



Jefferson Project at Chautauqua Lake: Lake Management and HABs

17 June 2023

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Agenda

Introduction

HABs Overview

- Algae
- Mechanisms
- Stream intrusion
- High-frequency measurements
- Cyberinfrastructure and computer modeling

Advances in genomic research

Plans and the view forward



Harmful Algal Bloom (HAB) common thinking

Nutrients

+

Warm Temperatures/Sun

=

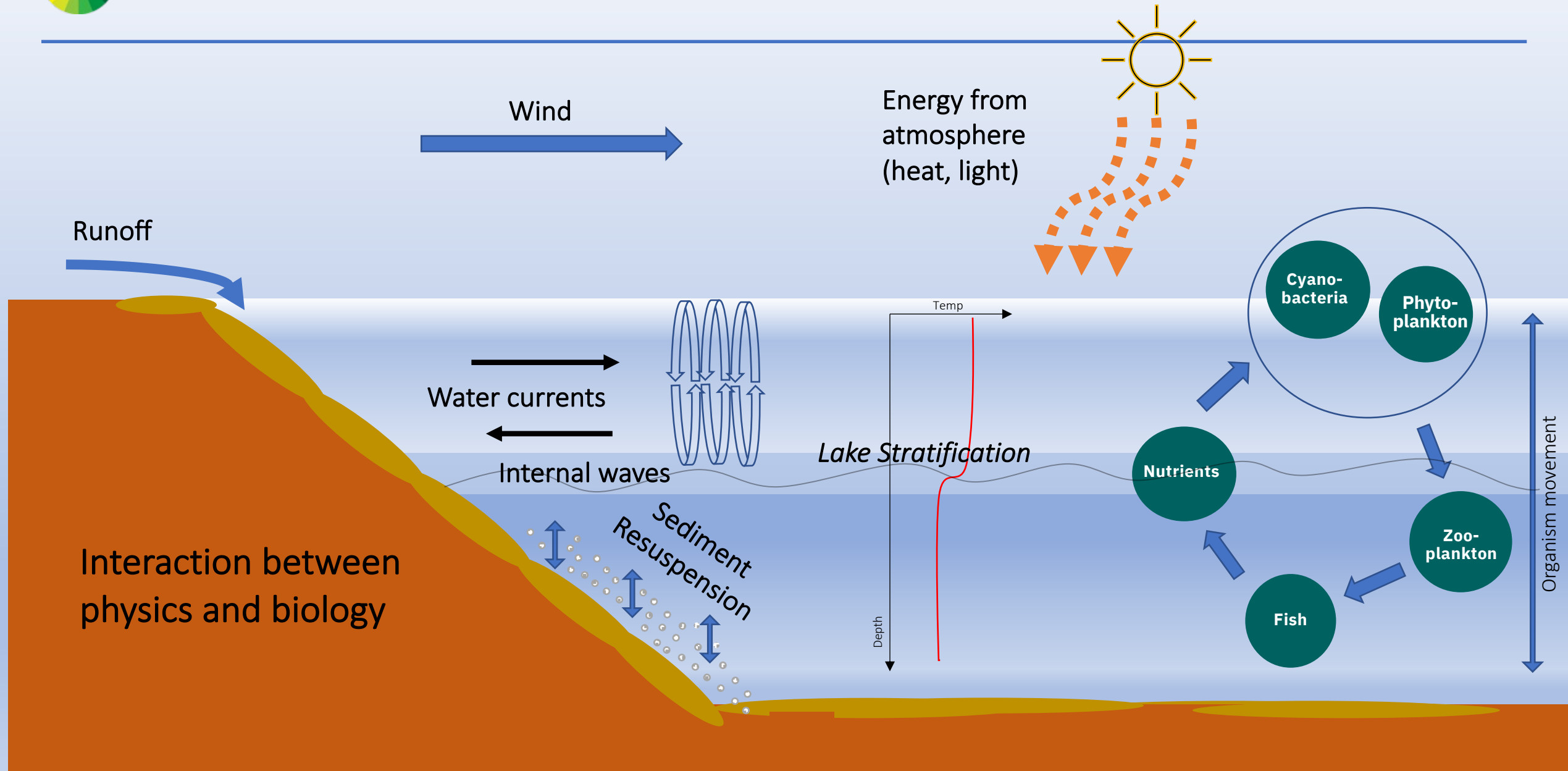
[Surface] HAB



It's not that simple...



