Zoological Synthesis
eISSN: 3122-7112
https://zs.cultechpub.com/index.php/zs
Copyright: © 2025 by the authors. This article is published by the Cultech Publishing Sdn. Bhd. under the terms of the Creative Commons Attribution4.0 International License (CC BY 4.0): https://creativecommons.org/licenses/by/4.0/

Modern Taxonomic Tools in the Race Against Anthropogenic Extinction

Lea Angela Mercado*

Department of Ecology, Bicol University, Legazpi City, Albay, Philippines

*Corresponding author: Lea Angela Mercado, angelaMercado@bicol-u.edu.ph

Abstract

The ongoing anthropogenic extinction crisis, characterized by unprecedented rates of biodiversity loss, demands a similarly unprecedented response from the scientific community. A fundamental, yet historically rate-limiting, challenge is the incomplete inventory of life on Earth-the "taxonomic impediment." Many species are disappearing before they are even discovered and described, crippling conservation prioritization and action. This review argues that we are in the midst of a renaissance in taxonomic science, driven by a suite of integrative, high-throughput tools that are radically accelerating species discovery, delimitation, and monitoring. We synthesize the transformative impact of genomic techniques (e.g., ultra-conserved elements, whole-genome sequencing), high-throughput methods (eDNA metabarcoding, digital imaging, bioacoustics), and cyber-infrastructure (integrative databases, AI-driven image/sound recognition). We present a comparative analysis of these tools (Table 1) and a conceptual framework for an integrated taxonomic workflow (Figure 1). Case studies from global biodiversity hotspots illustrate how these tools are moving taxonomy from a reactive, descriptive discipline to a proactive, predictive, and foundational pillar of conservation biology. However, we also critically examine persistent challenges, including data integration, equitable access, and the need for parallel training in morphological and molecular skills. Ultimately, modern taxonomy, empowered by technological convergence, provides the essential data pipeline to document biodiversity, identify threats, and inform timely conservation interventions in the race against extinction.

Keywords

Taxonomy, Biodiversity Crisis, Species Discovery, eDNA, Conservation Prioritization, Anthropocene, Integrative Methods

1. Introduction

The Crisis and the Impediment

Planet Earth is experiencing a sixth mass extinction event, driven unequivocally by human activities-habitat destruction, climate change, pollution, and overexploitation. Current extinction rates are estimated to be 100 to 1,000 times higher than background rates, with profound consequences for ecosystem function and resilience. In this urgent context, a stark paradox emerges: we are losing biodiversity faster than we can catalogue it [1]. This is known as the "taxonomic impediment"-the critical gap between the number of species existing and the number formally described by science. It is estimated that of the approximately 8.7 million eukaryotic species on Earth, only about 1.5 million have been described. For many hyperdiverse groups like insects, fungi, and deep-sea organisms, the deficit is staggering [2].

Traditional taxonomy, based primarily on comparative morphology, is meticulous but slow. The process of collection, expert examination, illustration, and description is a bottleneck in the face of exponential biodiversity loss. Furthermore, cryptic species complexes-groups of morphologically similar but genetically distinct species-are often overlooked, leading to severe underestimations of diversity and misdirected conservation efforts. The consequence is that conservation resources may be allocated to a single named species that actually represents several, each with potentially different ecological requirements and threat levels [3].

This review posits that overcoming the taxonomic impediment is the first and most critical strategic step in effective conservation. We are no longer limited to scalpels and microscopes alone. A new, integrative taxonomy is emerging, powered by technological convergence across genomics, sensor technology, and informatics. This article synthesizes these modern tools, evaluates their applications and limitations through comparative analysis, and demonstrates how they are transforming taxonomy into a high-throughput, data-rich science capable of meeting the demands of the Anthropocene extinction crisis [4].

2. The Genomic Revolution in Species Delimitation and Phylogenetics

The application of molecular data has already revolutionized taxonomy over recent decades, but contemporary genomic tools offer orders of magnitude more power and resolution.

