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Review Article

Integrative Zoology in the 21st Century: Unifying Genomics, eDNA, Morphology, Behavior, Biologging, Bioacoustics, Remote Sensing, and AI for Global Biodiversity Discovery and Conservation

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Abstract

Descriptive morphology and taxonomy That is because zoology is rapidly evolving to be a multi-modal science that operates on the organismic to molecular scale (i.e., it extends beyond the level of the ecosystem). To address that global crisis in biodiversity, scientists have combined genomics and environmental DNA (eDNA) analysis with morphometrics and imagery, behavior studies through biologging, trail cameras, and vocal monitoring, and landscape studies using remote-sensing tools. These varied approaches are now joined together by artificial intelligence and open data platforms and are opening new avenues to real-time biodiversity discovery and predictive conservation. However, questions also remain: the knowledge gap in taxonomy, bias in occurrence data, incomplete validation of models using either eDNA or acoustics data, and the lack of standards addressing blending multi-modal data. Moral imperatives such as animal welfare in tracking, fairness in international partnerships and data sovereignty are still burning. This paper presents an outline of Integrative Zoology and presents case studies of how it is transforming our basic understanding of the cryptic species, how it tracks movement and decline, and how it can inform conservation analysis. By integrating the traditional study of zoology with the newest of technologies, the discipline can transform into a science of awareness of biodiversity, infrastructure that is ready to directly assist the conservation policy and resilience of the planet.

Keywords: Integrative Zoology, Biodiversity, Genomics, eDNA, Bioacoustics, Biologging, Remote Sensing, AI, Conservation Biology, One Health.

1. INTRODUCTION

Biodiversity is currently facing an unprecedented crisis, marked by mass species extinctions, widespread habitat loss, and the accelerating impacts of climate change. Alarmingly, it is estimated that less than 25% of eukaryotic species have been formally described by science, even as many undiscovered species continue to disappear due to environmental degradation (Novaes *et al.,* 2023). In this context, the urgency to catalogue and understand Earth's biodiversity has never been greater. This urgency is driving the rise of integrative biology—a multidisciplinary approach that unifies classical biological disciplines with cutting-edge technologies like genomics, transcriptomics, proteomics, remote sensing, and artificial intelligence. Integrative biology enables researchers to bridge molecular, organismal, and ecological scales to better understand complex life systems (Steinicke *et al.,* 2014; Joshi & Agarwal, 2021).

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Traditionally, zoology has relied heavily on morphological data and classical taxonomy to describe and classify organisms. While these methods laid the foundation for our understanding of animal life, they are often inadequate for resolving complex evolutionary patterns or identifying cryptic species. Morphology alone can miss subtle differences or evolutionary signals that are now detectable through molecular and computational methods (Dayrat, 2005; Sukumaran & Gopalakrishnan, 2015). Modern zoological science has undergone a transformation, now embracing multi-omics approaches, AI-assisted species delimitation, high-throughput bioinformatics, and global sensing networks. These tools not only accelerate biodiversity discovery but also increase the objectivity, accuracy, and reproducibility of taxonomic decisions (Streicher & Meik, 2018; Karbstein *et al.,* 2024).

Despite this progress, the field still faces critical bottlenecks. Taxonomic expertise is in global decline, creating a "taxonomic impediment" that limits our capacity to identify and monitor biodiversity. This shortage of skilled taxonomists is especially problematic at a time when high-resolution biodiversity data is most needed (Boxshall, 2020). In addition, the biological data landscape is deeply fragmented across disciplines, institutions, and databases, resulting in poor interoperability and duplication of effort. Biodiversity datasets also exhibit biases—geographical, taxonomic, and methodological—that limit their utility for global conservation planning and ecosystem management (Sigwart *et al.,* 2023). Without integration, the full potential of new technologies in zoological research cannot be realized.

This review proposes a conceptual roadmap for what we call Integrative Zoology 4.0—a new paradigm that leverages multi-omics data, artificial intelligence, and cross-disciplinary integration to unify biodiversity research across scales, from genes to ecosystems. The aim is to identify practical strategies for bridging knowledge gaps, reducing data silos, and enhancing the predictive power of zoological science. We will explore the tools, frameworks, and case studies that demonstrate how integrative approaches can improve species discovery, monitoring, and conservation outcomes. Ultimately, this paper advocates for a unified and technologically empowered future for zoology—one that is capable of responding to the urgent challenges of the biodiversity crisis.

2. Zoology's Expanding Fields (Theoretical Framework)

Zoology, as a discipline, has traditionally been organized around a set of classical subfields that have served as its intellectual foundation for over a century. These include taxonomy and systematics, which focus on the identification, naming, and classification of organisms; morphology, which examines form and structure; physiology, which studies the functional processes within animals; ethology, which investigates animal behavior; ecology, which explores interactions between organisms and their environments; and evolution, which provides the framework for understanding biological change over time (Dayrat, 2005; Sukumaran & Gopalakrishnan, 2015). Together, these core areas have shaped the development of zoology as a rigorous and descriptive science centered on organismal biology and biodiversity.

In recent decades, however, zoology has undergone significant conceptual and methodological expansion. A number of emerging subfields have blurred the lines between disciplines and introduced new interfaces of inquiry. Disease ecology, for example, integrates principles of parasitology, immunology, and ecosystem dynamics to understand how pathogens move through animal populations. Conservation biology, driven by the global biodiversity crisis, brings together ecological, genetic, and management approaches to prevent species extinctions (Novaes *et al.,* 2023). The field of eco-evo-devo (ecological evolutionary developmental biology) explores how environmental factors influence developmental processes and evolutionary trajectories, offering a systems-level view of organismal change (Streicher & Meik, 2018). Urban ecology investigates how animals adapt to and interact with increasingly anthropogenic environments, while the One Health paradigm recognizes the interconnectedness of animal, human, and environmental health, creating a transdisciplinary framework for addressing zoonotic diseases and ecological sustainability (Sigwart *et al.,* 2023).

Zoology's intellectual landscape is also increasingly shaped by its connections to other scientific and societal domains. Bioinformatics and data science now play essential roles in managing and analyzing the vast datasets generated by genomics, transcriptomics, and remote sensing (Steinicke *et al.,* 2014; Joshi & Agarwal, 2021). Computational tools enable the modeling of ecological networks, prediction of species distributions, and inference of evolutionary relationships. Beyond the laboratory, zoology intersects with environmental policy, influencing how governments manage natural resources and respond to ecological threats. Ethical considerations are also becoming central, especially as research methods grow more invasive or as zoologists work in conservation contexts that impact local communities and indigenous rights. These cross-disciplinary connections signal a shift toward a more integrative, applied, and socially engaged zoology—one that not only seeks to understand animal life but also to inform action in a rapidly changing world.

3. Techniques and Modalities (Core Toolkit of Integrative Zoology)

3.1. Genomics & eDNA: Unveiling the Hidden Code of Biodiversity

Genomic technologies have transformed integrative zoology by enabling detection, identification, and monitoring of biodiversity at multiple scales. DNA barcoding, which uses short standardized genetic regions such as COI for animals, provides a reliable framework for species-level identification and has been expanded into global reference databases to aid taxonomic consistency (Cristescu, 2018). Building on this, DNA metabarcoding applies universal primers and next-generation sequencing to mixed community samples, yielding high-resolution snapshots of species assemblages across entire ecosystems (Compson, McClenaghan, Singer, Fahner, & Hajibabaei, 2020). Environmental DNA (eDNA) has further revolutionized biodiversity research by capturing trace genetic material shed into soil, sediment, air, or water, enabling the detection of rare, cryptic, or elusive species without direct observation or capture (Taberlet, Bonin, Zinger, & Coissac, 2018; Sepulveda, Nelson, Jerde, Luikart, & Lodge, 2020). These approaches have already proved critical in monitoring invasive species, such as invasive carps in North America, and informing conservation strategies by allowing early detection and rapid management response.

Beyond species detection, population genomics provides insights into adaptive variation, demographic history, and patterns of connectivity that are essential for managing species under environmental change. For instance, genomic markers can reveal genetic resilience or vulnerability to habitat loss, overexploitation, and climate stressors (Hoban *et al.,* 2020; Hohenlohe, Funk, & Rajora, 2021). Ancient DNA (aDNA) pushes this toolkit into the past by reconstructing evolutionary processes and ecosystem dynamics through genetic analysis of historical, archaeological, or subfossil remains. Recent advances have allowed near-complete genome recovery from extinct species and the reconstruction of past community structures, offering critical baselines for conservation in the Anthropocene (Orlando, Allaby, Skoglund, & Sinding, 2021; Pääbo, 2022).

At an even finer scale, single-cell transcriptomics dissects gene expression at the cellular level, revealing heterogeneity within tissues, developmental transitions, and molecular mechanisms that underpin phenotypic traits in model and non-model organisms alike. This frontier provides mechanistic insights into how organisms respond to environmental stressors, infection, or ecological interactions at the molecular scale (Stuart & Satija, 2019; Gerber, Taniguchi, & Tarashansky, 2021). Together, these genomic and molecular approaches form a synergistic toolkit for zoology, spanning from micro-level cellular mechanisms to macro-level ecosystem surveillance.

Figure 1 illustrates a typical eDNA workflow, emphasizing the pipeline from environmental sample collection (e.g., water, sediment, animal traces) through DNA extraction and amplification, sequencing, and taxonomic assignment, to the final analysis of species presence across sites (Schallenberg, Wood, Pochon, & Pearman, 2020). This stepwise process demonstrates how trace DNA becomes a powerful biodiversity signal, linking genomics directly to field ecology. By integrating barcoding, metabarcoding, eDNA, population genomics, ancient DNA, and single-cell approaches, integrative zoology can both monitor current biodiversity crises and reconstruct historical baselines to inform future conservation strategies.

Genomic tools such as DNA barcoding, metabarcoding, and eDNA unlock species identities from trace materials in the environment. Population genomics and ancient DNA provide insights into evolutionary histories and adaptive variation. These methods are revolutionizing monitoring of cryptic and invasive species at unprecedented scales.

3.2. Morphology & Imaging: Seeing Form in High Resolution

Modern zoology increasingly depends on quantitative imaging pipelines that convert anatomy into analyzable numbers and manipulable three-dimensional models. Geometric morphometrics (GM) provides the statistical framework for quantifying shape, testing hypotheses about form–function relationships, and visualizing differences among taxa or treatments. Landmark-based workflows begin with careful selection of homologous points or curves, followed by generalized Procrustes alignment to remove nonshape variation (position, scale, rotation), multivariate ordination (e.g., PCA), and subsequent hypothesis testing in shape space (Adams & Collyer, 2018; Baken, Collyer, Kaliontzopoulou, & Adams, 2021). Current best practice emphasizes transparent reporting of sampling decisions and statistical power because effect sizes in high-dimensional datasets are sensitive to sample size and view choice (Rummel, Arbour, & Anderson, 2024). In parallel, GM has expanded beyond discrete landmarks: semilandmarks along curves and surfaces preserve complex geometry, and “landmark-free” or surface-based pipelines (e.g., dense alignment and deformation fields) are gaining traction for structures where strict homology is hard to establish (Collyer, Davis, & Adams, 2020; Viacava, Gamarra, & Püschel, 2023). These developments allow zoologists to quantify subtle phenotypic variation—from shell coiling to skull vaulting—and relate it to ecology, development, and performance.

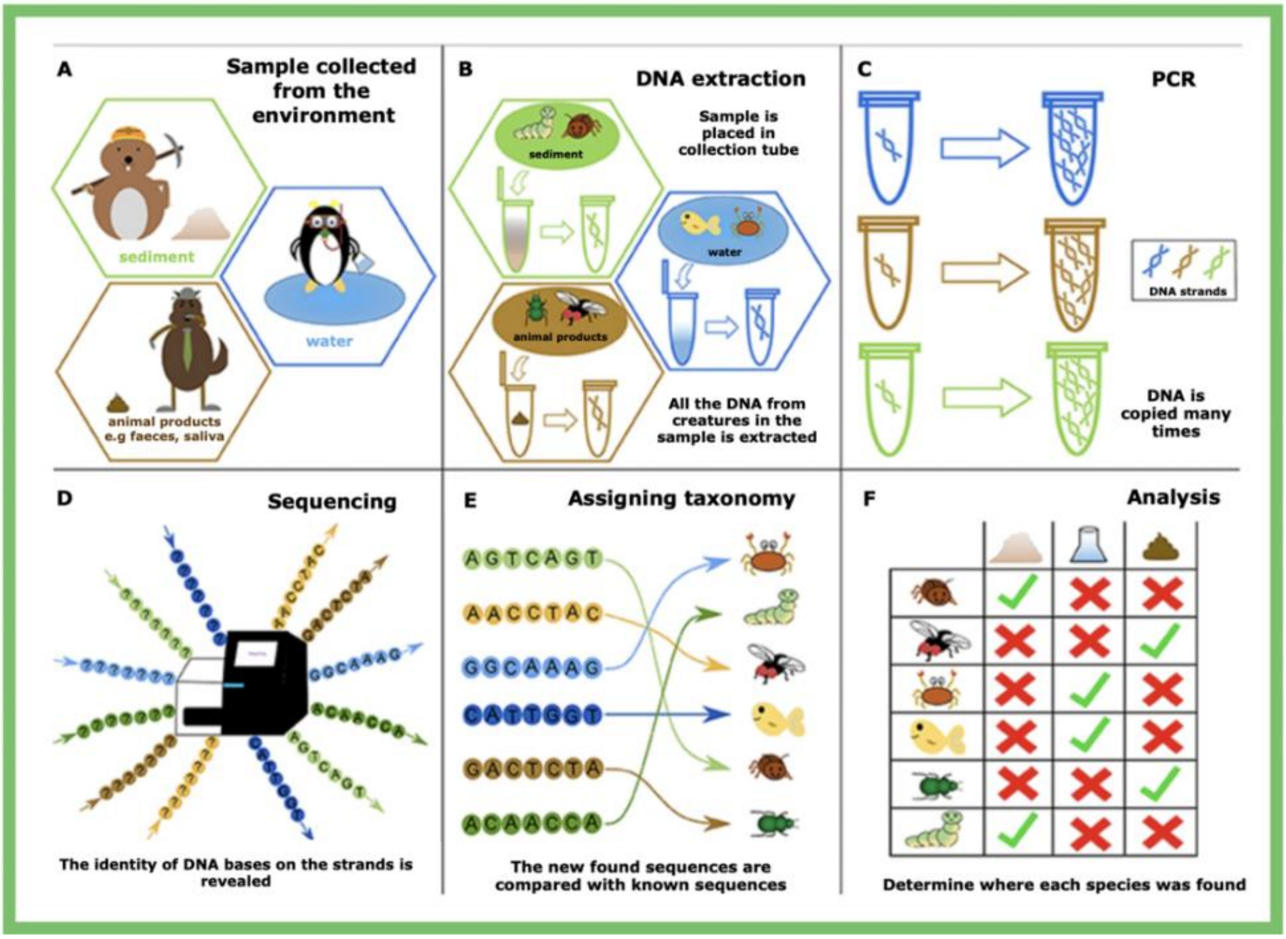

Figure 1: Genomics & eDNA: Unveiling the Hidden Code of Biodiversity

Micro-computed tomography (micro-CT) has become the non-destructive engine that feeds GM and other quantitative analyses with volumetric data at micron-level resolution. Unlike traditional histology, micro-CT images intact specimens, preserving spatial context and enabling virtual sectioning and segmentation of bones, teeth, soft tissues (with contrast agents), and even parasites embedded within host structures (Keklikoglou *et al.,* 2021). Protocol advances since 2018 have improved contrast for soft tissues in ethanol-preserved material; for example, phosphotungstic acid (PTA) provides strong, uniform staining for central nervous system visualization without critical-point drying, offering realistic in situ morphologies for downstream 3D reconstructions (Rivera-Quiroz, Vega-Ruiz, & Castañeda-Valdez, 2022). For studies requiring standardized reporting, CT "Primers" now outline instrument settings (voltage, current, filter), acquisition strategies (helical vs. step-and-shoot), and reconstruction parameters (beam hardening correction, ring artifact suppression) that affect voxel size and downstream morphometrics (Nature Research, 2021). These guidelines make micro-CT data more reproducible across laboratories and compatible with FAIR data practices.