The lake is a complex environment comprised of a “systems of systems”

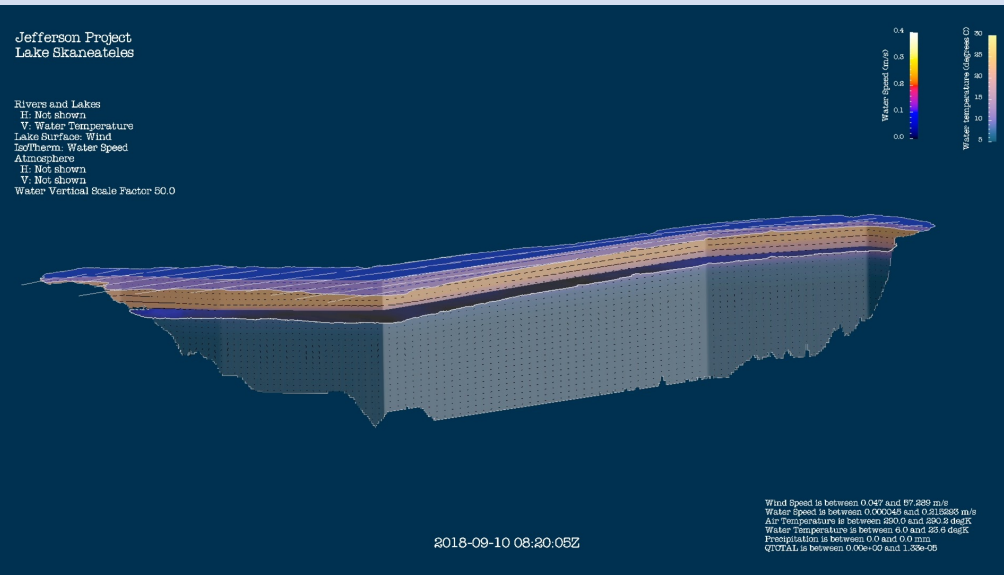


Mechanisms

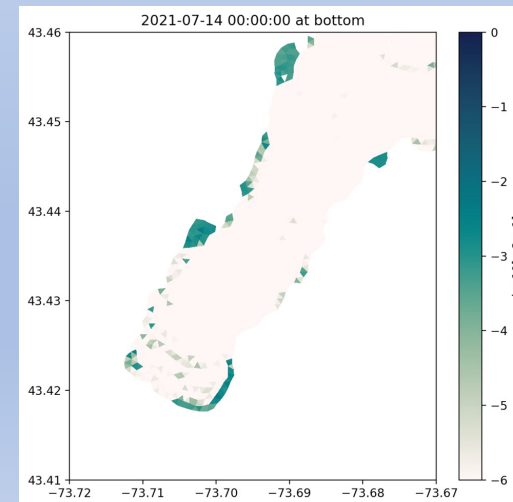
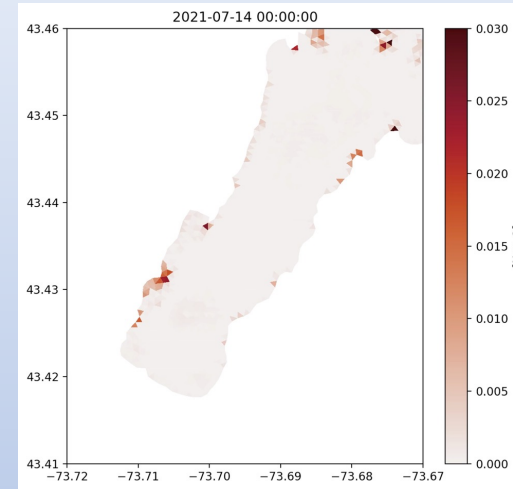


