**Annotated Bibliography CG2 Lina Raubold**

Lu, J., Rincon, N., Wood, D. E., Breitwieser, F. P., Pockrandt, C., Langmead, B., Salzberg, S. L. & Steinegger, M. (2022). Metagenome analysis using the Kraken software suite. *Nature protocols*, *17*(12), 2815-2839.

*Great walk-through for using kraken2 and bracken for metagenomic analyses followed by Pavian for data visualization.*

Madison, J. D., LaBumbard, B. C., & Woodhams, D. C. (2023). Shotgun metagenomics captures more microbial diversity than targeted 16S rRNA gene sequencing for field specimens and preserved museum specimens. *Plos one*, *18*(9), e0291540.

*The authors of this study compare metagenomics (medium-depth shotgun sequencing) and metabarcoding (16S) for both fresh specimens and museum specimens. Metagenomic analyses resulted in higher predicted diversity than metabarcoding analyses. This difference was even more pronounced in museum specimens compared to fresh specimens. The authors further demonstrate the effect of reference databases and sequencing methods on the predicted diversity and community diversity metrics (alpha- and beta-diversity).*

Moore, G., Tessler, M., Cunningham, S. W., Betancourt, J., & Harbert, R. (2020). Paleo‐metagenomics of North American fossil packrat middens: Past biodiversity revealed by ancient DNA. *Ecology and Evolution*, *10*(5), 2530-2544.

*Metagenomic analyses of fossil packrat middens reveal changes in ecosystem assemblages through time for vascular plants. Next to vascular plants, ascomycete fungi, arthropods, chordates, nematodes could be identified among other eukaryotic taxa as well as microbiota. Metagenomics outperformed amplicon sequencing by far. Taxonomic resolution of shotgun metagenomics was more or less consistent with morphological identification of microfossils.*

Serite, C. P., Emami-Khoyi, A., Ntshudisane, O. K., James, N. C., Jansen van Vuuren, B., Bodill, T., Cowley, P. D., Whitfield, A. K. & Teske, P. R. (2023). eDNA metabarcoding vs metagenomics: an assessment of dietary competition in two estuarine pipefishes. *Frontiers in Marine Science*, *10*, 1116741.

*This study is a nice case example showcasing how metagenomics can be used as a non-invasive approach of diet monitoring in conservation biology. The authors extracted DNA from two pipefish feces, one of which is critically endangered, and compared the taxonomic resolution and inferred dietary composition between targeted metabarcoding and untargeted metagenomic analyses, with metagenomics outperforming metabarcoding. The taxonomic resolution of metabarcoding analyses was much lower, most likely due to an amplification bias.*