The synergy between GM and micro-CT is perhaps best illustrated by applications that bridge taxonomy and functional anatomy. In taxonomy, micro-CT eliminates the trade-off between precision and preservation: type material or rare specimens can be scanned, virtually dissected, and digitally shared while remaining intact. Quantitative diagnoses can then be formulated with explicit GM characters (surface or curve semilandmarks) rather than subjective descriptors, and public 3D models enable reanalysis and replication (Baken *et al.,* 2021). For functional anatomy, 3D reconstructions derived from micro-CT can be exported to computational pipelines—e.g., beam theory approximations, inertial property estimation, or finite-element analysis—where GM-derived shape variables serve as predictors of mechanical performance or kinematics. This linkage tightens inference about adaptation by integrating measured shape differences with modeled or observed function.

Figure 2 exemplifies how these tools converge. The figure presents a micro-CT-based 3D reconstruction of a helicoid gastropod shell and a close-up of features on the inner shell surface that correspond to encapsulated nematodes. Panel A shows the exterior shell rendered as a triangulated surface from the volume, with arrows indicating the viewing direction of subsequent panels.

Panel B provides a high-magnification virtual surface view where a torus-like structure (≈1 mm) marks the encapsulated parasite; because micro-CT preserves the undisturbed internal surfaces, the morphology and spatial orientation of the capsule can be measured directly. Panel C pairs two closely spaced slices (or shaded-surface renderings) to emphasize the three-dimensionality of the capsule walls. Together, the panels demonstrate three strengths that are central to this section: (1) micro-CT allows non-destructive visualization of internal host–parasite interfaces; (2) 3D reconstruction translates these volumetric data into metrically accurate surfaces suitable for morphometrics; and (3) the same reconstructed geometry can be used for functional inference (e.g., stress distribution in the shell around the capsule) and quantitative taxonomy (Falkingham & Rae, 2021). In short, Figure 2 illustrates the complete path from imaging to biological interpretation: volumetric acquisition → segmentation and surface reconstruction → quantitative measurement and hypothesis testing.

Recent case studies highlight how 3D reconstructions transform inference in zoology. Micro-CT has clarified developmental trajectories by tracking organ or skeletal element rearrangements across ontogeny with minimal handling, producing longitudinal datasets unattainable with destructive methods (Keklikoglou *et al.,* 2021). In malacology, micro-CT reconstructions of shell interiors expose growth lines, muscle scars, and parasitic encapsulations that rarely fossilize or are obscured in traditional preparations; these features become measurable characters in species descriptions or phylogenetic matrices (Falkingham & Rae, 2021). In vertebrates, high-contrast staining and synchrotron-based micro-CT resolve cartilaginous and soft-tissue morphology of delicate embryos, enabling GM of previously intractable structures and facilitating cross-species comparisons at matched developmental stages (Rivera-Quiroz *et al.,* 2022; Nature Research, 2021). Each of these applications leverages the same core concept: a digital anatomy that can be measured, shared, and reused.

As 3D datasets proliferate, reproducibility and automation have become focal points. New software releases in the GM ecosystem (e.g., geomorph v4.0 and the gmShiny interface) add robust effect-size metrics, trajectory analyses, and interactive visualization that make complex multivariate results more interpretable and less prone to misuse (Baken *et al.,* 2021). Landmarking remains a critical source of variance; protocols now provide detailed anatomical guidelines for difficult structures (e.g., reptile endocasts), and semi-automated tools can propagate landmarks across specimens while preserving biological homology (Allemand *et al.,* 2023). Studies explicitly benchmarking linear, 2D, and 3D approaches show that 3D GM generally improves classification performance and biological signal, especially for curved or asymmetric shapes where 2D projections lose information (Viacava *et al.,* 2023). At the same time, careful experimental design—adequate sample sizes, consistent positioning, and repeated digitization for error estimation—is essential to avoid overconfident inferences (Rummel *et al.,* 2024).

The data life cycle is also changing. Micro-CT volumes and derivative mesh are increasingly deposited in open repositories, and journals encourage submission of segmentation files alongside raw data to support reanalysis. This has practical impacts: teaching collections and museum drawers can be "digitally liberated," allowing taxonomists worldwide to re-examine the same specimen virtually, propose alternative landmark schemes, and test new hypotheses without shipping fragile material. For regulatory and conservation contexts, digital surrogates provide audit trails for species diagnoses and facilitate forensic identification when physical access is restricted.

Looking ahead (2018–2025), several trends are reshaping morphology and imaging in integrative zoology. First, "landmark-free" morphometrics that align full surfaces using dense correspondence or deformable registration offer scalable alternatives when homology is diffuse; recent evaluations suggest these methods can approach or match landmark-based accuracy when preprocessing and mesh standardization are rigorous (Collyer *et al.,* 2020; Viacava *et al.,* 2023). Second, multimodal fusion—combining micro-CT with optical photogrammetry, confocal stacks, or MRI—yields datasets that capture both external texture and internal architecture, enabling richer functional models and facilitating field-to-lab pipelines in which photogrammetry provides specimen-level context and micro-CT supplies internal detail (Keklikoglou *et al.,* 2021). Third, advances in staining chemistry and scanning hardware extend micro-CT to soft tissues at submicron resolution, narrowing the gap between "3D histology" and traditional sectioning while preserving the ability to reanalyze the same specimen (Rivera-Quiroz *et al.,* 2022). Finally, community standards are coalescing around transparent metadata (voxel size, energy, filter, reconstruction algorithm), segmentation provenance, and analytic scripts, which together make morphometric conclusions reproducible and comparable across studies (Nature Research, 2021; Baken *et al.,* 2021).

In practice, the combined toolkit empowers zoologists to address questions that were previously inaccessible. With GM, one can quantify how shape covaries with ecology—e.g., whether shell curvature predicts microhabitat or predator regime—and test those relationships with robust multivariate statistics. With micro-CT, one can visualize the internal structures that causally link shape to function—e.g., shell thickness gradients or internal buttressing that determine fracture resistance. With 3D reconstructions, one can move seamlessly from qualitative description to quantitative diagnosis, simulate performance, and disseminate models for critique. The result is a more integrative discipline where taxonomy, development, biomechanics, and evolutionary biology share a common digital language of shape.

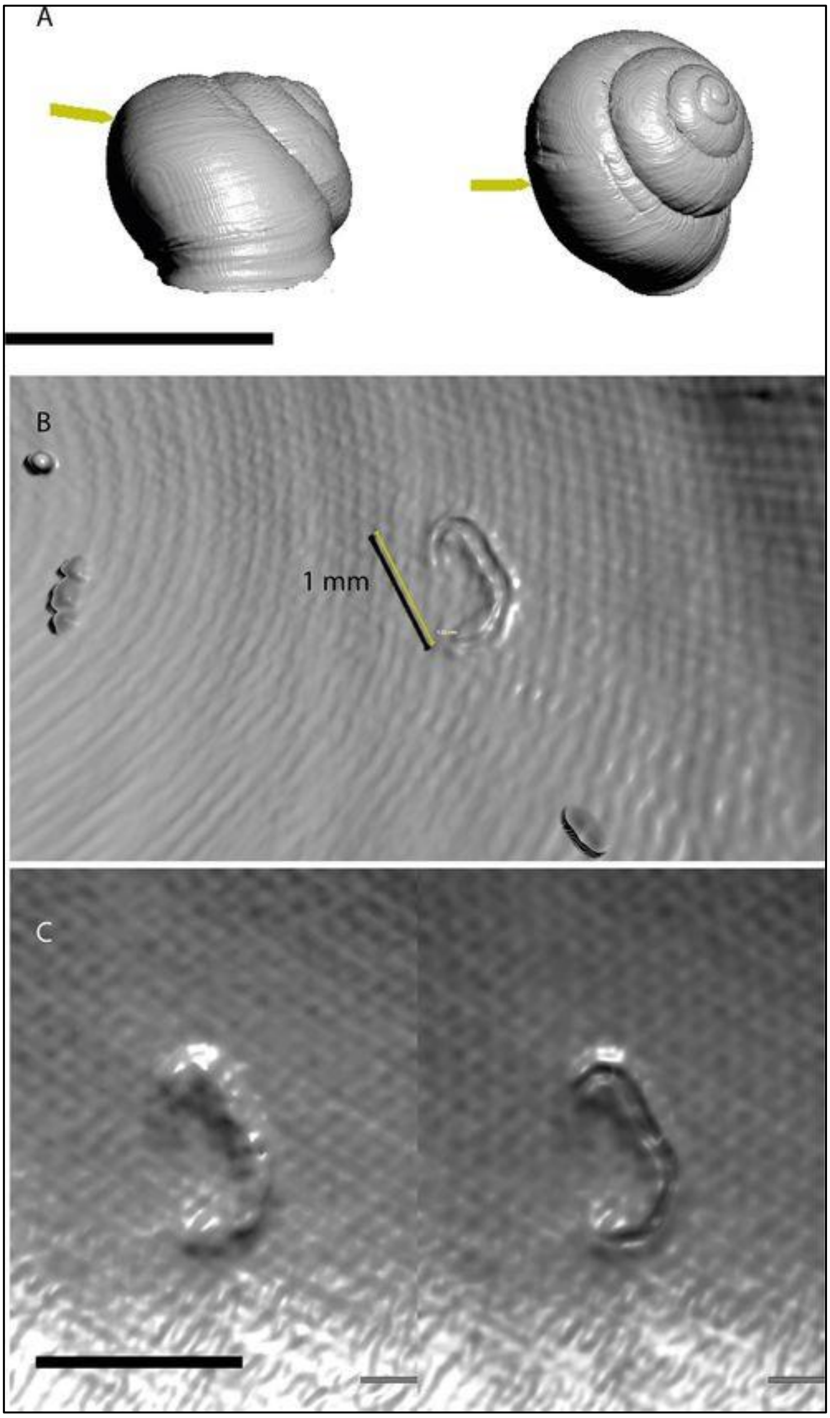

Figure 2: Morphology & Imaging: Seeing Form in High Resolution

Modern imaging—from geometric morphometrics to micro-CT scanning—captures organismal form with precision. 3D reconstructions allow functional and taxonomic analysis beyond traditional morphology. Together, these approaches bridge anatomy, biomechanics, and evolutionary biology.

3.3. Behavior & Movement: Tracking Life in Motion

Biologging and remote telemetry have transformed behavioral ecology by coupling fine-scale animal movements with environmental context in near–real time. Miniaturized tags now integrate GPS for positions, pressure sensors for dive depth, tri-axial accelerometers for posture and activity, and ancillary channels such as temperature, conductivity, heart rate, and even dissolved oxygen. When fused along a track, these streams reveal where and when animals switch among commuting, resting, and foraging, and how those state changes covary with features like currents, mixed-layer depth, prey fields, and surface conditions—exactly the multi-sensor pairing illustrated in our figure (Watanabe & Papastamatiou, 2023). Analytical pipelines increasingly translate raw accelerometry into ethograms and energetic proxies, with recent benchmarks showing that deep learning models outperform classical, hand-crafted features for behavior classification across multiple species and logger types (Hoffman *et al.,* 2024). Together, multi-sensor tags and improved inference methods have made it routine to quantify fine-scale behavior and bioenergetics at population scales (English *et al.,* 2024).

In parallel, camera traps augmented with modern computer vision are shifting from passive recorders to "smart" field instruments. On-device models can now filter empty frames, flag species or behaviors, and adapt to deployment-specific conditions, lowering annotation burdens and enabling near–real-time ecological signals (Velasco-Montero *et al.,* 2024). Field evaluations show that vision-equipped traps improve detections for challenging taxa (e.g., small or ectothermic fauna) when compared with conventional pipelines, and they complement general detectors such as MegaDetector within semi-automated labeling workflows that accelerate curation of million-image datasets (Mulero-Pázmány *et al.,* 2025; Pestell *et al.,* 2025).

Recent case studies underscore how these tools illuminate migration, foraging, and predator–prey dynamics. A global synthesis of marine megavertebrate telemetry mapped thousands of routes across ocean basins, revealing functional connectivity that spans national jurisdictions and highlighting the need for transboundary governance of migratory corridors (Bentley *et al.,* 2025). At the foraging scale, GPS–CTD–accelerometer deployments on Weddell seals linked dive behavior to seasonal water-mass structure and prey use, illustrating how biologging ties energy acquisition to dynamic physical habitats (Chung *et al.,* 2024). On land, predator–prey interactions have been quantified by aligning ungulate paths with spatially explicit predation risk derived from carnivore movements and kill locations; elk, for example, exhibit seasonally varying risk avoidance and activity trade-offs across diel cycles, directly measurable from high-resolution telemetry (Farley *et al.,* 2024; Thompson *et al.,* 2025). Collectively, GPS/accelerometer tags and AI-assisted camera traps now provide a coherent, multi-modal view of "life in motion," turning movement paths into testable models of behavior, energetics, and species interactions across environments (Watanabe & Papastamatiou, 2023; English *et al.,* 2024).