HABs germination and recruitment

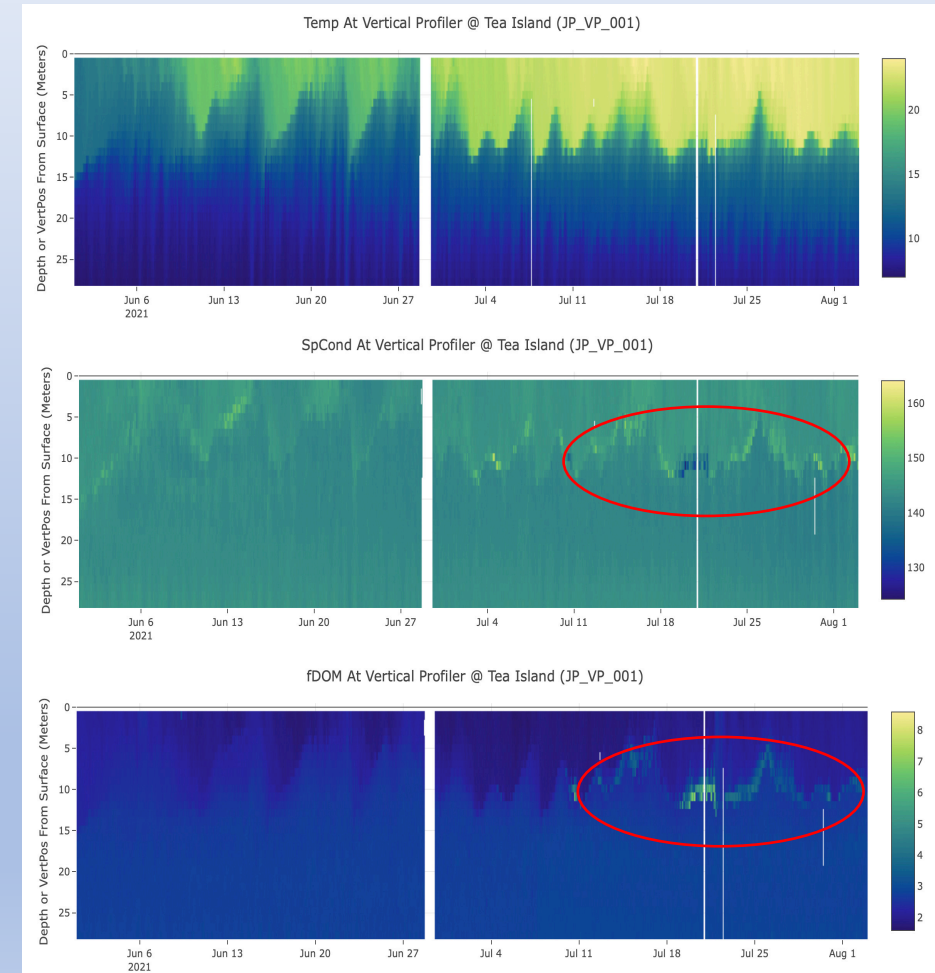
Internal waves



Lake bottom Interactions



Stream intrusion and contaminants

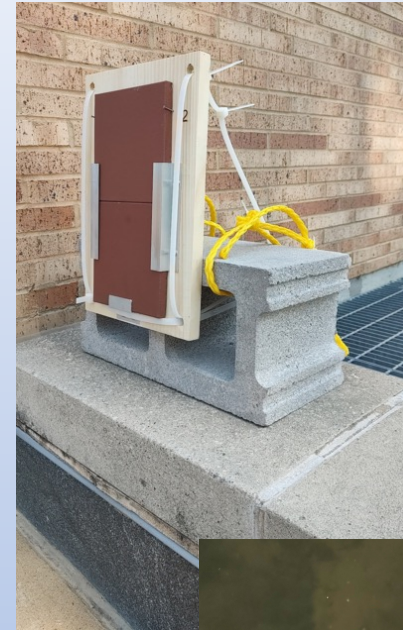


Sampling program



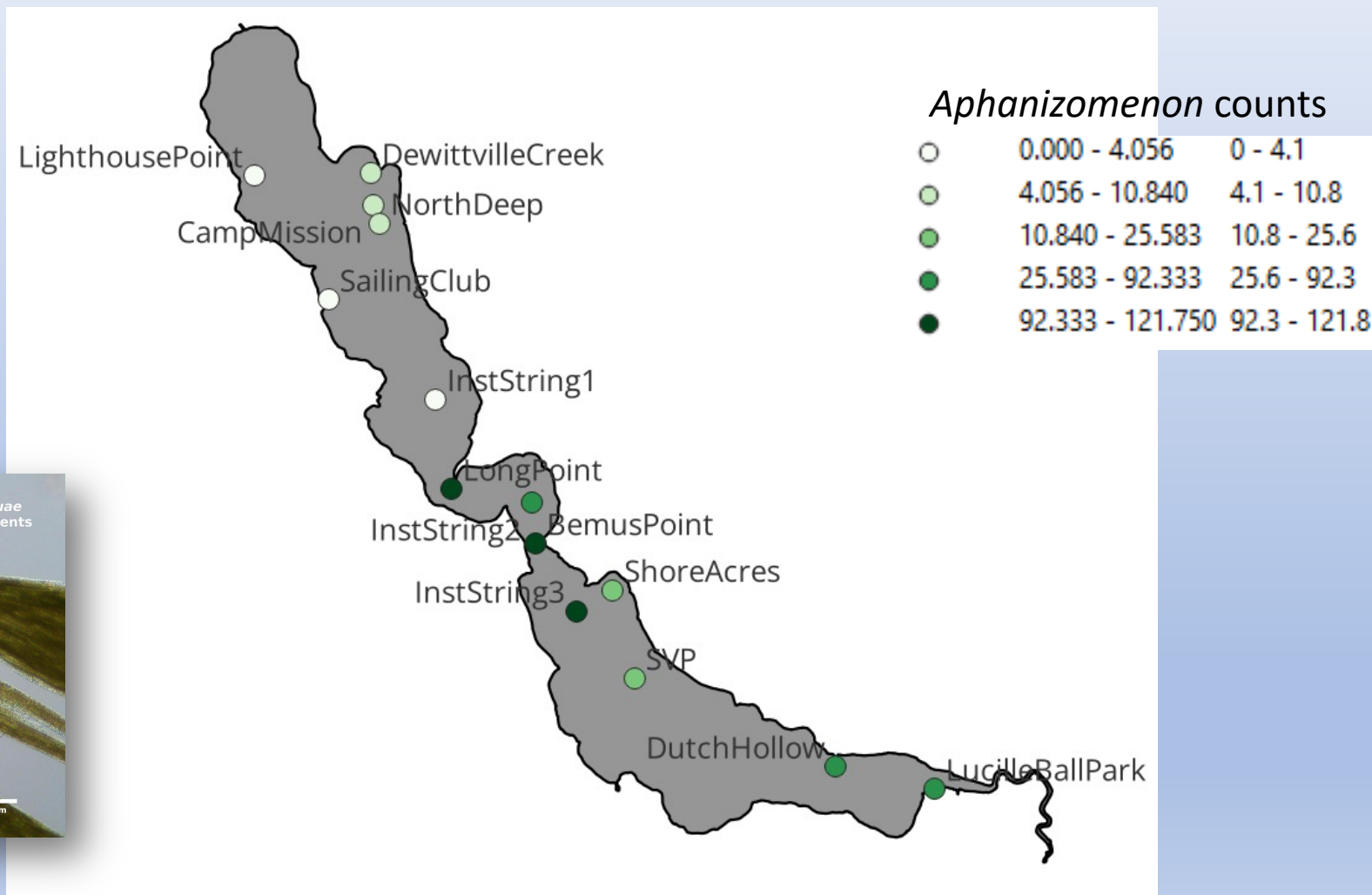
Sampling is underway!

