806_final

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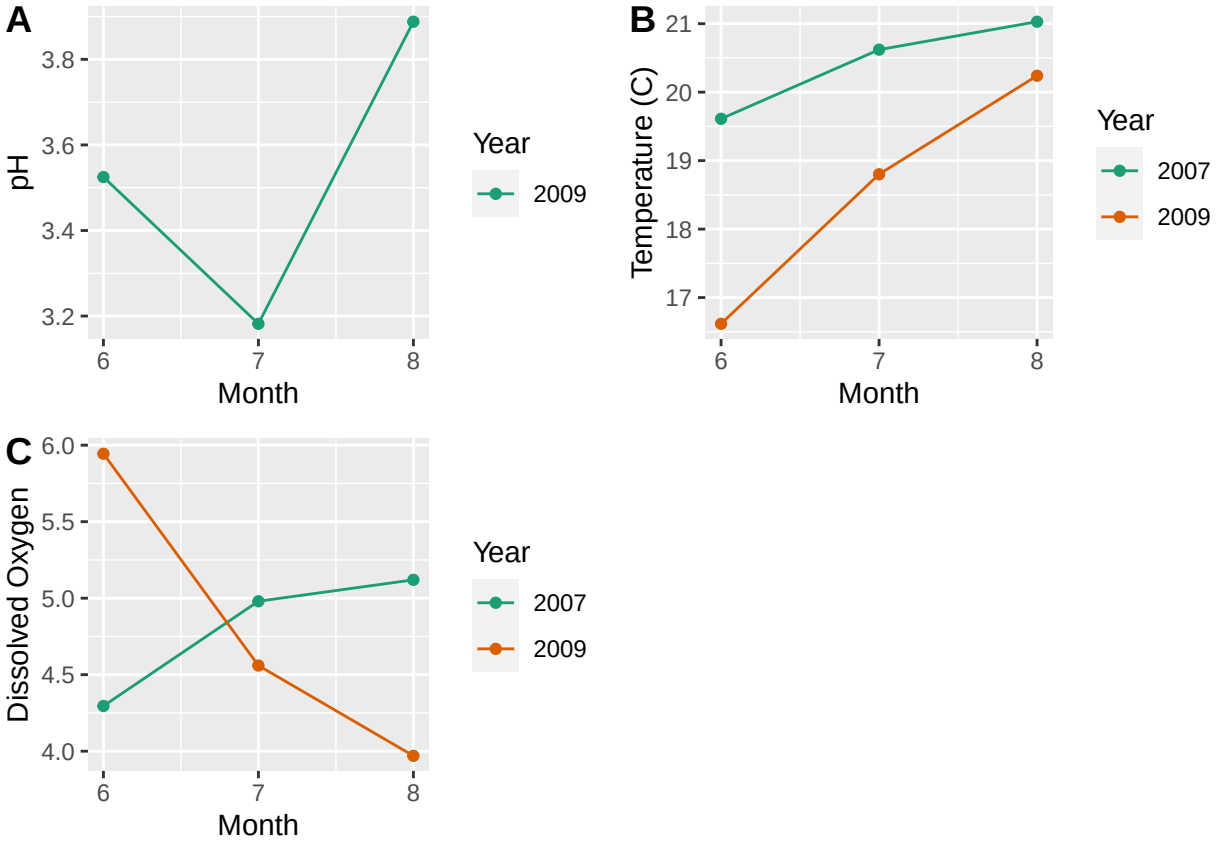
Introduction

