STREAMS guidelines: Standards for technical reporting in environmental and host-associated microbiome studies

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Abstract

The interdisciplinary nature of microbiome research, coupled with the generation of complex multi-omics data, makes knowledge sharing challenging. The Strengthening the Organization and Reporting of Microbiome Studies (STORMS) guidelines provide a checklist for the reporting of study information, experimental design, and analytical methods within a scientific manuscript on human microbiome research. In this Consensus Statement, we present the Standards for Technical Reporting in Environmental and host-Associated Microbiome Studies (STREAMS) guidelines. The guidelines expand on STORMS and include 67 items to support the reporting and review of environmental (e.g., terrestrial, aquatic, atmospheric, engineered), synthetic, and non-human host-associated microbiome studies in a standardized and machine-actionable manner. Based on input from 248 researchers spanning 28 countries, we provide detailed guidance, including comparisons to STORMS, and case studies that demonstrate the usage of the STREAMS guidelines. STREAMS, like STORMS, will be a living community resource updated by the Consortium with consensus-building input of the broader community.

Main

Microbiome research is inherently interdisciplinary, spanning hosts (humans, animals, or plants) and environments and capturing impacts ranging from health and disease, to ecosystem function, agriculture, and food security[1–4]. While human microbiome research has flourished due to heavy investment in research infrastructure and broad public recognition, resourcing for microbiome science outside human health has lagged[5]. Environmental microbiome research necessitates unique considerations, as it combines cross-disciplinary techniques, field sampling campaigns, and insights from microbiology, data science, bioinformatics, and ecology, among other areas. The data and metadata associated with microbiome studies continue to be difficult to capture and report, especially as utilization of multi-omics methodologies have advanced, which generate large, complex datasets[6]. Furthermore, ensuring data are deposited and available for reuse according to the Findable, Accessible, Interoperable, and Reusable (FAIR) principles presents challenges for many researchers when navigating data repository submissions and when working with incomplete metadata[7]. While there have been consistent calls from the community to promote more standardization across the entire microbiome research lifecycle, several barriers remain[8–12]. Researchers, publishers, funders, and data repositories must be brought together to establish consensus guidelines that address the unique complexities of environmental and synthetic microbiome data generation, analysis, and sharing.

Community-driven efforts to develop best practices, reporting guidelines, and standards have advanced how microbiome data are shared and reused. When the Genomic Standards Consortium (GSC) developed the *Minimum Information about any (x) Sequence* (MIxS) standards for metadata management in 2011, it quickly became a foundation for standardized microbiome metadata capture[13–15]. More recently, several genome-based community driven efforts have advanced cross-study comparisons, including standards for viral and prokaryotic genomes[16,17]. The *Strengthening the Organization and Reporting of Microbiome Studies* (STORMS) checklist leverages the MIxS standards as well as the *Strengthening the Reporting of Observational Studies in Epidemiology* (STROBE) and *STrengthening the REporting of Genetic Association Studies* (STREGA) guidelines to provide a framework for the reporting of human microbiome studies[18–20]. The microbiome research community has already widely adopted the STORMS checklist. However, these guidelines only apply to human-associated microbiome studies, and there has been no equivalent generated for environmental microbiomes.

To address the current gaps in comprehensive guidelines for environmental (e.g., terrestrial, aquatic, atmospheric, or engineered), non-human host-associated (e.g., animal- or plant-associated), and synthetic microbiome research, we present the *Standards for Technical Reporting in Environmental and host-Associated Microbiome Studies* (STREAMS) guidelines. These guidelines were constructed using the STORMS checklist as a framework and were iterated using extensive community feedback. The STREAMS guidelines and associated materials provide authors with clear, actionable recommendations for manuscript preparation and data sharing, while offering reviewers a structured framework for evaluating methodology and data quality. The STORMS checklist and its subsequent iterations will continue to support human-associated microbiome studies, whereas the STREAMS guidelines provide guidance to microbiomes not directly associated with human subjects. The STORMS and STREAMS guidelines will be collaboratively updated to maintain synergy. These guidelines were created to lower barriers to proper microbiome data management and reporting by providing a clear and structured framework. They are designed to foster greater standardization and promote FAIR data principles, ultimately maximizing the utility and impact of microbiome data for the broader scientific community.