•Beyond DNA Barcoding: High-Resolution Markers. While the COI mitochondrial gene ("DNA barcoding") remains a useful tool for specimen identification and preliminary diversity screening, its limitations for species delimitation, especially in recently diverged groups or those with complex histories, are well-known. Modern approaches employ Ultra-Conserved Elements (UCEs) and anchored hybrid enrichment (AHE). These techniques sequence hundreds to thousands of conserved genomic regions flanked by variable sequences, providing a massive dataset of orthologous loci ideal for resolving difficult phylogenetic relationships and establishing robust species boundaries with statistical support [5].

•The Power of Whole Genomes. Decreasing costs are making whole-genome sequencing (WGS) a feasible tool for taxonomy. WGS allows for the analysis of gene flow, demographic history, and adaptive divergence, moving beyond simple delimitation to understanding the evolutionary processes that generate and maintain species. For conservation, this can identify evolutionarily significant units (ESUs) and adaptive genetic variation critical for population viability under environmental change [6].

•Reference Libraries and the Genomic Gap. The utility of all genomic tools depends on accessible reference databases. Major initiatives like the Earth BioGenome Project aim to sequence the genomes of all eukaryotic life. For taxonomy, building comprehensive, voucher-linked genomic reference libraries is paramount to turn sequence data into actionable taxonomic and conservation insights.

•The Democratization of Genomics and Emerging Challenges. The precipitous drop in sequencing costs has democratized access to genomic tools, enabling research teams in biodiversity-rich regions to conduct sophisticated analyses. However, this accessibility unveils new challenges. The choice between targeted sequencing (e.g., UCEs, AHE) and whole-genome sequencing (WGS) now hinges on specific research questions rather than merely budget. Targeted approaches remain superior for phylogenetic studies across broad taxonomic scales due to their cost-effectiveness and ability to recover data from degraded museum specimens. In contrast, WGS is indispensable for studying local adaptation, demographic history, and the genetic basis of traits critical for survival in changing environments [7]. A pressing issue emerging from this data deluge is “phyloinformatic” literacy-the ability to process, analyze, and interpret massive genomic datasets. The field is grappling with a shortage of taxonomists equipped with the bioinformatic skills necessary to translate raw sequence data into evolutionary insights and conservation recommendations. Furthermore, the management, storage, and long-term curation of genomic data require infrastructure and policies that many institutions, especially in the Global South, are still developing.

•Beyond Macro-Organisms: The Frontier of Microbial and Micro-Eukaryote Taxonomy. While genomic tools have revolutionized the taxonomy of animals and plants, their application to microbial and micro-eukaryotic diversity-the “unseen majority”-is perhaps even more transformative. Traditional microscopy-based identification of bacteria, archaea, protists, and micro-fungi is severely limited by morphological convergence and cryptic diversity. Metagenomic and metatranscriptomic sequencing of environmental samples now allows for the reconstruction of nearly complete genomes of uncultured organisms, leading to the discovery of entirely new phyla and candidate species. Even more precise, single-cell genomics enables the sequencing of individual microbial cells sorted from environmental samples, bypassing cultivation and providing genomic context for organisms known only from marker gene surveys.

Emerging spatial genomic techniques, such as Fluorescence In Situ Hybridization (FISH) coupled with next-generation sequencing, allow researchers to link phylogenetic identity with physical location in a microbial mat, soil aggregate, or host tissue. This moves microbial taxonomy from a list of sequences to a spatially explicit understanding of community structure and function. For conservation, this is critical: microbial communities drive ecosystem processes like nutrient cycling, soil formation, and coral health. Monitoring changes in microbial taxonomic and functional diversity can serve as an early-warning indicator of ecosystem degradation long before macrofauna decline is evident. Thus, extending the genomic revolution to the microbial world is not merely an exercise in completeness; it is essential for understanding and preserving the functional foundations of all ecosystems.

