

As open as possible, as protected as necessary: Proportionate governance for environmental DNA under the BBNJ Agreement

Erin E. Hahn^{a*}, Justin I. McDonald^b, Clare I. M. Adams^c, Maarten De Brauwer^d, Dianne Gleeson^e, Miwa Takahashi^f, Cecilia Villacorta-Rath^g, Anastasija Zaiko^h

a – Commonwealth Scientific and Industrial Research Organisation, National Research Collections Australia, Canberra, ACT, Australia

b – Aquatic Biosecurity, WA Department of Primary Industries and Regional Development, Perth, WA, Australia

c – Coastal People, Southern Skies and the Maurice Wilkins Centre, Department of Mathematics and Statistics, University of Otago, Dunedin, New Zealand

d – Faculty of Science and Engineering, National Marine Science Centre, Southern Cross University, Coffs Harbour, NSW, Australia

e – National eDNA Reference Centre, University of Canberra, Canberra, ACT, Australia

f – Commonwealth Scientific and Industrial Research Organisation, National Collections and Marine Infrastructure, Crawley, WA, Australia

g – Centre for Tropical Water and Aquatic Ecosystem Research (TropWATER), James Cook University, Townsville, QLD, Australia

h – Sequench Ltd, Nelson, New Zealand

* Corresponding author: erin.hahn@csiro.au

Abstract

The Agreement on the Conservation and Sustainable Use of Marine Biological Diversity of Areas Beyond National Jurisdiction (BBNJ Agreement) establishes new arrangements for activities involving marine genetic resources and the sharing of resulting benefits. Direct pathways to resource utilisation are most apparent in conventional genetic workflows where whole organisms or tissues are collected for biodiscovery and analysed to generate high-resolution genomic or biochemical information. By comparison, routine environmental DNA (eDNA) research generally uses non-invasive sampling to infer species presence and characterise biological communities from mixed genetic material. Evolving genomic technologies are expanding the information recoverable from both tissue-based and environmental samples, making sample source alone an insufficient indicator of intended use, information sensitivity, or potential for resource utilisation. This perspective identifies proportionate, use-based governance as an approach to fulfilling applicable BBNJ obligations while recognising routine eDNA observation as shared environmental knowledge infrastructure and supporting timely data exchange and responsive biodiversity monitoring. Managed openness offers a science-informed framework for maintaining access to routine biodiversity information while applying targeted safeguards where warranted. Drawing on marine biosecurity examples and Indo-Pacific regional experience, we outline how existing infrastructure, cooperation, and capacity building could support equitable BBNJ implementation.

Keywords: environmental DNA, marine genetic resources, BBNJ Agreement, ocean governance, biodiversity monitoring, benefit sharing

Introduction

The BBNJ Agreement and its implementation

Areas beyond national jurisdiction (ABNJ) encompass the high seas, covering approximately two-thirds of the global ocean, and the international seabed Area, together supporting substantial marine biodiversity [1]. These regions are central to global ecological connectivity, climate regulation, fisheries productivity, and planetary health, yet their vast spatial scales and costly access, particularly in the deep ocean, make biodiversity observation and management especially challenging [2]. Historically, biodiversity governance in ABNJ has been fragmented, with limited coordination of conservation, scientific access, and sustainable use [3].

The Agreement under the United Nations Convention on the Law of the Sea on the Conservation and Sustainable Use of Marine Biological Diversity of ABNJ (BBNJ Agreement), adopted in 2023 and in force since 2026, marks a major development in ocean governance [4]. It establishes processes for marine genetic resource activities and benefit sharing, alongside measures for area-based management, environmental impact assessments, scientific capacity building, and marine technology transfer [4].

Many operational aspects remain under development [5]. Implementation decisions will shape how provisions on application (Article 10), notification (Article 12), and benefit sharing (Article 14) operate for marine genetic resources and associated digital sequence information [4,5]. Scientific and practitioner communities can inform implementation by explaining genomic technologies' capabilities, limitations, and uses in marine research and biodiversity observation, alongside the practical consequences of implementation options. This input can help advance the Agreement's objectives while avoiding unintended barriers to research and observation.