Methodology

In June 2024, we convened the *Microbiome Data Management in Action* workshop in Atlanta, USA, that brought together 50 invited microbiome researchers, publishers, funders, and data repository representatives to discuss the current state of microbiome data management and reporting[21]. More details regarding the workshop agenda, participants, panels, presentations, and discussions are available in the *Microbiome Data Management in Action* workshop report[21]. A large focus of the workshop was adapting the human-associated microbiome STORMS checklist to make it applicable to these systems. A preliminary review of the STORMS guidelines revealed that many of its Items would need to be revised based on differences in terminology, data access requirements, metadata standards, and conventions within environmental microbiome research compared to human-associated studies. Several limitations with the STORMS checklist such as the limited information about metabolomics and proteomics, varied interpretations of STORMS Item 6.0 related to causal inference, and the fact that several Items may be outdated, were also presented by the STORMS lead author. Six breakout groups worked on the checklist, and the suggested changes were discussed and concatenated. This led to a first draft version of the STREAMS guidelines.

Obtaining community feedback was a priority for the STREAMS effort, and therefore, the first draft of the guidelines was circulated across the broader microbiome research community through targeted emails, social media posts, microbiome-relevant newsletters, and through the STREAMS website (streamsmicrobiome.org). A modified Delphi methodology was implemented, featuring multiple rounds of community feedback reviewed by a working group formed by attendees of the workshop. We designed and distributed a feedback form which included prompts about suggested changes, revisions, and Items to consider as “must-keep” in the STREAMS draft, or respondents could comment directly in the Google Sheet with the STREAMS draft. From the first round of community feedback via direct comments and responses to the feedback form, we obtained over

700 comments that were discussed and implemented, or were deemed to be infeasible (e.g., the feedback was too prescriptive or did not align with existing reporting guidelines or standards). All comments from this first round were responded to by the members of the STREAMS working group that continued to meet bi-weekly. Subsequently, an updated second draft of the STREAMS guidelines was then circulated, which received 400 additional comments, all of which were responded to and implemented into the consensus guidelines whenever possible and when agreed upon by the working group. A few examples of comments that were received during the rounds of feedback that were incorporated into the final guidelines are, "Software: would be good to specify actual parameters used rather than 'default parameters' as the defaults can change over time"; "Item 3: For agricultural studies, greenhouse studies sometimes serve as an in-between for field and laboratory studies. Greenhouse or semi-controlled spaces could be added as a category."; "Similar to the STORMS checklist, having exemplary checklists for recent or past studies would be very helpful.". There were very few instances of conflicting comments, and in those cases, the STREAMS working group and expert researchers in the microbiome research field were consulted to determine the optimal course of action. Overall, 248 researchers from 28 countries provided feedback, although we acknowledge the lack of representation from researchers in Africa and parts of Asia and South America. Together, this group spans a range of career stages, works with various sample and data types, and represents varied facets of microbiome research.

Checklist

The STREAMS guidelines (Supplementary Table 1) consist of 67 Items organized into six sections aligned with the architecture of a scientific manuscript, reflecting which section they pertain to (Figure 1). The guidelines are also publicly available through Zenodo[22], on the STREAMS website, and as a machine-actionable data management plan (DMP) building tool within a free, publicly available web resource hosted by the California Digital Library called "DMP Tool"[23] (available under Templates, as "STREAMS Microbiome Guidelines DMP Tool template"). Each STREAMS Item comprises 8 elements: its number, name, the recommendation, where the Item derived from (e.g., if derived from another existing standard), additional guidance, example(s), and two manuscript-associated columns to be used by authors or reviewers for noting if the Item is reported in the manuscript, and if so in which section. The "Item Source" column references STORMS, the National Center for Biotechnology Information (NCBI), MIxS, the Environment Ontology (ENVO), the Open Biomedical Ontologies (OBO) Foundry, the Chemical Analysis Working Group (CAWG) of the Metabolomics Standards Initiative (MSI), STROBE, STREGA, or denotes if the Item is considered new for STREAMS. While not all studies may capture all reporting information, the intent of the STREAMS guidelines is to be broadly descriptive and inclusive of various use cases spanning environmental, synthetic, and non-human host-associated microbiomes. STREAMS is intended to act as a reflective framework for assessing manuscripts, and the content, Item order, and organization are not designed to be strict requirements.