- Bi-weekly sampling at 18 lake stations
- Algal tile survey at 11 dock sites
- Cyanobacteria sensor from a dock in Celoron
- Vertical profilers and phosphorus sensors to be launched soon





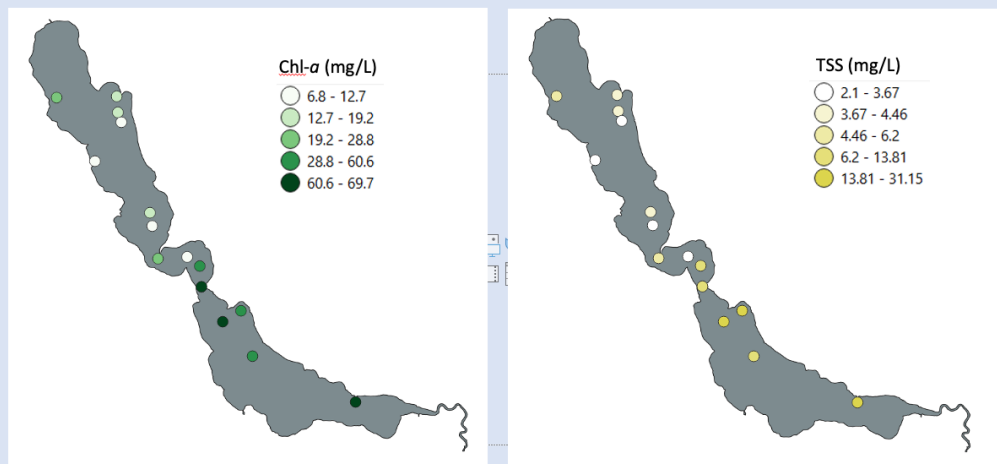
Cyanobacteria - more abundant in the southern and central parts of the lake





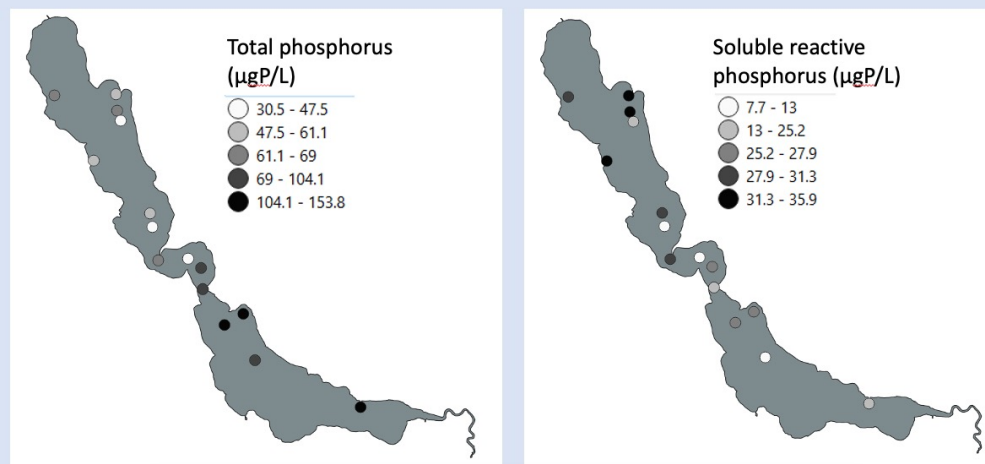
Select sampling survey early results - 2022