Environmental DNA in marine biodiversity observation

Environmental DNA (eDNA) is genetic material recovered from environmental samples such as seawater and sediments, originating from microorganisms, shed cells, mucus, faeces, gametes, and decaying tissue [6]. Analysis of eDNA enables non-invasive detection without directly capturing or observing organisms and can reveal species occurrence, community composition, and ecological change across taxa and habitats that may be difficult to observe using conventional methods [6-8]. Most contemporary eDNA analyses use targeted species

assays or metabarcoding for observational purposes, supporting biodiversity assessment, conservation monitoring, biosecurity surveillance, fisheries management, and ecosystem research [8-9]. Emerging approaches, including population genetic, metagenomic, genome-resolved, co-occurrence, network and functional analyses, are expanding the information recoverable from environmental samples within the broader field of environmental genomics [10-11].

Environmental DNA can complement conventional approaches and extend the geographic, temporal, and taxonomic coverage of marine biodiversity observation in ANBJ [9]. Relatively simple sample collection can enable citizen scientist participation and opportunistic sampling by commercial and recreational vessels, provided appropriate protocols and quality controls are in place [12-13]. The United States National Oceanic and Atmospheric Administration [14] and Australia's Integrated Marine Observing System [15] are adopting eDNA methods for large-scale biodiversity observation, while the Ocean Biomolecular Observing Network seeks to integrate biomolecular data into international ocean observing systems [16]. These developments highlight the expanding scientific and operational relevance of eDNA to BBNJ implementation.

The BBNJ implementation challenge for eDNA

A central implementation question for eDNA is how BBNJ obligations can be fulfilled across activities that vary in purpose, information sensitivity, and downstream use. UK implementation guidance explicitly includes eDNA sampling within marine genetic resource collection requirements [17], demonstrating that non-invasive sampling and observational purposes do not automatically confer exemption. Effective implementation calls for attention to scientific and operational differences between routine eDNA observation and genomic research directed towards commercial development or resource utilisation. Uniform implementation protocols could impose costs and delays on routine monitoring, disproportionately affecting remote and under-sampled regions [9,18].

Here, the Board of the Southern eDNA Society offers a scientific perspective on proportionate, use-based governance that meets BBNJ requirements while supporting biodiversity observation. Routine eDNA observation could be recognised as shared environmental knowledge infrastructure supporting conservation, stewardship, and marine biosecurity. Managed openness makes biodiversity information as open as possible, as protected as necessary, with safeguards proportionate to its intended use, sensitivity, and credible pathways

to resource utilisation. This framework could support equitable benefit sharing while maintaining timely biodiversity observation and data exchange across ABNJ.

Why intended use matters for eDNA governance

Effective BBNJ implementation depends on accommodating scientific and operational diversity in sampling, attribution, information characteristics, and intended use. Routine eDNA monitoring differs from conventional marine genetic resource collection across these dimensions in ways relevant to governance (**Figure 1**).

Conventional marine genetic resource sampling generally involves whole organisms or tissues linked to identifiable specimens and collection locations. Physical material can be controlled and transferred through permits and material transfer agreements under access and benefit-sharing frameworks such as the Nagoya Protocol [19,20]. By contrast, eDNA samples typically contain mixed, fragmented genetic material from multiple taxa [7]. Although eDNA sampling location can be recorded precisely, oceanographic transport and DNA persistence may make the geographic and temporal origins of detected material probabilistic [21,22].

Environmental DNA commonly generates community-scale datasets with extensive reuse potential. Both specimens and environmental samples can produce digital sequence information for storage, reanalysis, and sharing through global scientific networks consistent with FAIR (Findable, Accessible, Interoperable, and Reusable) data principles [23-25]. A single eDNA dataset may support biodiversity assessment, ecosystem modelling, invasive species surveillance, fisheries management, and climate adaptation research without further sampling or access to physical material [26]. These data are non-rivalrous, meaning use by one party does not diminish their availability to others [26,27]. Subsequent reuse for research and development may trigger additional obligations under the Agreement.

Organisms and tissues may be collected and analysed for purposes ranging from taxonomy and biochemical characterisation to biodiscovery and commercial development [10,28]. Emerging approaches, including long-read and single-cell sequencing and genome-resolved metagenomics, can recover functional or individual-level information from environmental samples, extending the range of analyses traditionally based on organism or tissues [29-32]. Together, sampling, information characteristics, and the intended use of material and resulting data underpin the proportionate, use-based framework shown in **Figure 2**.