Figure 1. Overview of the STREAMS guidelines. **(a)** The guidelines encompass microbiomes ranging from terrestrial and aquatic (environmental), synthetic, and non-human host-associated environments. **(b)** The six key sections include (1) abstract, (2) introduction, (3) methods, (4) results, (5) discussion, and (6) other information. Figure created using BioRender.com and Canva.

Abstract (1.0-1.5)

The Abstract section (Items 1.0-1.5) provides guidance on how to organize and report sufficient information in an abstract for environmental, non-human host-associated, or synthetic microbiome studies. Abstracts are often replicated across platforms (e.g., associated with the data in a data repository), magnifying their importance as independent summaries of key study elements. Overall guidance for the abstract organization is provided along with notes regarding graphical abstracts (Item 1.0). Items 1.1, 1.2, 1.4, and 1.5 encompass the study design, environments and samples, experiments or methodology (including specific information about omics methods utilized), the analyses performed, and the overall results of the study and their significance. As is noted throughout the guidelines, there are several Items that are only applicable to host-associated studies and the first instance of this is indicated in Item 1.3 which requests a summary of host information.

Introduction (2.0-2.1)

The Introduction section (Items 2.0-2.1) parallels that of the original STORMS checklist. This section requests that authors describe the background and rationale for their study (Item 2.0) in the context of previous work that has been conducted in their specific field. The synthesis of previous publications and datasets in their area of research should highlight any knowledge gaps. Researcher hypotheses, objectives, or research questions are also requested to be included in the Introduction (Item 2.1), which are encouraged to relate to the aforementioned knowledge gaps and broader significance of the reported study.

Methods (3.0-8.5)

Methods comprise a majority of the checklist, as outlined below.

Study & Sample Information (3.0-3.6)

The Study & Sample Information Items (3.0-3.6) request detailed information on the study design, any associated host(s), any datasets that were reused for the study, and the samples that were analyzed. This section is designed to capture sufficient contextual information about the study. The overall study design should be stated (Item 3.0) and should acknowledge if the study includes meta-analyses, combined analyses, or involves datasets derived from previously published work. The sample type(s) as well as any associated sample metadata are requested in Item 3.1 which also necessitates the inclusion of specific information on how any relevant synthetic communities (SynComs) were generated, and accurate citation information on datasets that have been reused[12]. The Environmental Context & Geographic Location Item (Item 3.2) requires that the author states where the samples originated. This Item generated a lot of discussion amongst the STREAMS Consortium as many researchers would prefer to require geographic coordinates, while others suggested that certain ethical and privacy considerations prevent this from being possible. The consortium decided on strongly encouraging the inclusion of coordinates and requiring a justification if they cannot be provided. The MIxS standards as well as ENVO are referenced in this Item to standardize how the environmental context and the geographic location are reported[24]. Item 3.3 requests any relevant dates including when samples were collected, over what time period, the frequency of sampling, and other temporal factors (e.g., seasonality). Item 3.4 only applies to host-associated studies and is intended to capture as much detailed information about the host(s) as possible. Comprehensive, well-researched, and detailed information on the ethics of the study design must be reported (Item 3.5). This Item includes guidance on reporting permits, permissions, and sampling ethics. The CARE principles for Indigenous data governance (Collective Benefit, Authority to Control, Responsibility, and Ethics) are referenced here, and researchers are expected to adhere to these guidelines and ensure Indigenous data sovereignty whenever applicable[25]. Item 3.6 refers to any treatments or conditions that the sampling environment(s) or host(s) were subjected to, and the relevant MIxS references are included in the additional guidance for this Item[26–28].

Sample Collection (3.7-3.9)

Authors should report detailed information regarding sample collection methods and metadata, including if previously published protocols were followed (Item 3.7). Specifics regarding the tools that were used, the host body site or environmental niche sampled, and potential sample destruction can be critical to a comprehensive understanding of the samples and the reproducibility of the methods and should also be provided. Information on sample eligibility/selection criteria should also be included (Item 3.8), which leads to reporting on the final analytic sample size (Item 3.9).

