**Community analysis by metabarcoding and metagenomics**

Metabarcoding describes the targeted PCR amplification and next generation sequencing of short DNA barcode markers (typically ~300-500 bp) from community samples (Ji et al. 2013; Yu et al. 2012). The resulting amplicon sequences are clustered into operational taxonomic units (OTUs), based on sequence similarity and compared to reference databases for taxonomic assignment. Even minute traces of taxa in environmental samples can be detected using metabarcoding (Bohmann et al. 2014). At the same time, amplicon sequencing is cheap, requires a small workload and thus allows rapid inventories of species composition and species interactions in whole ecosystems (Gibson et al. 2014; Leray & Knowlton 2015, Pompanon et al. 2012). However, the phylogenetic resolution offered by short barcode markers is limited. And the preferential amplification of some taxa during PCR can lead to highly skewed abundance estimates (Elbrecht & Leese 2015) or the complete loss of some taxa (Yu et al. 2012) from metabarcoding libraries. Recent work (Saitoh et al. 2016) suggests the application of taxon specific read abundance correction factors to account for amplification bias and derive accurate estimates for taxa from amplicon sequencing data.

Metagenomic approaches, in contrast, avoid marker specific amplification bias by sequencing libraries constructed either from untreated genomic DNA (Dodsworth 2015; Linard et al. 2015; Tang et al. 2014), or after targeted enrichment of genomic regions (Liu et al. 2016). While being more laborious, expensive and computationally demanding than metabarcoding, metagenomics thus offers improved accuracy in detecting species composition and abundance (Zhou et al. 2013). Moreover, the assembly of high coverage metagenomic datasets recovers large contiguous sequence stretches, even from rare members in a community, offering high phylogenetic resolution at the whole community level (Coissac et al. 2016). Due to large genome sizes and high genomic complexity, metazoan metagenomics is currently mostly limited to the assembly of fairly short high copy regions. Particularly mitochondrial and chloroplast genomes as well as nuclear ribosomal clusters are popular targets (Dodsworth 2015; Coissac et al. 2016). In contrast, microbial metagenomic studies now routinely assemble complete genomes and characterize gene content and metabolic pathways even from complex communities (Nielsen et al. 2014). This allows unprecedented insights into functional genetic process underlying community assembly and evolutionary change of communities to environmental stress.

**References**

|  |
| --- |
|  |
|  |

Bohmann, Kristine, Alice Evans, M. Thomas P. Gilbert, Gary R. Carvalho, Simon Creer, Michael Knapp, Douglas W. Yu, und Mark de Bruyn. Environmental DNA for wildlife biology and biodiversity monitoring. *Trends in Ecology & Evolution* 29, Nr. 6 (Juni 2014): 358–67. doi:10.1016/j.tree.2014.04.003.

Coissac, Eric, Peter M. Hollingsworth, Sébastien Lavergne, und Pierre Taberlet. From Barcodes to Genomes: Extending the Concept of DNA Barcoding. *Molecular Ecology* 25, Nr. 7 (1. April 2016): 1423–28. doi:10.1111/mec.13549.

Dodsworth, S. (2015). Genome skimming for next-generation biodiversity analysis. *Trends in plant science*, *20*(9), 525-527.

Elbrecht, Vasco, und Florian Leese. Can DNA-Based Ecosystem Assessments Quantify Species Abundance? Testing Primer Bias and Biomass—Sequence Relationships with an Innovative Metabarcoding Protocol. *PLOS ONE* 10, Nr. 7 (8. Juli 2015): e0130324. doi:10.1371/journal.pone.0130324.

Ji, Yinqiu, Louise Ashton, Scott M. Pedley, David P. Edwards, Yong Tang, Akihiro Nakamura, Roger Kitching, u. a. Reliable, Verifiable and Efficient Monitoring of Biodiversity via Metabarcoding. *Ecology Letters* 16, Nr. 10 (1. Oktober 2013): 1245–57. doi:10.1111/ele.12162.

Gibson, J., Shokralla, S., Porter, T. M., King, I., van Konynenburg, S., Janzen, D. H., ... & Hajibabaei, M. (2014) Simultaneous assessment of the macrobiome and microbiome in a bulk sample of tropical arthropods through DNA metasystematics. *Proceedings of the National Academy of Sciences*, **111**, 8007-8012.

Leray, Matthieu, und Nancy Knowlton. DNA Barcoding and Metabarcoding of Standardized Samples Reveal Patterns of Marine Benthic Diversity. *Proceedings of the National Academy of Sciences* 112, Nr. 7 (17. Februar 2015): 2076–81. doi:10.1073/pnas.1424997112.

Linard, B., Crampton-Platt, A., Gillett, C. P., Timmermans, M. J., & Vogler, A. P. (2015). Metagenome skimming of insect specimen pools: potential for comparative genomics. *Genome biology and evolution*, *7*(6), 1474-1489.

Liu, S., Wang, X., Xie, L., Tan, M., Li, Z., Su, X., ... & Niehuis, O. (2016). Mitochondrial capture enriches mito‐DNA 100 fold, enabling PCR‐free mitogenomics biodiversity analysis. *Molecular ecology resources*, *16*(2), 470-479.

Nielsen, H. Bjørn, Mathieu Almeida, Agnieszka Sierakowska Juncker, Simon Rasmussen, Junhua Li, Shinichi Sunagawa, Damian R. Plichta, u. a. Identification and Assembly of Genomes and Genetic Elements in Complex Metagenomic Samples without Using Reference Genomes. *Nature Biotechnology* 32, Nr. 8 (August 2014): 822–28. doi:10.1038/nbt.2939.

Pompanon, Francois, Bruce E. Deagle, William O. C. Symondson, David S. Brown, Simon N. Jarman, und Pierre Taberlet. Who Is Eating What: Diet Assessment Using next Generation Sequencing. *Molecular Ecology* 21, Nr. 8 (April 2012): 1931–50. doi:10.1111/j.1365-294X.2011.05403.x.

Saitoh, S., Aoyama, H., Fujii, S., Sunagawa, H., Nagahama, H., Akutsu, M., ... & Nakamori, T. (2016) A quantitative protocol for DNA metabarcoding of springtails (Collembola) 1. *Genome*, **59**, 705-723.

Tang, Min, Meihua Tan, Guanliang Meng, Shenzhou Yang, Xu Su, Shanlin Liu, Wenhui Song, u. a. Multiplex sequencing of pooled mitochondrial genomes—a crucial step toward biodiversity analysis using mito-metagenomics. *Nucleic Acids Research* 42, Nr. 22 (16. Dezember 2014): e166–e166. doi:10.1093/nar/gku917.

Yu, D. W., Ji, Y., Emerson, B. C., Wang, X., Ye, C., Yang, C., & Ding, Z. (2012) Biodiversity soup: metabarcoding of arthropods for rapid biodiversity assessment and biomonitoring. *Methods in Ecology and Evolution*, **3**, 613-623.

Zhou, Xin, Yiyuan Li, Shanlin Liu, Qing Yang, Xu Su, Lili Zhou, Min Tang, Ribei Fu, Jiguang Li, und Quanfei Huang. Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. *GigaScience* 2 (2013): 4. doi:10.1186/2047-217X-2-4.