High chlorophyll-*a* and total suspended solids

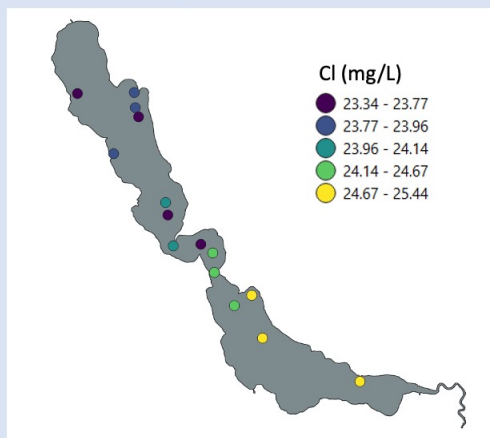


All values are epilimnetic means from 2021-2022

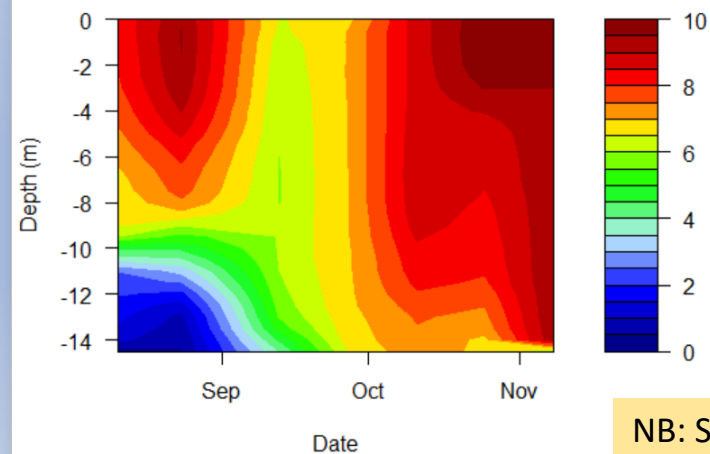
Potential SRP uptake in South Basin



Chloride is higher in the south basin



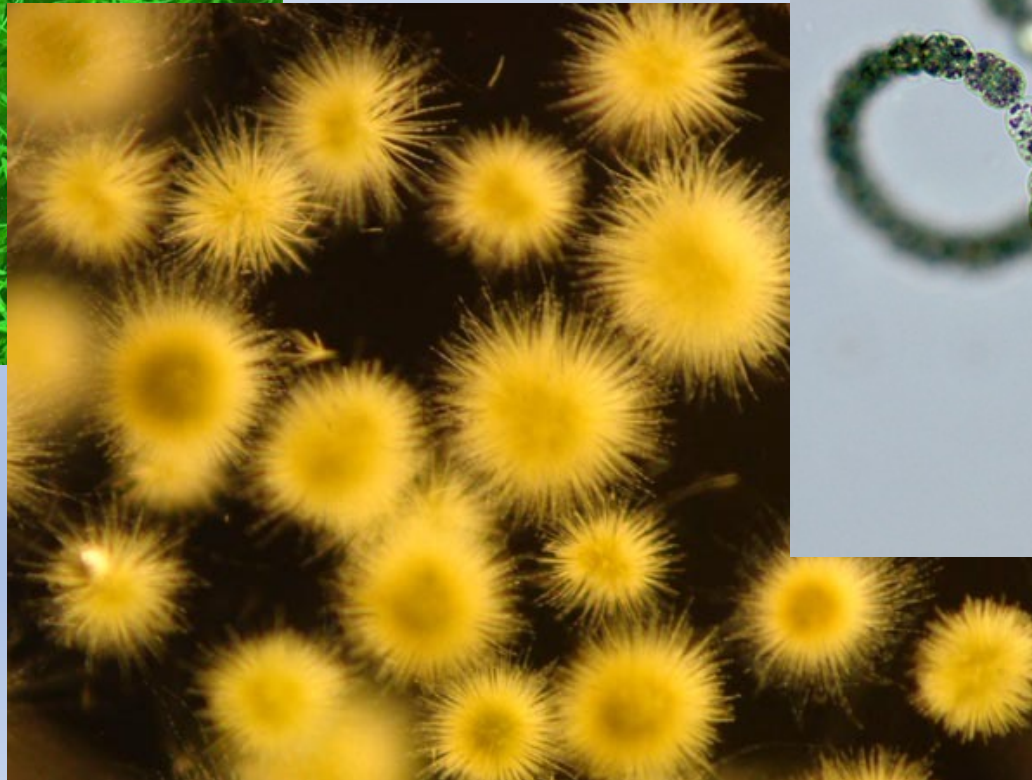
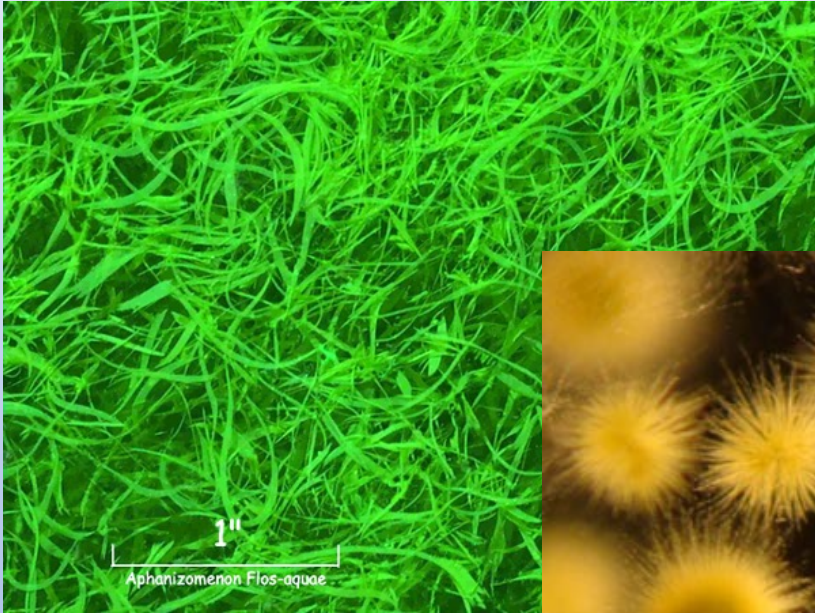
Long Point - Dissolved oxygen (mg/L)



