



Function from populations to communities

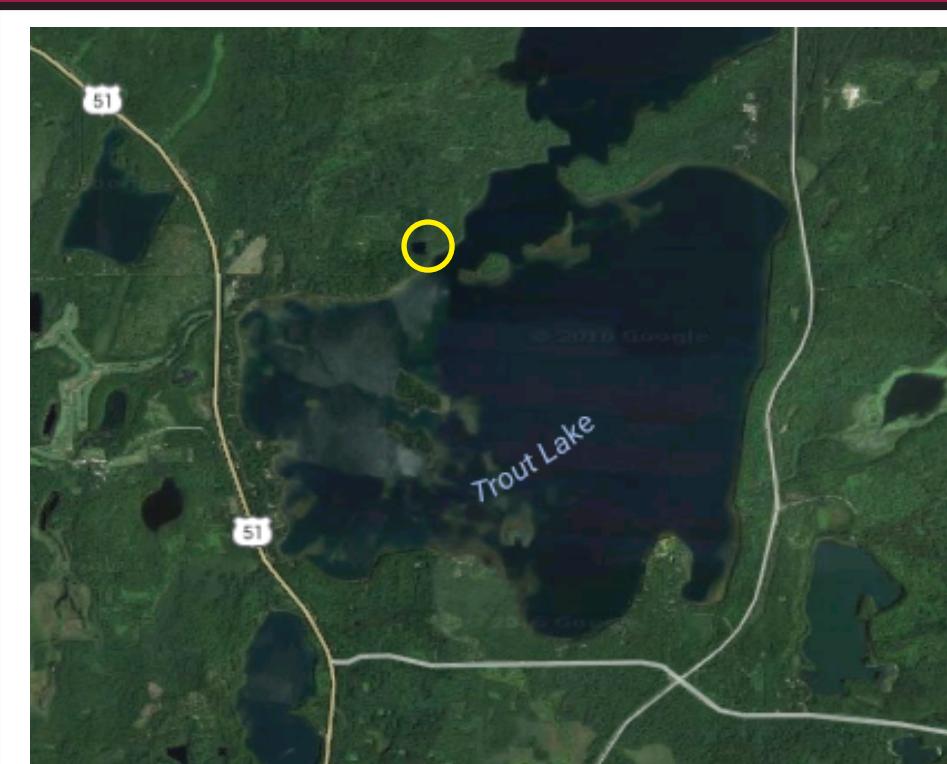
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Introduction/Objectives

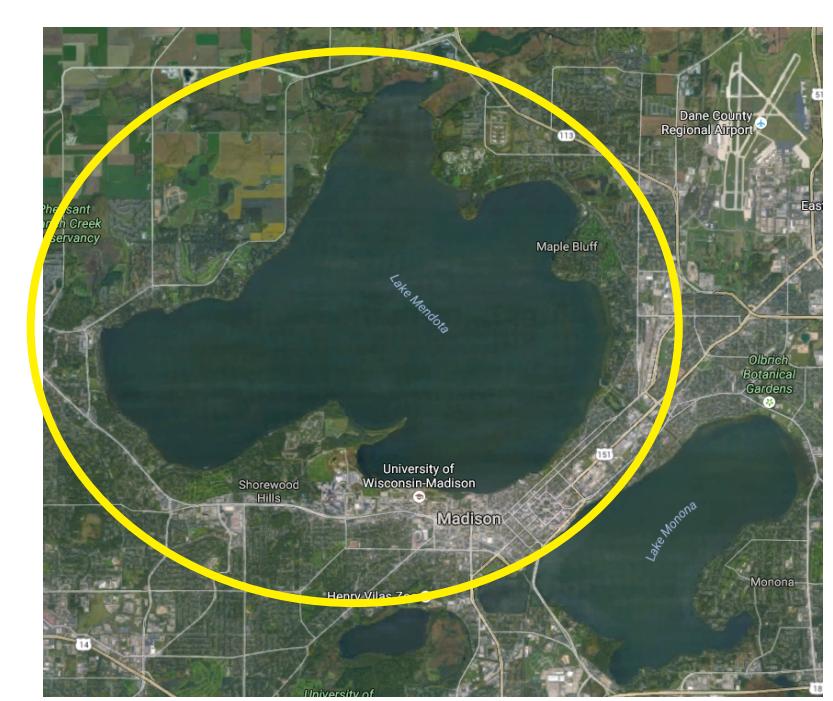
Bacteria form the base of freshwater ecosystems because of their importance in nutrient cycling. By comparing the metabolic capability of bacterial communities in two lakes with different nutrient regimes, we can link function at the population scale to the ecosystem scale.