Experimental Information (4.0-4.6)

Information on sample storage, preservation, transportation, and shipping should be included (Items 4.0 and 4.1). In terms of experimental steps, nucleic acid, protein, and/or metabolite extraction methods should be reported (Item 4.2), along with steps relating to experimental manipulations, sample processing, and culturing (Item 4.3). Information on nucleic acid library preparation protocols was separated into another Item to better align with submission requirements to data repositories such as the NCBI Sequence Read Archive (SRA)[29] (Item 4.4). Methods for enriching or depleting samples should be discussed in depth (Item 4.5), including if amplification was used and if so, the targeted region and primer sequences (Item 4.6). These Items are of particular importance to microbiome samples, as each depletion or enrichment method could exclude signatures from some members of the microbial community and can have particular biases.

Controls & Quality Information (5.0-6.2)

Feedback from the community suggested that the guidelines be extremely explicit for Items referring to controls and replicates. Therefore, the Control and Quality Information categories were split into several Items (Items 5.0-6.2). Any positive (Item 5.0) and negative (Item 5.1) controls should include detailed descriptions including what exactly they were and what stage they were implemented. Justification should be provided if no positive or negative controls were included. Information on quantity and quality assessments of samples, nucleic acids, proteins, and metabolites should be included in Item 6.0, referencing any pre-existing protocols. Any laboratory-based strategies utilized to minimize and identify contamination can be specifically stated (Item 6.1) or discussed throughout the Methods at each step. Biological and technical replicates should be discussed (Item 6.2) and the additional guidance recommends that authors describe why certain replicates were included and include how they factor into bioinformatics and statistical analyses.

Omics Data Generation (6.3-6.6)

Items 6.3-6.6 encompass omics data generation, specifically for sequencing (Item 6.3) and mass spectrometry (Item 6.4) applications[30]. Specificity in the information provided in this section is paramount as these metadata can directly affect results and interpretations. Vendor and kit information as well as established protocols should be referenced whenever possible. For the sequencing information, synergy with specific NCBI SRA submission fields and requirements is noted to assist researchers. Item 6.5 requests information on other contextual or linked datasets and how these relate to the study and the omics data. Other omics types or data types may not be encompassed by the guidelines and additional information would be required for other analyses. Anticipated or potential batch effects (Item 6.6) should also be reported for the sampling and processing steps outlined in earlier Items as well as for the omics and data generation Items in this section (Items 6.3-6.5).

Data Analysis (7.0-7.9)

Feedback from the community indicated that a key challenge for microbiome data reuse has been a lack of transparency regarding specifics about bioinformatics tools, workflows, parameters, and code in associated publications. Therefore, we split the bioinformatics, data analysis, and statistical processing steps into ten detailed Items. Information regarding all bioinformatics analyses and steps included in the study should be reported as noted in Item 7.0[31]. Standardization between workflow runs is encouraged, and all relevant processing metadata should be included so that any researcher can fully replicate all bioinformatics steps. Quality control information should be reported, including how low-quality data were filtered out and the performance of any negative or positive controls that were included (Item 7.1). Normalization processes can often differ between studies, and this information should be specifically reported (Item 7.2). Many STREAMS Consortium members appreciated the inclusion of database information in the STORMS guidelines but requested that this be expanded to its own Item with more guidance. Item 7.3 captures database information for taxonomic classifications as well as metabolite and protein identification. Database names, versions, dates of creation and access, Digital Object Identifiers (DOIs), citations, and/or relevant links are requested. Information on the construction of custom databases should also be included.

The statistical methods used in the study should be exhaustively reported (Item 7.4) and should include details about how calculations were performed, any transformations that were performed, and why particular statistical tests were chosen[32]. Item 7.5 is critical for research transparency relating to missing information. The potential for biases and confounding variables as well as methods utilized to minimize these effects are suggested to be included here in the Methods (Item 7.6), and can be expanded upon in the Discussion (Item 11.2) in the context of overall study limitations[33]. If any subgroups were formed during analysis, Item 7.7 should detail how and why these subgroups were created. Information on any sensitivity analyses that were performed, in particular those that may impact results, should be reported in Item 7.8. Significance thresholds should be included as described in Item 7.9, and false discovery assessments are also recommended for reporting.