NB: Stratification @ 11m



Nitrogen-fixing cyanobacteria are common





Summary of 2022 sampling findings

- Different conditions in 2021 vs. 2022
 - SRP, nitrate, and perhaps ammonium were much higher later in the season in 2022
 - Higher chlorophyll in 2022
- Chloride dynamics are not unexpected (road salt incursion) and may be worth further investigation
- Evidence of nitrogen limitation

Advanced technology and
supporting cyberinfrastructure



JP technologies have been essential tools to better understand HABs



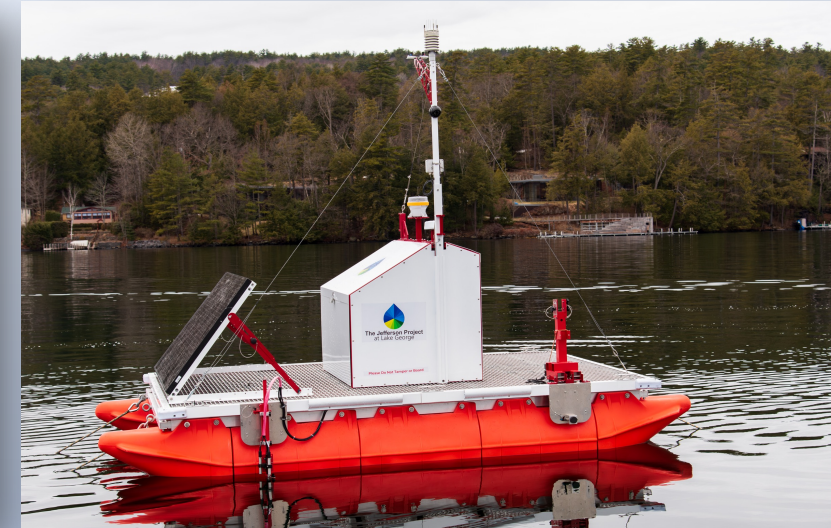
YSI 6951

- Standard sensor payload with limited sensor expandability and integration
- Coarse spatial profiling
- 135 W solar capacity
- 200 Ah battery capacity
- No water current monitoring capability



RPI CATS V1

- Enhanced sensor payload
- High frequency profiling with precise depth acquisition
- 300 W solar capacity
- 300 Ah battery capacity
- Single water current sensor (ADCP)



RPI CATS V2

- Enhanced sensor payload
- High frequency profiling with precise depth acquisition
- Integrated triple ADCP and surface WQ sensor mounts
- Larger, more stable platform
- 300 W solar capacity
- 400 Ah battery capacity
- Improved visibility and safety
- Increased flotation and deck space

