LLNL-JRNL-2012610

Lawrence Livermore National Laboratory

Clarifying Terminology in Microbial Ecology: A Call for Precision in Scientific Communication

G Trubl, A Probst

October 2025

Environmental Microbiology

Disclaimer

This work performed under the auspices of the U.S. Department of Energy by Lawrence Livermore National Laboratory under Contract DE-AC52-07NA27344.

LLNL-JRNL-2012610

Clarifying Terminology in Microbial Ecology: A Call for Precision in Scientific Communication

Gareth Trubl[1,*] & Alexander J. Probst[2,*]

[1] Physical and Life Sciences Directorate, Lawrence Livermore National Laboratory, Livermore, CA, 94550, USA
[2] Environmental Metagenomics, Research Center One Health Ruhr of the University Alliance Ruhr, Faculty of Chemistry, University of Duisburg-Essen, Germany

*To whom the correspondence should be addressed: Trubl1@llnl.gov and alexander.probst@uni-due.de

Key words: Standardization, Microbiology, Virology, Microbiome, Definitions, Miscommunication, Evolution of Terms

Abstract

The rapid evolution of microbiology as a field of research has led to the introduction of new terminology and the adaptation of existing terms. However, inconsistencies in the use of these terms, including variations across different scientific disciplines, can lead to confusion and miscommunication within the scientific community. This article discusses the importance of precise terminology in microbiome research, highlighting examples where terms have been misused or redefined without clear justification. We also present a list of frequently used terms in microbial ecology along with their specific definitions. We argue that the misuse of terminology can hinder scientific progress by creating ambiguity and misunderstanding. To address this, we propose a set of guidelines for the consistent use of key terms and provide clear definitions for some of the most commonly misused or newly introduced terms in the field. The definitions provided herein will also function as a guide for young researchers new to the field of microbial ecology. Accurate and consistent use of terminology is crucial for effective communication and collaboration in microbiology research. By adhering to standardized definitions, researchers can ensure that their work is clearly communicated and contributes meaningfully to the progress of science.

Main

The semantics of scientific terms, including neologisms and redefinitions, are key to proper science communication. They can involve simple disputes, for example, about the plural of a certain term like phage or phages (Ackermann 2011) which do not alter the meaning of the message conveyed. However, neologisms like the introduction of the term ‘archaellum’ instead of ‘archaeal flagellum’ (Jarrell and Albers 2012), both referring to the same cellular surface structure, can result in extensive discussions (Wirth 2012). While the neologism was ultimately grandfathered in (Albers and Jarrell 2018), such discussions are necessary as they shape science and its communication among peers. While the evolution of the science language has generally been quite conservative in the past century, neologisms have become a trend in recent years, particularly during the ’omics era of biological sciences. The field of microbiology has also seen

significant advancements in recent years, accompanied by an influx of neologisms and the redefinition of existing terms. As microbiology increasingly intersects with other scientific disciplines, certain terms can take on different meanings depending on the context. While such evolution is a natural part of scientific progress, it also presents challenges in ensuring consistent communication across research communities. This article highlights the importance of precise and consistent use of microbiological terminology, particularly in cases where interdisciplinary variations exist. By examining key areas where terminology may be ambiguous or evolving, we aim to emphasize the value of clear definitions in maintaining the integrity and clarity of scientific discourse.

The Importance of Terminology in Microbiology and beyond

Precise terminology is the backbone of effective scientific communication. In microbiology, where new conceptual discoveries are constantly reshaping our understanding, the accurate use of terms is essential to avoid confusion and ensure that findings are properly interpreted. Moreover, as microbiology overlaps with fields such as ecology, genetics, and bioinformatics, certain terms may evolve or carry different meanings depending on the disciplinary context. Recognising and addressing these variations is crucial for interdisciplinary collaboration and knowledge dissemination. Beyond science communication via publications, proper metadata deposition is often key for driving data mining studies. While standards on metadata have been emphasised in the past (Cernava et al. 2022; Rimet et al. 2021), proper metadata terminology usage might sometimes be harder to achieve for metadata than for the actual data. To address this, the scientific community should engage with resources developed across disciplines. For example, the National Institutes of Health's National Human Genome Research Institute Talking Glossary of Genomic and Genetic Terms provides clear, standardised explanations of nearly 250 terms to support both public understanding and professional consistency (National Human Genome Research Institute, n.d.). Similarly, the National Institute of Standards and Technology's Bioeconomy Lexicon (National Institute of Standards and Technology, n.d.), developed through interagency collaboration, offers harmonised definitions for key bioeconomy concepts by standardising language across scientific, governmental and industrial sectors to facilitate communication, measurement development, and machine learning applications. Leveraging such resources, combined with cross-disciplinary collaboration, will strengthen metadata practices and promote consistency in terminology as microbial ecology continues to advance (Liu et al. 2024).

