# Title

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# Abstract

# Introduction

Why nutrient cycling in lakes is important globally (lakes as integrators of the landscape, lakes as hotspots of carbon cycling, small lakes disproportionately active in carbon cycle, lakes as sentinels of change)

Description of study sites

How can metagenomic/genome analysis shed light on ecosystems?

Review other papers that have used this dataset (and why this paper is novel)

# Results/Discussion

**Overview of Dataset**

Analyzing the genomes of uncultured microbes can provide insight into the potential metabolic functions of those organisms. 205 bacterial metagenome assembled genomes (MAGs) were recovered from a metagenomic time series in Trout Bog and Lake Mendota as described in Bendall, et al (Bendall et al. 2016). These MAGs range in completeness from 50 to 99% complete, and passed quality checks for contamination using CheckM (Parks et al. 2015) (supp table). Of the 205 MAGs, 102 were recovered from Lake Mendota, 31 were recovered from the epilimnion of Trout Bog, and 69 were recovered from the hypolimnion of Trout Bog. Several MAGs in the epilimnion and hypolimnion of Trout Bog appeared to be from the same population based on high average nucleotide identities (supp table). The phylogenetic distribution of MAGs was consistent with the classifications of 16S ribosomal rRNA gene amplicon sequencing results (Figure 1). These results are consistent with other 16S-based studies in these sites (Hall et al. 2017; Linz et al. 2017).

<Fig 1a Barchart of MAG phyla>

<Fig 2b Barchart of 16S phyla>

**Figure 1. How representative are the MAGs of the microbial community?** The taxonomic classifications of MAGs (A) reflect the community composition observed via 16S rRNA ribosomal amplicon sequencing (B).

## Photosynthesis and Carbon Fixation

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**Fig 2. Carbon degradation in Mendota vs Trout Bog.**

**A close up of a map

Description generated with high confidenceFigure 3. Methylotrophy in freshwater.** *Methylococcaceae* and *Methylotenera* are taxa capable of methylotrophy in both Lake Mendota and Trout Bog.

# A screenshot of a cell phone Description generated with very high confidenceNitrogen Cycling

**A close up of a map

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**Fig 3. Nitrogen cycling in Trout Bog vs Mendota.** A) Number of marker genes for nitrogen cycling metabolisms in each lake B) Phylogeny of nitrogen fixers by lake

# Sulfur Cycling

# Unusual microbes

A picture containing text, map

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**Figure 6B. Proposed functions of Planctomycetes in freshwater.** Observation of genes annotated as glycoside hydrolases and sulfatases suggest a role for Planctomycetes as polysaccharide degraders.