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# Understanding practical barriers to the global adoption of environmental DNA (eDNA) methods, tools, and standards

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## Abstract

**Objective** Environmental DNA (eDNA) is a rapidly emerging data source with the potential to support environmental monitoring and biodiversity conservation around the world. Current efforts to standardize eDNA methods and reporting are aimed at strengthening credibility and supporting adoption. In doing this, however, researchers must be mindful of diverse capacities and ecological contexts both regionally and around the world. The objective of our research is to understand how international standards for eDNA may support or hinder the uptake of eDNA methods and tools for conservation and biodiversity work. This was accomplished through two interactive workshops that brought together eDNA researchers and practitioners from around the world to surface broad and specific barriers to uptake of eDNA methods and tools.

**Results** The most prevalent concern across all stages of the workflow was affordability. Workshop participants found the sampling and bioinformatics workflow stages to be the largest barriers. Participants also identified substantial hurdles: (1) the need for more clarity around eDNA methods and appropriate applications and protocols, (2) lack of access to suitable laboratories, (3) the need for different standards for diverse systems, species, and locations, and (4) the lack of trained experts in bioinformatics.

**Keywords** Metabarcoding, Scientific capacity, Qualitative methods, Standardization, Emerging technology, Global South

## Introduction

The eDNA Collaborative at the University of Washington is a program that disseminates, accelerates, and reinforces science to bring environmental DNA (eDNA) analysis and techniques out of the lab and into routine practice around the world. As eDNA emerges as an important source for biodiversity data [1–3], and is subsequently adopted into monitoring programs [4, 5] and regulatory practice [6, 7], standards for eDNA research are being developed at multiple regional and global scales [8–11]. Yet, researchers working with eDNA in the Global South, remote areas, or less-well-resourced institutions may not have access to the same materials and technologies as those in countries with more access, thus making standards challenging to implement under resource constraints [12]. To date, no study has captured real-time practitioner feedback on standards development, leaving a disconnect between standard-setters and end-users.

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To meet our goal of bringing the tools of eDNA to more people, we have been investigating why researchers may, or may not, reach for eDNA as a tool for biodiversity monitoring. These reasons include standards that might support, or hinder, access to and use of eDNA in routine conservation practice. To this end, we convened two workshops that brought eDNA researchers and practitioners together to facilitate a conversation around the potentials and concerns of eDNA standards for research. Workshops were held during scientific conferences held in Kigali - Rwanda, and Belém- Brazil. Data from these workshops was gathered from participants through a series of activities and then coded using a grounded theory methodology [13, 14]. This resulted in a series of qualitative findings including common barriers to using eDNA and recommendations to overcome them.

## Methods

In order to gather a broad range of views from researchers outside of the Global North, the workshops were held at two international conservation conferences in 2024: (1) the Association for Tropical Conservation Biology Annual Meeting in Kigali, Rwanda and (2) the International Barcode of Life Conference in Belém, Brazil. At each conference, we conducted a 90–120 min workshop using interactive methods for eliciting user opinions and concerns. Anyone attending the conference was encouraged to attend, and estimated numbers of workshop attendees were: 30 in Kigali and 50 in Belém. There was no requirement for prior knowledge or use of eDNA, and the conferences drew diverse audiences of conservation professionals from around the world. At each conference, the majority of the attendees were from the continent where the conference was held, but participants attended from around the world. The in-person and interactive nature of this event was important to its success, as putting researchers from around the world, in the same room, in the same time-zone, and face-to face was key to eliciting diverse perspectives across varying cultures and language differences.

Both workshops followed the same format and used a series of interactive discussions and gallery walks (see below) to elicit user experiences of eDNA workflows from sample collection to data and bioinformatics. After a brief introduction to the broad concept of standards and eDNA standards development internationally, we held a brief, open discussion about individuals' use of standards. Following this we convened a "gallery-walk," in which participants could move around the room to engage with posters at different stations representing each stage of the eDNA workflow (Fig. 1). At each stage, participants were encouraged to contribute their thoughts by writing into and pasting post-it notes onto posters. Red post-it notes were used to represent barriers, problems or concerns, while green or blue were used to represent positive outcomes or questions respectively. There was no limit to the number of notes/comments an individual could contribute. After a brief facilitated discussion, a "vote" was held, with a limit of 4 votes per participant. Each vote represented a barrier, three yellow stickers represented important barriers, and one blue sticker to represent the most impactful barrier. These materials (post-it notes, posters, stickers) form the data for this study and were analyzed using the following method.