Efforts to improve terminology standardisation in microbiology are increasingly recognised as critical by the broader research community. For example, a recent editorial by the Senior Editors of Microbiome (Bindels et al. 2025) highlighted widespread misuse and confusion around foundational terms such as ‘microbiome’, ‘microbiota’, ‘16S rRNA gene amplicon sequencing’ and ‘metagenomics’, stressing that inaccurate language impedes understanding both within the scientific community and in communication with the public. Their call for precise, standardised usage of these and other terms aligns with the focus of this paper, highlighting that terminology is not just a semantic issue but a barrier to effective knowledge transfer, reproducibility and scientific progress. While their editorial does not function as a glossary, it

explicitly discusses the consequences of terminology misuse in the field, reinforcing the need for continued community-level efforts to establish clearer definitions and best practices.

Examples of Misused and Reinterpreted Terms

Scientific terminology is not static; it evolves as new discoveries are made and as different fields of study intersect. For example, the transition from alchemy to chemistry was accompanied by the introduction of new terms like ‘hydrogen’ (introduced as ‘hydrogène’; Lavoisier 1789). Similarly, in computer sciences, there exist multiple discrepancies when it comes to terminologies, yet systematizing terminology beyond object-oriented modelling was proposed for improving the clarification of terminology (Hasselbring 1997). In microbiology, this evolution can be seen in terms such as ‘microbiome’, ‘pathogen’ and ‘symbiosis’ which have taken on varied meanings in different contexts. For example, the term ‘microbiome’ sometimes refers to the collective genomes of microorganisms in a specific environment but is also frequently expanded to include the microorganisms themselves. One of the most common references, however, defines the human microbiome as ‘the totality of microbes, their genetic information, and the milieu in which they interact’ (Cho and Blaser 2012), which is very much in agreement with the environmental definition of microbiome (Berg et al. 2020). Such shifts in meaning are natural but can create confusion if not explicitly addressed in scientific discourse.

A notable example of terminology misuse is the application of the term ‘16S metagenomics’ where it is not accurate. While 16S rRNA gene surveys and other amplicon-based approaches are valuable for identifying microbes based on a marker gene and providing taxonomic insights, they do not represent metagenomics. Metagenomics involves sequencing all the DNA from a sample, enabling a comprehensive analysis that extends beyond identification and relative abundances of biological entities. This approach allows for in-depth exploration of genetic potential, including assessing codon usage bias, GC content and evaluating genome features (Chuckran et al. 2025). It also facilitates the detection of viruses and other mobile genetic elements, offering insights into microbial physiology, adaptation strategies and evolutionary history. The incorrect use of ‘16S metagenomics’ can cause confusion, particularly among early-career scientists and the general public, potentially hindering accurate understanding and learning.

Another example of terminology misuse refers to derivatives of the term ’omics itself, which means the application of one type of ’omics such as genomics to a pure culture. For the application of such ’omics techniques to communities of two or more biological entities, scientists introduced the prefix meta-, as in metagenomics, for the collective analysis of multiple genomes from a single sample (Rondon et al. 1998). When multiple different ’omics techniques are applied, scientists call such a combination multi’omics; however, it is not always clearly specified whether the data were generated from pure cultures or mixed communities. Strictly using the discrete definitions of ’omics, multi’omics, multi-omics, meta’omics, meta-omics or multi-meta’omics can substantiate clarity particularly when reading abstracts or reviews of extensive studies. The National Institute of Standards and Technology Bioeconomy Lexicon defines omics as the study of biomolecules within a cell or a cellular system and multi-omics as the combined analysis of multiple omics data types (National Institute of Standards and

Technology, n.d.), supporting the need for precise application of these terms in microbial ecology.

