins for enhanced ocean understanding. *Remote Sensing Applications: Society and Environment, 36*, 101268. https://doi.org/10.1016/j.rsase.2024.101268

Mora, C., Tittensor, D. P., Adl, S., Simpson, A. G. B., & Worm, B. (2011). How many species are there on Earth and in the ocean? *PLOS Biology, 9*(8), e1001127. https://doi.org/10.1371/journal.pbio.1001127

Ricklefs, R. E. (2012). Natural history and the nature of biological diversity. *American Naturalist, 179*(4), 423–435. https://doi.org/10.1086/664622

Rivetti, I., Fraschetti, S., Lionello, P., Zambianchi, E., & Boero, F. (2014). Global warming and mass mortalities of benthic invertebrates in the Mediterranean Sea. *PLOS ONE, 9*(12), e115655. https://doi.org/10.1371/journal.pone.0115655

Sánchez, P., Coutinho, F. H., Sebastián, M., Pernice, M. C., Rodríguez-Martínez, R., Salazar, G., Cornejo-Castillo, F. M., Pesant, S., López-Alforja, X., López-García, E. M., Agustí, S., Gojobori, T., Logares, R., Sala, M. M., Vaqué, D., Massana, R., Duarte, C. M., Acinas, S. G., & Gasol, J. M. (2024). Marine picoplankton metagenomes and MAGs from eleven vertical profiles obtained by the Malaspina Expedition. *Scientific Data, 11*, 154. https://doi.org/10.1038/s41597-024-02974-1

Sunagawa, S., Coelho, L. P., Chaffron, S., Kultima, J. R., Labadie, K., Salazar, G., Djahanschiri, B., Zeller, G., Mende, D. R., Alberti, A., Cornejo-Castillo, F. M., Costea, P. I., Cruaud, C., D'Ovidio, F., Engelen, S., Ferrera, I., Gasol, J. M., Guidi, L., Hildebrand, F., Lima-Mendez, G., Poulain, J., Poulos, B. T., Royo-Llonch, M., Sarmento, H., Vieira-Silva, S., Dimier, C., Picheral, M., Searson, S., Kandels-Lewis, S., Boss, E., Follows, M., Karp-Boss, L., Krzic, U., Reynaud, E. G., Sardet, C., Sieracki, M., Velayoudon, D., Bowler, C., De Vargas, C., Gorsky, G., Grimsley, N., Hingamp, P., Iudicone, D., Jaillon, O., Not, F., Ogata, H., Pesant, S., Speich, S. (2015). Structure and function of the global ocean microbiome. *Science, 348*(6237), 1261359. https://doi.org/10.1126/science.1261359

Valzano, V,.& Sartor, G. (2024). Biodiversity and Literature, Music and Technological Applications. *SCIRES-IT - SCIentific RESearch and Information Technology, 14*(Special Issue), 71-90. http://www.sciresit.it

Wilson, E. O., & Frenkel, E. (2013). Two views: How much math do scientists need? *Notices of the American Mathematical Society, 60*(7), 837–838.

Woese, C. R. (2004). A new biology for a new century. *Microbiology and Molecular Biology Reviews*, *68*(2), 173–186. https://doi.org/10.1128/MMBR.68.2.173-186.2004