Environmental DNA as shared environmental knowledge infrastructure

Routine eDNA applications generate biodiversity knowledge for conservation, environmental stewardship, and decision-making, providing societal value beyond resource utilisation [26,33]. Environmental DNA is increasingly incorporated into biodiversity monitoring, conservation assessments, biosecurity surveillance, and marine observing systems [34-37]. By enabling observation of ecological change across broad spatial and temporal scales, routine eDNA monitoring can be understood as shared environmental knowledge infrastructure.

This infrastructure gains value when observations can be aggregated and compared across locations, institutions, and time periods [38]. Common reporting standards, rich metadata, and accessible repositories enable reuse and can improve regional and global monitoring [23,39]. Fragmented or unnecessarily restrictive systems can duplicate effort and constrain data exchange [40], particularly in ABNJ, where integrating observations across international programs can strengthen biodiversity assessments [9]. Open science can broaden participation, but data access alone does not ensure equitable participation. Investment in infrastructure, training, and technical and institutional capacity alongside access could advance the Agreement's objectives for capacity building, technology transfer, and equitable benefit sharing [4,9,41].

Recognising the public value of routine eDNA data does not imply unrestricted openness. Safeguards may be appropriate for culturally significant biodiversity knowledge, endangered-species locations, and biosecurity detections requiring verification or coordinated response [42-44]. Additional consideration may be warranted where information has a credible pathway to resource utilisation. Managed openness accommodates these considerations through targeted safeguards proportionate to intended use, sensitivity, and potential future reuse opportunities.

Implications for marine biosecurity

International shipping connects coastal ecosystems through routes traversing ABNJ, transporting non-native species in ballast water and through hull fouling [45,46]. Much routine marine biosecurity surveillance occurs within national jurisdictions, but cross-jurisdictional data sharing and interoperability support coordinated surveillance and are relevant to BBNJ implementation [46]. Environmental DNA can complement conventional surveys by providing

early indications of invasive species or aquatic pathogens that warrant follow-up, while extending surveillance coverage and responsiveness [37,47-49].

Effective eDNA surveillance depends on timely comparison of observations across programs, locations, and jurisdictions [50]. Delayed exchange or fragmented data may weaken early warning and coordinated response [51]. However, detections with significant operational consequences may require verification or coordination prior to wider dissemination or management action, particularly where false positives are possible [44,52]. Marine biosecurity illustrates managed openness in practice: facilitating timely access to surveillance information while applying targeted safeguards where uncertainty, sensitivity, or risk warrants them.

Regional perspectives: Australia, New Zealand, and the Indo-Pacific

Ratification of the BBNJ Agreement by countries including Australia, Fiji, Indonesia, Papua New Guinea, Samoa, and Solomon Islands [53] highlights growing Indo-Pacific participation. Across the region, marine research and monitoring span large geographic areas, institutions, and data systems, making interoperability and sustained collaboration important for effective biodiversity observation [54-56]. Existing eDNA capability, biodiversity and biosecurity programs, and regional partnerships across Australia, Aotearoa New Zealand, and the wider Indo-Pacific can contribute to BBNJ implementation [57,58].

Regional BBNJ implementation will encounter diverse Indigenous rights and data governance contexts. In Aotearoa New Zealand, biodiversity and genomic information governance engages with Māori concepts of kaitiakitanga (guardianship and stewardship), mana motuhake (self-determination), and rangatiratanga (authority and self-governance) [59]. Aboriginal and Torres Strait Islander data sovereignty and custodianship are important considerations in Australia [60]. Indigenous Peoples across the Indo-Pacific maintain diverse customary relationships with and systems of authority over marine biodiversity [61]. The CARE Principles (Collective benefit, Authority to control, Responsibility, and Ethics) provide an international reference point [42], but cannot replace locally grounded rights, governance frameworks, or practices. Because local contexts differ, no single access model can be assumed appropriate across jurisdictions.

Regional researchers and institutions already collaborate on eDNA methods, best-practice guidance, and data sharing for biodiversity assessment and invasive species detection [23,35].

Although these initiatives were not developed in the context of the BBNJ Agreement, they illustrate collaborative networks that could provide a foundation for its future implementation. Continued cooperation could strengthen interoperable observing networks, improve regional taxonomic and molecular reference coverage, and broaden equitable access to sequencing, bioinformatics, and analytical capability. Co-development with Pacific Island nations and Indigenous partners could align these efforts with regional priorities while supporting capacity building and non-monetary benefit sharing under the BBNJ Agreement [4,54,59,62]. These experiences can inform implementation elsewhere without prescribing a single governance model.