Consequently, we summarized frequently used terms in microbial ecology in Tables 1 and 2, differentiating taxonomy and name-related terminology from techniques and conceptual terminology in microbial ecology. One example relates to viruses infecting Prokaryotes, which are differentiated into bacteriophages (often abbreviated as phages) and archaeal viruses (Abedon and Murray 2013; Trubl et al. 2020), which is a consequence of the introduction of Archaea as a separate domain of life by Carl Woese and George Fox (Woese and Fox 1977). While the word phage originates from the Greek word 'phagein', meaning 'to eat' or 'to devour' (Chanishvili 2016), there are also other biological terms like macrophage that include the term 'phage'. Consequently, the term 'phage' should be avoided as an abbreviation for bacteriophages in at least interdisciplinary studies and when use to describe viruses it should refer exclusively to viruses that infect bacteria. This usage traces back to Félix d'Hérelle, who discovered bacteriophages in 1917 (d'Hérelle 1917) and pioneered phage therapy using these viruses to selectively target bacterial pathogens (d'Hérelle 1921; d'Hérelle 1926). To prevent confusion, phage should remain reserved for bacterial viruses, not archaeal viruses.

Another example relates to the concept of 'virome', which has been expanded to include multiple meanings, leading to inconsistencies in its application and prompting researchers to adopt new terminology. The term 'virome' has been used to refer both to a virus-targeted metagenomics approach and to all the viruses in a sample or system. This duality is notable given the history of the field. The work of Breitbart et al. (2002) marked a significant turning point, being the first to use shotgun metagenomic sequencing to characterize an entire viral community from an environmental sample. While that initial paper didn't explicitly use the word 'virome' to describe its methodology, it effectively laid the groundwork for the concept of studying the collective genetic material of viruses within a given environment, which is precisely what 'virome' came to represent in the context of metagenomics. Indeed, subsequent publications from the same research group (Angly et al. 2006), and others that followed, began to formally adopt and popularize the term 'virome' for these viral metagenomic datasets. Meanwhile, the definition of 'virome' as 'all the viruses in a sample or system' significantly overlaps with the term 'virosphere', which was originally coined for that broader meaning (Condit 2001; Mayo 2001). These variations, while reflecting the dynamic nature of scientific language, can cause misunderstandings if not clearly defined within each study's context. In an attempt to address this ambiguity, some researchers have introduced the term 'metaviromics' to specify that a 'virome' refers to viruses derived from a virus-targeted metagenome. However, rather than resolving confusion, this additional term has further complicated the terminology by introducing another layer of distinction that may not be necessary. Instead of clarifying the meaning of 'virome', it risks fragmenting the field's terminology further, making consistent communication more challenging.

The use of the term algae in relation to cyanobacteria is a more complex scenario. Historically, all unicellular and multicellular organisms capable of photosynthesis that do not belong to plants were unified in the term algae, although polyphyletic. However, cyanobacteria as photosynthetic microbes belong to the domain bacteria, while the rest are Eukaryotes. The debate about the inclusion of cyanobacteria in the term algae is still ongoing (Novis and Broady 2014; Garcia-Pichel et al. 2020). Further complicating the term, some organisms classified as

algae no longer perform photosynthesis but are believed to have once had this capacity (Suzuki et al. 2018). Given this confusion, we argue that the term algae should not contain cyanobacteria as there are also other prokaryotic phototrophs that are not included in this heterogeneous term (Imhoff 2021).

While science is interdisciplinary in nature, it can be very segmented, leading to terms evolving different meanings. A great example of this is the term 'virus-like particle' (VLP) which has been used for over 80 years, originally referring to particles resembling viruses in electron microscope images but lacking proven viral functionality. Over time, its meaning has diverged, with VLP now referring to either virus-sized particles with nucleic acids that could be functional viruses in viral ecology or to viral structures intentionally devoid of genomes in vaccine and biotechnology contexts (Hyman et al. 2021) (Table 1).