Access & Reproducibility (8.0-8.5)

Access to the metadata, host data, raw data, processed data, software, and code are all critical for adhering to the FAIR principles and ensuring reproducibility and reusability of microbiome studies. The metadata standards that were followed (e.g., MIxS) and how the metadata can be accessed should be reported as indicated in Item 8.0, and justification should be provided if not all metadata are made publicly available[34]. If applicable, host information, data, and metadata should also be directly linked in the publication and details should be provided on how to link host data to the microbiome data (Item 8.1). All raw data (Item 8.2) and processed data (when applicable; Item 8.3) should also be made publicly available in robust long-term databases. Item 8.4 outlines recommended details to include when reporting on the software, tools, workflows, and code used to perform assessments and analyses, which should all be made publicly available whenever possible[35]. Item 8.5 closely matches the STORMS checklist to request information regarding the reproducibility of the methodologies and analyses used in the study[36].

Results (9.0-10.3)

While microbiome research results can be presented in a myriad of ways, Items 9.0-10.3 provide recommendations for proper manuscript reporting of common types of results. Results and information relating to the environment(s), host(s), and sample(s), including the variables of interest (as well as potential confounding variables to the results) are requested in Item 9.0. Results, specifically from sequencing analyses, are encapsulated in Item 10.0, and results from positive and negative controls should be referenced. Results from other omics analyses (e.g., metabolomics and proteomics) should also be reported in the context of any standards that were used to identify metabolites and proteins (Item 10.1). Item 10.2 relates to the methods reported in Item 7.4 and includes guidelines for reporting on the results of statistical analyses performed on the data. Item 10.3 provides overall guidance for figures, tables, and captions.

Discussion (11.0-13.0)

The Discussion section is meant to be minimally prescriptive, and we recognize that each journal, researcher, and group have unique approaches to Discussion sections. The STREAMS guidelines request a summary of the key results and how they relate to the overall study objective(s) (Item 11.0). This can also include if any hypotheses have been rejected or supported. Item 11.1 describes how interpretations of results can be reported, and how the results fit into the broader context of the field and other existing datasets. It is noted that caution should be used when including certain terms and language, and that formal definitions may need to be included or referenced[37]. The overall limitations of the study should be included, with an emphasis on areas of potential bias (Item 11.2). The generalizability of the study results should also be reported (Item 11.3): for example, how the results are expected to change or remain the same in different hosts or environments. Guidelines are also provided for the reporting of ongoing or future work (Item 12.0) and for overarching conclusions (Item 13.0).

Other information (14.0-18.0)

The *Other information* section encompasses Items that are typically required during journal submission. Journals may have different thresholds for awarding an acknowledgement, but typically acknowledgements are provided to researchers that did not meet the criteria for authorship, or for other groups, facilities, or institutions that provided assistance to the study (Item 14.0). As permitted by the publisher and authors' affiliates, Indigenous land acknowledgments may also be reported here along with other information described in Item 3.5. Item 14.1 provides guidance for how funding statements should be reported for each author. Any known or potentially perceived conflicts of interest must be reported to the journal following publisher guidance (Item 15.0). Proper management and reporting of supplementary information (Item 16.0) is often necessary to ensure FAIRness of the research, and this can often be overlooked by authors, reviewers, and readers. Links to DOIs and external supplemental information should be provided, and metadata, supplemental figures, and data processing information should all be properly reported in this section. Similarly, information on how all the samples and data associated with the study can be accessed should be reported, along with information on how disparate datasets and information can be linked (Item 17.0). fFinally, many journals now require the reporting of any machine learning or artificial intelligence (AI) methods that were utilized throughout the study (Item 18.0). We encourage authors to include this information in the Methods, as well as in this supplemental information section. Authors should describe the exact ways in which AI was used (e.g., language translations, writing assistance, figure generation) and refer to journal-specific guidance for acceptable usage. We expect the guidance for this Item to continuously evolve as AI usage becomes more prevalent, and as guidance and restrictions change.

Implementation

Throughout the process of creating STREAMS, it became clear that providing these guidelines during the manuscript writing process may be too late in the research process to ensure that the information and metadata noted in the STREAMS Items are captured. Therefore, we constructed a STREAMS template through an existing data management plan-building resource, the DMP Tool. While this template is not meant to be used directly as a data management plan, it can assist in the creation of information recommended in the STREAMS guidelines. Any researcher can access the "STREAMS Microbiome Guidelines" DMP Tool template to help craft a machine-actionable template, automating the process of pulling institutional information and linking persistent identifiers, for work they plan to perform or have already conducted.