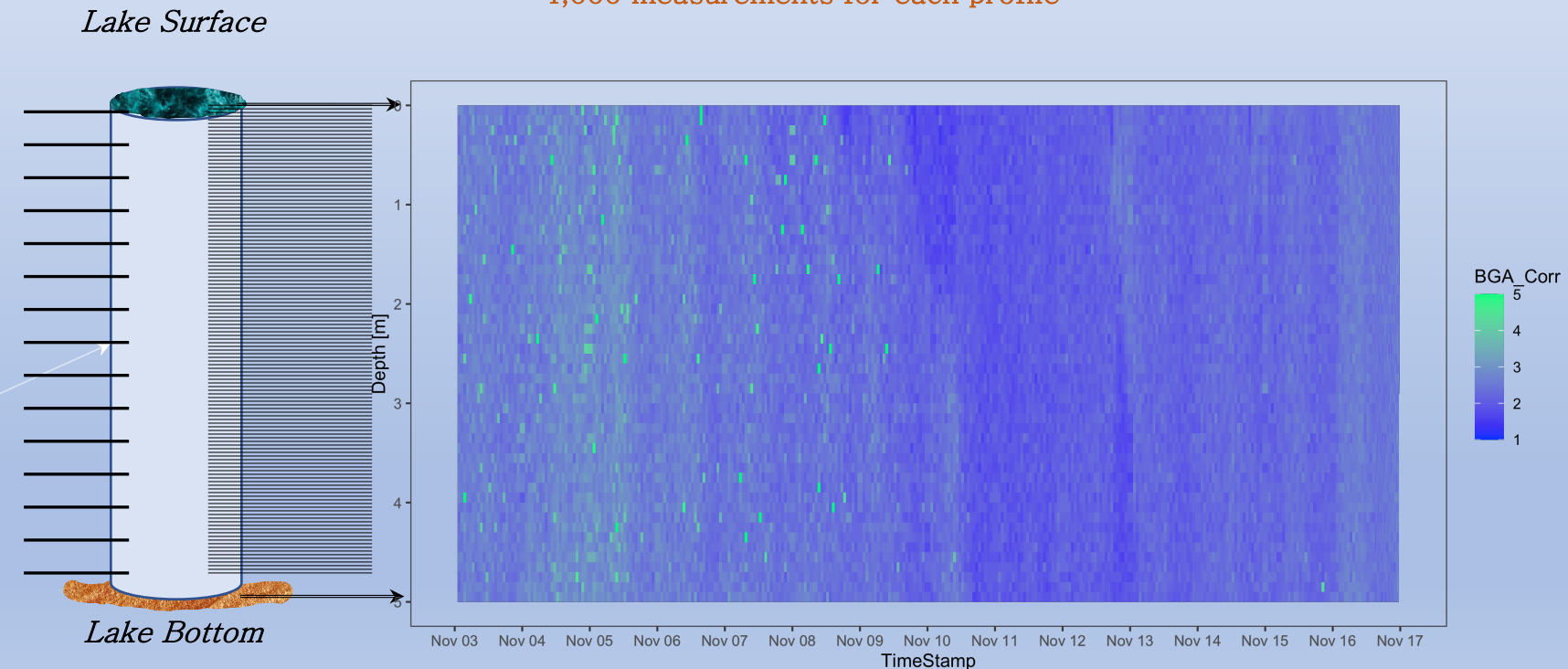
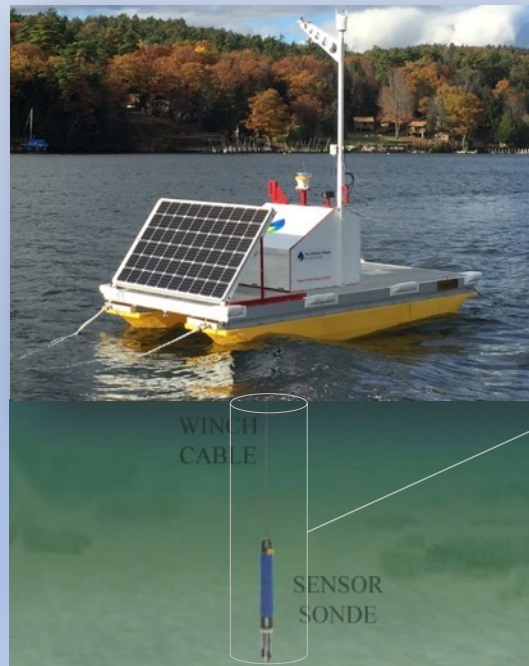


HABs are more than a surface phenomenon

Jefferson Project Advanced Technology

Detecting Blue-Green Algae (BGA) in the water column via high-resolution measurements

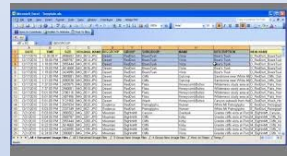
30 minutes to profile surface to bottom
4,000 measurements for each profile



Lake George



A coupled observatory and modeling System at Lake George



~39 years of
historical
water
quality data

Analytics Platform

Visualization

Scenario Engine

Analytics

Data &
Semantics

Operational Model Forecasting Platform

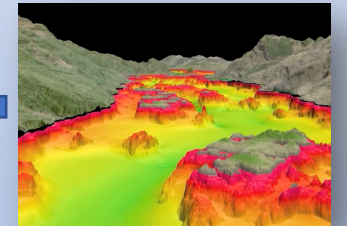
Chemistry/Biology

Circulation/Ice/Particle

Runoff/Pollutants

Weather/Land Surface

Bathymetric &
topographic
survey data



IoT Edge Nodes (Sensors with real time, autonomous edge analytics and AI)



