Processing amoA amplicons from sequencing data

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2023-11-10

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16S rRNA gene amplicon sequences were trimmed with TrimGalore ([Krueger et al. 2021](#ref-krueger2021)), a wrapper using CutAdapt ([Martin 2011](#ref-EJ200)) for trimming of sequencing primers and adapters and FastQC ([Andrews et al. 2012](#ref-andrews2012)) for quality control. Trimmed reads were merged and assigned to amplicon sequence variants (ASVs) using dada2([Callahan et al. 2016](#ref-callahan2016)), with quality filtering and chimera removal using the default settings (Table S7). Taxonomy was assigned to ASVs in dada2 using the Silva rRNA database (SSU Ref NR 99 v138.1)([Quast et al. 2012](#ref-quast_silva_2012)). Community diversity (Table S8) and relative abundance (Table S9) of all sample replicates and fractions were calculated using phyloseq([McMurdie and Holmes 2013](#ref-mcmurdie_phyloseq_2013)).

Andrews, Simon, Felix Krueger, Anne Segonds-Pichon, Laura Biggins, Christel Krueger, and Steven Wingett. 2012. “FastQC.” Babraham, UK: Babraham Institute.

Callahan, Benjamin J., Paul J. McMurdie, Michael J. Rosen, Andrew W. Han, Amy Jo A. Johnson, and Susan P. Holmes. 2016. “DADA2: High-Resolution Sample Inference from Illumina Amplicon Data.” *Nature Methods* 13 (7): 581–83. <https://doi.org/10.1038/nmeth.3869>.

Krueger, Felix, Frankie James, Phil Ewels, Ebrahim Afyounian, and Benjamin Schuster-Boeckler. 2021. “FelixKrueger/TrimGalore: V0.6.7 - DOI via Zenodo.” Zenodo. <https://doi.org/10.5281/zenodo.5127899>.

Martin, Marcel. 2011. “Cutadapt Removes Adapter Sequences from High-Throughput Sequencing Reads.” *EMBnet.journal* 17 (1): 10–12. <https://doi.org/10.14806/ej.17.1.200>.

McMurdie, Paul J., and Susan Holmes. 2013. “Phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data.” *PloS One* 8 (4): e61217. <https://doi.org/10.1371/journal.pone.0061217>.

Quast, Christian, Elmar Pruesse, Pelin Yilmaz, Jan Gerken, Timmy Schweer, Pablo Yarza, Jörg Peplies, and Frank Oliver Glöckner. 2012. “The SILVA Ribosomal RNA Gene Database Project: Improved Data Processing and Web-Based Tools.” *Nucleic Acids Research* 41 (D1): D590–96. <https://doi.org/10.1093/nar/gks1219>.