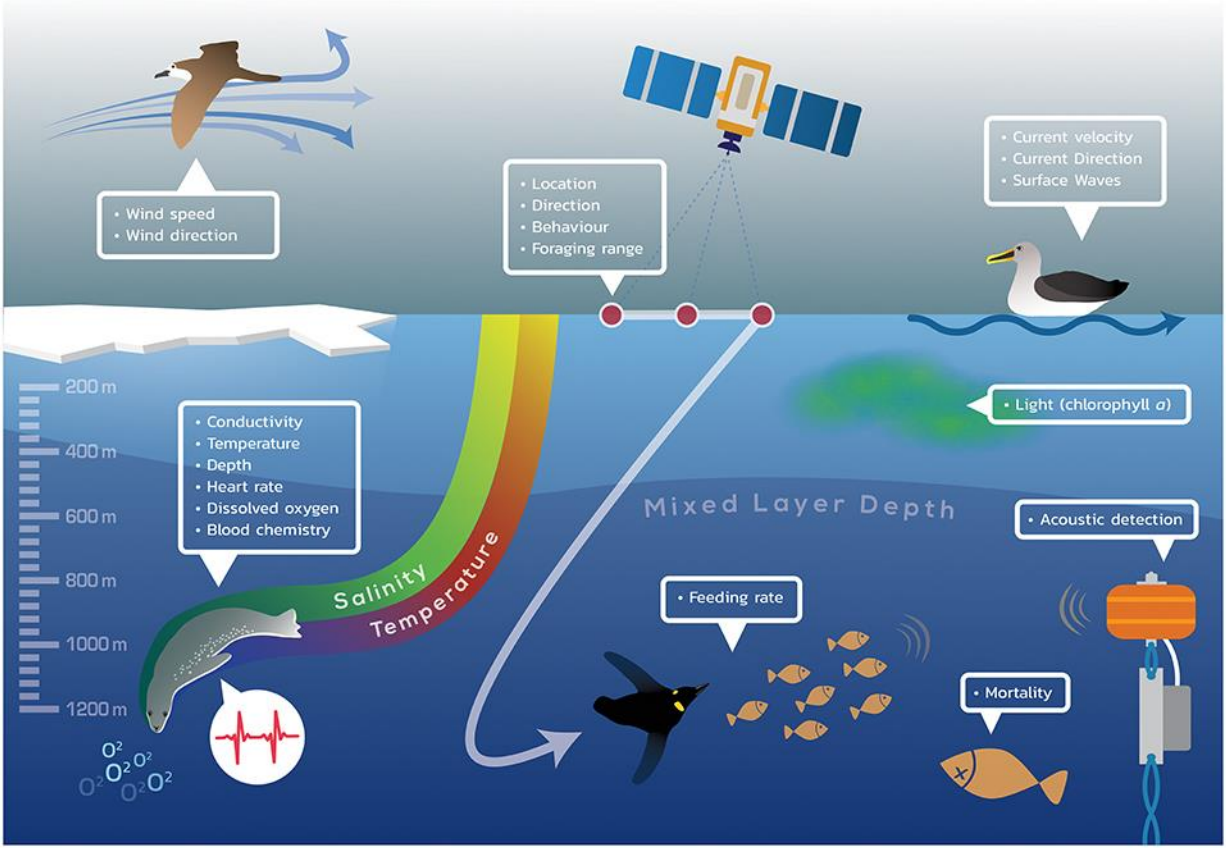

Figure 3: B & M-1. Animal-borne telemetry captures movement and behavior

Schematic of biologging packages attached to free-ranging animals showing how multiple sensors (e.g., GPS for locations/paths, tri-axial accelerometers for activity/behavioral states, and environmental sensors) log data and relay it via satellite or acoustic links. Such integrated tags quantify migrations, foraging routes, and fine-scale behaviors in near-real time, providing the backbone for modern movement ecology; analogous systems are used in terrestrial wildlife tracking. Source: Harcourt *et al., Frontiers in Marine Science* (2019).

3.4. Bioacoustics

Passive acoustic monitoring (PAM) has matured into a core tool for observing wildlife at scales and resolutions that were impossible with traditional surveys, because it records the full soundscape—biophony from animals, geophony from ice, wind, waves, and rain, and anthropophony from ships, sonar, drilling, and seismic exploration—continuously and without disturbing organisms. Figure 4 depicts this triad of sources in a marine setting and highlights why any bioacoustic inference must begin with careful characterization of local propagation conditions and background-noise regimes across seasons, tides, and weather events: the same whale call or fish chorus can exhibit very different detectability as wind seas rise, as rain adds broadband energy, or as distant shipping lanes shift (Duarte *et al.,* 2021). In practice, PAM deployments range from low-cost single hydrophones or AudioMoth-class loggers to sparse arrays and cabled observatories; they may be fixed to the seafloor or shoreline, moored in the water column, towed behind vessels, or carried by gliders, floats, and animal-borne tags. These platforms trade off power, storage, sampling rate, and duty cycle. Long-term ecological questions (“When do seasonal choruses begin?” “How do diel calling patterns track lunar phase?”) often favor months-long, low-maintenance recorders with scheduled duty cycles, whereas questions about behavior and density require higher sampling rates, synchronized arrays for time-difference-of-arrival localization, and robust clock drift correction (Gibb *et al.,* 2019). The raw waveform stream is typically converted into time–frequency representations (short-time Fourier spectrograms or mel/log-mel spectrograms), band-limited to the taxa of interest, then segmented into manageable windows (e.g., 5–30 s). Detections can be rule-based (energy thresholds in species-specific bands), matched-filter (template correlation for stereotyped signals), or learned by data-driven models; detections then feed occupancy models, activity indices, encounter-rate estimators, or full density estimators if cue rates and detection functions are available (Marques *et al.,* 2013). For marine mammals or other taxa with localized cues (clicks, songs), arrays provide hyperbolic localization and sometimes tracking; for chorusing fishes and invertebrates, the unit of analysis may be sound level or chorus metrics rather than individual calls, yet those metrics still reveal seasonal reproduction and habitat quality.

Deep learning has transformed species recognition and call-type classification by learning robust features directly from spectrograms. Convolutional neural networks (CNNs) remain strong baselines for many tasks (spectrotemporal filters emulate expert visual scanning), while attention mechanisms and transformer encoders capture long-range temporal structure such as phrase order, bouts, and alternating duets (Stowell, 2022). Performance hinges on data curation: representative training across sites, seasons, devices, and noise regimes; strong augmentations (time/frequency masking, additive noise, pitch/time shifts, mixup) that encourage invariances; and label quality controls to limit confirmation bias. BirdNET exemplifies how curated training and pragmatic engineering can deliver high precision/recall for hundreds of avian taxa at continental scales, with models that run on laptops, cloud servers, and even embedded devices (Kahl *et al.,* 2021). For marine applications, CNNs trained on click envelopes or cepstral features discriminate odontocete species and sometimes individuals; for baleen whales, detectors combine harmonic-stack templates with learned classifiers to handle variable song modes. Increasingly, teams export intermediate embeddings (fixed-length vectors summarizing each audio window) to enable downstream ecological modeling without shipping raw audio, which reduces bandwidth, storage, and privacy risk while preserving signal structure for transfer learning. Edge-AI is accelerating this trend: quantized models (e.g., int8) execute on microcontrollers or single-board computers near the sensor, filter empty audio, and trigger event-based recordings—critical for power-limited stations that must operate for months.

Despite these advances, noisy and nonstationary environments remain the principal obstacle to reliable, generalizable inference. Because the soundscape is a superposition of geophony and anthropophony on top of biophony, the same species’ call recorded in different habitats, seasons, or sensor positions can vary in signal-to-noise ratio (SNR), reverberation, and apparent frequency content; models trained on one site often underperform at the next—a classic domain-shift problem (Gibb *et al.,* 2019; Stowell, 2022). Best practice therefore couples site-conditioned thresholds with transfer-learning strategies: fine-tuning on a small, locally labeled set; domain-adversarial training to learn site-invariant embeddings; and uncertainty-aware calibration so downstream occupancy or abundance estimates propagate model confidence rather than treating classifier outputs as truth. Robust denoising (spectral subtraction, Wiener filtering) helps at moderate SNR, but aggressive filtering can erase biologically meaningful harmonics or sidebands, producing false negatives; consequently, many pipelines favor conservative denoising coupled with augmentation-hardened models. Hardware heterogeneity—different hydrophone sensitivities, frequency responses, and pre-amp noise floors—adds variance; calibration tones and standard metadata (sensitivity, gain, sampling rate, deployment geometry) are indispensable for cross-project comparability. Where human verification is necessary, human-in-the-loop workflows prioritize clips with high uncertainty or ecological novelty (active learning), maximizing expert time and continuously improving the training set.

From inference to ecology, PAM enables multi-level questions: presence–absence and phenology (first/last calling dates); behavioral state (e.g., foraging buzzes vs. search clicks; song vs. social calls); habitat associations (chorus intensity vs. seagrass cover); and population processes (density estimation from cue rates and detection probabilities). For line-transect-style acoustic surveys, the distance-sampling framework connects detection probability to range via propagation models and empirical calibration, yielding unbiased density under stated assumptions (Marques *et al.,* 2013). For stationary sensors, repeated-measures occupancy models use detection histories to separate detection from availability, while passive acoustic density estimation infers absolute abundance if cue rate (calls per animal per unit time) is known or can be estimated—often the limiting parameter biologically rather than technically. Ethical and governance considerations accompany scale: even though PAM is non-invasive for wildlife, deployments near human activity can capture voices or sensitive operations; projects should follow data-minimization and privacy-preserving practices, document consent where applicable, and consider embargoes or location jitter for threatened species.

Returning to Figure 4**,** the schematic is more than an illustration: it encodes the causal web linking environmental forcing to acoustic observables. Ice cracking and wave action inject low-frequency energy; wind raises broadband hiss and modulates calling behavior; rain spikes mid-to-high frequencies; shipping produces narrow-band tonals that mask baleen whale song; seismic surveys generate impulsive, high-energy signals; drilling and sonar add structured noise; fishes and invertebrates chorus around crepuscular periods; and marine mammals vocalize for communication, navigation, and prey search. Effective study designs exploit this mapping: scheduling duty cycles to span dawn/dusk, choosing frequency bands that avoid local shipping tones, and colocating recorders with temperature or chlorophyll sensors so models can attribute calling changes to physical or biological drivers rather than to masking alone (Duarte *et al.,* 2021). In short, PAM turns sound into a quantitative, environmental sensor of life itself. The field's trajectory is clear: richer multi-sensor context (acoustic plus current meters, eDNA, or satellite layers), standardized metadata and FAIR archiving for comparability, uncertainty-aware AI that transfers across sites and devices, and edge deployments that move intelligence to the field. With these ingredients, bioacoustics is becoming a true "systems biology of sound," where automated detectors, calibrated propagation models, and ecological theory combine to reveal how animals use—and are constrained by—the changing soundscapes of the Anthropocene Ocean and beyond (Gibb *et al.,* 2019; Kahl *et al.,* 2021; Marques *et al.,* 2013; Stowell, 2022; Duarte *et al.,* 2021).

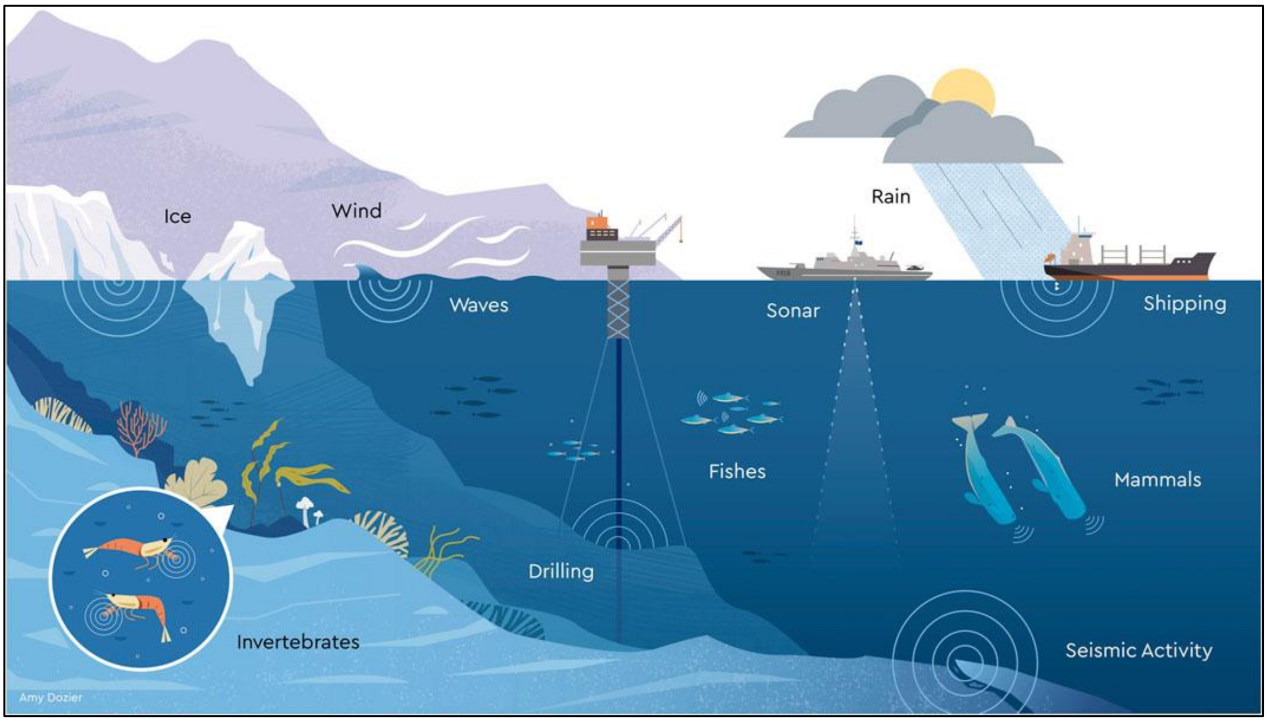

Figure 4: Sensing the Living Earth — Bioacoustics from Soundscapes to AI Pipelines

Panels illustrate the core pieces of modern bioacoustics. **(A) Soundscape sources**—biophony, geophony, and anthropophony—drive the signals PAM stations record; separating these is the first analytic challenge. **(B) A PAM workflow** shows spectrogram inspection paired with a trained classifier for automated click/call detection, reflecting typical QA steps in marine-mammal monitoring. **(C) Species-specific spectrograms** emphasize why time–frequency structure enables recognition but is sensitive to filtering/noise choices. **(D) Deep-learning architecture** for audio (multi-scale spectrogram features with self-attention) exemplifies current CNN/transformer approaches that power on-device or cloud inference for species presence, call types, and density indices.