Results/Conclusions



Trout Bog

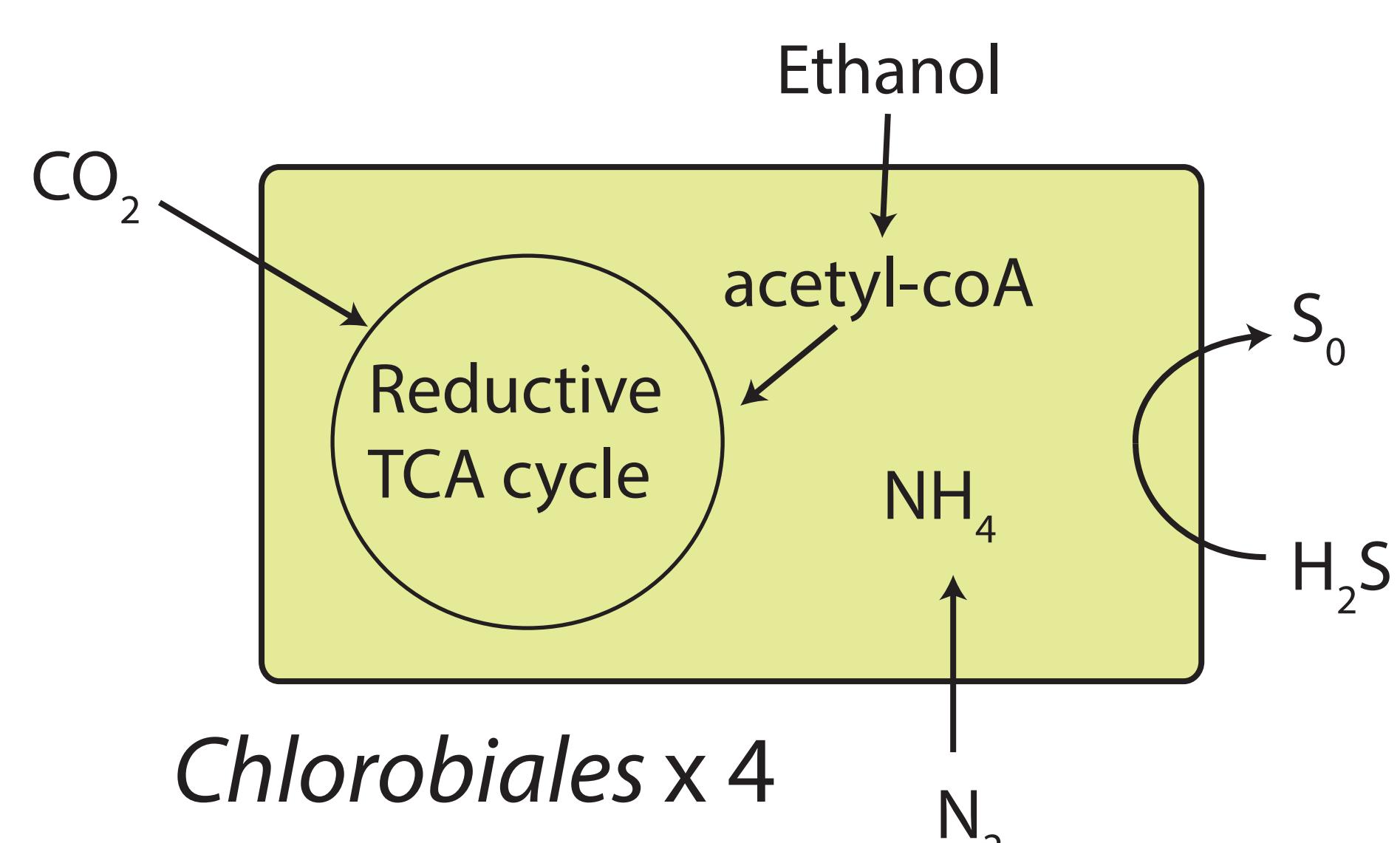
Small, humic lake near Minocqua, WI



Lake Mendota

Large, eutrophic lake in Madison, WI

Trout Bog Populations:



Primary Production

Anaerobic *Chlorobiiales* are the dominant primary producers in Trout Bog, while aerobic *Cyanobacteria* are dominant in Mendota.

Chlorobiiales uses the reductive TCA cycle instead of the Calvin-Benson-Bassham pathway to fix carbon, suggesting energy limitation.

One Carbon Compounds

Methylococcales in Trout Bog can fix nitrogen, while *Methylococcales* in Mendota cannot.

Despite being closely related to isolates of *Methylophilera versatilis* from Lake Washington, *Methylophilales* in both lakes do not appear to be able to degrade methylamines.

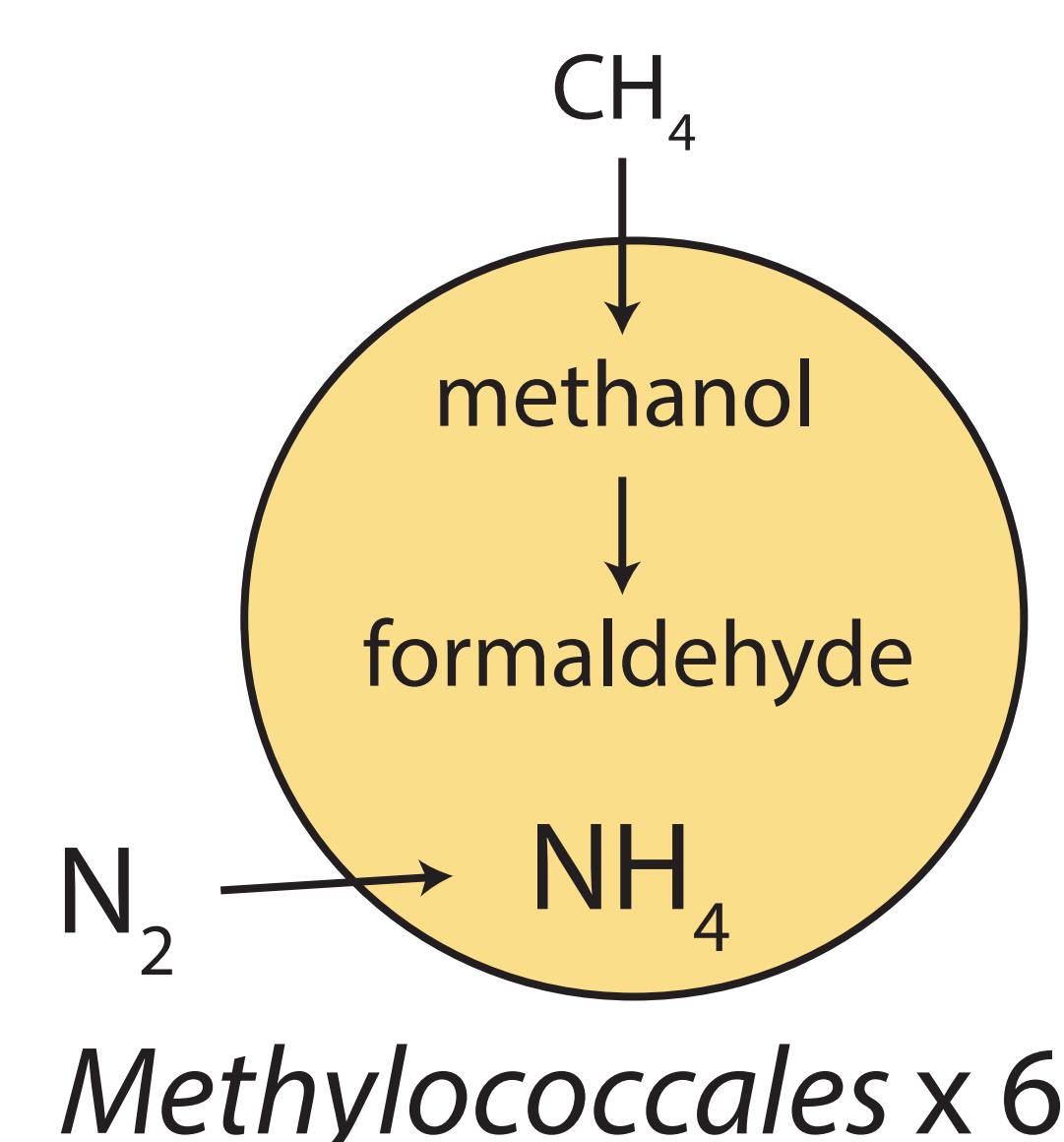
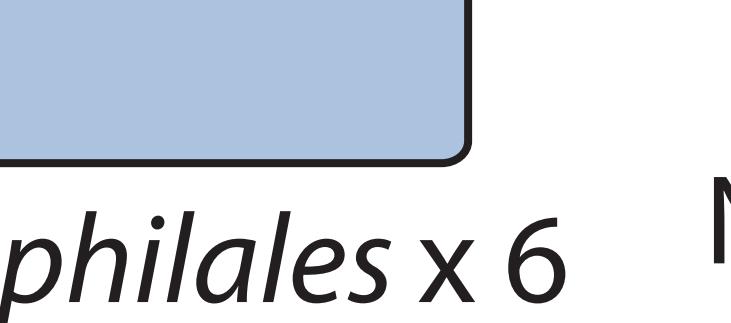
Complex Carbon Degradation