Proportionate BBNJ implementation

Existing institutions have complementary roles in supporting proportionate BBNJ implementation alongside routine eDNA observation (Table 1). Scientific advisory bodies can help clarify provenance, attribution, uncertainty, and information sensitivity. Integrating notification and reporting with existing observation and data infrastructure can support compliance without duplicating systems.

Established repositories can support data sharing for routine eDNA monitoring through standardised metadata, persistent identifiers, and attribution [23,25]. The Ocean Biodiversity Information System (OBIS), Global Biodiversity Information Facility (GBIF), Aotearoa Genomic Data Repository (AGDR), and other international sequence repositories offer infrastructure for storing, governing, sharing and integrating biodiversity and genomic information [63-65]. Interoperability, rather than a single prescribed repository, could support reuse while recognising data generators and stewards. Controlled access, spatial generalisation, delayed release, or case-by-case assessment could be reserved for information with demonstrated cultural, conservation, or biosecurity sensitivity, or a credible pathway to resource utilisation.

Benefit sharing for routine eDNA observation may be primarily non-monetary. Capacity to generate, manage, and interpret biodiversity data remains concentrated in high-resource countries, limiting participation in research and decision-making [41]. Targeted investment in sequencing and analytical infrastructure, training, data-stewardship expertise, and collaborative research networks could broaden access and complement other benefit-sharing arrangements while advancing capacity building and scientific participation under the BBNJ Agreement [4].

Conclusions

The BBNJ Agreement creates an important opportunity to strengthen international cooperation in marine biodiversity research, observation and the equitable benefit sharing. Effective implementation requires governance arrangements that recognise the scientific and operational diversity of activities involving marine genetic material, including routine eDNA biodiversity observation.

Proportionate governance does not imply exemption from the Agreement's requirements. Rather, it requires implementation mechanisms that fulfil applicable obligations while minimising unnecessary administrative barriers to research, monitoring and responsible data exchange. Managed openness offers a science-informed framework guided by the principle “as open as possible, as protected as necessary.” Existing observation systems and data infrastructure could support interoperable biodiversity information, reporting and benefit sharing mechanisms, with targeted safeguards applied where warranted.

By integrating implementation requirements with established scientific infrastructure, investing in quality-assured observation and reference data, and supporting equitable participation and regional capacity, Parties can advance the Agreement's objectives while maintaining the accessibility and scientific value of marine biodiversity information.