3.5. Remote Sensing & Environmental Layers

Figure 5 illustrates a modern, end-to-end workflow for ecological prediction that begins with global species records and proceeds through satellite time-series preprocessing, deep convolutional training (here, an Inception-style architecture), and evaluation with a particular focus on the value of temporal information. In the figure's orchid case study, nearly one million GBIF occurrences are geographically and taxonomically filtered to reduce noise and bias, monthly Sentinel-2 image stacks are prepared at appropriate spatial resolutions, and a convolutional species-distribution model (SDM) is trained to learn habitat context directly from imagery; this pipeline demonstrates how seasonal greenness trajectories, moisture signals, and disturbance histories can encode the ecological niches that static snapshots miss (Zizka *et al.,* 2020; Drusch *et al.,* 2012; Elith & Leathwick, 2009). In general, satellite and UAV sensors now map habitat structure, productivity, water, and disturbance from plot to planet: multispectral platforms (e.g., Sentinel-2, Landsat) provide surface reflectance and vegetation indices for phenology and primary productivity; thermal sensors resolve surface temperature for heat stress and water balance; synthetic aperture radar (SAR) penetrates clouds and is sensitive to canopy water and structure, enabling humid-tropics monitoring where optical data are persistently cloudy; and laser altimeters and airborne/UAV LiDAR translate canopy geometry into canopy height models (CHMs), roughness, and gap metrics that quantify microhabitats and structural connectivity (Pettorelli *et al.,* 2014; Wulder *et al.,* 2019; Coomes *et al.,* 2017; Dubayah *et al.,* 2020). On the ground or at low altitude, drones fill the scale gap with centimeter-level orthomosaics and point clouds that validate spaceborne products and capture fine-scale features (e.g., nest substrates, small canopy openings, riparian complexity) that often govern occupancy and detection (Maxwell *et al.,* 2018). These physical layers, when combined with hydroclimate, edaphic, and disturbance products (e.g., fire, logging), create a rich environmental "cube" onto which biological data can be projected.

Integration with species data is the heart of predictive modeling. Occurrence data from community repositories (GBIF, iNaturalist), curated atlases, and museum records can be filtered, spatially thinned, and bias-corrected (e.g., target-group background, bias grids) before modeling to reduce the outsized influence of collector accessibility (Fourcade *et al.,* 2014; Phillips *et al.,* 2009). Telemetry yields presence tracks and utilization distributions that can be coupled to dynamic environmental layers to infer step selection, corridor use, and behavioral states; eDNA detections add presence signals in aquatic and soil systems that can be co-modeled with imagery to reveal otherwise cryptic distributions (Kays *et al.,* 2015; Deiner *et al.,* 2017). Classical SDMs—generalized additive models, boosted trees, and MaxEnt—remain powerful baselines, especially when environmental layers are carefully chosen to represent mechanistic constraints, collinearity is handled, and spatial cross-validation prevents optimistic error estimates (Elith & Leathwick, 2009; Phillips *et al.,* 2006). Increasingly, deep learning complements these tools by ingesting image patches or time-series directly, learning spatial–temporal features linked to habitat quality (as in Figure 5), and enabling transfer across regions with fine-tuning; importantly, interpretable saliency methods and permutation tests can quantify which phenological or structural signals drive predictions (Lorieul *et al.,* 2019; Zizka *et al.,* 2020). Crucially, these models now operate within cloud geocompute ecosystems such as Google Earth Engine, which make petabyte-scale archives (Landsat, Sentinel) and climate reanalyses accessible for continental modeling and rapid re-runs under alternative scenarios (Gorelick *et al.,* 2017).

Once species and environment are fused, remote sensing informs connectivity and conservation design. Resistance surfaces derived from LiDAR (e.g., canopy height continuity), SAR (flooded vs. dry states), and multispectral indices (NDVI/NDWI dynamics) can be combined with circuit theory or least-cost path modeling to identify movement corridors, stepping-stone habitats, and bottlenecks, guiding protected-area placement and restoration priorities (Keeley *et al.,* 2018; Coomes *et al.,* 2017). Joint SDMs and hierarchical occupancy frameworks extend from single species to assemblages, pooling information and enabling community-level forecasts such as expected richness or functional diversity under changing environments (Norberg *et al.,* 2019). Importantly, these predictions should be delivered with calibrated uncertainty—stemming from sampling bias, model choice, and environmental data errors—so that decision-makers can weigh risk when allocating scarce resources. Best practice therefore includes spatial block cross-validation, out-of-region transfer tests, and explicit propagation of uncertainty from environmental predictors (e.g., cloud contamination, BRDF artifacts) through to ecological endpoints (Elith & Leathwick, 2009; Wulder *et al.,* 2019).

Climate and land-use change are the dominant drivers of distributional dynamics, and remote sensing supplies both the historical baselines and the forward-looking layers that power forecasts. Long Landsat and Sentinel records establish phenological trends, greening/browning patterns, and disturbance histories that contextualize present niches; coupling these with downscaled climate projections (temperature, precipitation, drought metrics) and scenarios of land conversion or fire regime shift allows forecasts of range movement, contraction, or fragmentation (Pettorelli *et al.,* 2014; Wulder *et al.,* 2019). Decades of synthesis show that many taxa have already shifted poleward and upslope in response to warming, with phenological advancement creating mismatches between consumers and resources; forecasting these dynamics demands models that are dynamic in time, not just correlative snapshots (Parmesan, 2006; Thackeray *et al.,* 2016). Land-use, particularly the conversion and intensification of human-dominated landscapes, remains a primary pressure on biodiversity, with measurable impacts on local species richness and community composition; pairing satellite-derived land-use change with SDMs quantifies how fragmentation and edge effects amplify climate stress (Newbold *et al.,* 2015; IPBES, 2019). In tropical forests, LiDAR-based structure and SAR-based moisture detect selective logging and degradation that optical sensors may miss under clouds, improving forecasts for forest-dependent fauna (Coomes *et al.,* 2017). At global scale, GEDI's spaceborne lidar is revolutionizing estimates of aboveground biomass and vertical structure, yielding mechanistic predictors that are directly relevant to animal energetics, nesting niches, and predator–prey encounter rates (Dubayah *et al.,* 2020). These structural layers, combined with climate trajectories, sharpen predictions of extinction risk by distinguishing mere habitat loss from functional habitat collapse.

Because high-capacity models can be confidently wrong outside their training domain, the community is converging on standards to ensure transparency and reuse. FAIR principles and community vocabularies (e.g., Darwin Core for occurrences; STAC for spatiotemporal assets) facilitate interoperability among institutions and projects, while open repositories hosting training data, code, and pre-trained weights enable rigorous comparison and iterative improvement (Pettorelli *et al.,* 2014; Gorelick *et al.,* 2017). Bias diagnostics and corrective strategies—spatial thinning, environmental filtering, target-group background selection, and explicit sampling-effort covariates—should be reported alongside accuracy metrics to avoid spurious certainty where observers simply did not go (Fourcade *et al.,* 2014; Phillips *et al.,* 2009). Finally, as imagery sharpens and telemetry densifies, privacy and biosecurity considerations escalate: locations of threatened species, nesting trees, or rookeries identified from high-resolution products may require coarsening or embargo policies to prevent misuse, balancing openness with protection (IPBES, 2019). In sum, the Figure-5 paradigm—global occurrences distilled and de-biased, time-resolved satellite stacks, LiDAR/SAR structure, and deep yet interpretable models—underpins a new predictive ecology capable of mapping hotspots and corridors today and forecasting tomorrow's ranges, phenology, and extinction risk under coupled climate and land-use change.

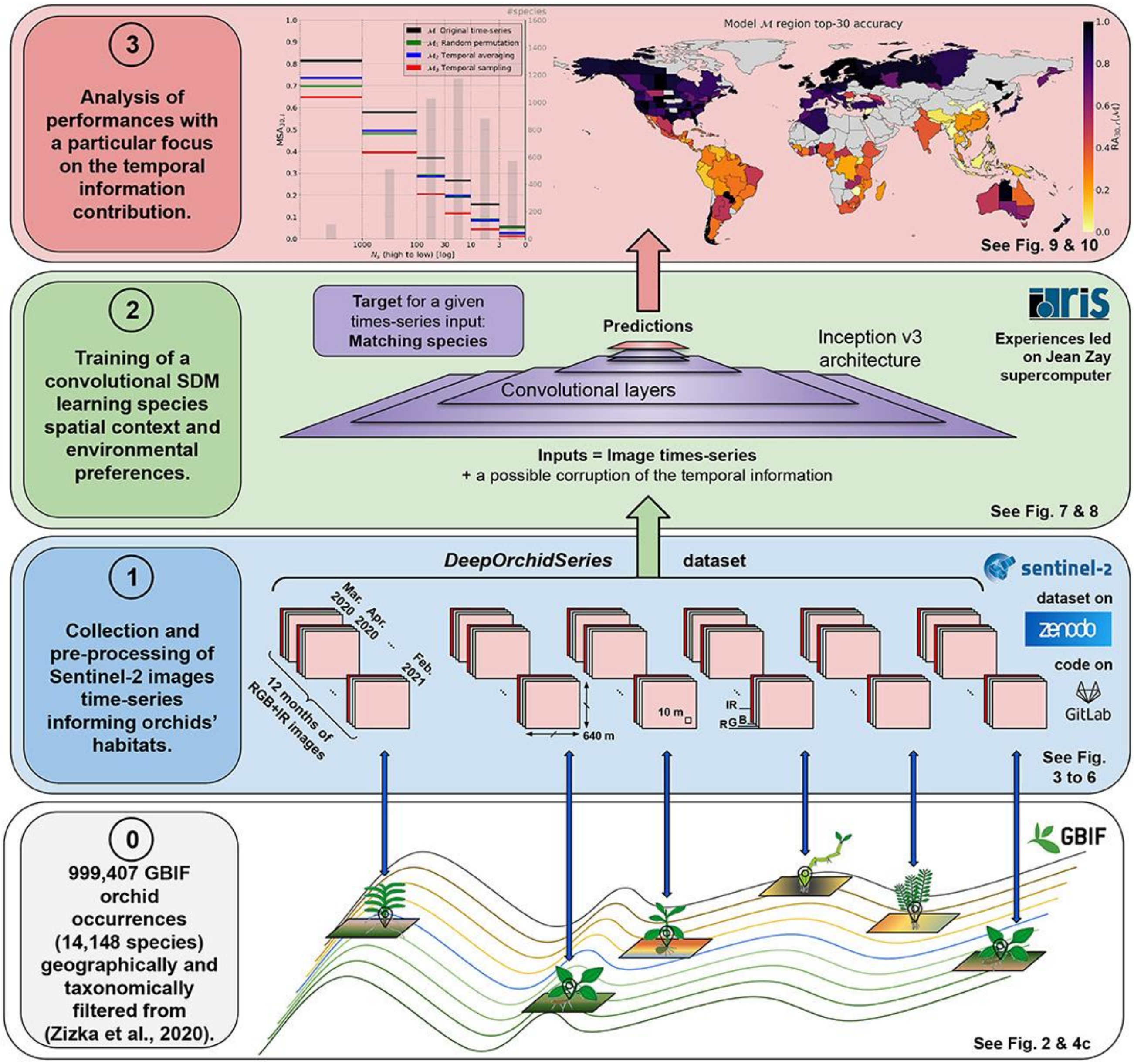

Figure 5: RS-1. Remote Sensing & Environmental Layers — from pixels to predictive ecology

Caption. (A) Satellite time-series + species data → SDMs. Visual abstract of a deep species-distribution pipeline pairing Sentinel-2 image stacks with GBIF orchid occurrences to learn spatio-temporal habitat signals and generate global predictions; it exemplifies fusing occurrence data with environmental layers for hotspot mapping. (B) UAV–LiDAR mapping. Schematic of a drone LiDAR survey producing dense point clouds and canopy-height surfaces, the fine-scale layers used to quantify microhabitats, gaps, and structural connectivity. (C) Multi-platform sensing. Conceptual overview of spaceborne, airborne/UAV, and ground systems jointly measuring canopy traits (e.g., LAI, height) and biomass—illustrating how orthomosaics, multispectral/SAR/thermal data, and LiDAR complement one another from plot to region. (D) Climate/land-use scenarios → extinction risk. Workflow linking environmental predictors, model uncertainty, and IUCN risk categories to forecast range change and extinction probability under future climate/land-use, highlighting why uncertainty quantification matters for policy.

3.6. Computational Advances

Figure 6 illustrates the backbone of modern biodiversity informatics: a Darwin Core "event core" that nests samples within sampling events and links each *occurrence* to standardized measurements (e.g., abundance, body length) via extensions such as ExtendedMeasurementOrFact. This schema—together with Audubon Core for multimedia—operationalizes the FAIR ideal (Findable, Accessible, Interoperable, Reusable) by binding observations, methods, and traits to persistent identifiers and controlled vocabularies, so datasets from community portals can feed directly into machine-learning pipelines without ad-hoc wrangling

(Wieczorek *et al.,* 2012; Morris *et al.,* 2013; Wilkinson *et al.,* 2016). On the modeling side, convolutional/transformer architectures now power automated taxonomy from images and audio, with large-scale bird sound recognition (e.g., BirdNET) and high-throughput camera-trap classifiers demonstrating expert-level accuracy under field conditions (Kahl *et al.,* 2021; Van Horn *et al.,* 2018). In predictive ecology, species-distribution models increasingly fuse occurrence archives with satellite time series and LiDAR/SAR structure, while joint/ensemble approaches propagate uncertainty and improve transferability across regions and climates (Elith & Leathwick, 2009; Araújo & New, 2007; Norberg *et al.,* 2019). Open repositories supply the fuel: GBIF aggregates billions of standardized occurrences; BOLD couples sequences and vouchers for DNA barcoding; Movebank curates animal tracking with rich metadata and privacy controls; and VertNet federates vertebrate museum records—together providing training data, covariates, and benchmarks for recognition, occupancy, abundance, and movement-aware models (Ratnasingham & Hebert, 2007; Constable *et al.,* 2010; Kranstauber *et al.,* 2011; GBIF Secretariat, 2023). Priorities now include rigorous bias correction (spatial thinning, target-group backgrounds), calibrated uncertainty in downstream ecological metrics, reproducible and versioned pipelines (containers, workflow languages), and safeguards for sensitive species locations, all documented within the same standardized schemas that Figure 6 encapsulates (Phillips *et al.,* 2009; Fourcade *et al.,* 2014; Wilkinson *et al.,* 2016).