There are many similarities in this category between lakes. However, phenol degradation is present in Trout Bog but not Mendota, and no members of *Bacteriodales* able to degrade chitin were identified in Mendota.

Inorganic Nutrients

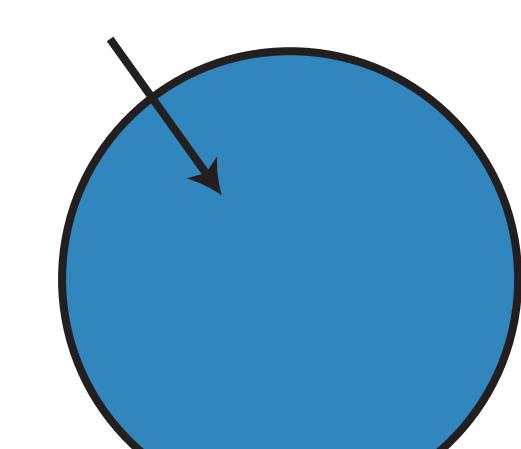
Nitrogen fixation is widespread in Trout Bog, but limited to *Cyanobacteria* in Mendota. This may contribute to Mendota's frequent *Cyanobacteria* blooms.

Sulfur oxidation is common in Trout Bog, but rare in Mendota. Sulfur reduction is found in both lakes.