The Impact of Inconsistent Terminology

Inconsistent use of terminology can lead to misinterpretation of data, misalignment of research objectives, and challenges in cross-disciplinary collaboration. This is particularly problematic in an era where collaborative efforts across different fields are becoming increasingly common. For instance, a term defined in a genomic context may differ when used in ecological studies, potentially causing confusion among researchers from different backgrounds.

Proposing Guidelines for Terminology Use

To mitigate these issues, we propose a set of guidelines for the consistent use of key microbiology terms, while allowing for necessary interdisciplinary variations. These guidelines include:

- Standardized definitions: Adhering to widely accepted definitions within the microbiology community to maintain consistency.
- Contextual clarification: When terms have different meanings in various disciplines, clearly defining them within the context of each study.
- Avoiding unnecessary neologisms: Refraining from creating new terms without clear justification, unless they provide significant clarity or advancement.
- Use of glossaries: Encouraging the inclusion of glossaries in publications to clarify terminology for readers from diverse backgrounds.

By implementing these guidelines, researchers can enhance the clarity and precision of their communication, facilitating better understanding and collaboration across disciplines.

Encouraging Best Practices and community efforts

To mitigate the risks of miscommunication, we recommend that journals, reviewers and researchers adopt best practices for terminology usage. This includes providing clear definitions of key terms in manuscripts, being mindful of the potential for terms to be understood differently across disciplines and fostering an environment where questioning and refining terminology is encouraged. Additionally, educational efforts should be made to ensure that new and evolving

terms are understood by young scientists in classrooms as well as the broader scientific community.

Beyond the scientific community, we also appeal to companies and science communicators to present microbial ecology accurately to young scientists and the public. For example, the abovementioned term '16S metagenomics' which clearly is a neologism combining two very different technologies (16S rRNA gene sequencing and metagenomics) is heavily advertised by certain companies. Such marketing can result in the propagation of misleading terms in secondary literature and even within scientific discourse itself. While we are aware of specific companies and publications contributing to this confusion, we intentionally do not name them here, as our goal is not to point fingers but to raise awareness and promote greater clarity and consistency in the future. Therefore, raising awareness within the scientific community is equally important to ensure accurate science communication and prevent the misrepresentation of technologies and findings to broader audiences.

In addition to promoting proper terminology use in publications and outreach, the microbial ecology community should pursue consensus-building around new terms. Regular roundtables or workshops at international conferences, such as those organised by the International Society for Microbial Ecology, could help develop shared standards and incorporate diverse perspectives. We view this article as an appeal for the community to engage actively in setting clear, consistent terminology to support accurate science education and communication in the long term.

Conclusion

The use of consistent and accurate terminology, while acknowledging interdisciplinary variations, is vital for advancing the field of microbiology. Misuse or unclear definition of terms can create barriers to understanding and collaboration, ultimately hindering scientific progress. By adhering to standardized definitions, providing contextual clarifications and following proposed guidelines, researchers can contribute to a more cohesive and effective scientific discourse. This commitment to precise language ensures that all members of the scientific community, regardless of their disciplinary background, can engage in meaningful and productive exchanges of knowledge.

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and material

Not applicable

Competing interests

The authors declare that they have no competing interests.

Funding

This study was performed within the Collaborative Research Center (CRC) RESIST funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) – CRC 1439/1 and CRC 1439/2 – project number: 426547801. GT was supported by the U.S. Department of Energy Office of Biological and Environmental Research through the Genomic Science Program and the Lawrence Livermore National Laboratory "Microbes Persist" Soil Microbiome Scientific Focus Area (SCW1632). Work conducted by GT at LLNL was conducted under the auspices of the US Department of Energy under Contract DE-AC52-07NA27344.

Authors' contributions

GT and AJP conceptualized the study, performed literature research, and wrote the manuscript.