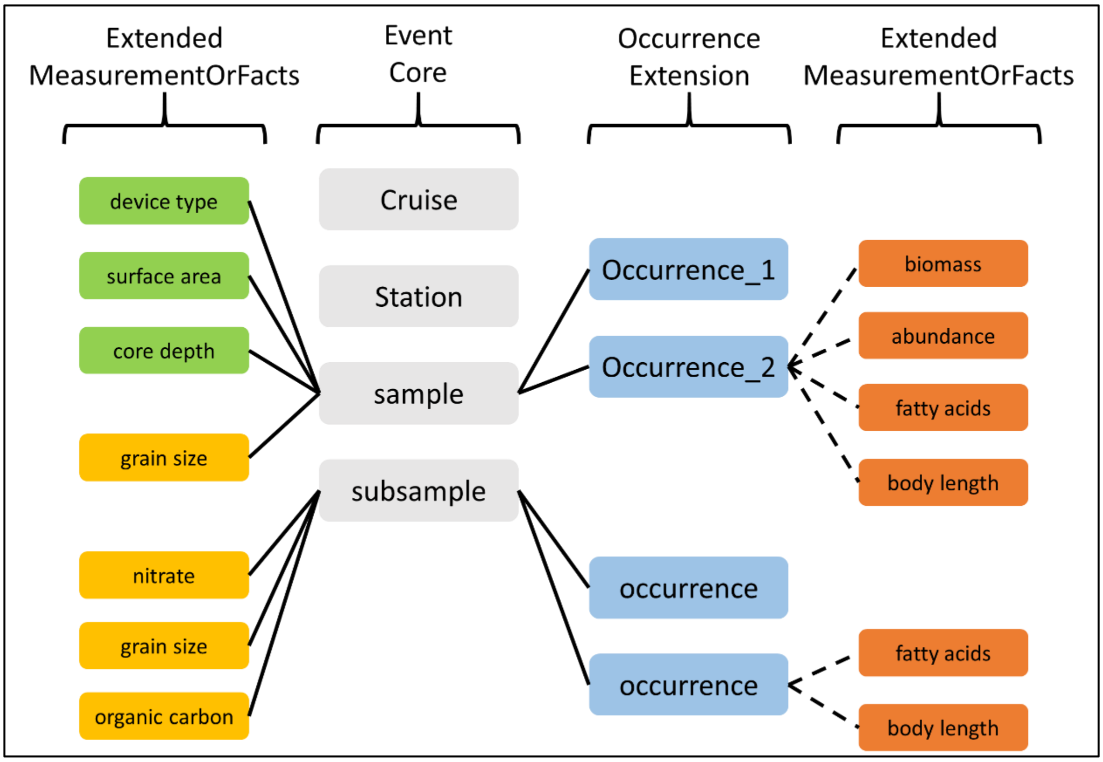

Figure6 CA-1. Computational Advances — Standards-to-Models Pipeline

Caption. Diagram of a Darwin Core Archive "star schema," where an Event/Occurrence core is linked to extensions (e.g., Extended Measurement Or Fact) via stable IDs. This structure underpins FAIR-aligned biodiversity workflows: occurrences from platforms like GBIF/OBIS are packaged with standardized metadata (Darwin Core/Audubon Core), enabling machine-learning tasks such as taxonomy/image–audio ID, occupancy and abundance modeling, and movement-aware predictive ecology using interoperable, reusable datasets. The same principles extend to tracking repositories (e.g., Move bank/Move Apps) and data-processing scripts (e.g., GBIF pipelines), which rely on standard schemas and versioned workflows to support bias correction, uncertainty quantification, and privacy-preserving data release.

4. Research Gaps and Challenges

Biodiversity science is advancing rapidly, yet fundamental frictions persist across data collection, modeling, governance, and equity. The first bottleneck is the enduring taxonomic impediment—the shortage of trained identifiers and curators relative to the volume of new samples, images, audio, and eDNA reads flowing into repositories. Although machine learning is accelerating preliminary identifications, authoritative names, synonym resolution, and type-based revisions still depend on expert taxonomists and well-resourced collections. Recent assessments highlight the backlog of undescribed diversity and the growing need for sustainable career pathways, voucher digitization, and training programs that connect taxonomic expertise to modern pipelines (Acerbi *et al.,* 2022; Engel *et al.,* 2021). The problem is acute in hyperdiverse clades and regions where collections infrastructure and long-term funding are limited (Amano *et al.,* 2021).

A second, cross-cutting challenge is bias in biodiversity data. Community occurrence archives (e.g., GBIF) and camera-trap or acoustic datasets are geographically skewed toward accessible, affluent, and temperate regions; they are also taxonomically biased toward charismatic and easily detectable species, and temporally biased toward recent years and specific seasons. These biases inflate apparent richness and model confidence in well-sampled places while degrading transferability elsewhere. Systematic evaluations between 2018 and 2025 show that spatial sampling intensity, observer accessibility, and road density strongly structure what is "known," and that failure to correct for these biases leads to misleading species–environment relationships (Amano *et al.,* 2018; Zizka *et al.,* 2021). Recommended mitigations include spatial thinning of points, target-group backgrounds, explicit effort covariates, and spatial block cross-validation to obtain realistic predictive skill (Fourcade *et al.,* 2014; Valavi *et al.,* 2019).

Third, validation for eDNA and bioacoustic models remains a frontier. For eDNA, uncertainties arise from variable shedding/decay rates, taxon- and habitat-specific detection probabilities, contamination, and incomplete reference libraries; metabarcoding pipelines differ in primer choice, clustering, and error filtering, making cross-study comparability difficult (Zinger *et al.,* 2019; Beng *et al.,* 2022). Ground-truth designs that pair eDNA with independent methods (visual surveys, telemetry, traditional nets) and that report detection histories are essential for robust occupancy or abundance inference (Bessey *et al.,* 2023). In computational bioacoustics, deep networks achieve high accuracy in lab and "seen" sites but can falter under domain shift—new habitats, microphones, or noise regimes. Reviews emphasize uncertainty quantification, domain adaptation, and standardized metadata for microphones and deployments to ensure reliable ecological estimates rather than just classifier scores (Stowell, 2022; Gibb *et al.,* 2019).

A fourth gap concerns multi-modal integration and standards. Ecologists increasingly fuse images, audio, trajectories, eDNA, and environmental layers, yet standards for cross-modal metadata, identifiers, and provenance are still patchy. Darwin Core and Audubon Core cover occurrences and media, and Movebank provides a structured schema for tracking, but there is no universally adopted "fusion standard" that binds an observed individual (or event) to synchronized audio, imagery, genetic reads, and sensor covariates with versioned workflows and uncertainty fields (Kranstauber *et al.,* 2011; Morris *et al.,* 2013; GBIF Secretariat, 2023). FAIR principles guide data stewardship, but practical, interoperable implementations for multi-modal pipelines—especially at edge devices that perform on-sensor inference—are still emerging. Community calls prioritize persistent identifiers across modalities, standardized confidence scoring, and machine-readable provenance linking raw signals to derived ecological quantities (Wilkinson *et al.,* 2016; Lorieul *et al.,* 2019).

Fifth, ethics, safety, and rights require sustained attention. Tagging and telemetry can impose mass, drag, or attachment effects that alter behavior and survival; studies urge explicit welfare assessments, species- and life-stage-specific payload limits, and reporting checklists for tag effects (Bodey *et al.,* 2018; Lennox *et al.,* 2021). Indigenous data sovereignty is also central: many observations are gathered on Indigenous lands or concern culturally significant species, and the CARE Principles (Collective Benefit, Authority to Control, Responsibility, Ethics) complement FAIR by asserting community governance over data use and sharing (Carroll *et al.,* 2020). Open-data misuse remains a tangible risk when precise locations of threatened taxa enable poaching or disturbance; guidance recommends coordinate obfuscation, delayed release, or sensitive-data tiers to balance transparency with protection (Tulloch *et al.,* 2018).

Finally, major equity gaps persist in who collects, curates, models, and benefits from biodiversity data. The Global South is under-represented in authorship, funding, instrumentation, and training opportunities, which in turn amplifies geographic data gaps and model uncertainty in biodiversity hotspots. Analyses from 2018–2025 show that language barriers, limited infrastructure, and colonial legacies depress visibility of non-English research and constrain participation in global syntheses (Amano *et al.,* 2018; Meneghini & Packer, 2021). Addressing equity is not just ethical: improving participation and infrastructure in under-sampled regions is the most effective way to reduce bias and increase the reliability of global predictions.

The table1 summarizes key pain points, their consequences, and practical remedies that teams can implement now while community-level standards continue to evolve.

Gap (2018–2025)	Why it matters	Typical consequence	Practical remedies (near-term)
Taxonomic impediment	Vouchers and names anchor all downstream models	Misidentifications; unstable labels	Invest in taxonomic hires and fellowships; fund digitization; mandate voucher deposition; pair ML pre-ID with expert review (Acerbi *et al.,* 2022; Engel *et al.,* 2021)
Sampling bias (geo/tax/temporal)	Models learn biases, not biology	Overconfident SDMs; poor transfer	Spatial thinning; effort covariates; target-group background; spatial block CV; prioritized sampling in gaps (Zizka *et al.,* 2021; Valavi *et al.,* 2019)
eDNA validation	Pipeline choices alter detections	False positives/negatives; incomparable studies	Co-deploy traditional surveys; report detection histories; expand reference libraries; blind controls (Zinger *et al.,* 2019; Beng *et al.,* 2022)
Acoustic model generalization	Domain shift across sites/devices	Degraded accuracy; biased occupancy/abundance	Domain adaptation; calibrated uncertainty; device metadata; human-in-the-loop QA (Stowell, 2022; Gibb *et al.,* 2019)
Multi-modal fusion standards	Linking audio–image–eDNA–tracks is ad-hoc	Lost provenance; irreproducibility	Persistent IDs for entities/events; harmonized schemas across DwC/Audubon/Movebank; machine-readable provenance (Morris *et al.,* 2013; Kranstauber *et al.,* 2011; GBIF Secretariat, 2023)
Ethics & rights	Harm or misuse undermines conservation	Tag-related mortality; poaching risk	Welfare checklists; payload limits; CARE-aligned governance; coordinate obfuscation for sensitive taxa (Bodey *et al.,* 2018; Carroll *et al.,* 2020; Tulloch *et al.,* 2018)
Global equity	Under-sampled hotspots; lost expertise	Uncertain forecasts; dependency	Fund South-led observatories; multilingual publishing; equitable data agreements; capacity building (Amano *et al.,* 2018; Meneghini & Packer, 2021)

5. Integrative Case Studies

Case 1: Combining eDNA + camera traps + acoustics for cryptic mammals. Coordinating environmental DNA (eDNA) with autonomous camera traps and passive acoustics closes detection gaps for elusive or nocturnal species. Comparative field tests show that terrestrial eDNA can recover many of the same mammals recorded by cameras while adding species that seldom trigger sensors, especially when catchment-scale river samples integrate signals across heterogeneous habitats (Leempoel, Hebert, & Pellissier, 2020; Chacko, Leempoel, Buri, & Pellissier, 2023). Airborne eDNA extends coverage to the air column and has detected dozens of vertebrates around trails and enclosures, offering a non-invasive complement to cameras and microphones (Lynggaard *et al.,* 2022). In an integrated design, monthly soil/river/air eDNA collections anchor presence, continuous acoustic recorders capture bats and vocal carnivores, and camera grids provide individual-level imagery and behavior; cross-validation comes from co-detections and temporal concordance across methods (Beng, Corlett, & Núñez-Mir, 2022).

Case 2: Linking biologging with trait databases to predict species' climate resilience. Tracking data quantify exposure (thermal histories, drought encounters, phenological timing), but resilience also depends on species traits (body size, fecundity, trophic strategy, thermal niche breadth). Integrating global tracking archives with trait compilations enables trait–environment models that forecast climate vulnerability and reveal corridor or stopover dependencies (Hays *et al.,* 2019; Beltran, Abrahms, Costa, *et al.,* 2025). Trait-aware analyses suggest species with constrained movement and slow life histories struggle to track shifting isotherms, whereas highly mobile taxa with broad niches show greater adaptive capacity. Practical pipelines estimate exposure metrics from tracks, join them with trait tables, and fit hierarchical models to predict sensitivity and adaptive potential across related taxa.

Case 3: AI-based bioacoustic monitoring in tropical bird conservation. Deep learning on long-duration audio produces near–real-time indicators for tropical forest birds where visual surveys are logistically difficult. BirdNET and similar models deliver high precision/recall across hundreds of species, and embeddings enable few-shot searches for rare targets (Kahl, Wood, Eibl, & Klinck, 2021; Van Horn *et al.,* 2018). Recent tropical deployments show that ARU+AI workflows scale across protected areas and seasons; fusing ARU detections with citizen-science records improves species-distribution models and trend detection for rainforest birds (Rumelt, Mere Roncal, Basto, Buřivalová, & Searcy, 2025; Winiarska *et al.,* 2025). Best practice includes dawn/dusk duty cycles, site-specific threshold calibration, domain adaptation to mitigate "site shift," and human-in-the-loop audits for uncertainty control.

Case 4: Remote sensing + genomics for tracking insect decline. Satellite time series reveal phenology, greening/browning, and heat extremes that can be coupled to population genomics to diagnose mechanisms of decline. Space-observed environmental trajectories have been linked to temporal genomic change and predicted genomic vulnerability ("genomic offsets") under future climates in alpine and montane systems (Theodoridis *et al.,* 2025). Museum-to-modern genomes of threatened butterflies document historical declines and inbreeding, providing baselines to interpret contemporary range contractions (de-Dios *et al.,* 2024). At landscape scales, long Landsat records contextualize habitat loss and fragmentation that interact with heat extremes to drive declines (Wulder *et al.,* 2019). An RS-genomics workflow pairs annual vegetation/thermal metrics with SNP datasets, identifies environment-associated loci, and maps vulnerability to guide micro-refugia protection or assisted gene flow.

6. Towards a Unified Framework for Zoology 4.0

Zoology 4.0 connects molecular mechanisms to planetary patterns through a single, testable scaffold: genes shape phenotypes in individuals, whose behaviors and life histories aggregate to populations, whose interactions and flows of energy/matter organize communities and ecosystems. A unified framework treats these levels as coupled state variables linked by constraints and feedbacks—e.g., genotype–phenotype maps and plasticity at the individual level; demography, dispersal, and trait distributions at the population level; and interaction networks, disturbance regimes, and environmental filters at ecosystem scales. Practically, this means defining cross-scale quantities that are both biologically meaningful and observable: genomic diversity and functional alleles (genes), movement/physiology and behavior (individuals), vital rates and connectivity (populations), and compositional/functional turnover plus structural habitat metrics (ecosystems). Joint models then propagate information upward and downward—for instance, trait distributions inferred from genomes and bioacoustics inform population growth/decline, while remote-sensing indicators of habitat structure feedback to predict selection and gene flow (Elith & Leathwick, 2009; Norberg *et al.,* 2019).