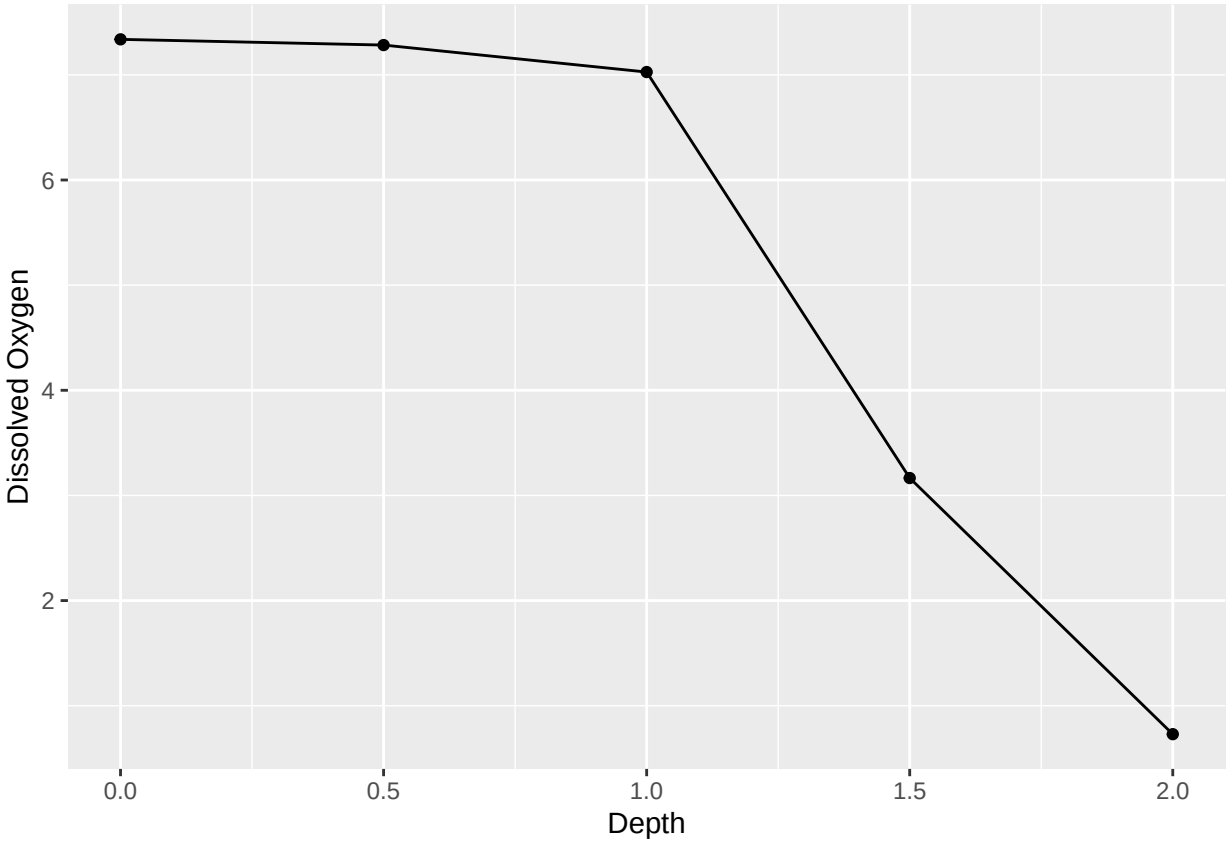
Microbial communities are responsible for carrying out crucial ecosystem functions and processes, and are therefore essential to life on Earth (Li et al., 2015). Specifically, in aquatic systems, bacterial communities play vital roles in biogeochemical cycling (Monard et al., 2016). Knowledge of the composition, structure, and distribution of microbial communities can be utilized to predict how an ecosystem may respond to environmental changes over time (Monard et al., 2016; Sieber et al., 2020). The North Temperate Lakes Long Term Ecological Research (LTER) program located in Vilas County, Wisconsin has collected a myriad of data from lakes and bogs in the area. In 2007 and 2009, data on pH, dissolved oxygen (DO), and temperature were collected from Crystal Bog. Additionally, samples were collected and analyzed to identify members of the microbial community by 16S rRNA sequencing (McMahon et al., 2019). This dataset was analyzed using R v. 4.1.1 to gain an understanding of the influence these environmental factors (pH, DO, temperature) may have had on microbial community composition between Summer 2007 and Summer 2009.