Acknowledgements

n/a

References

1. Abedon, S. T., and K. L. Murray. 2013. “Archaeal Viruses, Not Archaeal Phages: An Archaeological Dig.” Archaea 2013, no. 1: 251245.
2. Ackermann, H. W. 2011. “Phage or Phages.” Bacteriophage 1, no. 1: 52–53.
3. Albers, S. V., and K. F. Jarrell. 2018. “The Archaellum: An Update on the Unique Archaeal Motility Structure.” Trends in Microbiology 26, no. 4: 351–362.
4. Angly, F. E., B. Felts, M. Breitbart, et al. 2006. “The Marine Viromes of Four Oceanic Regions.” PLoS Biology 4, no. 11: e368.
5. Berg, G., D. Rybakova, D. Fischer, et al. 2020. “Microbiome Definition Re-Visited: Old Concepts and New Challenges.” Microbiome 8: 1–22.
6. Bindels, L. B., J. E. Watts, K. R. Theis, et al. 2025. “A Blueprint for Contemporary Studies of Microbiomes.” Microbiome 13, no. 1: 1–9.
7. Breitbart, M., P. Salamon, B. Andresen, et al. 2002. “Genomic Analysis of Uncultured Marine Viral Communities.” Proceedings of the National Academy of Sciences 99, no. 22: 14250–14255.
8. Cernava, T., D. Rybakova, F. Buscot, et al. 2022. “Metadata Harmonization–Standards Are the Key for a Better Usage of Omics Data for Integrative Microbiome Analysis.” Environmental Microbiomes 17, no. 1: 33.
9. Chanishvili, N. 2016. “Bacteriophages as Therapeutic and Prophylactic Means: Summary of the Soviet and Post Soviet Experiences.” Current Drug Delivery 13, no. 3: 309–323.
10. Cho, I., and M. J. Blaser. 2012. “The Human Microbiome: At the Interface of Health and Disease.” Nature Reviews Genetics 13, no. 4: 260–270.
11. Chuckran, P. F., K. Estera-Molina, A. M. Nicolas, et al. 2025. “Codon Bias, Nucleotide Selection, and Genome Size Predict In Situ Bacterial Growth Rate and Transcription in Rewetted Soil.” Proceedings of the National Academy of Sciences of the United States of America 122, no. 3: e2413032122.
12. Condit, R. C. 2001. “Principles of Virology.” In Fields Virology, vol. 1. ASM Press.
13. d'Hérelle, F. 1917. Sur Un Microbe Invisible Antagoniste Des Bacilles.
14. d’Hérelle, F. 1921. Le bacteriophage. La Nature (Paris). 49: 219–222.
15. d’Hérelle, F. 1926. Le Bactériophage et Son Comportement. Paris: et Cie.

16. Garcia-Pichel, F., J. P. Zehr, D. Bhattacharya, and H. B. Pakrasi. 2020. “What's in a Name? The Case of Cyanobacteria.” Journal of Phycology 56, no. 1: 1–5.
17. Hasselbring, W. 1997. “Technical Opinion: On Defining Computer Science Terminology.” Communications of the ACM 40, no. 5: 97–98.
18. Hyman, P., G. Trubl, and S. T. Abedon. 2021. “Virus-Like Particle: Evolving Meanings in Different Disciplines.” Therapy, Applications, and Research 2, no. 1: 11–15.
19. Imhoff, J. F. 2021. “Editorial for the Special Issue: Advances in the Biology of Phototrophic Bacteria.” Microorganisms 9, no. 10: 2119.
20. Jarrell, K. F., and S. V. Albers. 2012. “The Archaellum: An Old Motility Structure With a New Name.” Trends in Microbiology 20, no. 7: 307–312.
21. Lavoisier, A. L. 1789. Traité élémentaire de Chimie (Elementary Treatise of Chemistry). Cuchet.
22. Liu, R., J. Mao, G. Li, and Y. Cao. 2024. “Characterizing Structure of Cross-Disciplinary Impact of Global Disciplines: A Perspective of the Hierarchy of Science.” Journal of Data and Information Science 9: 53–81.
23. Mayo, M. A. 2001. “Report of the 29th Meeting of the Executive Committee of the International Committee on Taxonomy of Viruses (ICTV).” Archives of Virology 146, no. 7: 1437–1439.
24. National Human Genome Research Institute. n.d. Talking Glossary of Genomic and Genetic Terms Accessed July 14, 2025. https:// www. genome. gov/ genet ics-gloss ary# O.
25. National Institute of Standards and Technology. n.d. NIST Bioeconomy Lexicon Accessed July 14, 2025. https:// www. nist. gov/ biosc ience/ nist-bioec onomy -lexicon.
26. Novis, P., and P. Broady. 2014. “Reclaiming the Term Algae for the Cyanobacteria.” New Zealand Journal of Botany 52, no. 4: 446–448.
27. Rimet, F., E. Aylagas, A. Borja, et al. 2021. Metadata Standards and Practical Guidelines for Specimen and DNA Curation When Building Barcode Reference Libraries for Aquatic Life.
28. Rondon, M. R., J. Handelsman, R. M. Goodman, J. Clardy, and S. F. Brady. 1998. “Cloning the Soil Metagenome: A Strategy for Accessing the Genetic and Functional Diversity of Uncultured Microorganisms.” Proceedings of the National Academy of Sciences of the United States of America 95, no. 11: 6566–6571.
29. Suzuki, S., R. Endoh, R. I. Manabe, M. Ohkuma, and Y. Hirakawa. 2018. “Multiple Losses of Photosynthesis and Convergent Reductive Genome Evolution in the Colourless Green Algae Prototheca.” Scientific Reports 8, no. 1: 940.
30. Trubl, G., P. Hyman, S. Roux, and S. T. Abedon. 2020. “Coming-Of- Age Characterization of Soil Viruses: A User's Guide to Virus Isolation, Detection Within Metagenomes, and Viromics.” Soil Systems 4, no. 2: 23.
31. Wirth, R. 2012. “Response to Jarrell and Albers: Seven Letters Less Does Not Say More.” Trends in Microbiology 20, no. 11: 511–512.
32. Woese, C. R., and G. E. Fox. 1977. “Phylogenetic Structure of the Prokaryotic Domain: The Primary Kingdoms.” Proceedings of the National Academy of Sciences 74, no. 11: 5088–5090.