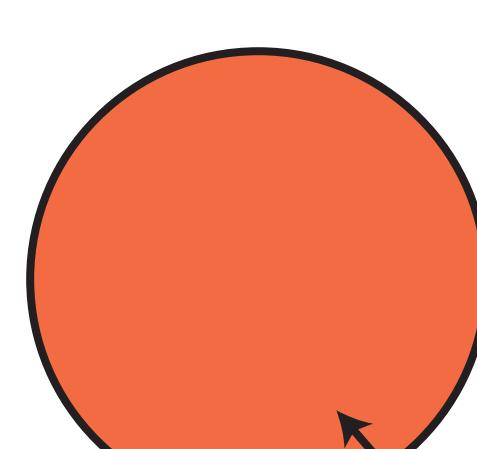


salicylate
phenol

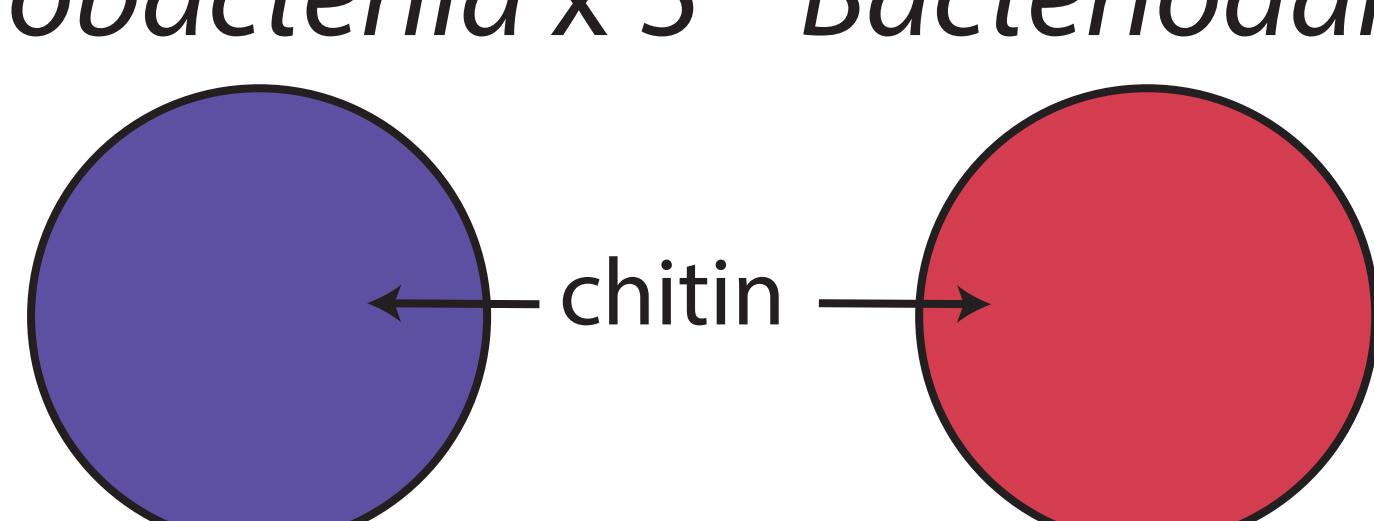
