Environmental DNA variability in lake sediment cores

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Introduction

Lake sediments - information about lake communities and their surrounding catchments

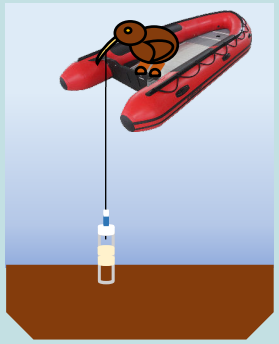
Molecular techniques – can target soft-bodied organisms and bacteria

Aims

Investigate bacterial community heterogeneity within depth slices of sediment cores

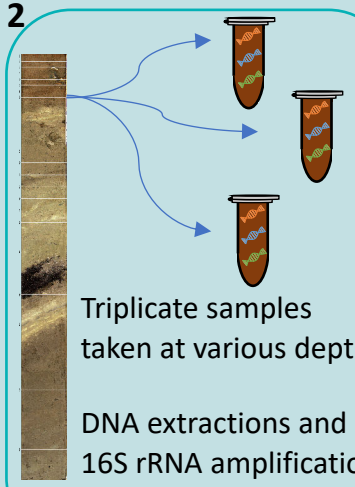
Methods

1



Sediment core collected – three lakes
Represents ~1200 years

2



Triplicate samples taken at various depths

DNA extractions and 16S rRNA amplification

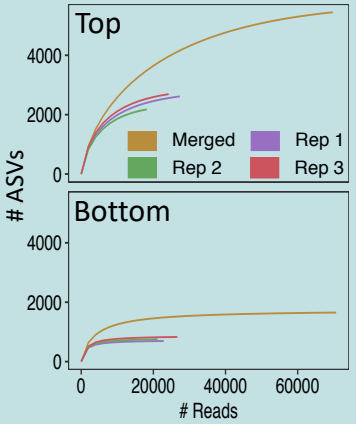
3

Illumina Miseq sequencing

4

Dada2 processing of Amplicon Sequence Variants (ASVs)

Results

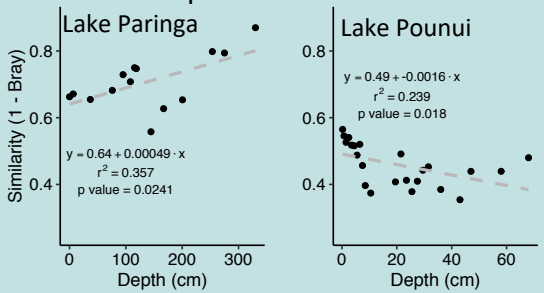


Triplicates insufficient to reveal total richness at surface

Richness plateaus in deeper samples

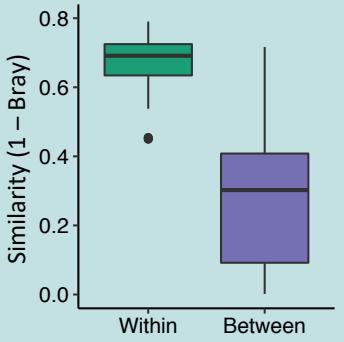
DNA degradation? Community shifts?

Inconsistent patterns in similarity with depth across lakes

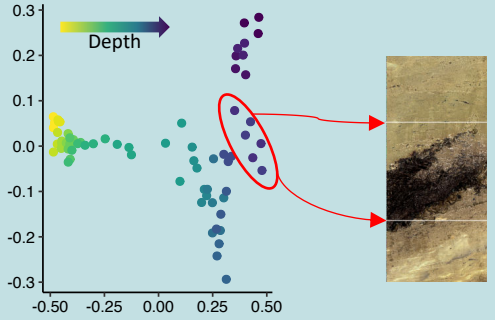


Increased similarity in deeper samples could be due to removal of rare ASVs by degradation

Increased variation in replicates
- Sampling across the stratigraphy



Replicates within a depth have a higher similarity than samples between depth slices



Conclusion

Single samples from a depth slice sufficient when assessing shifts in abundant members of microbial community
- Replication improved the detection of rare species in the sediment samples

Similarity higher within slices than between
- exceptions related to bioturbation or sediment heterogeneity
- stratigraphy needs to be accounted for in sampling