338 33. Xu, X., and W. Liu. 2017. “The Global Distribution of Earth's Critical Zone and Its
339 Controlling Factors.” Geophysical Research Letters 44, no. 7: 3201–3208.

340 Table 1. Frequently used taxonomic and name-related terms in microbial ecology and potential sources of confusion.

Term	Definition	Do not confound with	Explanation of related/confounded term	NIST/NIH Definition
Algae	Unicellular or multicellular, non-flowering aquatic eukaryotes.	Cyanobacteria	Photosynthetic bacteria; once grouped with algae as "blue-green algae" but now recognized as Bacteria.	
Archaea	A domain of single-celled microorganisms distinct from Bacteria and Eukarya.	Archaebacteria	Outdated term for archaea.	
Archaeal viruses	Viruses infecting archaea, previously grouped as bacteriophages but now recognized separately.	Bacteriophage / phage	Viruses infecting bacteria only.	
Cyanobacteria	Phylogenetic lineage of Bacteria capable of oxygenic photosynthesis.	Algae; blue-green algae	Algae are eukaryotic and may not be able to perform photosynthesis	
Eubacteria	Outdated term for Bacteria, but still found in probe names (e.g., EUB338).	Bacteria	Modern term encompassing all bacterial lineages.	
Key species	Species (often abundant) playing essential roles in ecosystems.	Keystone species	Species typically of low abundance but exerting disproportionate ecosystem effects.	
Microbe	Any microscopic biological entity (e.g., bacteria, archaea, protists, viruses) so small it cannot be observed by naked eye and necessitates a microscopy of any type for visualization.	Microorganism	Restricted to cellular entities, excluding viruses.	

Microbiome	Totality of microbial communities (bacteria, archaea, viruses, protists) and their environment in a sample, encompassing both genetic and functional information.	Microbiota	The viable microbial community present in a sample.	NIH: The microbiome is the community of microorganisms (such as fungi, bacteria and viruses) that exists in a particular environment. In humans, the term is often used to describe the microorganisms that live in or on a particular part of the body, such as the skin or gastrointestinal tract. These groups of microorganisms are dynamic and change in response to a host of environmental factors, such as exercise, diet, medication and other exposures.
Protist	Diverse, mostly unicellular eukaryotic organisms not classified as animals, plants, or fungi.	Protozoa	A specific group of protists, often referred to as animal-like protists.	
Virosphere	The totality of viruses in an environment, including those infecting all domains of life.	Virome	A targeted metagenome that collects genetic material from the virus size fraction.	