Verrucomicrobia x 10



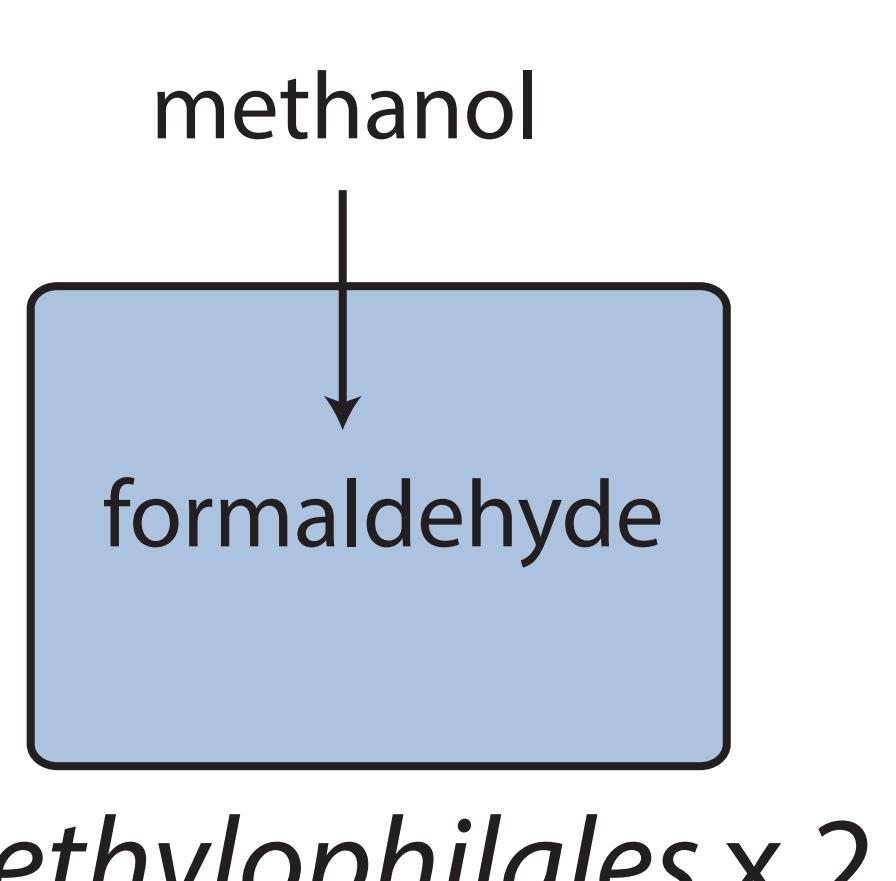