To ensure these guidelines are broadly comprehensible and user-friendly, we created an overall STREAMS User Guide document (Supplementary Note 1), as well as a tutorial video that is available on the STREAMS website (https://streamsmicrobiome.org). A simplified STREAMS document is also available on the website to be used as a quick checklist for those who are already familiar with the more comprehensive guidelines, or for those who would prefer a document that is less overwhelming and can then reference the main STREAMS guidelines for context. A list of acronyms used in STREAMS along with relevant links is also available (Supplementary Note 2).

To demonstrate how the STREAMS guidelines can be applied, we selected eight publications spanning various environmental, synthetic, and non-human host-associated microbiome studies (Table 1, Supplementary Tables 2-9). Examples for each STREAMS Item, where applicable, as well as their respective locations in the manuscripts were manually recorded on a STREAMS template. Each completed exemplar was internally reviewed for accuracy and made available here and on the STREAMS website.

Discussion

Reporting guidelines and checklists have demonstrated their efficacy across various disciplines, and the STORMS checklist continues to be adopted across human microbiome research and by funding agencies and publishers[18]. Using STORMS as the template for STREAMS leverages the successes seen with STORMS, while aiming to provide an effective checklist for necessary study, experimental design, and analytical methods reporting for environmental, non-human host-associated, and synthetic microbiomes. We also recognize the impact and utility of previously generated standards such as STROBE, STREGA, ENVO and MIxS, which were implemented throughout the STREAMS guidelines whenever possible[14,19,20,24]. A more detailed explanation of the Item Source column of STREAMS including the connections to these other standards and initiatives, as well as a comparison between STORMS & STREAMS is also available (Supplementary Note 3).

While the Items listed in the guidelines do not capture information relevant to every study, they are designed to be generalizable without being exhaustive. There are several noted limitations of these guidelines. There is the possibility of "checklist-fatigue" due to the length and amount of content captured in the STREAMS guidelines. The simplified version of STREAMS (https://streamsmicrobiome.org) was designed to help with this, however, we recognize that these guidelines may still appear overwhelming. The order of the Items may also be perceived as a strict recommendation for manuscript ordering and flow, which could potentially hinder creativity and prevent non-traditional manuscript formatting. Additionally, STREAMS may be interpreted by some as a set of strict requirements to assess compliance, rather than a reflective framework as it is intended. It can also be difficult to retroactively obtain the information or perform steps recommended by STREAMS. If researchers are not aware of these guidelines until the manuscript submission step, critical reporting information could be missed. We also recognize that the specific caveats associated with various research areas, environments, experiments, or contexts may not be captured in sufficient detail by these guidelines.

Throughout the development of STREAMS, we prioritized community feedback to generate consensus. The inherent interdisciplinarity of microbiome research necessitates feedback from across the field which in turn also supports adoption. We broadly circulated the draft guidelines with the intent to reach researchers around the world, however, we recognize that many research groups and countries are not represented in the Consortium, specifically researchers from Africa and parts of Asia and South America, which currently limits the generalizability. We also emphasize that these guidelines are not meant to be prohibitive to those in less well-resourced areas. We will continue to involve the global microbiome research community in future iterations of the STREAMS guidelines and will continue to expand the STREAMS Consortium. Furthermore, the lead author of the STORMS checklist is co-author here and a core member of the STREAMS Consortium, and we will continue to work synergistically with the STORMS team on iterations to both sets of guidelines. An ongoing feedback form (https://forms.gle/WgEpBAEAnx3m9o5UA) is publicly available on the STREAMS website for any researcher to provide their input. Updated versions are planned, with new versions being posted publicly on the STREAMS website and through Zenodo[22].

We believe the STREAMS guidelines will be valuable for researchers writing manuscripts and can help to streamline the peer review process for both the authors and reviewers. The DMP Tool template guidance will also assist with proper writing, reviewing, and reporting on aspects of data management plans for funding agencies and is a machine-actionable implementation of these guidelines. Future efforts include the development of a STREAMS large language model that could be used by researchers to quickly assess microbiome manuscripts. Together, the STREAMS guidelines and accompanying resources will advance the ways in which microbiome research is reported and reviewed, increasing the short- and long-term value of these studies.