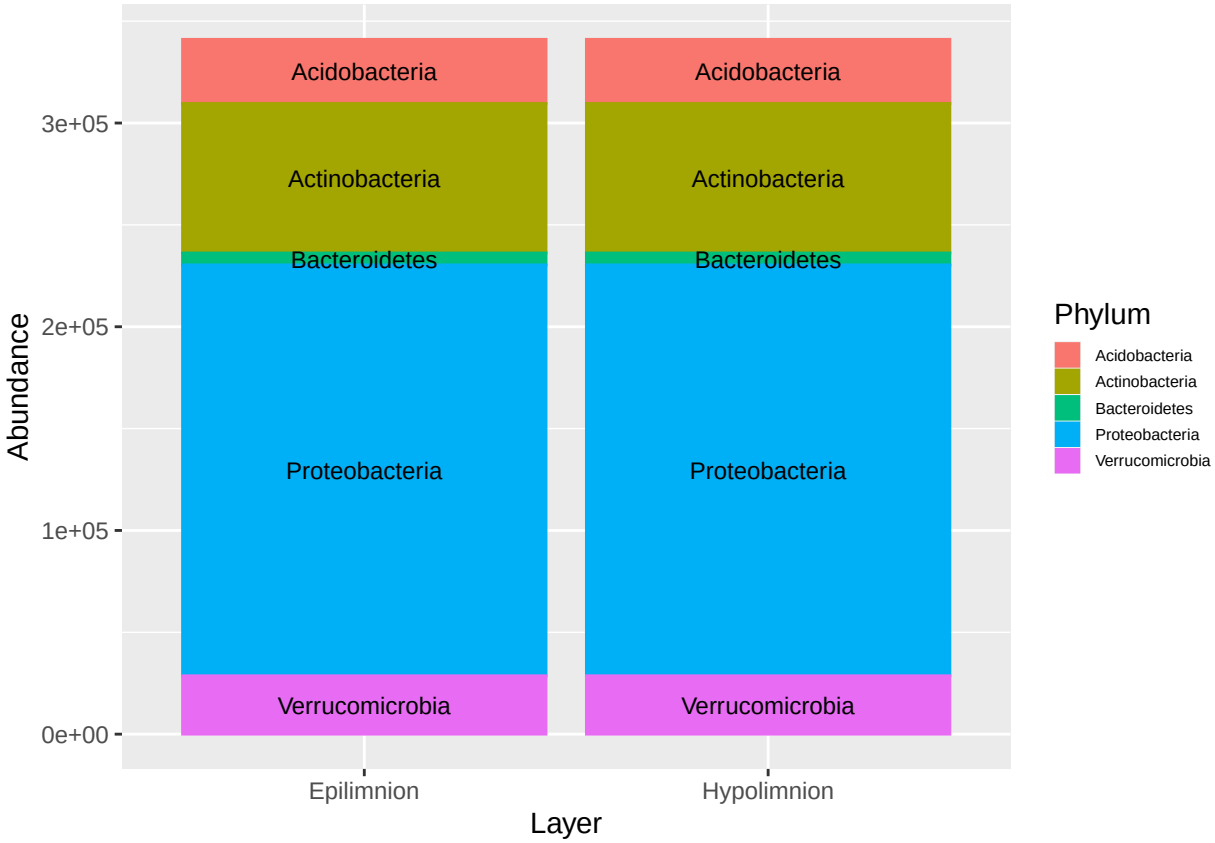
Methods

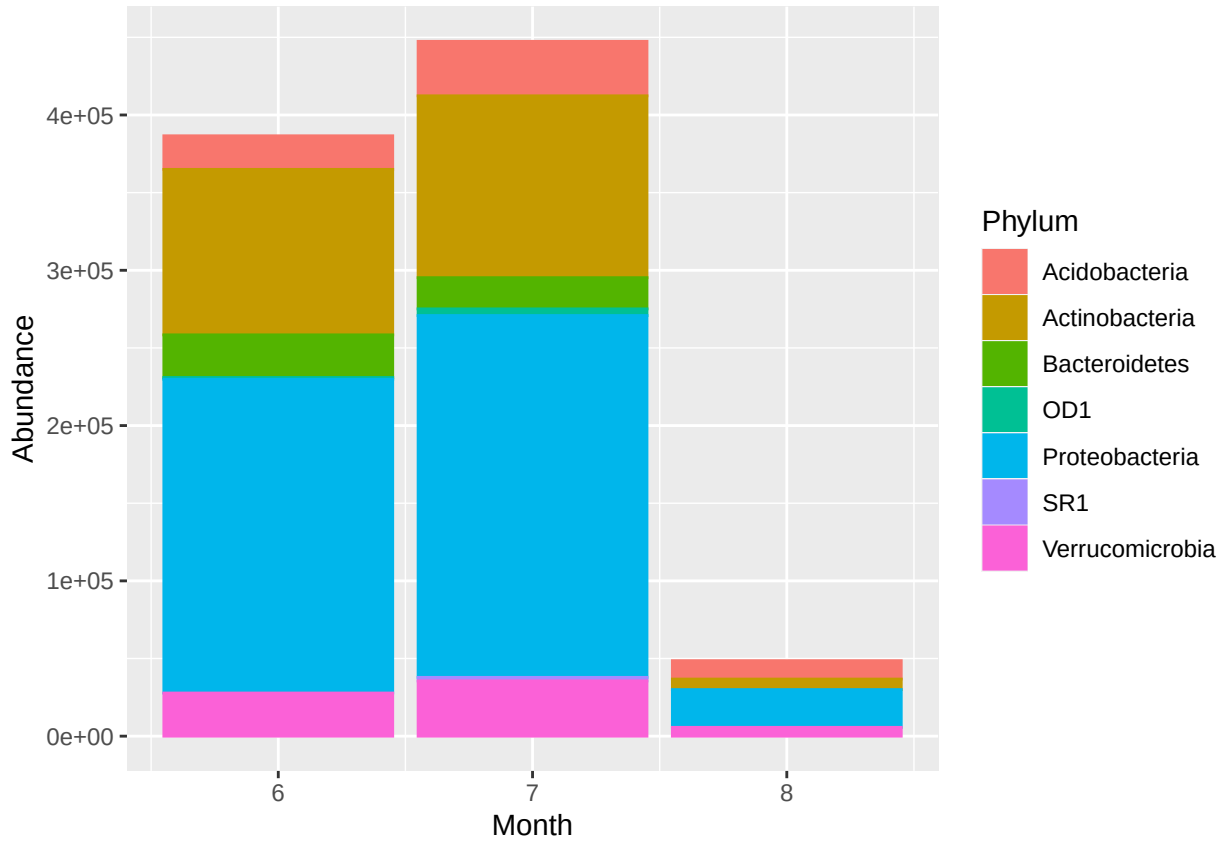
Data was collected by researchers through the North Temperate Lakes LTER in Vilas County, Wisconsin. Freshwater samples were collected from Crystal Bog in 2007 and 2009 and 16S rRNA sequencing was performed. Data was analyzed using R v. 4.1.1.