The gallery walk portion of the workshop. Each stage was represented by a poster at the gallery walk, in which participants wrote their thoughts and voted for the most meaningful among them.

Analysis of the data followed the following protocol, based on qualitative grounded-theoretical coding in

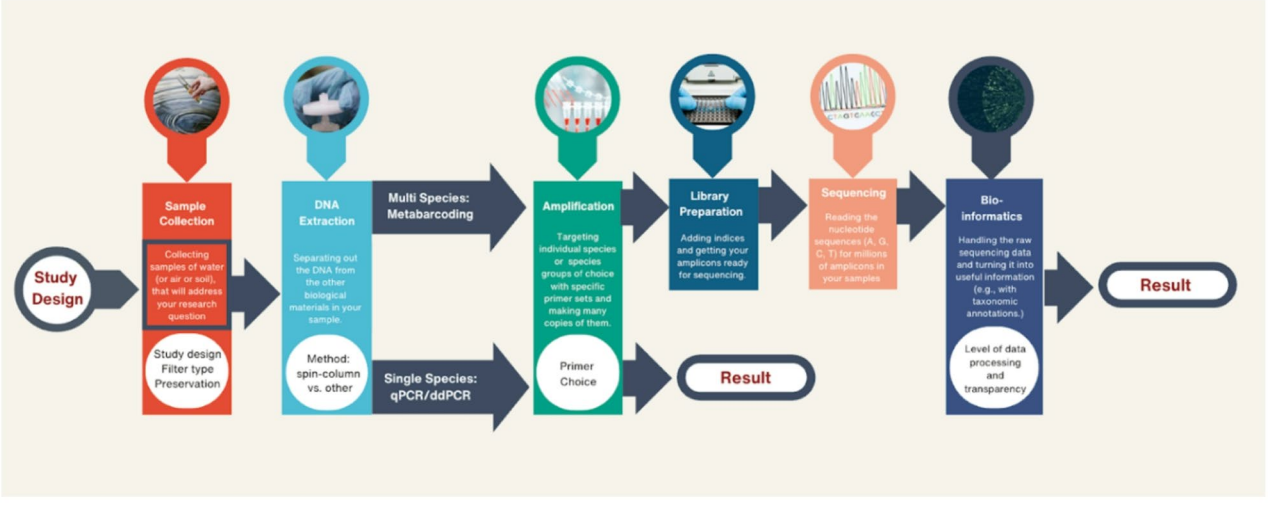


**Fig. 1** Simplified eDNA workflow with six "stages" used in

which the text of the post-it notes served as data. This text was systematically coded using patterns emerging from the text itself [13]. For each workshop, the text from each note was entered into a spreadsheet according to the workflow stage and the color (representing positive/negative), along with the number of "votes" each note or stage had in total. To weigh the importance of the final votes, one point (vote) was given for each yellow sticker, and three points (votes) to each blue sticker. Finally, all entries were coded using an iterative process whereby the coder grouped each entry into similar themes, both per stage and as a whole. The data was then explored using several visualizations [14] including "heat-mapping" of most "important" themes and notes, as well as bar graphs of each stage and theme (Figs. 2 and 3).

## Results

Differences between the results from the two conferences vary slightly (see Figs. 2 and 3), although we hesitate to make regional assumptions based on these differences because both conferences were international in attendance. Due to differences in conference topics, we assume that there were generally more participants familiar with eDNA methods participating in the Belém workshop. While the work stages (as outlined in Fig. 1) supported gathering data about all aspects of an eDNA study, the results from the different stages were overlapping, although some stages appeared to be more problematic than others.

Affordability is the most prevalent concern combined across all stages of the workflow (45 code count out of 344 coded comments). Affordability ranked very high as a barrier in all stages except bioinformatics. It is important to note that we distinguish *affordability* (cost) from *accessibility* (cold chain/logistics). Although related, some items might be inaccessible due to reasons such as logistics or cold chain shipping, whereas the issue of affordability denotes that cost is the foremost barrier. Examples of affordability issues include concerns around the cost of sampling campaigns, analysis, reagents, and equipment, and prohibitive shipping fees. The cost of sending samples to a service provider for analysis may also be beyond the budget of many practitioners. Economic disparities, including unequal exchange rates between countries are cited by participants as a major contributing factor to lack of affordability for researchers.

