



# Function from populations to communities

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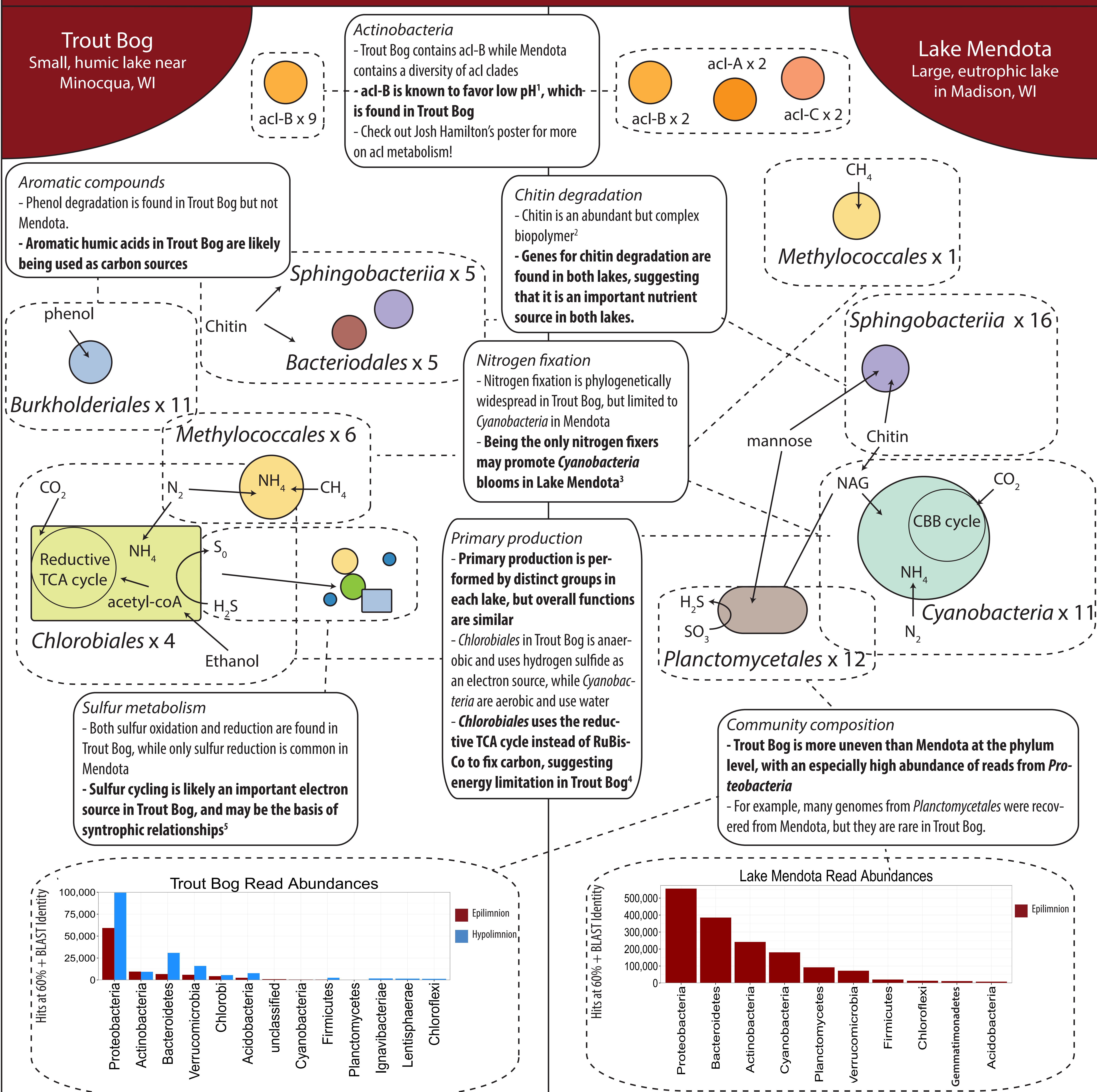
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## Introduction/Objectives

Bacteria form the base of freshwater ecosystems because of their importance in nutrient cycling. We used genomes assembled from metagenomes to assess gene content in bacterial populations in two lakes, Lake Mendota and Trout Bog. We know that environmental parameters and bacterial community composition differ between these lakes, but do not know how function compares. Analyzing potential function at the population level allows us to integrate phylogenetic and metabolic information. By comparing the metabolic capability of bacterial communities in two lakes with different nutrient regimes, we can link function at the population scale to the ecosystem scale.

## Results/Conclusions



## Methods

**Methods:** Integrated water samples were collected from the epilimnion of Lake Mendota and the epilimnion and hypolimnion of Trout Bog multiple times during the ice-free seasons in 2005 - 2009. Bacteria were collected on a 0.22 micron filter and DNA was extracted from each filter using a FastDNA spin kit. DNA was sequenced on Illumina MiSeq at the Joint Genome Institute. Samples from across the time series were pooled by lake and co-assembled using MetaBat, as described in Stevens, et al.<sup>6</sup> Contigs were grouped into metagenome-assembled genomes (MAGs) based on taxonomy and read coverage over the time series. Metapathways was run on each MAG to assess metabolic capability.



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