Delivering on this vision requires multi-modal data-fusion pipelines that bind occurrences, traits, tracks, acoustic and image evidence, eDNA reads, and environmental layers into reproducible workflows. At ingestion, standardized schemas (Darwin Core/Audubon Core for occurrences and media; Movebank for tracking) and persistent identifiers ensure that observations, devices, and analytical steps are machine-joinable across projects and time (Wieczorek *et al.,* 2012; Kranstauber *et al.,* 2011; Morris *et al.,* 2013). At the modeling layer, three families of tools dominate and interoperate: (i) *recognition models* (convolutional/transformer architectures for image/audio ID) that convert raw signals to species/individual probabilities; (ii) *integration models* that connect detections to environment and process—ranging from hierarchical occupancy/abundance models to joint species distribution models (JSDMs) and movement-aware step-selection models; and (iii) *forecast engines* that run scenarios under climate and land-use change with uncertainty propagation (Kahl, Wood, Eibl, & Klinck, 2021; Norberg *et al.,* 2019; Wulder *et al.,* 2019). Technically, fusion means aligning time and space (e.g., co-registering acoustic detections with canopy height or temperature), learning shared representations (embeddings) that transfer across sites and sensors, and versioning every transformation from raw data to ecological metric so results are auditable and repeatable (Lorieul *et al.,* 2019; Wilkinson *et al.,* 2016). Edge-to-cloud designs further reduce costs and bias by running lightweight models on recorders or collars, transmitting embeddings or events rather than raw data, and syncing with cloud pipelines for calibration and validation.

Equally central are ethical and reproducible research practices. Adopting the 3Rs—*Replacement, Reduction, Refinement*—in wildlife research means (i) replacing invasive methods with non-invasive alternatives where possible (e.g., eDNA, camera traps, autonomous recorders), (ii) reducing sample sizes and handling through power-aware designs and re-use of open datasets, and (iii) refining procedures to minimize stress (e.g., payload-to-mass limits, hydrodynamic tag shapes, quick-release fittings) with transparent reporting of tag effects (Bodey *et al.,* 2018; Lennox, Diserud, Thorstad, & Cooke, 2021). Reproducibility depends on preregistered protocols; containerized, version-controlled code; open benchmarks; and FAIR data publication so analyses are *findable, accessible, interoperable, and reusable* (Wilkinson *et al.,* 2016). Where data concern threatened species or culturally significant places, CARE principles (collective benefit, authority to control, responsibility, ethics) and Indigenous data sovereignty must guide governance, including sensitive-data tiers, coordinate generalization, and co-stewardship agreements (Carroll *et al.,* 2020). Together, FAIR+CARE transforms raw signals into trustworthy, shareable evidence while safeguarding welfare and rights.

Finally, a Zoology-4.0 program reaches beyond academia by integrating with policy and practice. Models should emit indicators that map directly to conservation levers: occupancy and abundance trends for protected-area management; connectivity and resistance surfaces for corridor design; demographic and genomic vulnerability for prioritizing translocations or assisted gene flow; and ecosystem-function proxies (e.g., acoustic energy, pollinator activity) that track restoration success. These outputs should align with global targets and reporting frameworks so they are actionable: the Kunming–Montreal Global Biodiversity Framework under the Convention on Biological Diversity sets measurable goals for 2030 and 2050; IPBES assessments synthesize drivers and options; and Essential Biodiversity Variables provide an observation-to-indicator bridge adopted by monitoring networks (IPBES, 2019; CBD, 2022). Remote-sensing time series (Landsat/Sentinel), coupled with field and community data streams (GBIF, BOLD, Movebank, VertNet), enable consistent baselines and near-term updates against which progress can be scored (Wulder *et al.,* 2019; GBIF Secretariat, 2023). To support uptake, every model run should carry calibrated uncertainty and decision-relevant summaries (e.g., probability of falling below a population threshold), and workflows should be packaged as reusable, well-documented pipelines that agencies can execute without rebuilding the stack. Critically, the framework must be equitable: capacity building, co-authorship, and funding for field observatories in under-represented regions are as important as algorithms for closing data gaps and ensuring that benefits—knowledge, credit, careers—are shared (Amano, González-Varo, Sutherland, & Edwards, 2021).

In sum, Zoology 4.0 is not a single tool but a disciplined way of linking scales, sensors, and society. It treats genes-to-ecosystems as a coherent system, fuses heterogeneous evidence with transparent, versioned pipelines, embeds the 3Rs and FAIR+CARE into everyday practice, and outputs decision-ready indicators aligned to CBD/IPBES goals. With these pillars in place, the field can move from fragmented case studies to cumulative, policy-relevant science that anticipates change and guides conservation where it is most needed.

7. DISCUSSION

Integrative zoology demonstrates that stitching together multi-modal evidence—genomes, traits, images, audio, tracks, and environmental layers—can produce ecological inferences that classical, single-method approaches rarely achieve. First, fusion across scales closes persistent detectability gaps: pairing eDNA with autonomous recorders and camera traps elevates true occupancy estimates for cryptic taxa and delivers convergent lines of evidence, reducing method-specific false negatives and enabling stronger causal claims about presence, behavior, and habitat use (Beng, Corlett, & Núñez-Mir, 2022; Stowell, 2022). Second, remote-sensing time series (optical, SAR, thermal, LiDAR) supply dynamic habitat context—phenology, disturbance, structural change—so species–environment relationships are learned on the backdrop of real variability rather than static climatic means (Wulder *et al.,* 2019; Dubayah *et al.,* 2020). Third, joint and hierarchical models link individual behavior to population processes and community assembly, allowing uncertainty to be propagated from raw detections through to forecasts of abundance, connectivity, and resilience (Norberg *et al.,* 2019). Finally, standardization and FAIR practices turn ad-hoc analyses into reusable pipelines, making it possible to compare results across regions and years, replicate findings, and accumulate evidence into policy-relevant indicators (Wieczorek *et al.,* 2012; Wilkinson *et al.,* 2016). In effect, integrative zoology operationalizes a genes→individuals→populations→ecosystems chain where evidence flows both upward (from signals to systems) and downward (from habitat dynamics to predicted behavior and gene flow)—a synthesis that classical, siloed approaches struggle to reproduce.

Looking forward, three directions can move the field from powerful case studies to operational, global observatories. The first is real-time biodiversity dashboards that couple streaming data with decision-ready analytics. Edge devices already filter audio and images on-site, transmitting only events or embeddings; paired with cloud geocompute platforms, this enables near-real-time occupancy and activity indices for priority species, with spatial block cross-validation and calibrated uncertainty baked in (Gorelick *et al.,* 2017; Kahl, Wood, Eibl, & Klinck, 2021). Mature exemplars in allied domains—forest loss alerts, fire detections—show how to render model outputs as actionable maps; integrative zoology can analogously publish live indicators of corridor use, breeding phenology, or acoustic energy as early-warning signals for managers (Wulder *et al.,* 2019). To be credible, such dashboards must expose data lineage, model versions, and "health checks" (coverage, sensor uptime) so users can judge reliability at a glance (Wilkinson *et al.,* 2016).

The second direction is AI foundation models for ecology. Modern recognition systems excel within domain bounds, but transfer across sites, sensors, seasons, and species remains uneven. Foundation models—large, pre-trained networks that learn universal audio–image–text embeddings and can be adapted with small, local datasets—offer a path to robust, few-shot ecological inference. In acoustics, embeddings learned from billions of audio snippets can power few-shot detectors for rare species and yield calibrated uncertainty that downstream occupancy models can ingest (Stowell, 2022). In imagery, transformer backbones pre-trained on massive, biodiversity-focused datasets (e.g., iNaturalist) already approach expert-level identification; with standardized, Darwin Core–anchored metadata and Audubon Core media descriptors, these backbones can be fine-tuned for regional faunas while preserving provenance (Van Horn *et al.,* 2018; Wieczorek *et al.,* 2012; Morris *et al.,* 2013). Crucially, ecological foundation models must be *interpretable* and *constrained*: saliency, counterfactuals, and process-guided loss functions should make feature use biologically sensible, avoiding spurious correlations with sampling bias (Elith & Leathwick, 2009; Fourcade, Engler, Röder, & Secondi, 2014).

The third direction is spaceborne biodiversity monitoring that moves beyond proxies toward mechanistic habitat signals. Long-running optical programs (Landsat, Sentinel-2) now integrate with spaceborne LiDAR (GEDI) and upcoming/global SAR time series to estimate vertical structure, biomass, moisture, and disturbance with continuity and global reach (Wulder *et al.,* 2019; Dubayah *et al.,* 2020). These layers, when fused with trait and movement datasets, can quantify corridor permeability and energetic costs—inputs directly relevant to fitness and demography—while hyperspectral missions add biochemical sensitivity for mapping plant functional diversity, host–parasite risks, and pollinator resources. Spaceborne cadence also provides the temporal baselines necessary to judge progress against the Kunming–Montreal targets and IPBES indicators, supporting recurring, standardized reporting (CBD, 2022; IPBES, 2019). The frontier is not only better sensors but also harmonized, open products (with STAC metadata and uncertainty layers) that interoperate with occurrence archives and tracking repositories (Gorelick *et al.,* 2017; GBIF Secretariat, 2023).

Delivering this future requires people, culture, and partnerships. The taxonomic impediment remains binding: integrative pipelines falter without authoritative names, diagnoses, and type-anchored revisions. A call to action is therefore to train and fund a new generation of taxonomists, embed them in data-intensive teams, and resource collections for digitization and genomic barcoding so machine learning rests on a stable nomenclatural backbone (Engel *et al.,* 2021; Ratnasingham & Hebert, 2007). Equally, we must cultivate an open-science culture that normalizes preregistration, containerized workflows, registered reports, and FAIR+CARE data stewardship—particularly for sensitive species and Indigenous lands (Wilkinson *et al.,* 2016; Carroll *et al.,* 2020). Openness is not merely ethical; it is pragmatic: reproducible, versioned pipelines are easier to adopt by agencies and NGOs, shorten time-to-decision, and transform one-off projects into living observatories.

Finally, global collaborations should shift resources and authorship toward under-represented regions. The spatial and linguistic skew of biodiversity research is well documented and directly undermines model transferability and conservation equity (Amano, González-Varo, Sutherland, & Edwards, 2021). Investments in South-led observatories, shared training curricula, hardware grants, and bilingual publishing will close data gaps and diversify the talent building ecological foundation models and dashboards. With these elements—cross-scale fusion, real-time systems, interpretable AI, spaceborne context, ethical openness, and equitable partnerships—Zoology 4.0 can move from promise to practice, producing decision-grade knowledge at the speed and scale demanded by the biodiversity crisis.

8. CONCLUSION

The evidence across this review converges on a simple imperative: integration is no longer optional. To understand and safeguard life in motion, zoology must fuse signals from genes, organisms, populations, and ecosystems—uniting eDNA, images, acoustics, biologging, and remote sensing within transparent, reproducible pipelines. Such fusion closes long-standing detection and inference gaps, turning disparate observations into decision-ready indicators of occupancy, abundance, connectivity, resilience, and ecosystem function. It also transforms case studies into scalable observatories where uncertainty is quantified, ethics are embedded, and results are comparable across sites and years.

This integrated agenda creates practical opportunities to tackle the field's toughest bottlenecks. Joint deployments of cameras, ARUs, and eDNA can overcome method-specific blind spots; bias-aware models and standardized metadata can correct geographic and taxonomic skews; cross-modal standards can link audio, imagery, tracks, and genomes with clear provenance; and FAIR+CARE practices can protect sensitive species and Indigenous rights while enabling reuse. Aligning trait databases with tracking and spaceborne structure opens new paths to anticipate climate vulnerability, while foundation-model AI and edge-to-cloud workflows promise real-time biodiversity dashboards that guide rapid management responses.

Positioned this way, zoology is not merely a descriptive discipline—it is central to addressing the biodiversity and sustainability crises. By delivering timely, credible, and equitable evidence to conservation actors and policy frameworks (from protected-area planning to global CBD/IPBES targets), an integrative Zoology 4.0 can help societies prioritize corridors, recover populations, maintain ecosystem functions, and adapt to accelerating climate and land-use change. The task ahead is collective: train and empower the next generation of taxonomists and data-literate field scientists, invest in South-led observatories, and normalize open, versioned, uncertainty-aware analyses. Done well, integration will turn today's fragmented signals into tomorrow's durable solutions.

REFERENCE

- Acerbi, E., Hardisty, A., Kissling, W. D., … Robertson, T. (2022). Integrating taxonomy into the digital age of biodiversity: Opportunities and challenges. *Trends in Ecology & Evolution, 37*(12), 1011–1021.
- Amano, T., Berdejo-Espinola, V., Christie, A. P., … Sutherland, W. J. (2018). Tapping into non-English-language science for the conservation of global biodiversity. *PLOS Biology, 16*(10), e2000933.
- Amano, T., González-Varo, J. P., Sutherland, W. J., & Edwards, D. P. (2021). Global distribution of

biodiversity research effort. *Nature Ecology & Evolution, 5*(6), 678–687.