Across all stages, there is a call for more clarity around eDNA methods and tools due to widespread and fundamental confusion creating a barrier. Lack of information about choosing primers, the appropriate applications of each sequencing technology, and comparability across these technologies were all highly ranked barriers. Standards are sometimes cited as a way to increase clarity, especially in terms of sampling protocols and comparability across regions, study sites, and laboratories. It should be noted, however, that "clarity," is one perspective related to a broader lack of knowledge and can thus be addressed in different ways (i.e. courses vs. standards). Clarity also extends to a concern many people had around the transparency of service providers (i.e. Laboratories that analyze samples and return data).

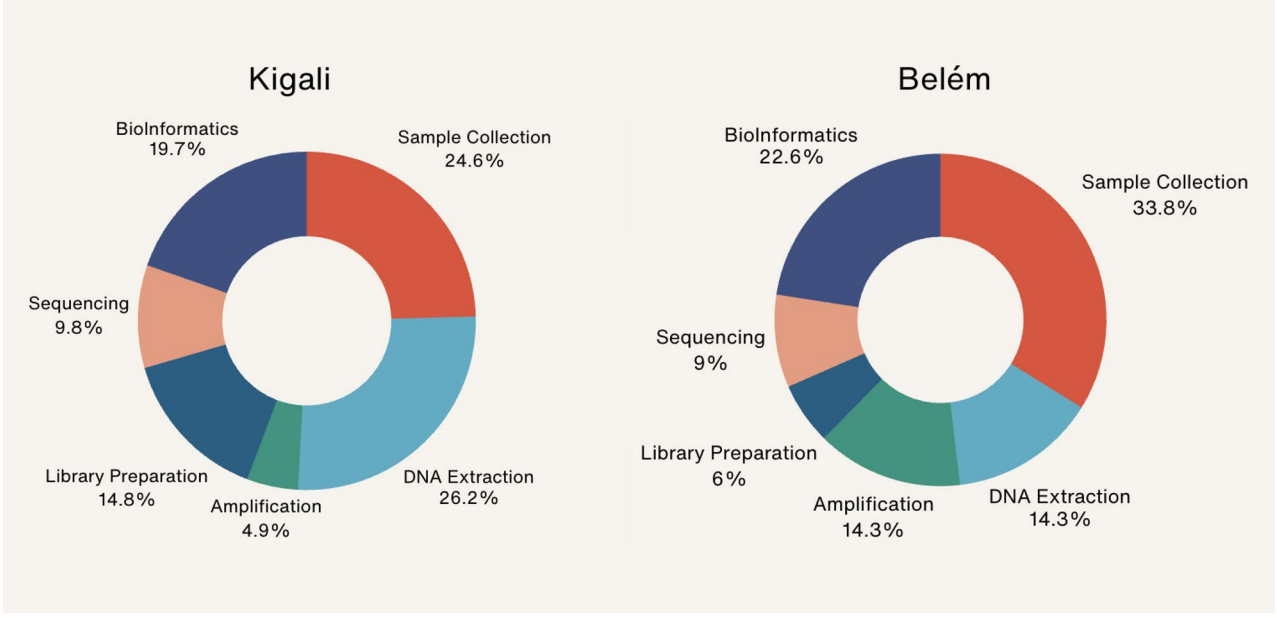


**Fig. 2** Total "vote" count for each eDNA workflow stage across each workshop when asked "What is the *most* impactful barrier?" Each participant was given one (blue dot) vote for this question

