

References

1. Kaye J, Heeney C, Hawkins N, De Vries J, Boddington P. Data sharing in genomics—re-shaping scientific practice. *Nat Rev Genet.* 2009;10: 331–335.
2. Maxmen A. One million coronavirus sequences: popular genome site hits mega milestone. *Nature.* 2021;593: 21. doi:10.1038/d41586-021-01069-w
3. Colavizza G, Hrynaskiewicz I, Staden I, Whitaker K, McGillivray B. The citation advantage of linking publications to research data. *PLoS One.* 2020;15: e0230416. doi:10.1371/journal.pone.0230416
4. Langille MGI, Ravel J, Fricke WF. “Available upon request”: not good enough for microbiome data! *Microbiome.* 2018;6: 8. doi:10.1186/s40168-017-0394-z
5. Kozlov M. NIH issues a seismic mandate: share data publicly. *Nature.* 2022;602: 558–559. doi:10.1038/d41586-022-00402-1
6. Collins FS, Tabak LA. Policy: NIH plans to enhance reproducibility. *Nature.* 2014;505: 612–613. doi:10.1038/505612a
7. Christian T-M, Gooch A, Vision T, Hull E. Journal data policies: Exploring how the understanding of editors and authors corresponds to the policies themselves. *PLoS One.* 2020;15: e0230281. doi:10.1371/journal.pone.0230281
8. Fenner M, Crosas M, Grethe JS, Kennedy D, Hermjakob H, Rocca-Serra P, et al. A data citation roadmap for scholarly data repositories. *Sci Data.* 2019;6: 28. doi:10.1038/s41597-019-0031-8

9. Cousijn H, Kenall A, Ganley E, Harrison M, Kernohan D, Lemberger T, et al. A data citation roadmap for scientific publishers. *Sci Data*. 2018;5: 180259. doi:10.1038/sdata.2018.259
10. Hodson S, Molloy L. Current best practice for research data management policies. CODATA; 2014. Available: <https://apo.org.au/sites/default/files/resource-files/2014-05/apo-nid58192.pdf>
11. Altman M Director o, Borgman C Professor, Crosas M Director o, Matone M Co-Directo. An introduction to the joint principles for data citation. *Bull Am Soc Inf Sci*. 2015;41: 43–45. doi:10.1002/bult.2015.1720410313
12. Data Citation Synthesis Group. Joint declaration of data citation principles. *Force11*; 2014. doi:10.25490/a97f-egyk
13. Schloss PD. Identifying and Overcoming Threats to Reproducibility, Replicability, Robustness, and Generalizability in Microbiome Research. *MBio*. 2018;9. doi:10.1128/mBio.00525-18
14. Ravel J, Wommack KE. All hail reproducibility in microbiome research. *Microbiome*. 2014;2: 8. doi:10.1186/2049-2618-2-8
15. Wilkinson MD, Dumontier M, Aalbersberg IJJ, Appleton G, Axton M, Baak A, et al. The FAIR Guiding Principles for scientific data management and stewardship. *Sci Data*. 2016;3: 160018. doi:10.1038/sdata.2016.18
16. Silvello G. Theory and practice of data citation. *J Assoc Inf Sci Technol*. 2018;69: 6–20. doi:10.1002/asi.23917

17. Starr J, Castro E, Crosas M, Dumontier M, Downs RR, Duerr R, et al. Achieving human and machine accessibility of cited data in scholarly publications. *PeerJ Comput Sci.* 2015;1. doi:10.7717/peerj-cs.1
18. National Research Council, Policy and Global Affairs, Board on Research Data and Information. *For Attribution: Developing Data Attribution and Citation Practices and Standards: Summary of an International Workshop.* National Academies Press; 2012. Available: <https://play.google.com/store/books/details?id=-CF1AgAAQBAJ>
19. Langham-Putrow A, Bakker C, Riegelman A. Is the open access citation advantage real? A systematic review of the citation of open access and subscription-based articles. *PLoS One.* 2021;16: e0253129. doi:10.1371/journal.pone.0253129
20. Shilatifard A, Yeagle P. Editorial expression of concern. *Sci Adv.* 2021;7. doi:10.1126/sciadv.abh0587
21. Integrative HMP (iHMP) Research Network Consortium. The Integrative Human Microbiome Project. *Nature.* 2019;569: 641–648. doi:10.1038/s41586-019-1238-8
22. Ding T, Schloss PD. Dynamics and associations of microbial community types across the human body. *Nature.* 2014;509: 357–360. doi:10.1038/nature13178
23. Sze MA, Schloss PD. Looking for a Signal in the Noise: Revisiting Obesity and the Microbiome. *MBio.* 2016;7. doi:10.1128/mBio.01018-16
24. Sze MA, Schloss PD. Leveraging Existing 16S rRNA Gene Surveys To Identify Reproducible Biomarkers in Individuals with Colorectal Tumors. *MBio.* 2018;9. doi:10.1128/mBio.00630-18