347 Table 2. Frequently used technical and conceptual terms in microbial ecology and potential sources of confusion.

Term	Definition	Do not confound with	Explanation of related/confounded term	NIST/NIH Definition
Aerobic / Anaerobic	Organismal lifestyles dependent on presence (aerobic) or absence (anaerobic) of oxygen.	Oxic / Anoxic	Environmental conditions of oxygen presence or absence, respectively.	
Amplicon analysis	Sequencing and analysis of PCR-amplified marker genes from mixed populations.	Metagenomics	Untargeted shotgun sequencing, covering entire genomes.	
Barcode	Short, standardized marker gene (e.g., rRNA gene) used for identifying organisms.	Barcode (of primers)	Short nucleotide sequences used as identifiers in multiplex sequencing reactions.	
Chronic infections	Viral infection cycles where host cells continuously release virions without undergoing cell lysis.	Lytic infection; Lysogenic infection; Pseudolysogenic infection; dormant	Lytic infection kills host immediately; lysogenic infection integrates into host genome or plasmid; pseudolysogenic persists without integration or active replication; dormant maintains ability to perfrom infection and no other activity.	
Community analysis	Analysis of microbial diversity, structure, or composition from environmental samples.	Population genomics	Focused on genetic diversity within a single species or population.	

Core microbiome	Genetic and taxonomic features consistently shared across multiple samples (cutoffs for sharing are arbitrary, however).	Core microbiota	Focused only on viable organisms.	
Cultureomics	High-throughput cultivation approaches for isolating microbial diversity.	Culturomics (in social sciences)	Originally a term in sociology (existed around 1960s); now repurposed for microbial ecology.	
Critical zone	Earth's near-surface zone, extending from vegetation canopy through soil and groundwater to bedrock (~0.7 to 223.5 meters depth; (Xu and Liu, 2017).	Surface ecosystems	Excludes deeper subsurface environments.	
Environmental genomics	Analysis of DNA from environmental samples; may refer to metagenomics or the recovery of MAGs or SAGs.	Metagenomics; Genomics of metagenome-assembled genomes or single amplified genomes (MAGs / SAGs)	Metagenomics is untargeted sequencing; MAGs/SAGs refer to genomes reconstructed from metagenomes or single cells.	
Indicator species	Species signaling ecological change or ecosystem health.	Sentinel species	Sentinel species specifically relate to hazards for human health.	
Lysogenic	The infection cycle of temperate viruses that are integrated into the host and can become virulent.	Temperate	Temperate viruses can use lysogenic or lytic infection cycles.	

Lytic	The infection cycle that can be done by virulent and temperate viruses, during which host machineries are hijacked for reproducing the virus resulting in host lysis and viral release.	Virulent	Virulent viruses use the lytic infection cycle to reproduce.	
Meta-omics / Meta‘omics	Application of omics techniques (genomics, transcriptomics, proteomics, etc.) to mixed biological communities.	Omics / ‘omics /multi-omics	The application of one or multiple methods characterizing an isolate.	
Metabolomics	Analysis of metabolites from a pure culture.	Meta-metabolomics	Analysis of metabolites from environmental samples or mixed communities.	NIST: The study of all or a significant portion of metabolites within an organism or biological material
Metacommunity	Assemblage of multiple biological communities connected across space or time.	Local community	A single population or community in a defined site.	

Metagenomics	Untargeted sequencing of environmental DNA, followed by genome- or gene-centric analyses.	Amplicon sequencing; 16S rRNA gene sequencing	Amplicon sequencing targets specific genes; metagenomics captures entire genomic information.	NIST: The study of nucleic acids and their function(s) from all or a significant portion of the organisms within a collection. NIH: Metagenomics is the study of the structure and function of entire nucleotide sequences isolated and analyzed from all the organisms (typically microbes) in a bulk sample. Metagenomics is often used to study a specific community of microorganisms, such as those residing on human skin, in the soil or in a water sample.
Meta-metabolomics	Analysis of metabolites from mixed communities or environmental samples.	Metabolomics	From pure cultures.	
Metaviromics	Redundant term for "viromics"; refers to viral metagenomics.	Viromics	Standard term for sequencing viral DNA/RNA fraction from environmental samples.	