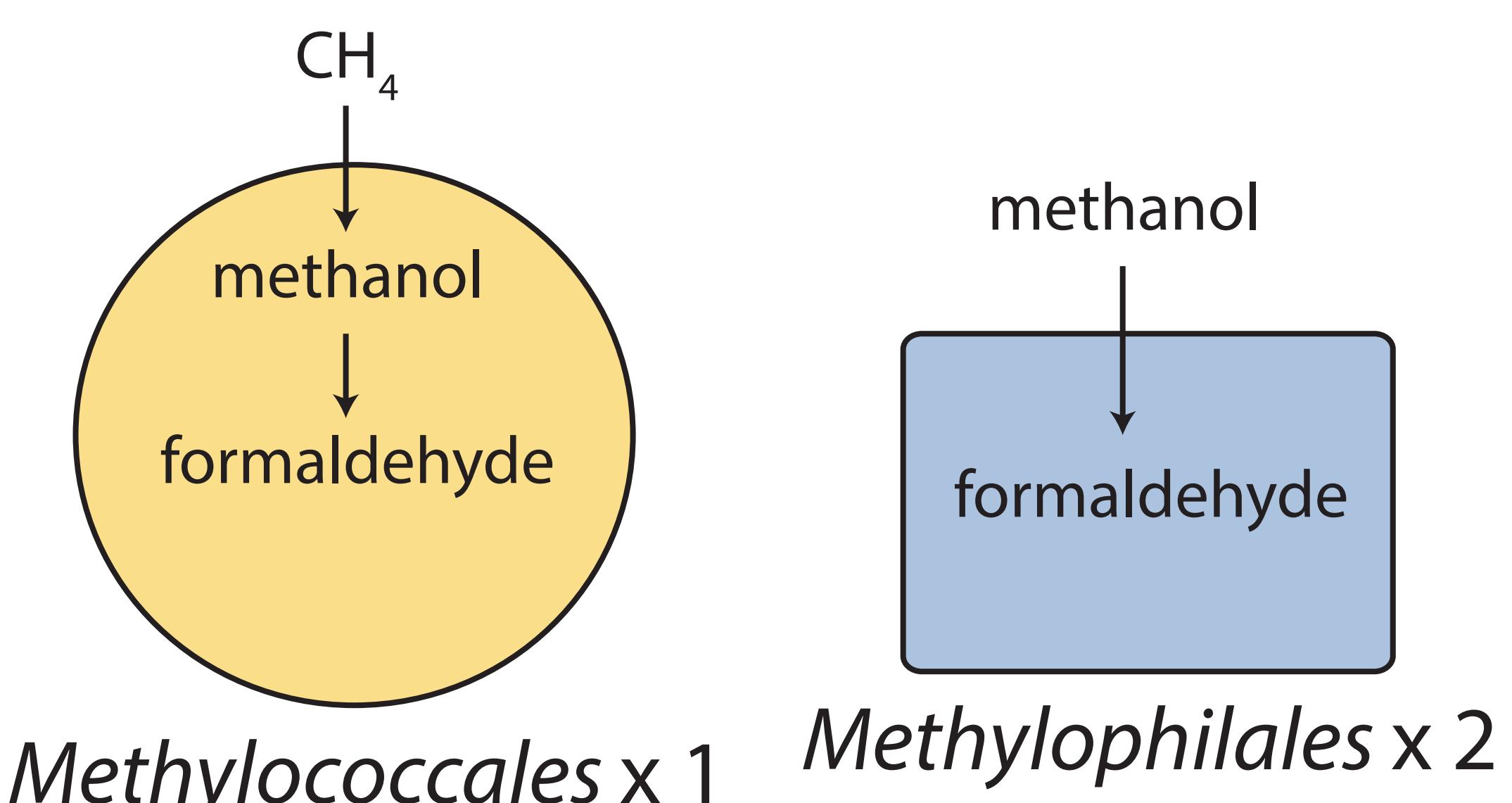
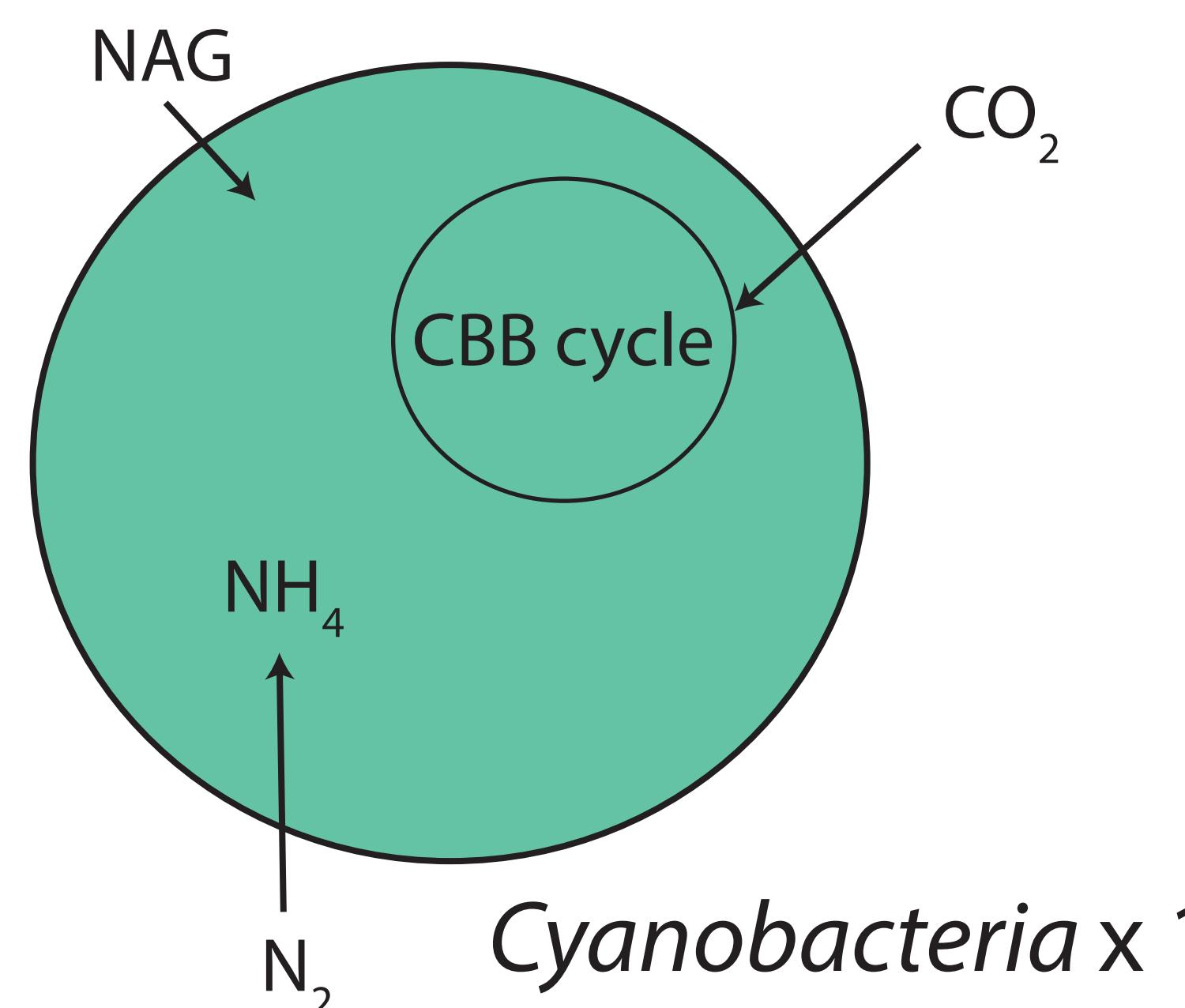
Burkholderiales x 11