3. High-Throughput Tools for Biodiversity Discovery and Monitoring

A suite of non-invasive or minimally invasive tools now allows for rapid biodiversity assessment across vast spatial and temporal scales, often without the need to capture or even see the target organisms [8].

•Environmental DNA (eDNA) Metabarcoding. This technique involves extracting DNA from environmental samples (water, soil, air, gut contents). By metabarcoding this eDNA, researchers can create an inventory of species present in a habitat. It is exceptionally powerful for detecting rare, elusive, or cryptic species and for conducting rapid biodiversity surveys in inaccessible areas. Its application ranges from monitoring amphibian pathogens in ponds to assessing fish diversity in murky rivers and detecting invasive species early [9].

•Refining the eDNA Toolkit: From Detection to Quantification. While eDNA metabarcoding has proven revolutionary for presence-absence data, its path toward reliable biomass or abundance quantification remains complex. Factors such as DNA shedding rates, transport dynamics, and degradation vary by species and environment, complicating the relationship between DNA concentration and organismal abundance. Current research is focusing on quantitative PCR (qPCR) and digital droplet PCR (ddPCR) for target species to gain semi-quantitative insights, and on experimenting with meta-barcoding read counts calibrated with controlled experiments. Another frontier is the move from passive detection to functional assessment through metagenomics-sequencing all DNA in a sample to infer not just species identity, but also potential functional genes related to ecosystem processes or pathogen load. This evolution positions eDNA not just as a discovery tool, but as a holistic ecosystem health monitor [10].

•Digital Imaging and AI. Digital specimen imaging (e.g., micro-CT scanning, focus-stacked macrophotography) creates high-resolution, shareable digital vouchers. Coupled with machine learning algorithms, these images can be used for automated species identification and even the discovery of morphologically cryptic patterns not discernible to the human eye. Platforms like iNaturalist leverage citizen-scientist photos and AI to create massive, real-time occurrence datasets.

•Bioacoustics and Passive Acoustic Monitoring (PAM). Automated recording units can collect vast amounts of audio data in the field. Sophisticated software (e.g., Arbimon, Kaleidoscope) uses acoustic indices and convolutional neural networks (CNNs) to identify species by their calls, monitor phenology, and estimate population density. This is transformative for monitoring vocally active species like birds, frogs, bats, and insects in dense forests over long periods [11].

•Remote Sensing and Satellite Technology: Landscape-Scale Biodiversity Assessment. Complementing ground-based sensors, remote sensing provides a synoptic, landscape-to-continental scale perspective on biodiversity that is unattainable through plot-based methods alone. Multispectral and hyperspectral satellite imagery can characterize vegetation composition, structure, and phenology, allowing for the mapping of habitat types, the detection of invasive species, and the monitoring of deforestation or habitat fragmentation in near real-time. More recently, LiDAR (Light Detection and Ranging) from aircraft or satellites creates high-resolution three-dimensional maps of forest canopy structure, enabling precise estimation of above-ground biomass, habitat complexity, and even the identification of tree species based on crown architecture.

These data streams are increasingly integrated with species occurrence data from GBIF and eDNA surveys through Species Distribution Models (SDMs) and Essential Biodiversity Variables (EBVs) frameworks. For example, remote sensing-derived metrics of habitat heterogeneity can predict the diversity of understory plants or arthropods. In marine systems, satellite-derived sea surface temperature, chlorophyll concentration, and ocean color are used to model phytoplankton diversity and predict coral bleaching events. While remote sensing does not directly identify species at the individual level, it provides the critical environmental context and spatial framework that guide and enhance targeted taxonomic and monitoring efforts. It transforms taxonomy from a point-based science to one that operates within an explicitly spatial and ecological landscape, enabling conservation prioritization at ecologically relevant scales.

Table 1. Comparative analysis of modern taxonomic tools.