25. Sovacool KL, Westcott SL, Mumphrey MB, Dotson GA, Schloss PD. OptiFit: an Improved Method for Fitting Amplicon Sequences to Existing OTUs. *mSphere*. 2022;7: e0091621. doi:10.1128/msphere.00916-21
26. Amann RI, Baichoo S, Blencowe BJ, Bork P, Borodovsky M, Brooksbank C, et al. Toward unrestricted use of public genomic data. *Science*. 2019;363: 350–352. doi:10.1126/science.aaw1280
27. Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, et al. Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Appl Environ Microbiol*. 2009;75: 7537–7541. doi:10.1128/AEM.01541-09
28. Yilmaz P, Kottmann R, Field D, Knight R, Cole JR, Amaral-Zettler L, et al. Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. *Nat Biotechnol*. 2011;29: 415–420. doi:10.1038/nbt.1823
29. Mirzayi C, Renson A, Genomic Standards Consortium, Massive Analysis and Quality Control Society, Zohra F, Elsafoury S, et al. Reporting guidelines for human microbiome research: the STORMS checklist. *Nat Med*. 2021;27: 1885–1892. doi:10.1038/s41591-021-01552-x
30. Lapp Z, Sovacool KL, Lesniak N, King D, Barnier C, Flickinger M, et al. Developing and deploying an integrated workshop curriculum teaching computational skills for reproducible research. *J Open Source Educ*. 2022;5. doi:10.21105/jose.00144

31. Hagan AK, Lesniak NA, Balunas MJ, Bishop L, Close WL, Doherty MD, et al. Ten simple rules to increase computational skills among biologists with Code Clubs. PLoS Comput Biol. 2020;16: e1008119. doi:10.1371/journal.pcbi.1008119
32. Schloss PD. The Riffomonas Reproducible Research Tutorial Series. J Open Source Educ. 2018;1. doi:10.21105/jose.00013
33. Westcott SL, Schloss PD. OptiClust, an Improved Method for Assigning Amplicon-Based Sequence Data to Operational Taxonomic Units. mSphere. 2017;2. doi:10.1128/mSphereDirect.00073-17
34. Schloss PD. A high-throughput DNA sequence aligner for microbial ecology studies. PLoS One. 2009;4: e8230. doi:10.1371/journal.pone.0008230
35. Hannigan GD, Duhaime MB, Koutra D, Schloss PD. Biogeography and environmental conditions shape bacteriophage-bacteria networks across the human microbiome. PLoS Comput Biol. 2018;14: e1006099. doi:10.1371/journal.pcbi.1006099
36. Gevers D, Pop M, Schloss PD, Huttenhower C. Bioinformatics for the Human Microbiome Project. PLoS Comput Biol. 2012;8: e1002779. doi:10.1371/journal.pcbi.1002779
37. Schloss PD, Gevers D, Westcott SL. Reducing the effects of PCR amplification and sequencing artifacts on 16S rRNA-based studies. PLoS One. 2011;6: e27310. doi:10.1371/journal.pone.0027310
38. Abubucker S, Segata N, Goll J, Schubert AM, Izard J, Cantarel BL, et al. Metabolic

reconstruction for metagenomic data and its application to the human microbiome.

PLoS Comput Biol. 2012;8: e1002358. doi:10.1371/journal.pcbi.1002358

39. Jumpstart Consortium Human Microbiome Project Data Generation Working Group.

Evaluation of 16S rDNA-based community profiling for human microbiome research. PLoS One. 2012;7: e39315. doi:10.1371/journal.pone.0039315

40. Human Microbiome Project Consortium. A framework for human microbiome research. Nature. 2012;486: 215–221. doi:10.1038/nature11209

41. Human Microbiome Project Consortium. Structure, function and diversity of the healthy human microbiome. Nature. 2012;486: 207–214. doi:10.1038/nature11234

42. Schloss PD. Preprinting Microbiology. MBio. 2017;8. doi:10.1128/mBio.00438-17

43. Hagan AK, Topçuoğlu BD, Gregory ME, Barton HA, Schloss PD. Women Are Underrepresented and Receive Differential Outcomes at ASM Journals: a Six-Year Retrospective Analysis. MBio. 2020;11. doi:10.1128/mBio.01680-20

44. Schloss PD, Junior M, Alvania R, Arias CA, Baumler A, Casadevall A, et al. The ASM Journals Committee Values the Contributions of Black Microbiologists. J Virol. 2020;94. doi:10.1128/JVI.01473-20

45. Topçuoğlu BD, Lapp Z, Sovacool KL, Snitkin E, Wiens J, Schloss PD. mikropml: User-Friendly R Package for Supervised Machine Learning Pipelines. J Open Source Softw. 2021;6. doi:10.21105/joss.03073

46. Topçuoğlu BD, Lesniak NA, Ruffin MT 4th, Wiens J, Schloss PD. A Framework for

Effective Application of Machine Learning to Microbiome-Based Classification

Problems. MBio. 2020;11. doi:10.1128/mBio.00434-20