- Adams, D. C., & Collyer, M. L. (2018). Multivariate phylogenetic comparative methods: Evaluations, comparisons, and recommendations. *Methods in Ecology and Evolution, 9*(1), 26–35.
- Allemand, R., Houssaye, A., Boistel, R., Bardin, J., & Laurin, M. (2023). A landmarking protocol for geometric morphometric analysis of squamate endocasts. *The Anatomical Record, 306*(12), 3713–3726.
- Amano, T., González-Varo, J. P., Sutherland, W. J., & Edwards, D. P. (2021). Global distribution of biodiversity research effort. *Nature Ecology & Evolution, 5*(6), 678–687.
- Amano, T., González-Varo, J. P., Sutherland, W. J., & Edwards, D. P. (2021). Global distribution of biodiversity research effort. *Nature Ecology & Evolution, 5*(6), 678–687.
- Araujo, M. B., & New, M. (2007). Ensemble forecasting of species distributions. *Trends in Ecology & Evolution, 22*(1), 42–47.
- Araújo, M. B., & New, M. (2007). Ensemble forecasting of species distributions. *Trends in Ecology & Evolution, 22*(1), 42–47.
- Constable, H., Guralnick, R., Wieczorek, J., Spencer, C., & Peterson, A. T. (2010). VertNet: A new model for biodiversity data sharing. *PLoS Biology, 8*(2), e1000359.
- Elith, J., & Leathwick, J. R. (2009). Species distribution models: Ecological explanation and prediction across space and time. *Annual Review of Ecology, Evolution, and Systematics, 40*, 677–697.
- Fourcade, Y., Engler, J. O., Röder, D., & Secondi, J. (2014). Mapping species distributions with MaxEnt using a geographically biased sample of presence data. *PLoS ONE, 9*(5), e97122.
- Baken, E. K., Collyer, M. L., Kaliontzopoulou, A., & Adams, D. C. (2021). geomorph v4.0 and gmShiny: Enhanced analytics and a new graphical interface for a comprehensive morphometric experience. *Methods in Ecology and Evolution, 12*(12), 2355–2363.
- Beltran, R. S., Abrahms, B., Costa, D. P., *et al.,*(2025). Integrating animal tracking and trait data to facilitate global ecological discoveries. *Journal of Experimental Biology, 228*(Suppl 1), JEB247981.
- Beng, K. C., Corlett, R. T., & Nunez-Mir, G. (2022). The rise of environmental DNA for biodiversity monitoring: Opportunities, challenges and best practices. *Biological Conservation, 268*, 109520.
- Beng, K. C., Corlett, R. T., & Núñez-Mir, G. (2022). The rise of environmental DNA for biodiversity monitoring: Opportunities, challenges and best practices. *Biological Conservation, 268*, 109520.
- Beng, K. C., Corlett, R. T., & Núñez-Mir, G. (2022). The rise of environmental DNA for biodiversity monitoring: Opportunities, challenges and best practices. *Biological Conservation, 268*, 109520.
- Bentley, L. K., Dunn, D. C., Kot, C. Y., … Game, E. T. (2025). Marine megavertebrate migrations connect the global ocean. *Nature Communications*.
- Bessey, C., Stat, M., & Bunce, M. (2023). Towards robust eDNA-based ecological inference. *Molecular Ecology Resources, 23*(1), 1–16.
- Bodey, T. W., Cleasby, I. R., Bell, F., Parr, N., Schultz, A., Votier, S. C., & Bearhop, S. (2018). A phylogenetically controlled meta-analysis of biologging device effects on birds. *Methods in Ecology and Evolution, 9*(4), 946–955.
- Bodey, T. W., Cleasby, I. R., Bell, F., Parr, N., Schultz, A., Votier, S. C., & Bearhop, S. (2018). A phylogenetically controlled meta-analysis of biologging device effects on birds. *Methods in Ecology and Evolution, 9*(4), 946–955.
- Boxshall, G. (2020). Self-help for taxonomists: three things we must do for taxonomy to survive. *Megataxa, 1*(1), 39-42.
- Carroll, S. R., Garba, I., Figueroa-Rodríguez, O. L., Holbrook, J., Lovett, R., Materechera, S., … Hudson, M. (2020). The CARE Principles for Indigenous Data Governance. *Data Science Journal, 19*(43), 1–12.
- Carroll, S. R., Garba, I., Figueroa-Rodríguez, O. L., Holbrook, J., Lovett, R., Materechera, S., … Hudson, M. (2020). The CARE Principles for Indigenous Data Governance. *Data Science Journal, 19*(43), 1–12.
- Carroll, S. R., Garba, I., Figueroa-Rodríguez, O. L., Holbrook, J., Lovett, R., Materechera, S., … Hudson, M. (2020). The CARE Principles for Indigenous Data Governance. *Data Science Journal, 19*(43), 1–12
- CBD — Convention on Biological Diversity. (2022). *Kunming–Montreal Global Biodiversity Framework*. Montreal: CBD Secretariat.
- Chacko, M. R., Leempoel, K., Buri, A., & Pellissier, L. (2023). Catchment-based sampling of river eDNA integrates biodiversity signals across heterogeneous habitats. *Ecological Indicators, 149*, 110204.
- Chung, H., Smee, S., Lee, S., Kim, T., Kim, S., & Choi, Y. (2024). Seasonal foraging behavior of Weddell seals in the southern Weddell Sea (2021–2023). *Biogeosciences, 21*, 1921–1946.
- Collyer, M. L., Davis, M. A., & Adams, D. C. (2020). Making heads or tails of combined landmark configurations in geometric morphometrics. *Evolutionary Biology, 47*(2), 137–159.
- Compson, Z. G., McClenaghan, B., Singer, G., Fahner, N. A., & Hajibabaei, M. (2020). Metabarcoding from microbes to mammals: Comprehensive bioassessment across the tree of life. *Environmental DNA, 2*(2), 125–141.
- Convention on Biological Diversity (CBD). (2022). *Kunming–Montreal Global Biodiversity Framework*. Montreal: CBD Secretariat.

- Coomes, D. A., Dalponte, M., Jucker, T., Asner, G. P., Banin, L., Burslem, D. F. R. P., … Phillips, O. L. (2017). Area-based vs tree-centric approaches to mapping forest carbon in Southeast Asian forests from airborne laser scanning. *Remote Sensing of Environment, 194*, 77–88.
- Deiner, K., Bik, H. M., Mächler, E., Seymour, M., Lacoursière-Roussel, A., Altermatt, F., … Bernatchez, L. (2017). Environmental DNA metabarcoding: Transforming how we survey animal and plant communities. *Molecular Ecology, 26*(21), 5872–5895.
- Cristescu, M. E. (2018). From barcoding to metabarcoding: Advances in the use of DNA sequences for biodiversity research. *Genome, 61*(9), 736–745.
- Dayrat, B. (2005). Towards integrative taxonomy. *Biological Journal of the Linnean Society, 85*, 407–415.
- Dayrat, B. (2005). Towards integrative taxonomy. *Biological Journal of the Linnean Society, 85*(3), 407–415.
- de-Dios, T., *et al.,*(2024). Whole genomes from the extinct Xerces Blue butterfly reveal historical declines and inbreeding. *eLife, 13*, e87928.
- Drusch, M., Del Bello, U., Carlier, S., Colin, O., Fernandez, V., Gascon, F., … Bargellini, P. (2012). Sentinel-2: ESA's optical high-resolution mission for GMES operational services. *Remote Sensing of Environment, 120*, 25–36.
- Duarte, C. M., Chapuis, L., Collin, S. P., Costa, D. P., Devassy, R. P., Eguiluz, V. M., … Wensveen, P. J. (2021). The soundscape of the Anthropocene Ocean. *Science, 371*(6529), eaba4658.
- Dubayah, R., Blair, J. B., Goetz, S. J., Fatoyinbo, L., Hansen, M., Healey, S., … Armston, J. (2020). The Global Ecosystem Dynamics Investigation: High-resolution laser ranging of the Earth's forests and topography. *Science of Remote Sensing, 1*, 100002.
- ecosystem restoration, and nanoparticle applications. Scholars Academic Journal of Biosciences, 13(4). Peer-reviewed. https://doi.org/10.36347/sajb.2025.v13i04.005
- Elith, J., & Leathwick, J. R. (2009). Species distribution models: Ecological explanation and prediction across space and time. *Annual Review of Ecology, Evolution, and Systematics, 40*, 677–697.
- GBIF Secretariat. (2023). *GBIF science review 2023*. Copenhagen: GBIF.
- Kahl, S., Wood, C. M., Eibl, M., & Klinck, H. (2021). BirdNET: A deep learning solution for avian diversity monitoring. *PLOS Computational Biology, 17*(7), e1008954.
- Elith, J., & Leathwick, J. R. (2009). Species distribution models: Ecological explanation and prediction across space and time. *Annual Review of Ecology, Evolution, and Systematics, 40*, 677–697.
- Engel, M. S., Ceríaco, L. M. P., Daniel, G. M., … Schwarzhans, W. (2021). The taxonomic impediment: A 21st-century perspective. *Megataxa, 6*(1), 1–113.
- GBIF Secretariat. (2023). *GBIF science review 2023*. Copenhagen: GBIF.
- Gorelick, N., Hancher, M., Dixon, M., Ilyushchenko, S., Thau, D., & Moore, R. (2017). Google Earth Engine: Planetary-scale geospatial analysis for everyone. *Remote Sensing of Environment, 202*, 18–27.
- Elith, J., & Leathwick, J. R. (2009). Species distribution models: Ecological explanation and prediction across space and time. *Annual Review of Ecology, Evolution, and Systematics, 40*, 677–697. Fourcade, Y., Engler, J. O., Rödder, D., & Secondi, J. (2014). Mapping species distributions with MAXENT using a geographically biased sample of presence data: A performance assessment of methods for correcting sampling bias. *PLoS ONE, 9*(5), e97122.
- Engel, M. S., Ceríaco, L. M. P., Daniel, G. M., … Schwarzhans, W. (2021). The taxonomic impediment: A 21st-century perspective. *Megataxa, 6*(1), 1–113.
- English, H. M., Börger, L., Kane, A., & Ciuti, S. (2024). Advances in biologging can identify nuanced energetic costs and gains in predators. *Movement Ecology, 12*, 7.
- Falkingham, P. L., & Rae, R. (2021). 3D morphology of nematode encapsulation in snail shells revealed by micro-CT imaging. *Scientific Reports, 11*, 2523.
- Farley, Z. J., Thompson, C. J., Boyle, S. T., Tatman, N. M., & Cain, J. W. III. (2024). Behavioral trade-offs by elk in relation to predation risk from Mexican gray wolves. *Ecology and Evolution, 14*(5), e11383.
- GBIF Secretariat. (2023). *GBIF science review 2023*. Copenhagen, Denmark: GBIF. Kranstauber, B., Cameron, A., Weinzerl, R., Fountain, T., Tilak, S., Wikelski, M., & Kays, R. (2011). The Movebank data model for animal tracking. *Environmental Modelling & Software, 26*(6), 834–835.*
- GBIF Secretariat. (2023). *GBIF science review 2023*. Copenhagen: GBIF. Kahl, S., Wood, C. M., Eibl, M., & Klinck, H. (2021). BirdNET: A deep learning solution for avian diversity monitoring. *PLOS Computational Biology, 17*(7), e1008954.
- Gerber, T., Taniguchi, Y., & Tarashansky, A. (2021). Single-cell transcriptomics for comparative and functional zoology. *Annual Review of Animal Biosciences, 9*, 21–40.
- Gibb, R., Browning, E., Glover-Kapfer, P., & Jones, K. E. (2019). Emerging opportunities and challenges for passive acoustics in ecological assessment and monitoring. *Methods in Ecology and Evolution, 10*(2), 169–185.

- Gibb, R., Browning, E., Glover-Kapfer, P., & Jones, K. E. (2019). Emerging opportunities and challenges for passive acoustics in ecological assessment and monitoring. *Methods in Ecology and Evolution, 10*(2), 169–185.
- Gorelick, N., Hancher, M., Dixon, M., Ilyushchenko, S., Thau, D., & Moore, R. (2017). Google Earth Engine: Planetary-scale geospatial analysis for everyone. *Remote Sensing of Environment, 202*, 18–27.
- Haidar, S. H. (2025). Emerging nanoparticle technologies for targeted disease therapy. In A comprehensive review of microbiology (pp. 411–426). Empyreal Publishing House. Book chapter. ISBN: 978-81-194XX-XX-X https://www.researchgate.net/publication/389271893_A_COMPREHENSIVE_REVIEW_OF_MICROBIOLOGY
- Hays, G. C., Bailey, H., Bograd, S. J., *et al.,*(2019). Translating marine animal tracking data into conservation policy and management. *Trends in Ecology & Evolution, 34*(5), 459–473.
- Hoban, S., Bruford, M. W., D'Urban Jackson, J., *et al.,*(2020). Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework. *Conservation Genetics, 21*(3), 495–504.
- Hoffman, B., Cusimano, M., Baglione, V., … Friedlaender, A. (2024). A benchmark for computational analysis of animal behavior using animal-borne tags. *Movement Ecology, 12*, 78.
- Hohenlohe, P. A., Funk, W. C., & Rajora, O. P. (2021). Population genomics for wildlife conservation and management. *Molecular Ecology, 30*(1), 62–82.
- IPBES. (2019). *Global assessment report on biodiversity and ecosystem services*. Bonn: IPBES Secretariat.
  Kahl, S., Wood, C. M., Eibl, M., & Klinck, H. (2021). BirdNET: A deep learning solution for avian diversity monitoring. *PLOS Computational Biology, 17*(7), e1008954.
- IPBES. (2019). *Global assessment report on biodiversity and ecosystem services*. Bonn, Germany: IPBES Secretariat.
- Jalal, M., Haidar, S. H., *et al.,*(2025). Effect of silver nanoparticles on oxidative stress enzymes in D. melanogaster. Scholars Academic Journal of Biosciences, 13(5), 614–631. Peer-reviewed. https://doi.org/10.36347/sajb.2025.v13i05.015
- Joshi, J., & Agarwal, I. (2021). Integrative taxonomy in the Indian subcontinent: Current progress and prospects. *Journal of the Indian Institute of Science, 101*, 125–149.
- Joshi, J., & Agarwal, I. (2021). Integrative taxonomy in the Indian subcontinent: Current progress and prospects. *Journal of the Indian Institute of Science, 101*, 125–149.
- Kahl, S., Wood, C. M., Eibl, M., & Klinck, H. (2021). BirdNET: A deep learning solution for avian diversity monitoring. *PLOS Computational Biology, 17*(7), e1008954.
- Kahl, S., Wood, C. M., Eibl, M., & Klinck, H. (2021). BirdNET: A deep learning solution for avian diversity monitoring. *PLOS Computational Biology, 17*(7), e1008954.
- Karbstein, K., Kösters, L. M., Hodač, L., Hofmann, M., Hörandl, E., Tomasello, S., ... & Wäldchen, J. (2024). Species delimitation 4.0: integrative taxonomy meets artificial intelligence. *Trends in Ecology & Evolution*.
- Keeley, A. T. H., Beier, P., Creech, T., Jones, K., Jongman, R. H. G., Stonecipher, G., & Tabor, G. M. (2018). Thirty years of connectivity conservation planning: An assessment of graph theory approaches. *Ecological Applications, 28*(1), 211–222.
- Keklikoglou, K., Tretiakow, D., Kardaras, D., & Tserevelakis, G. J. (2021). Micro-CT for biological and biomedical studies: A comparison of imaging techniques and emerging applications. *Microscopy and Microanalysis, 27*(6), 1189–1205.
- Kranstauber, B., Cameron, A., Weinzerl, R., Fountain, T., Tilak, S., Wikelski, M., & Kays, R. (2011). The Movebank data model for animal tracking. *Environmental Modelling & Software, 26*(6), 834–835.
- Kranstauber, B., Cameron, A., Weinzerl, R., Fountain, T., Tilak, S., Wikelski, M., & Kays, R. (2011). The Movebank data model for animal tracking. *Environmental Modelling & Software, 26*(6), 834–835.
- Leempoel, K., Hebert, T., & Pellissier, L. (2020). A comparison of eDNA to camera trapping for assessment of terrestrial mammal diversity. *Proceedings of the Royal Society B, 287*(1918), 20192353.
- Lennox, R. J., Diserud, O. H., Thorstad, E. B., & Cooke, S. J. (2021). Welfare considerations for tagging wild fish. *Reviews in Fish Biology and Fisheries, 31*(2), 221–241.
- Lennox, R. J., Diserud, O. H., Thorstad, E. B., & Cooke, S. J. (2021). Welfare considerations for tagging wild fish. *Reviews in Fish Biology and Fisheries, 31*(2), 221–241.
- Lorieul, T., *et al.,*(2019). Toward a global deep learning ecosystem for biodiversity monitoring. *Nature Ecology & Evolution, 3*(5), 671–673.
- Lorieul, T., Goodwin, Z. A., Güntsch, A., … Sosef, M. (2019). Toward a global deep-learning ecosystem for biodiversity monitoring. *Nature Ecology & Evolution, 3*(5), 671–673.
- Lorieul, T., Goodwin, Z. A., Güntsch, A., … Sosef, M. (2019). Toward a global deep-learning ecosystem for biodiversity monitoring. *Nature Ecology & Evolution, 3*(5), 671–673.
- Lynggaard, C., Bertelsen, M. F., Jensen, C. V., *et al.,*(2022). Airborne environmental DNA for

terrestrial vertebrate community monitoring. *Current Biology, 32*(3), 701–707.