Tool/Category	Primary Application(s)	Key Strengths	Key Limitations	Conservation Relevance
UCEs/AHE	Phylogenetics, delimiting cryptic species	High resolution, hundreds of loci, works with degraded DNA	Requires specialized probe design, higher cost than barcoding	Defines ESUs, clarifies conservation units in complexes
Whole-Genome Sequencing	Understanding speciation, adaptive variation	Ultimate data source, reveals functional diversity	Costly, computationally intensive, data management	Identifies adaptive alleles for climate resilience
eDNA Metabarcoding	Rapid biodiversity inventory, rare species detection	Non-invasive, high sensitivity, bulk sample processing	Does not provide abundance data, requires reference databases, prone to contamination	Early detection of invasives, monitoring degraded habitats
Digital Imaging + AI	Digitization, automated ID, morphometric analysis	Creates permanent digital voucher, enables global collaboration	AI models require large training datasets, can miss novel species	Rapid field ID, monitoring phenotypic changes (e.g., size)
Bioacoustics + AI	Monitoring vocal species, behavioral studies	Passive, long-term, covers large spatial scales	Species-specific, background noise interference, less useful for silent taxa	Population trend analysis, impact assessment of noise pollution
Integrative Databases	Data synthesis, predictive modeling	Links disparate data types, enables gap analysis	Data heterogeneity, requires curation & standardization	Spatial conservation planning, Red List assessments

Table 1 presents a comparative overview of modern taxonomic tools, emphasizing their primary applications, strengths, limitations, and relevance to biodiversity conservation. Each tool category is evaluated across multiple dimensions to illustrate how different technologies contribute to species discovery, identification, and long-term monitoring.

The first group of methods includes genomic tools such as UCEs/AHE and whole-genome sequencing. UCEs and AHE enable high-resolution phylogenetics and cryptic species delimitation using hundreds of loci, and they work well even with degraded DNA. However, these techniques require specialized probes and are more costly than simpler methods like barcoding. Whole-genome sequencing provides the most comprehensive picture of functional and adaptive variation but demands substantial computational resources and extensive data management. Both methods play crucial roles in defining evolutionarily significant units (ESUs), understanding adaptive traits, and informing conservation priorities.

The second group covers eDNA metabarcoding and digital imaging combined with AI. eDNA metabarcoding excels at non-invasive biodiversity surveys, providing high sensitivity and enabling large-scale, bulk-sample monitoring. Its limitations include an inability to quantify abundance accurately and susceptibility to contamination. Digital imaging and AI automate species identification and create permanent digital vouchers, though robust AI performance requires extensive training datasets. These tools support rapid field identification and real-time ecosystem monitoring.

The third section highlights bioacoustics + AI and integrative databases. Bioacoustics offers passive, long-term monitoring of vocal species across large spatial scales but is less effective for silent taxa and can be affected by noise interference. Integrative databases synthesize diverse data types and enable comprehensive analyses, though they require careful curation and standardization to avoid inconsistencies. Both methods contribute to conservation by assisting in population trend analysis, documenting ecological changes, and supporting Red List assessments and spatial planning.

The table illustrates how modern taxonomic tools complement one another, forming a multi-layered toolkit for biodiversity research, species discovery, and conservation decision-making.

4. Cyber-Taxonomy: Integration and Democratization

The data deluge from these tools necessitates a cyber-infrastructure to integrate, analyze, and disseminate information.

•Integrative Platforms and Digital Specimens. Platforms like the Global Biodiversity Information Facility (GBIF) aggregate occurrence data. The next step is "digital specimens" or "extended specimens," which link a physical voucher to its genomic data, digital images, field recordings, and ecological metadata in a permanent, accessible digital object . This creates a powerful resource for holistic analysis [12].