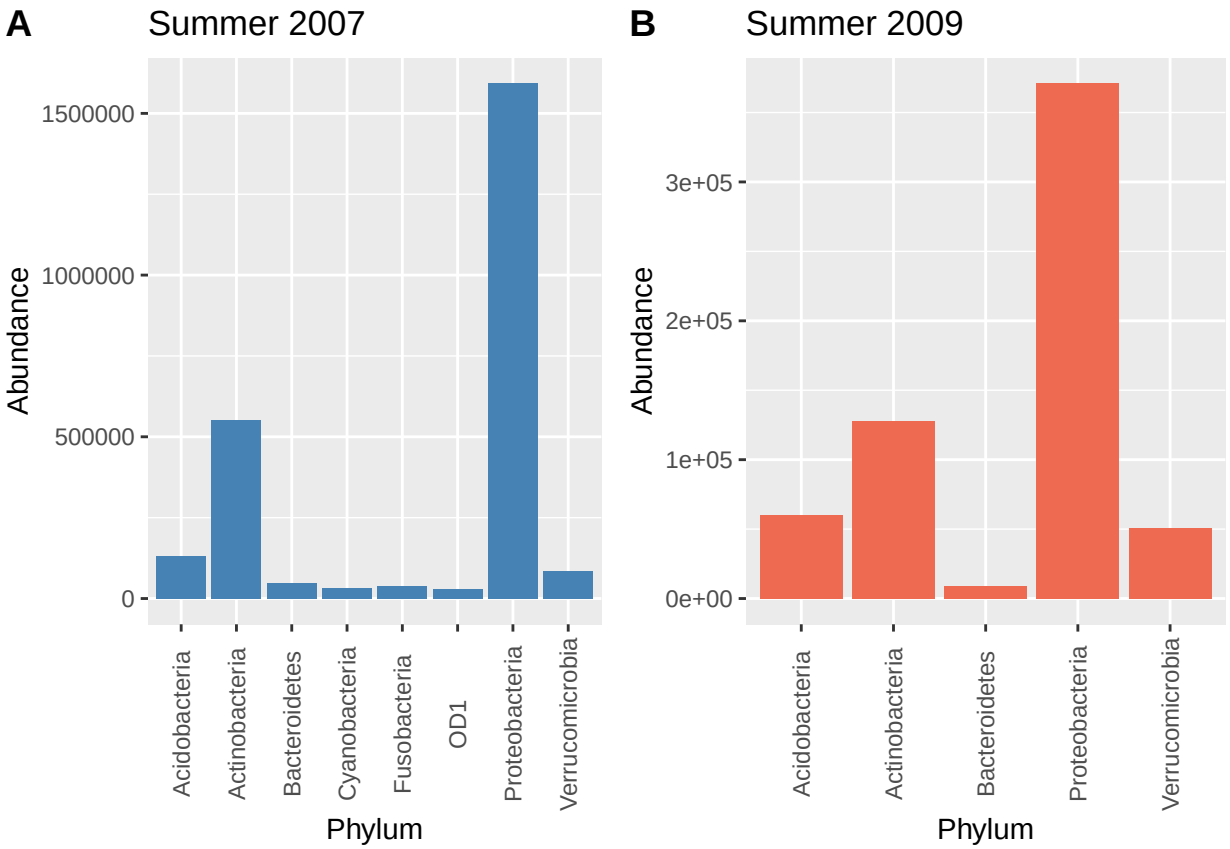
Results

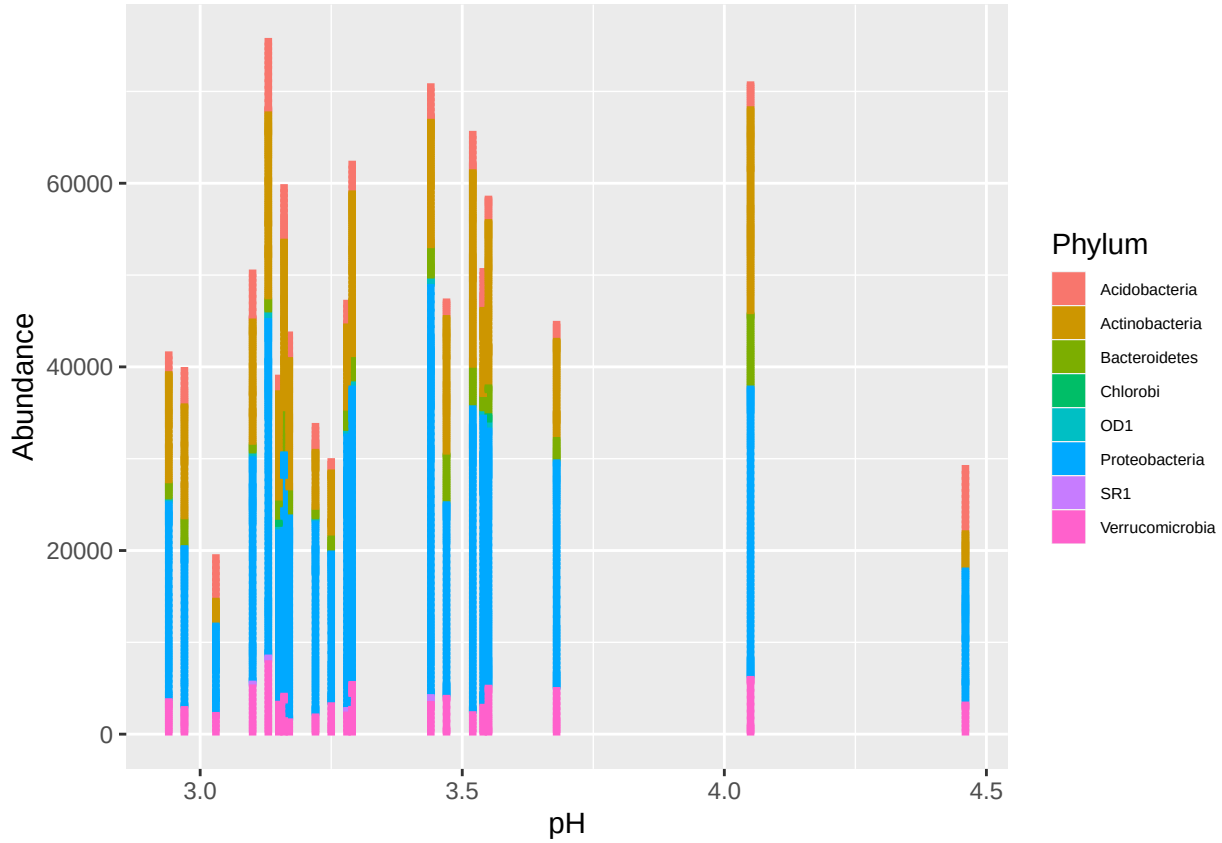

A
pH
3.8
3.6
3.4
3.2
6
7
8
Month
Year
2009
B
Temperature (C)
21
20
19
18
17
6
7
8
Month
Year
2007
2009
C
Dissolved Oxygen
6.0
5.5
5.0
4.5
4.0
6
7
8
Month
Year
2007
2009


Dissolved Oxygen
6
4
2
0.0
0.5
1.0
1.5
2.0
Depth


Acidobacteria
Actinobacteria
Bacteroidetes
Proteobacteria
Verrucomicrobia
3e+05
2e+05
1e+05
0e+00
Abundance
Epilimnion
Hypolimnion
Layer
Phylum
Acidobacteria
Actinobacteria
Bacteroidetes
Proteobacteria
Verrucomicrobia


Abundance
4e+05
3e+05
2e+05
1e+05
0e+00
6
7
8
Month
Phylum
Acidobacteria
Actinobacteria
Bacteroidetes
OD1
Proteobacteria
SR1
Verrucomicrobia


A
Summer 2007
Abundance
1500000
1000000
500000
0
Acidobacteria
Actinobacteria
Bacteroidetes
Cyanobacteria
Fusobacteria
OD1
Proteobacteria
Verrucomicrobia
Phylum
B
Summer 2009
Abundance
3e+05
2e+05
1e+05
0e+00
Acidobacteria
Actinobacteria
Bacteroidetes
Proteobacteria
Verrucomicrobia
Phylum



Discussion

References

Li P, Yang SF, Lv BB, Zhao K, Lin MF, Zhou S, Song X, Tang XM. 2015. Comparison of extraction methods of total microbial DNA from freshwater. Genet Mol Res. 14(1):730-8.

Monard, C., Gantner, S., Bertilsson, S., Hallin, S., & Stenlid, J. 2016. Habitat generalists and specialists in microbial communities across a terrestrial-freshwater gradient. Scientific reports, 6, 37719.

Sieber, G., Beisser, D., Bock, C., & Boenigk, J. 2020. Protistan and fungal diversity in soils and freshwater lakes are substantially different. Scientific reports, 10(1), 20025.

McMahon, K., S. Jones, A. Shade, R. Newton, E. Read, L. Beversdorf, R. Rohwer, B. Peterson, A. Linz, E. McDaniel, G. Wolf, and S. Schmitz. 2019. Microbial Observatory at North Temperate Lakes LTER High-resolution temporal and spatial dynamics of microbial community structure in freshwater bog lakes 2005 - 2009 original format ver 4. Environmental Data Initiative.