- Marques, T. A., Thomas, L., Martin, S. W., Mellinger, D. K., Ward, J. A., Moretti, D. J., … Tyack, P. L. (2013). Estimating animal population density using passive acoustics. *Methods in Ecology and Evolution, 4*(4), 361–369.
- Maxwell, A. E., Warner, T. A., & Fang, F. (2018). Implementation of machine-learning classification in remote sensing: An applied review. *International Journal of Remote Sensing, 39*(9), 2784–2817.
- Newbold, T., Hudson, L. N., Hill, S. L. L., Contu, S., Lysenko, I., Senior, R. A., … Purvis, A. (2015). Global effects of land use on local terrestrial biodiversity. *Nature, 520*(7545), 45–50.
- Norberg, A., Abrego, N., Blanchet, F. G., Adler, F. R., Anderson, B. J., Anttila, J., … Ovaskainen, O. (2019). A comprehensive evaluation of predictive performance of joint species distribution models. *Methods in Ecology and Evolution, 10*(3), 326–339.
- Parmesan, C. (2006). Ecological and evolutionary responses to recent climate change. *Annual Review of Ecology, Evolution, and Systematics, 37*, 637–669.
- Pettorelli, N., Laurance, W. F., O'Brien, T. G., Wegmann, M., Nagendra, H., & Turner, W. (2014). Satellite remote sensing for applied ecologists: Opportunities and challenges. *Journal of Applied Ecology, 51*(4), 839–848.
- Phillips, S. J., Anderson, R. P., & Schapire, R. E. (2006). Maximum entropy modeling of species geographic distributions. *Ecological Modelling, 190*(3–4), 231–259.
- Phillips, S. J., Dudík, M., & Schapire, R. E. (2009). A maximum entropy approach to species distribution modeling with presence-only data: Background and case studies. *Ecological Modelling, 220*(4), 480–492.
- Thackeray, S. J., Henrys, P. A., Hemming, D., Bell, J. R., Botham, M. S., Burthe, S., … Wanless, S. (2016). Phenological sensitivity to climate across taxa and trophic levels. *Nature, 535*(7611), 241–245.
- Dubayah, R., Blair, J. B., Goetz, S. J., Fatoyinbo, L., Hansen, M., Healey, S., … Armston, J. (2020). The Global Ecosystem Dynamics Investigation: High-resolution laser ranging of the Earth's forests and topography. *Science of Remote Sensing, 1*, 100002.
- Meneghini, R., & Packer, A. L. (2021). Bibliometric indicators for countries and institutions: Research in the Global South. *Scientometrics, 126*(4), 2899–2919.
- Morris, R. A., Walls, R. L., Guralnick, R., *et al.,*(2013). Audubon Core: A community-developed standard for biodiversity images and media. *Biodiversity Informatics, 8*(2), 1–12.*
- Morris, R. A., Walls, R. L., Guralnick, R., *et al.,*(2013). Audubon Core: A community-developed standard for biodiversity images and media. *Biodiversity Informatics, 8*(2), 1–12.
- Morris, R. A., Walls, R. L., Guralnick, R., *et al.,*(2013). Audubon Core: A community-developed standard for biodiversity images and media. *Biodiversity Informatics, 8*(2), 1–12.
- Morris, R. A., Walls, R. L., Guralnick, R., *et al.,*(2013). Audubon Core: A community-developed data standard for biodiversity images and media. *Biodiversity Informatics, 8*(2), 1–12.
- Mulero-Pázmány, M., Ruiz-Jiménez, L. A., Fernández-Gálvez, J., de la Torre, J., & Palomares, F. (2025). Deep learning for animal detection in camera-trap images: Addressing domain shift and annotation bottlenecks. *Scientific Reports*.
- Nature Research. (2021). X-ray computed tomography. *Nature Reviews Methods Primers, 1*, 75.
- Norberg, A., Abrego, N., Blanchet, F. G., *et al.,*(2019). A comprehensive evaluation of predictive performance of joint species distribution models. *Methods in Ecology and Evolution, 10*(3), 326–339.
- IPBES. (2019). *Global assessment report on biodiversity and ecosystem services*. Bonn: IPBES Secretariat.
  Wieczorek, J., Bloom, D., Guralnick, R., *et al.,*(2012). Darwin Core: An evolving community-developed biodiversity data standard. *PLOS ONE, 7*(1), e29715.
- Norberg, A., Abrego, N., Blanchet, F. G., *et al.,*(2019). A comprehensive evaluation of predictive performance of joint species distribution models. *Methods in Ecology and Evolution, 10*(3), 326–339.
- Ratnasingham, S., & Hebert, P. D. N. (2007). BOLD: The Barcode of Life Data System. *Molecular Ecology Notes, 7*(3), 355–364.
- Norberg, A., Abrego, N., Blanchet, F. G., *et al.,*(2019). A comprehensive evaluation of joint species distribution models. *Methods in Ecology and Evolution, 10*(3), 326–339.
- Novaes, R. L. M., Cláudio, V. C., & Moratelli, R. (2023). The integrative taxonomy driving conservation of cryptic species: an example of Neotropical Myotis. *Therya*.
- Novaes, R. L. M., Cláudio, V. C., & Moratelli, R. (2023). The integrative taxonomy driving conservation of cryptic species: An example of Neotropical Myotis. *Therya*.
- Orlando, L., Allaby, R., Skoglund, P., & Sinding, M.-H. S. (2021). Ancient DNA and paleogenomics in zoology: Insight into evolution, adaptation, and past ecosystems. *Annual Review of Animal Biosciences, 9*, 203–229.
- Pääbo, S. (2022). The human past from ancient DNA. *Science, 377*(6606), 803–805.
- Pestell, A. J. L., Rendall, A. R., Sinclair, R. D., Ritchie, E. G., Nguyen, D. T., Corva, D. M., …

Driscoll, D. A. (2025). Smart camera traps and computer vision improve detections of small fauna. *Ecosphere*.

- Phillips, S. J., Dudík, M., & Schapire, R. E. (2009). A maximum entropy approach to species distribution modeling with presence-only data. *Ecological Modelling, 220*(4), 480–492.
- Ratnasingham, S., & Hebert, P. D. N. (2007). BOLD: The Barcode of Life Data System. *Molecular Ecology Notes, 7*(3), 355–364.
- Rivera-Quiroz, F. A., Vega-Ruiz, C., & Castañeda-Valdez, F. (2022). Micro-CT visualization of the central nervous system: Performance of different contrast agents in ethanol-preserved specimens. *Journal of Anatomy, 241*(3), 653–667.
- Rumelt, R., Mere Roncal, C., Basto, A., Buřivalová, Z., & Searcy, C. (2025). Combining acoustic survey and citizen-science data yields enhanced SDMs for tropical rainforest birds. *PLOS ONE, 20*(7), e0327944.
- Rummel, A. D., Arbour, J. H., & Anderson, P. S. L. (2024). Sample size and geometric morphometrics methodology influence inference in macroevolutionary studies. *Evolutionary Biology, 51*(1), 1–16.
- Schallenberg, L., Wood, S. A., Pochon, X., & Pearman, J. K. (2020). What can DNA in the environment tell us about an ecosystem? *Frontiers for Young Minds, 8*, 150.
- Sepulveda, A. J., Nelson, N. M., Jerde, C. L., Luikart, G., & Lodge, D. M. (2020). Are environmental DNA methods ready for aquatic invasive species management? *Trends in Ecology & Evolution, 35*(8), 668–678.
- Sigwart, J., Chen, C., Tilic, E., Vences, M., & Riehl, T. (2023). Why is there no service to support taxonomy? *BioEssays, 45*.

- Sigwart, J., Chen, C., Tilic, E., Vences, M., & Riehl, T. (2023). Why is there no service to support taxonomy? *BioEssays, 45*.

- Steinicke, H., Tilch, S., Curtiss, J., Rosselló-Móra, R., Esporles, & Hacker, J. (2014). Challenges and opportunities of integrative taxonomy for research and society.

- Steinicke, H., Tilch, S., Curtiss, J., Rosselló-Móra, R., Esporles, & Hacker, J. (2014). Challenges and opportunities of integrative taxonomy for research and society.

- Stowell, D. (2022). Computational bioacoustics with deep learning: A review and roadmap. *IEEE Signal Processing Magazine, 39*(6), 120–131.

- Stowell, D. (2022). Computational bioacoustics with deep learning: A review and roadmap. *IEEE Signal Processing Magazine, 39*(6), 120–131.
- Stowell, D. (2022). Computational bioacoustics with deep learning: A review and roadmap. *IEEE Signal Processing Magazine, 39*(6), 120–131.

- Streicher, J. W., & Meik, J. (2018). Integrative taxonomy of squamate reptiles: A special issue. *Journal of Natural History, 52*(13–16), 767–770.

- Streicher, J. W., & Meik, J. (2018). Integrative taxonomy of squamate reptiles: A special issue. *Journal of Natural History, 52*(13–16), 767–770.

- Stuart, T., & Satija, R. (2019). Integrative single-cell analysis. *Nature Reviews Genetics, 20*(5), 257–272.
- Sukumaran, S., & Gopalakrishnan, A. (2015). Integrative taxonomy – Methods and applications.

- Sukumaran, S., & Gopalakrishnan, A. (2015). Integrative taxonomy – Methods and applications.

- Taberlet, P., Bonin, A., Zinger, L., & Coissac, E. (2018). *Environmental DNA: For biodiversity research and monitoring*. Oxford University Press.
- Theodoridis, S., *et al.,*(2025). Satellite-observed Mountain greening predicts genomic change in alpine populations. *Current Biology*. (In press/online ahead of print.)
- Thompson, C. J., Tatman, N. M., Farley, Z. J., Boyle, S. T., Greenleaf, A. R., & Cain, J. W. III. (2025). Spatiotemporal risk avoidance varies seasonally in a reestablishing predator–prey system. *Frontiers in Ecology and Evolution, 13*, 1613904.
- Tulloch, A. I. T., Possingham, H. P., Joseph, L. N., Szabo, J., & Martin, T. G. (2018). Realising the full potential of citizen science monitoring programs. *Biological Conservation, 208*, 113–120.
- Valavi, R., Elith, J., Lahoz-Monfort, J. J., & Guillera-Arroita, G. (2019). BlockCV: An R package for generating spatially or environmentally separated folds for k-fold cross-validation of species distribution models. *Methods in Ecology and Evolution, 10*(2), 225–232.
- Van Horn, G., Mac Aodha, O., Beery, S., *et al.,*(2018). The iNaturalist species classification and detection dataset. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition* (pp. 8769–8778).
- Van Horn, G., Mac Aodha, O., Song, Y., *et al.,*(2018). The iNaturalist species classification and detection dataset. *Proceedings of CVPR*, 8769–8778.
- Wieczorek, J., Bloom, D., Guralnick, R., *et al.,*(2012). Darwin Core: An evolving community-developed biodiversity data standard. *PLoS ONE, 7*(1), e29715.
- Wilkinson, M. D., Dumontier, M., Aalbersberg, I. J., *et al.,*(2016). The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data, 3*, 160018.
- Velasco-Montero, D., Fernández-Berni, J., Carmona-Galán, R., Sanglas, A., & Palomares, F. (2024). Integrating AI into camera traps via continual learning for reliable wildlife monitoring. *Ecological Informatics, 83*, 102815.
- Viacava, P., Gamarra, R., & Püschel, T. A. (2023). The relative performance of geometric morphometrics and linear morphometrics:

Implications for shape analysis. *Biology Letters, 19*(4), 20220564.*

- Watanabe, Y. Y., & Papastamatiou, Y. P. (2023). Biologging and biotelemetry: Tools for understanding the lives and environments of marine animals. *Annual Review of Animal Biosciences, 11*, 247–267.
- Wieczorek, J., Bloom, D., Guralnick, R., *et al.,*(2012). Darwin Core: An evolving community-developed biodiversity data standard. *PLOS ONE, 7*(1), e29715.
- Wilkinson, M. D., Dumontier, M., Aalbersberg, I. J., *et al.,*(2016). The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data, 3*, 160018.

- Wilkinson, M. D., Dumontier, M., Aalbersberg, I. J., *et al.,*(2016). The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data, 3*, 160018.
- Wilkinson, M. D., Dumontier, M., Aalbersberg, I. J., *et al.,*(2016). The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data, 3*, 160018.

- Winiarska, D., *et al.,*(2025). BirdNET provides superior diversity estimates compared to manual review under standardized protocols. *Ecological Indicators*.
- Wulder, M. A., Loveland, T. R., Roy, D. P., Crawford, C. J., Masek, J. G., Woodcock, C. E., … Zhu, Z. (2019). Current status of Landsat program, science, and applications. *Remote Sensing of Environment, 225*, 127–147.

- Wulder, M. A., Loveland, T. R., Roy, D. P., Crawford, C. J., Masek, J. G., Woodcock, C. E., … Zhu, Z. (2019). Current status of Landsat program, science, and applications. *Remote Sensing of Environment, 225*, 127–147.
- Wulder, M. A., Loveland, T. R., Roy, D. P., Crawford, C. J., Masek, J. G., Woodcock, C. E., … Zhu, Z. (2019). Current status of Landsat program, science, and applications. *Remote Sensing of Environment, 225*, 127–147.
- Wulder, M. A., Loveland, T. R., Roy, D. P., Crawford, C. J., Masek, J. G., Woodcock, C. E., … Zhu, Z. (2019). Current status of Landsat program, science, and applications. *Remote Sensing of Environment, 225*, 127–147.

- Zahoor, Z., Haidar, S. H., *et al.,*(2025). Biotechnological advances in wildlife conservation: Genetic engineering, cloning,
- Zinger, L., Bonin, A., Alsos, I. G., … Taberlet, P. (2019). DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. *Molecular Ecology, 28*(8), 1857–1862.
- Zizka, A., Silvestro, D., Andermann, T., *et al.,*(2021). Sampling bias in global plant occurrence data and its effect on species distribution modelling. *Ecography, 44*(4), 501–511.