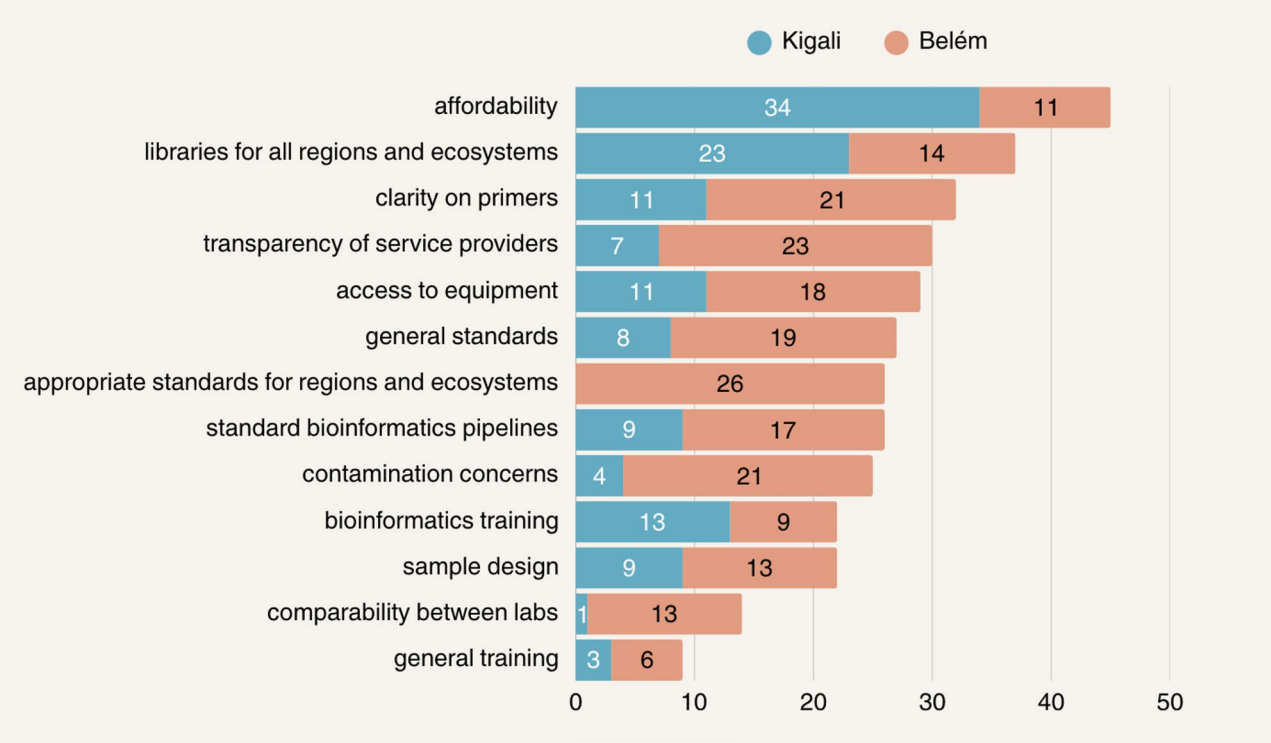


**Fig. 3** Number of coded comments and votes across all workflow stages in Kigali and Belém workshops

A lack of suitable laboratories is a major barrier for many participants. This barrier is characterized in different ways, described as a matter of access, such as access to sequencing laboratories capable of processing environmental samples (as opposed to human), or lack of access to other equipment such as cold storage or even stable electricity supply that may not exist in many remote and low-resourced areas of the world. Contamination was cited as the main concern for the "extraction" stage of the workflow. This barrier is also associated with the need for appropriate laboratory workspaces for extraction and analysis, but it can also be associated with credibility of the method. Increased false positives caused by contamination and the lack of appropriate laboratory infrastructure are not only barriers to implementing eDNA workflows but also threaten the credibility of the method as its use continues to expand.

Many participants were concerned about the applicability of standards to different systems, species, and locations. They highlighted the need to foreground this difference in any standards or sample designs that are developed. Related to difference is a particular concern that was highly ranked across both workshops: the need for comprehensive species libraries containing reference sequences from across the globe, especially in remote and lesser-studied areas such as the tropics, as sequencing data will be unusable without the appropriate libraries.

Finally, the entire stage of bioinformatics rose to the foreground as a major "pinch point" for participants who wanted to use eDNA in their research. Participants highlighted the need for trained experts, standards, and open-source pipelines. They also highlighted the computationally intensive nature of bioinformatics and the lack of capacity in many remote regions. For many participants, lack of access to bioinformatics expertise was a fundamental reason *not* to embrace eDNA methods and tools.

Although most of the gathered comments were barriers, some "positive" comments were also collected, notably several recommendations for self-made, open-source, or DIY protocols, buffers, or other tools. There were also many comments that highlighted the need for and importance of simple and accessible standards.

## Discussion/Recommendations

The findings from this study highlight individual and collective hesitations and structural barriers to useful uptake of eDNA by conservation practitioners around the world. We uncovered perspectives that went well beyond international standards. These findings should be considered when developing any standards for the field, as well as those working to make eDNA more accessible and useful. These issues and barriers outlined by workshop participants have been echoed in other studies and forums [12, 15, 16]. A discussion of some practical ways to support

the reduction of barriers when crafting eDNA standards or programs follows.

The most-commented on and highest-ranked stages as a barrier of the workflow were *sample collection*, *DNA extraction* and *bioinformatics* (Fig. 2). This may be due to the entry-point (sample collection/DNA extraction) and results (bioinformatics) being the most visible and engaged-with stages of the workflow. It is common for conservation scientists to gather samples (*sample collection*) and send them off to a service provider for processing (DNA extraction, amplification, library preparation, and sequencing) to receive the results in the form of bioinformatics data. Therefore, most of the participants were likely less familiar with the "black boxed," intermediate stages that would be executed by a service provider, resulting in more barriers encountered at the end stages.