•The Imperative of Standards and Interoperability. The vision of the “digital specimen” or “extended specimen” is contingent upon the development and universal adoption of data standards. Fragmented data stored in incompatible formats creates “digital silos” that hinder synthesis. Initiatives like Darwin Core for occurrence data, MIxS for genomic and environmental metadata, and ABCD (Access to Biological Collection Data) schema are critical. The true power of cyber-taxonomy will be realized when a genomic record from a repository like the Sequence Read Archive (SRA) can be seamlessly linked, via persistent identifiers (e.g., DOIs, ORCIDs for researchers, GGBN identifiers for samples), to a high-resolution image on MorphoSource, an occurrence record in GBIF, and a conservation assessment on the IUCN Red List. This level of interoperability requires ongoing collaboration between taxonomists, bioinformaticians, and data architects [13].

•Predictive Modeling and Gap Analysis. Integrated data can be used in ecological niche modeling (ENM) and spatial phylogenetics to predict where undiscovered diversity is likely to occur (targeted field work) and to identify geographic areas of high evolutionary distinctiveness and threat. This moves taxonomy from random discovery to a predictive science.

•Democratization and Capacity Building. Cloud-based analysis platforms and shared informatics pipelines are lowering barriers to entry. However, a critical challenge remains: ensuring equitable access to technology, training, and funding for taxonomists in the Global South, where biodiversity is highest.

5. Case Studies: Tools in Action in Biodiversity Hotspots

•Neotropical Amphibians: Combining targeted eDNA surveys with UCE phylogenomics has rapidly uncovered cryptic diversity in Amazonian frogs, some in areas immediately threatened by deforestation, allowing for pre-emptive conservation designation.

•Indo-Pacific Coral Reefs: PAM is used to assess reef health by monitoring soundscapes (the collective biophony). Changes in acoustic complexity index (ACI) provide a rapid proxy for biodiversity and coral cover decline, guiding marine protected area management [14].

•African Megafauna: Non-invasive fecal sampling coupled with metabarcoding and metagenomics is used to monitor diet, health, population structure, and pathogen load in elephant and great ape populations, informing anti-poaching and disease mitigation strategies.

•Southeast Asian Tropical Forests: Integrative Workflow in Action. The montane forests of Southeast Asia, hotspots of cryptic amphibian and reptile diversity, exemplify the integrated workflow. Initial bioacoustic surveys identify areas with high vocal diversity or unique calls. Follow-up eDNA sampling of stream water confirms the presence of aquatic and semi-aquatic taxa without disturbance. These guides targeted herpetological surveys to collect voucher specimens. These specimens then undergo UCE phylogenomics to delineate species boundaries within morphologically confusing groups, while micro-CT scanning reveals subtle skeletal distinctions. All data-location, call recordings, sequences, and digital morphology-are linked to the physical specimen in an institutional database [15]. This consolidated evidence package accelerates the formal description of new species and provides a robust, multi-evidence basis for immediate threat assessment and protected area advocacy.

•Paleogenomics and Sediment Ancient DNA (sedaDNA): Illuminating Past Biodiversity to Inform Future Trajectories. Modern taxonomic tools are not only forward-looking but can also resurrect the past. The analysis of ancient DNA (aDNA) from museum specimens, subfossils, and even historical environmental samples is filling critical gaps in our understanding of recent extinctions, species' historical ranges, and genetic diversity loss. More broadly, sediment ancient DNA (sedaDNA)-DNA preserved in lake, permafrost, or cave sediments-provides a multi-millennial record of entire ecosystems. By metabarcoding sedaDNA cores, scientists can reconstruct past plant, animal, and microbial community assemblages and track their responses to historical climate shifts and human arrival.

This "time-traveling" taxonomy has profound conservation implications. For instance, sedaDNA studies in the Arctic have revealed that mammoth steppe vegetation persisted longer than previously thought, informing debates about Pleistocene rewilding. In New Zealand, aDNA from museum kiwi specimens has revealed unrecognized genetic lineages lost to recent predation, refining conservation targets for remaining populations. By establishing historical baselines, these tools allow us to move beyond the "shifting baseline syndrome" and set more ecologically meaningful restoration goals. They answer not just "what is there?" but "what was there, and why did it disappear?"-providing a long-term lens through which to assess current biodiversity crises and model future scenarios under climate change.

