

Additional Readings

General papers on microbial diversity or methods to assess microbial diversity:

- Hughes, J. B., Hellmann, J. J., Ricketts, T. H., & Bohannan, B. J. M. (2001). MINIREVIEW Counting the Uncountable : Statistical Approaches to Estimating Microbial Diversity, *67*(10), 4399–4406.
<https://doi.org/10.1128/AEM.67.10.4399>
- Konopka, A. (2009). What is microbial community ecology? *The ISME Journal*, *3*(11), 1223–30.
<https://doi.org/10.1038/ismej.2009.88>
- Pace, N. R. (1997). A Molecular View of Microbial Diversity and the Biosphere. *Science*, *276*(5313), 734–740.
<https://doi.org/10.1126/science.276.5313.734>
- Pernthaler, J. (2017). Competition and niche separation of pelagic bacteria in freshwater habitats. *Environmental Microbiology*. Doi: 10.1111/1462-2920.13742
- Su, C., Lei, L., Duan, Y., Zhang, K. Q., & Yang, J. (2012). Culture-independent methods for studying environmental microorganisms: Methods, application, and perspective. *Applied Microbiology and Biotechnology*, *93*(3), 993–1003. <https://doi.org/10.1007/s00253-011-3800-7>

Metagenomics and 16S rRNA sequencing papers:

- Huse, S. M., Dethlefsen, L., Huber, J. A., Welch, D. M., Relman, D. A., & Sogin, M. L. (2008). Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. *PLoS Genetics*, *4*(11).
<https://doi.org/10.1371/journal.pgen.1000255>
- Ghurye, J. S., & Pop, M. (2016). Metagenomic Assembly : Overview, Challenges and Applications, *89*, 353–362
- Quince, C., Walker, A.W., Simpson, J.T., Loman, N.J., and Segata, N. (2017) Shotgun metagenomics, from sampling to analysis. *Nat. Biotechnol.* *35*: 833–844.
- Riesenfeld, C. S., Schloss, P. D., & Handelsman, J. (2004). Metagenomics: Genomic Analysis of Microbial Communities. *Annual Review of Genetics*, *38*(1), 525–552.
<https://doi.org/10.1146/annurev.genet.38.072902.091216>
- Sharpton, T.J. (2014) An introduction to the analysis of shotgun metagenomic data. *Front. Plant Sci.* *5*: 1–14.
- Shendure, J., & Ji, H. (2008). Next-generation DNA sequencing. *Nature Biotechnology*, *26*(10), 1135–1145.
<https://doi.org/10.1038/nbt1486>
- Wooley, J.C., Godzik, A., and Friedberg, I. (2010) A primer on metagenomics. *PLoS Comput. Biol.* *6*..

Microbial (bacteria, phytoplankton) ecology papers, lake focus:

- Ávila, M. P., Staehr, P. A., Barbosa, F. A. R., Chartone-Souza, E., & Nascimento, A. M. A. (2017). Seasonality of freshwater bacterioplankton diversity in two tropical shallow lakes from the Brazilian Atlantic Forest. *FEMS Microbiology Ecology*, *93*(1). <https://doi.org/10.1093/femsec/fiw218>
- Hampton, S.E., E Galloway, A.W., Powers, S.M., Ozersky, T., Woo, K.H., Batt, R.D., et al. (2016) Ecology under lake ice. *Ecol. Lett.* 98–111.
- Newton, R.J., Jones, S.E., Eiler, A., McMahon, K.D., and Bertilsson, S. (2011) A guide to the natural history of freshwater lake bacteria.

Measuring microbial activity:

- Singer, E., Wagner, M. and Woyke, T. (2017). Capturing the genetic makeup of the active microbiome in situ. *The ISME journal*. doi:10.1038/ismej.2017.59
- Radajewski, S., McDonald, I.R. and Murrell, J.C. (2003). Stable-isotope probing of nucleic acids: a window to the function of uncultured microorganisms. *Current opinion in Biotechnology*.
[https://doi.org/10.1016/S0958-1669\(03\)00064-8](https://doi.org/10.1016/S0958-1669(03)00064-8)