Figures

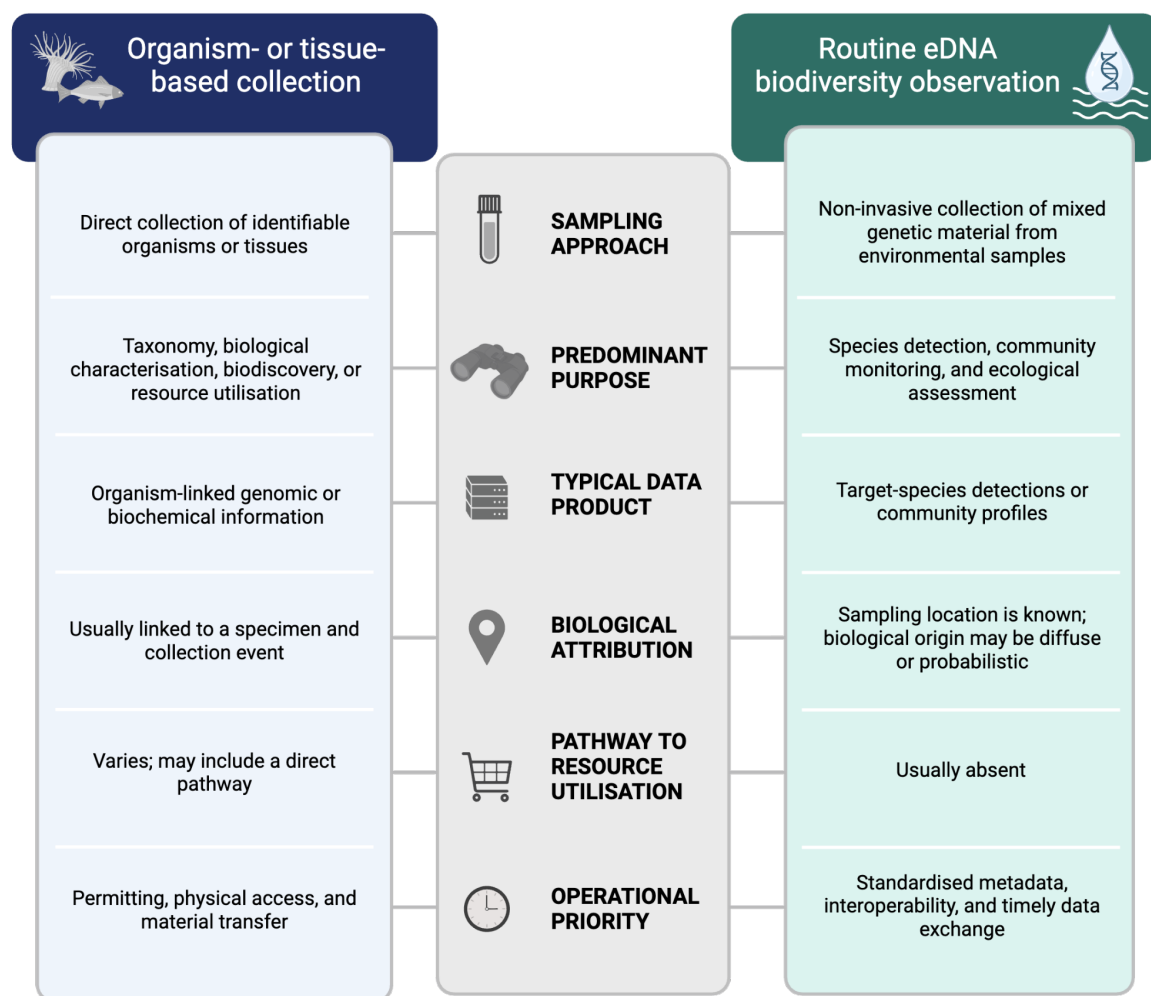


Figure 1. Typical characteristics of organism- or tissue-based marine genetic resource collection and routine eDNA biodiversity observation.

Organism- or tissue-based collection of marine genetic resources typically produces material and information linked to identifiable specimens and collection events, and may include direct pathways to resource utilisation, making physical access, permitting, and material transfer important considerations. Routine eDNA observation generally recovers mixed genetic material to generate species detections or community profiles, with biological origin sometimes diffuse and scientific value often enhanced through timely, interoperable data exchange. These differences are relevant to how arrangements for access, attribution, data sharing, and benefit sharing may apply under the BBNJ Agreement.