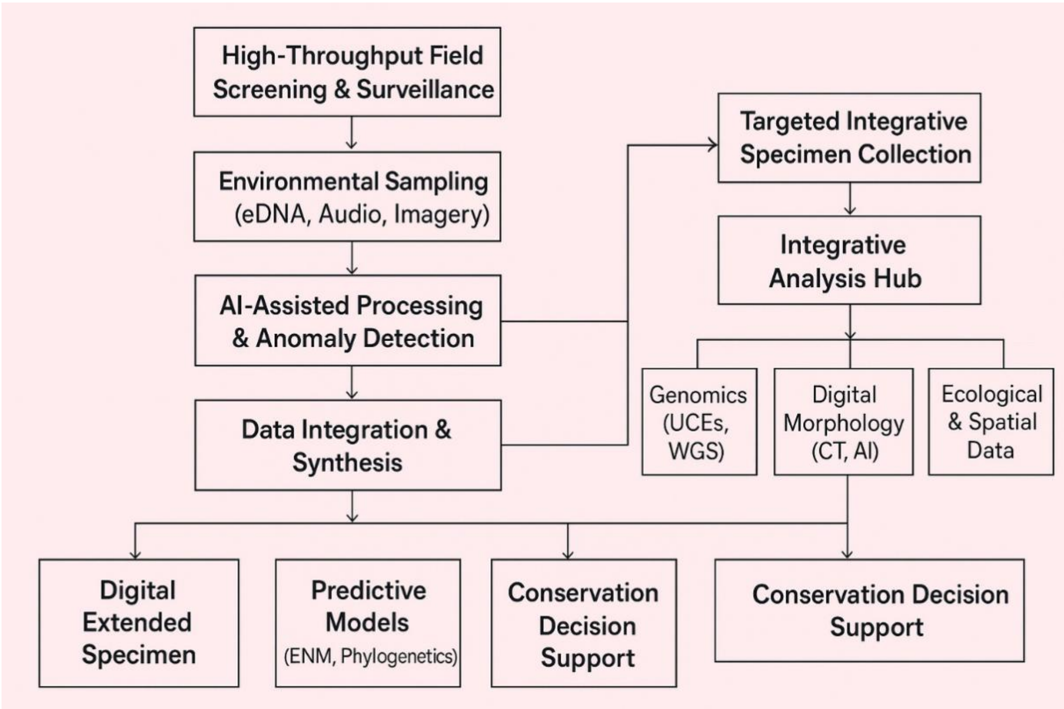

Figure 1. Conceptual framework of an integrated modern taxonomic workflow for conservation.

Figure 1 illustrates an integrated workflow for modern biodiversity monitoring, specimen analysis, and conservation decision-making. The left side of the chart represents large-scale, high-throughput field surveillance, which begins with environmental sampling methods such as eDNA collection, acoustic monitoring, and imagery. These data streams are processed using AI-assisted algorithms that detect anomalies or signals of interest. The processed information then moves into a data integration and synthesis stage, where diverse datasets are combined to generate digital extended specimens, predictive ecological or phylogenetic models, and conservation-relevant outputs.

The right side of the diagram focuses on targeted specimen-based research. Specimens collected through directed fieldwork are channeled into an integrative analysis hub, where several types of high-resolution data are generated, including genomic data (such as UCEs and whole-genome sequencing), digital morphological reconstructions (e.g., CT imaging and AI-based shape analysis), and ecological or spatial information. These datasets are subsequently fed into the same synthesis layer, reinforcing the conservation decision-support system. This system provides outcomes such as species assessments, habitat planning, and management recommendations.

The diagram conveys a dual-pipeline framework where broad environmental surveillance and targeted specimen analysis converge into a unified data integration process that guides biodiversity research and conservation action.