Bacteriodales x 5

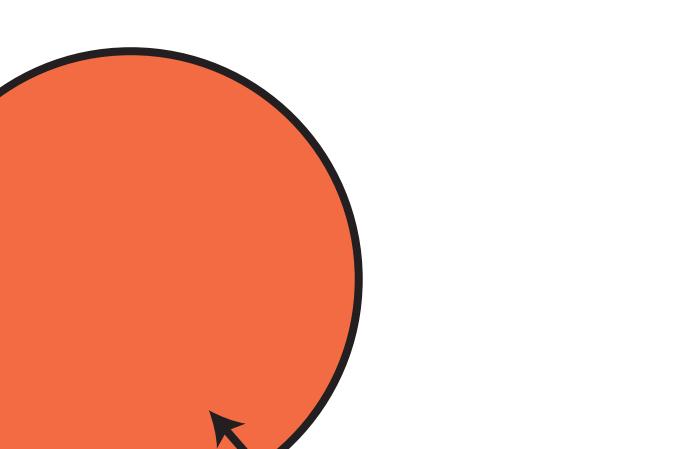
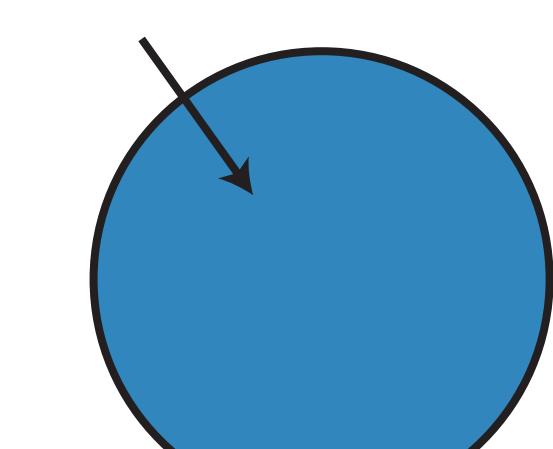


Lake Mendota Populations:

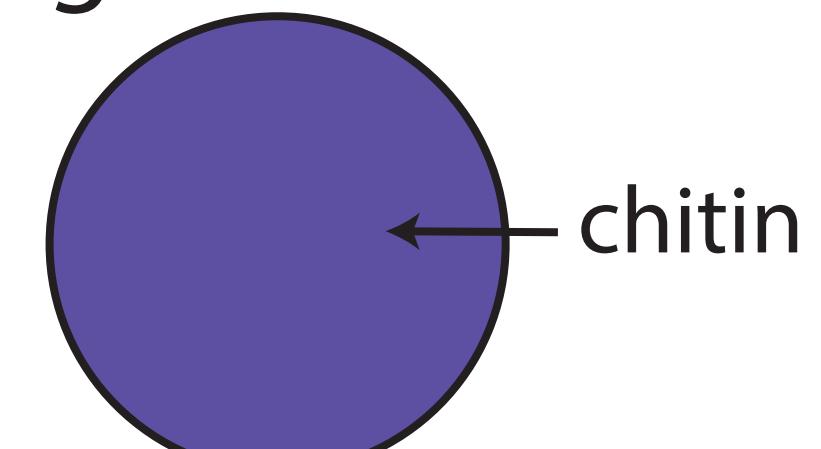


salicylate

Verrucomicrobia x 8



Sphingobacteriia x 16



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. 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.

Methods