MiSeq	Short-read sequencing platform by Illumina.	Long-read sequencing	A DNA sequencing technique that generates much longer DNA or RNA sequences (typically thousands of base pairs); long-read platforms (e.g., PacBio, Nanopore) produce longer reads.	NIH for long-read sequencing: DNA sequencing technologies determine the order of the base pairs in fragments of DNA known as “reads”. Scientists must then piece these reads together to assemble the sequences of full chromosomes. While some sequencing technologies produce reads that are only a few 100 nucleotides long, some methods can generate reads that are thousands to hundreds of thousands of nucleotides long known as long-read DNA sequencing. These long reads are easier to assemble because the sequence is broken into fewer fragments.
Mobilome	Totality of mobile genetic elements (plasmids, transposons, viruses) in a sample.	Virome	A targted metagenome of the virus size fraction.	

Omics / ‘Omics / Multi-omics	Application of large-scale molecular approaches (genomics, transcriptomics, proteomics) to single organisms.	Meta-omics / Multi meta-omics	Meta-omics applies omics methods to mixed populations.	NIST: Refers to combined information derived from data, analysis, and interpretation of multiple omics measurement technologies to identify or analyze the roles, relationships, and functions of biomolecules (including nucleic acids, proteins, metabolites) that make up a cell or cellular system. Omics are disciplines in biology that include genomics, transcriptomics, proteomics, and metabolomics
Opportunistic pathogen	Microorganisms that typically do not cause disease but can become pathogenic under certain conditions.	Pathogen	Organisms consistently associated with disease.	
Oxic / Anoxic	Environmental conditions of oxygen presence or absence.	Aerobic / Anaerobic	Refers to organismal metabolisms rather than environmental conditions.	
Phylogenomics	Phylogenetic analysis based on whole-genome data.	Multi-locus sequence analysis (MLSA)	Uses several conserved genes rather than whole genomes.	

Probe	Short oligonucleotide sequence used for detection or amplification of specific nucleic acid targets (e.g., primer in PCR).	Sample	Biological material from which nucleic acids are extracted.	
Pseudolysogenic virus	Virus persisting inside host without genome integration or lytic activity; can switch to lytic.	Lysogenic infection	An infection cycle done by temperate viruses where they integrate into the host genome or plasmid.	
Quasispecies	Collection of genetically related viral variants within a population, particularly in RNA viruses.	Population	More general term referring to a group of organisms or viruses defined in a specific manner (e.g., all viruses in a sample or all viruses sharing a speficic nucleotide identifty).	
rDNA	Ribosomal DNA; frequently used as synonym for rRNA gene, yet incorrect as there is no ribosome DNA (i.e. DNA in ribosomes).	rRNA gene	Gene encoding ribosomal RNA. Marker gene (e.g., 16S/18S rRNA gene) used for phylogenetic or taxonomic analyses.	
Replication rate	Frequency of organism reproduction or viral replication, typically expressed per unit time.	Growth rate	Sometimes used interchangeably, but "growth rate" may refer to increase in biomass or population size, not just reproduction events.	
Resilience	The capacity of a microbial community or biological entity to recover after disturbance.	Resistance	Resistance refers to the ability to withstand disturbance without changing.	

Suboxic	Environmental condition with low oxygen levels, between oxic and anoxic.	Oxic; Anoxic	Oxic: oxygen present; Anoxic: oxygen absent.	
Synteny	Conserved gene order along a genome or chromosome.	Gene similarity	Refers to gene sequence similarity, not gene order.	
Taxonomy	Science of classifying organisms based on shared characteristics and evolutionary relationships.	Classification; Naming	Classification refers to grouping organisms; naming (nomenclature) is the assignment of names following taxonomic rules.	
Temperate	Viruses capable of lysogenic infection or lytic i.	Lysogenic	An infection cycle used by temperate viruses.	
Virulent	Viruses with strictly lytic infection cycles.	Lytic	An infection cycle that is used by virulent viruses and temperate viruses.	

348