6. Synthesis, Challenges, and Future Directions

The integrated application of modern tools is creating a new taxonomic workflow (Figure 1). The path begins with broad-scale, high-throughput screening (eDNA, acoustics, imagery) to identify diversity hotspots and anomalies [16]. This guides targeted specimen collection for integrative study, where genomics delimits species and reveals relationships, and high-resolution imaging documents morphology. All data are linked in a digital specimen framework, feeding predictive models and, crucially, directly into conservation assessment platforms like the IUCN Red List.

Persistent challenges must be addressed:

1.Data Integration: Developing standards and platforms to seamlessly link genomic, morphological, and ecological data.

2.The "Taxonomist's Trinity": The field still requires experts trained in morphology, molecular biology, and bioinformatics-a rare combination. Training the next generation is critical [17].

3.Philosophical and Ethical Shifts: The community must reconcile rapid, sequence-based delimitation with the formal requirements of the International Code of Zoological Nomenclature (ICZN) [18]. Policies for data sharing and sovereignty, especially regarding sensitive location data for endangered species, are urgently needed.

Societal Taxonomy: Public Engagement, Citizen Science, and Integration of Local Knowledge

The taxonomic revolution is not confined to laboratories; it is increasingly a societal endeavor. Citizen science platforms like iNaturalist, eBird, and Mushroom Observer are generating massive, geo-referenced biodiversity datasets at a scale impossible for professional scientists alone. AI-assisted identification on these platforms empowers the public to contribute valid observations, while also providing real-time data on species phenology, range shifts, and rare species occurrences. This democratizes biodiversity monitoring and fosters public connection to nature-a key component of long-term conservation support.

However, the most profound integration may be with Indigenous and local ecological knowledge (ILK). Many communities possess deep, place-based knowledge of species identities, behaviors, and ecological relationships, often recognizing distinct biological entities that formal taxonomy has yet to describe. Modern tools can act as a bridge: bioacoustic recordings can validate distinct bird calls recognized by local experts; eDNA can confirm the presence of culturally significant but elusive species. Projects that collaboratively document biodiversity, respecting data sovereignty and intellectual property of Indigenous communities, lead to more robust, culturally grounded, and equitable conservation outcomes. The future of taxonomy lies not only in technological convergence but in its convergence with diverse knowledge systems, creating a more inclusive and comprehensive science of life.

Future directions point towards even greater integration: portable, real-time DNA sequencers (e.g., Oxford Nanopore) for field-based taxonomy and pathogen detection; AI that not only identifies but generates synthetic hypotheses about species limits from multimodal data; and a fully realized Internet of Natural History where environmental sensors, automated imagers/sound recorders, and sequenced data streams are continuously integrated. Perhaps the most profound shift will be the rise of predictive taxonomy, where machine learning models trained on known species distributions, traits, and genomic data will predict the existence, traits, and even potential conservation status of undiscovered taxa, directing finite exploration resources with unprecedented precision.

7. Conclusion

The race against anthropogenic extinction cannot be won blindfolded. We must know what exists, where it persists, and how it is related. Modern taxonomic tools-genomic, high-throughput, and cyber-enabled-are removing the blindfold at an accelerating pace. They are transforming taxonomy from a chronicler of the past into a vital, proactive informant for conservation action. By integrating these technologies into a cohesive workflow and addressing the associated socio-technical challenges, we can build a comprehensive, dynamic, and responsive map of planetary biodiversity. This map is not merely an academic exercise; it is the essential, real-time dashboard required to navigate and mitigate the biodiversity crisis of the Anthropocene. The tools are now in our hands; the imperative is to use them with speed, collaboration, and purpose.

