Processing amoA amplicons from sequencing data

Dylan Bodington

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Sequence data was 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 sequences were assigned to amplicon sequence variants (ASVs) using dada2([Callahan et al. 2016](#ref-callahan2016)), which includes quality filtering and chimera removal. Taxonomy was assigned to ASVs in dada2 using a custom database created from a highly-resolved phylogeny of ammonia-oxidising archaea ([Alves et al. 2018](#ref-alves2018)). ASVs were clustered at different cutoffs using the R package DECIPHER ([Wright 2016](#ref-RJ2016)).

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