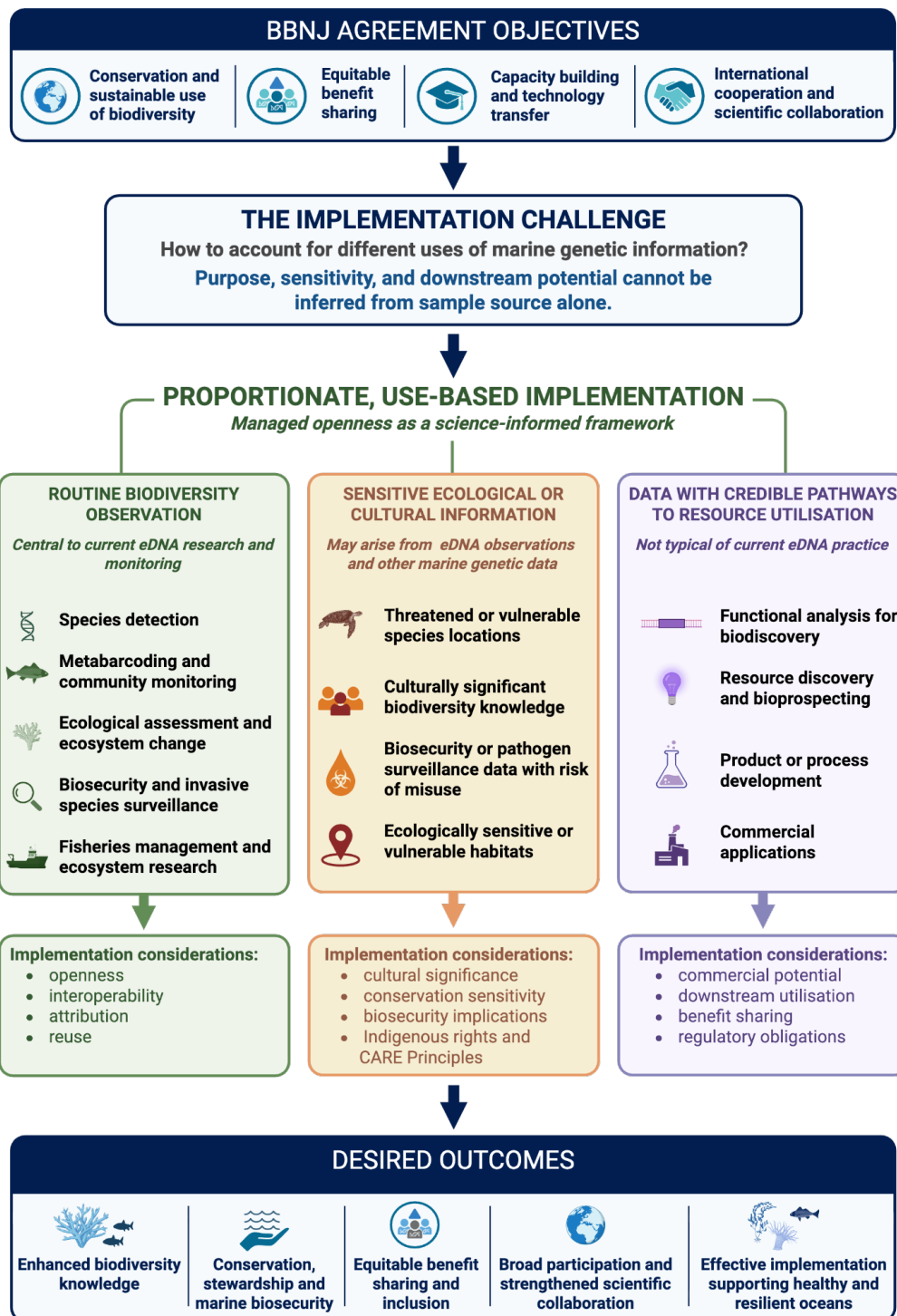


Figure 2. A proportionate, use-based framework for marine genetic information governance under the BBNJ Agreement.

The purpose, sensitivity, and downstream potential of marine genetic information cannot be inferred from sample source alone. Routine biodiversity observation represents the predominant use of eDNA and benefits from openness, interoperability, attribution, and reuse. Cultural, ecological, or biosecurity sensitivities may arise across eDNA observations and other

marine genetic data, while credible pathways to resource utilisation are not typical of current eDNA practice. Managed openness provides a science-informed framework for distinguishing these contexts and applying implementation measures proportionate to intended use and sensitivity. Such an approach could support the Agreement's objectives while enabling biodiversity observation, equitable participation, and scientific cooperation.

Tables

Table 1. Institutional contributions to proportionate BBNJ implementation

Illustrative ways in which institutions and scientific communities could support fulfillment of BBNJ requirements while sustaining routine biodiversity observation and applying proportionate safeguards.

Implementation actor	Potential contributions
Conference of the Parties (COP)	Develop implementation guidance that accommodates routine biodiversity observation and activities with different sensitivities or pathways to resource utilisation.
Scientific and technical advisory bodies	Provide evidence-based advice on provenance, attribution, uncertainty, metadata, reporting standards, and information sensitivity.
National governments	Translate BBNJ requirements into proportionate reporting, access, and benefit-sharing arrangements while supporting interoperable biodiversity observation.
Ethics committees	Review ethical considerations where relevant, including community engagement, consent, and culturally sensitive information.
Data repositories	Support persistent identifiers, standardised metadata, attribution, appropriate access controls, and interoperable data exchange.
Professional societies and scientific networks	Develop best-practice guidance, contribute technical expertise, support training, and communicate scientific perspectives during implementation.
Funding agencies	Invest in infrastructure, capacity building, and equitable scientific participation.
Researchers and institutions	Follow best-practice stewardship, metadata standards and responsible data sharing.

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