References

[1] Rosinger, H.S., Geraldes, A., Nurkowski, K.A., Battlay, P., Cousens, R.D., Rieseberg, L.H. and Hodgins, K.A. (2021), The tip of the iceberg: Genome wide marker analysis reveals hidden hybridization during invasion. Mol Ecol, 30: 810-825. https://doi.org/10.1111/mec.15768

[2] The Earth BioGenome Project. (2022). Sequence all eukaryotes. Proceedings of the National Academy of Sciences, 119(4). https://doi.org/10.1073/pnas.2115635118

[3] Deiner, K., et al. (2017). Environmental DNA metabarcoding: Transforming how we survey animal and plant communities. Molecular Ecology, 26(21), 5872-5895. https://doi.org/10.1111/mec.14350

[4] Weinstein, B. G. (2018). A computer vision for animal ecology. Journal of Animal Ecology, 87(3), 533-545. https://doi.org/10.1111/1365-2656.12780

[5] Sofie Meeus, Iolanda Silva-Rocha, Tim Adriaens, Peter M J Brown, Niki Chartosia, Bernat Claramunt-López, Angeliki F Martinou, Michael J O Pocock, Cristina Preda, Helen E Roy, Elena Tricarico, Quentin J Groom, More than a Bit of Fun: The

Multiple Outcomes of a Bioblitz, BioScience, Volume 73, Issue 3, March 2023, Pages 168–181, https://doi.org/10.1093/biosci/biac100
[6] Pimm, S. L., et al. (2014). The biodiversity of species and their rates of extinction, distribution, and protection. Science, 344(6187), 1246752. https://doi.org/10.1126/science.1246752
[7] Hebert, P. D. N., et al. (2003). Biological identifications through DNA barcodes. Proceedings of the Royal Society B: Biological Sciences, 270(1512), 313-321. https://doi.org/10.1098/rspb.2002.2218
[8] Beng, K. C., & Corlett, R. T. (2020). Applications of environmental DNA (eDNA) in ecology and conservation: opportunities, challenges, and prospects. Biodiversity and Conservation, 29, 2089-2121. https://doi.org/10.1007/s10531-020-01980-0
[9] Jetz, W., et al. (2019). Essential biodiversity variables for mapping and monitoring species populations. Nature Ecology & Evolution, 3, 539-551. https://doi.org/10.1038/s41559-019-0826-1
[10] Scheffers, B. R., et al. (2012). What we know and don't know about Earth's missing biodiversity. Trends in Ecology & Evolution, 27(9), 501-510. https://doi.org/10.1016/j.tree.2012.05.008
[11] Thomson, S. A., et al. (2018). Taxonomy based on science is necessary for global conservation. PLOS Biology, 16(3), e2005075. https://doi.org/10.1371/journal.pbio.2005075
[12] Gippet, J. M. W., & Bertelsmeier, C. (2021). Invasiveness is linked to greater commercial success in the global pet trade. Proceedings of the National Academy of Sciences, 118(14), e2016337118. https://doi.org/10.1073/pnas.2016337118
[13] DeSalle, R., & Goldstein, P. (2019). Review and interpretation of trends in DNA barcoding. Frontiers in Ecology and Evolution, 7, 302. https://doi.org/10.3389/fevo.2019.00302
[14] Stork, N. E. (2018). How many species of insects and other terrestrial arthropods are there on Earth? Annual Review of Entomology, 63, 31-45. https://doi.org/10.1146/annurev-ento-020117-043348
[15] Turvey, S. T., & Crees, J. J. (2019). Extinction in the Anthropocene. Current Biology, 29(19), R982-R986. https://doi.org/10.1016/j.cub.2019.07.040
[16] Kühl, H. S., & Burghardt, T. (2013). Animal biometrics: Quantifying and detecting phenotypic appearance. Trends in Ecology & Evolution, 28(7), 432-441. https://doi.org/10.1016/j.tree.2013.02.013
[17] Meineke, E. K., et al. (2019). Biological collections for understanding biodiversity in the Anthropocene. Philosophical Transactions of the Royal Society B, 374(1763), 20170386. https://doi.org/10.1098/rstb.2017.0386
[18] Ducarme, F., Flipo, F. and Couvet, D. (2021), How the diversity of human concepts of nature affects conservation of biodiversity. Conservation Biology, 35: 1019-1028. https://doi.org/10.1111/cobi.13639