Availability of data and materials

The guidelines are publicly available through Zenodo[22]: https://doi.org/10.5281/zenodo.15014818, on the STREAMS website: streamsmicrobiome.org, and through a data management plan (DMP) building site (https://dmptool.org): DMP Tool as the "STREAMS Microbiome Guidelines" template.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

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References

1. Alivisatos, A. P. *et al.* A unified initiative to harness Earth's microbiomes. *Science* **350**, 507–508 (2015).
2. Thompson, L. R. *et al.* A communal catalogue reveals Earth's multiscale microbial diversity. *Nature* **551**, 457–463 (2017).
3. Martiny, J. B. H. *et al.* The emergence of microbiome centres. *Nat. Microbiol.* **5**, 2–3 (2020).
4. Banerjee, S. & van der Heijden, M. G. A. Soil microbiomes and one health. *Nat. Rev. Microbiol.* **21**, 6–20 (2023).
5. Stulberg, E. *et al.* An assessment of US microbiome research. *Nat. Microbiol.* **1**, 1–7 (2016).
6. Jansson, J. K. & Baker, E. S. A multi-omic future for microbiome studies. *Nat. Microbiol.* **1**, 1–3 (2016).
7. Wilkinson, M. D. *et al.* The FAIR Guiding Principles for scientific data management and stewardship. *Sci. Data* **3**, 160018 (2016).
8. Berg, G. *et al.* Microbiome definition re-visited: old concepts and new challenges. *Microbiome* **8**, 103 (2020).
9. Hornung, B. V. H., Zwittink, R. D. & Kuijper, E. J. Issues and current standards of controls in microbiome research. *FEMS Microbiol. Ecol.* **95**, fiz045 (2019).
10. Cernava, T. *et al.* Metadata harmonization–Standards are the key for a better usage of omics data for integrative microbiome analysis. *Environ. Microbiome* **17**, 33 (2022).
11. Huttenhower, C., Finn, R. D. & McHardy, A. C. Challenges and opportunities in sharing microbiome data and analyses. *Nat. Microbiol.* **8**, 1960–1970 (2023).
12. Northen, T. R. *et al.* Community standards and future opportunities for synthetic communities in plant–microbiota research. *Nat. Microbiol.* **9**, 2774–2784 (2024).
13. Field, D. *et al.* The Genomic Standards Consortium. *PLoS Biol.* **9**, e1001088 (2011).
14. Yilmaz, P. *et al.* Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. *Nat. Biotechnol.* **29**, 415–420 (2011).
15. Eloe-Fadrosh, E. A. *et al.* A Practical Approach to Using the Genomic Standards Consortium MIxS Reporting Standard for Comparative Genomics and Metagenomics. *Methods Mol. Biol. Clifton NJ* **2802**, 587–609 (2024).
16. Parks, D. H. *et al.* A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. *Nat. Biotechnol.* **36**, 996–1004 (2018).
17. Roux, S. *et al.* Minimum Information about an Uncultivated Virus Genome (MIUViG). *Nat. Biotechnol.* **37**, 29–37 (2019).
18. Mirzayi, C. *et al.* Reporting guidelines for human microbiome research: the STORMS checklist. *Nat. Med.* **27**, 1885–1892 (2021).
19. Elm, E. von *et al.* The Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) statement: guidelines for reporting observational studies. *The Lancet* **370**, 1453–1457 (2007).
20. Little, J. *et al.* STrengthening the REporting of Genetic Association Studies (STREGA)—an extension of the STROBE statement. *Genet. Epidemiol.* **33**, 581–598 (2009).
21. Kelliher, J. *et al.* Microbiome Data Management in Action Workshop: Atlanta, GA, USA, June 12-13, 2024. Preprint at https://doi.org/10.5281/zenodo.13829669 (2024).
22. Kelliher, J. & Eloe-Fadrosh, E. STREAMS Guidelines. (2025) doi:10.5281/zenodo.15014818.
23. DMP Tool. https://dmptool.org/about_us.
24. Buttigieg, P. L. *et al.* The environment ontology: contextualising biological and biomedical entities. *J. Biomed. Semant.* **4**, 43 (2013).
25. Carroll, S. R. *et al.* The CARE Principles for Indigenous Data Governance. *Data Sci. J.* **19**, 43–43 (2020).
26. Glass, E. M. *et al.* MIxS-BE: a MIxS extension defining a minimum information standard for sequence data from the built environment. *ISME J.* **8**, 1–3 (2014).
27. Dundore-Arias, J. P. *et al.* Community-Driven Metadata Standards for Agricultural Microbiome

Research. *Phytobiomes J.* **4**, 115–121 (2020).