### Support knowledge transfer

One of the main issues identified was a need for clarity around how to use eDNA-driven techniques appropriately and in different contexts. Further, bioinformatics expertise is a fundamental gap that is preventing researchers from using eDNA methods and tools. Training in eDNA methods is therefore critically needed in both resourced and less-resourced parts of the world. This is especially the case in terms of bioinformatics training, as there is a lack of expertise internal to conservation fields, and even a lack of researchers to consult for bioinformatics support. Capacity for bioinformatics will need to be developed and training will need to be made available to a wide range of people from different disciplines and backgrounds. A good example of this capacity building has been taking place in a regional context in the Africa BioGenome Project, which has trained over 3500 African scientists in bioinformatics and other genetic methods [16–19].

However, while dedicated bioinformatics training remains essential, the growing accessibility of AI assistants and language models, which can help inexperienced users generate and troubleshoot code and bioinformatics pipelines, offers a valuable way to "level the playing field" potentially enabling broader participation in eDNA workflows [20, 21].

### Ensure affordability and accessibility

Affordability and accessibility of technologies and materials will remain an issue with eDNA until regional supply networks and laboratories are developed. Portable long-read sequencers (e.g., handheld/field-deployable units) can reduce shipping and cod-chain dependencies and enable near-field sequencing. However, cost-effectiveness and performance are use-case dependent and should be weighed against accuracy, throughput, and local expertise [23]. eDNA methods and tools span a wide range of low-tech (i.e. some filters) and high-tech (i.e. advanced sequencers) worlds. The rapid innovation within the eDNA community should be embraced and used to create low-cost, open-source technologies and protocols that can be used by almost anyone [22, 23].

### Strengthen reliability

Reliability should be demonstrated with platform-agnostic Quality assurance/Quality control metrics: contamination safeguards and field blanks, positive controls or mock communities, replicate concordance, and transparent, versioned analysis pipelines, alongside inter-laboratory ring trials. Technological innovation can improve access and speed, but workflow choices should be justified by performance metrics not instrument brand [8, 23]. Any workflow proposed on affordability or portability grounds should show comparable detection/error profiles and be reproduced across multiple laboratories before inclusion in standards.

## Conclusion

We urge funders and standard-setting bodies to co-develop tiered standards that align with regional capacity, ensuring equity in eDNA adoption. Conservation practitioners generally feel that standards will support the uptake of eDNA methods and tools. However, if different systems and capabilities are not considered, standards could hinder the uptake of eDNA tools by creating barriers to use. This means that eDNA technologies that are required or suggested for inclusion in standards and protocols should be globally accessible and cost as little as possible, while still being comparable. The results gathered from these workshops highlight the need for general capacity building alongside any efforts at standardization if eDNA methods and tools are to become accessible and useful to conservation practitioners around the world.

## Limitations

This study is qualitative and thus aligns with the general limitations of qualitative research. The sample size was not intended to support quantitative analysis, and thus all results should be read within the context of the two conference workshops in which the data was gathered. All participants were self-selected to participate in the workshops.

### Abbreviations

| | |
|---|---|
| ATBC | Association for tropical biology |
| eDNA | Environmental DNA |
| IBOL | International barcode of life |

## Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13104-026-07693-x.

Supplementary Material 1.

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**Author contributions**
SH, EA, and RK conceptualized the research. SH designed the methods and managed the data. AI and PB assisted in data collection. SH drafted the manuscript. All authors contributed to and approved the final manuscript.

**Data availability**
The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

## Declarations

**Ethics approval and consent to participate**
This study received an exempt determination from the University of Washington Institutional Review Board (IRB #00019295). The research involved anonymous, voluntary opinion surveys conducted with adult participants, after obtaining informed consent, during open workshops at an international scientific conference. No personal identifiers or health information were collected. Rwanda and Brazil served solely as the physical locations of the conference workshops; no research activities, recruitment, or institutional partnerships occurred within local institutions in either country. As confirmed by the University of Washington Human Subjects Division, no local ethics committee approval was required under these circumstances. All procedures were conducted in accordance with the principles of the Declaration of Helsinki..

**Consent for publication**
Not applicable.

**Competing interests**
The authors declare no competing interests.

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## Publisher's Note