28. Simpson, A. *et al.* MISIP: a data standard for the reuse and reproducibility of any stable isotope probing-derived nucleic acid sequence and experiment. *GigaScience* **13**, giae071 (2024).
29. Katz, K. *et al.* The Sequence Read Archive: a decade more of explosive growth. *Nucleic Acids Res.* **50**, D387–D390 (2022).
30. Sumner, L. W. *et al.* Proposed minimum reporting standards for chemical analysis. *Metabolomics* **3**, 211–221 (2007).
31. Schymanski, E. L. *et al.* Identifying Small Molecules via High Resolution Mass Spectrometry: Communicating Confidence. *Environ. Sci. Technol.* **48**, 2097–2098 (2014).
32. Willis, A. D. & Clausen, D. S. Planning and describing a microbiome data analysis. *Nat. Microbiol.* **10**, 604–607 (2025).
33. Vujkovic-Cvijin, I. *et al.* Host variables confound gut microbiota studies of human disease. *Nature* **587**, 448–454 (2020).
34. Kukutai, T. & Black, A. CARE-ing for Indigenous nonhuman genomic data — rethinking our approach. *Science* **385**, eadr2493 (2024).
35. Boettiger, C. An introduction to Docker for reproducible research. *SIGOPS Oper Syst Rev* **49**, 71–79 (2015).
36. Schloss, P. D. Identifying and Overcoming Threats to Reproducibility, Replicability, Robustness, and Generalizability in Microbiome Research. *mBio* **9**, 10.1128/mbio.00525-18 (2018).
37. Joos, R. *et al.* Examining the healthy human microbiome concept. *Nat. Rev. Microbiol.* **23**, 192–205 (2025).
38. Fonseca, A. *et al.* Investigating antibiotic free feed additives for growth promotion in poultry: effects on performance and microbiota. *Poult. Sci.* **103**, 103604 (2024).
39. Kellogg, C. A. & Pratte, Z. A. Unexpected diversity of Endozoicomonas in deep-sea corals. *Mar. Ecol. Prog. Ser.* **673**, 1–15 (2021).
40. Berg, M. *et al.* Host population diversity as a driver of viral infection cycle in wild populations of green sulfur bacteria with long standing virus-host interactions. *ISME J.* **15**, 1569–1584 (2021).
41. Tláskal, V. *et al.* Complementary Roles of Wood-Inhabiting Fungi and Bacteria Facilitate Deadwood Decomposition. *mSystems* **6**, 10.1128/msystems.01078-20 (2021).
42. Novak, V. *et al.* Multi-laboratory Study Establishes Reproducible Methods for Plant-Microbiome Research in Fabricated Ecosystems. 2024.10.02.615924 Preprint at https://doi.org/10.1101/2024.10.02.615924 (2024).
43. Becsei A. *et al.* Time-series sewage metagenomics distinguishes seasonal, human-derived and environmental microbial communities potentially allowing source-attributed surveillance. *Nat. Comm*. 2024;15:7551 (2024).
44. Chen, M. *et al*. Molecular mechanisms and environmental adaptations of flagellar loss and biofilm growth of Rhodanobacter under environmental stress. *ISME J. 18*(1), wrae151. (2024).
45. Fernandes, VMC *et al*. Rainfall pulse regime drives biomass and community composition in biological soil crusts. *Ecology,* 103(9):e3744, (2022).

Table 1. STREAMS exemplars serve as practical examples of how to apply the guidelines for a broad range of environmental, synthetic, and host-associated microbiome studies.

Environment / Host	**Microbiome Study**	**STREAMS Exemplar**
Agriculture / Broiler Chickens	Fonseca et al., 2024[38]	Supplementary Table 2
Deep-sea corals	Kellogg & Pratte, 2021[39]	Supplementary Table 3
Freshwater lake	Berg et al., 2021[40]	Supplementary Table 4

Deadwood	Tlaskal et al., 2021[41]	Supplementary Table 5
Synthetic community	Novak et al., 2025[42]	Supplementary Table 6
Wastewater	Becsei et al., 2024[43]	Supplementary Table 7
Subsurface groundwater & extreme conditions	Chen et al., 2024[44]	Supplementary Table 8
Soil	Fernandes et al., 2022[45]	Supplementary Table 9

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