Vertical Profilers



Weather Stations



Stream Stations

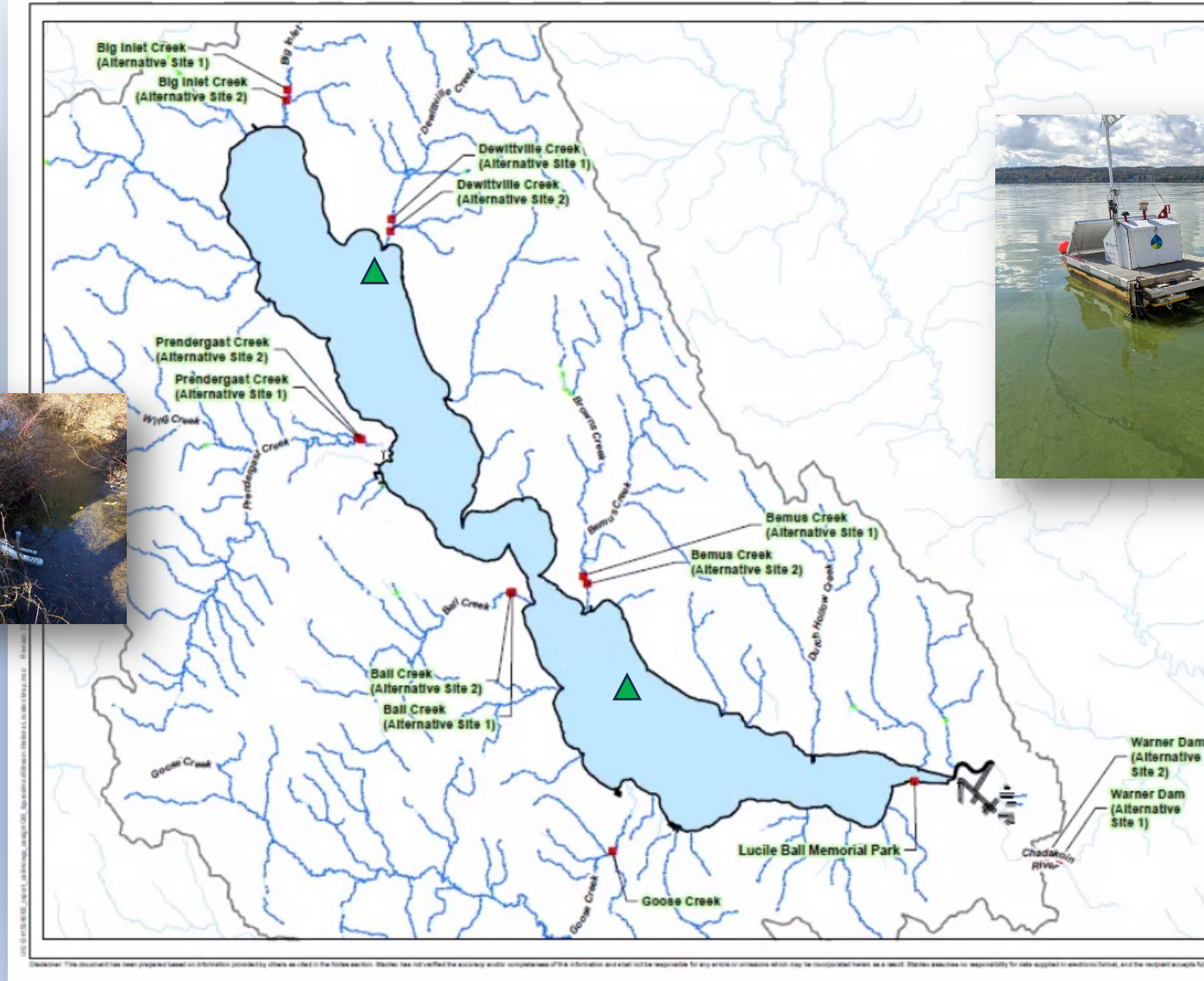
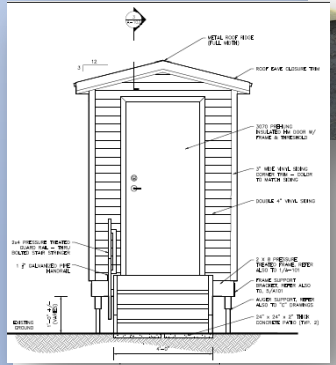


ADCPs

~50 sensor platforms, 500 sensors, 1.3 B observations

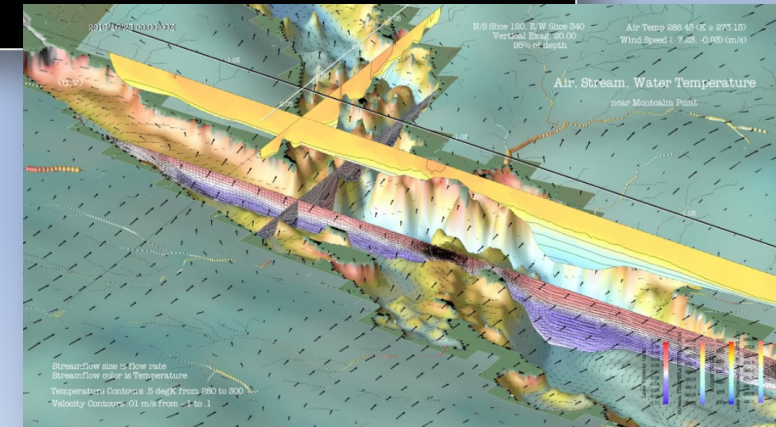
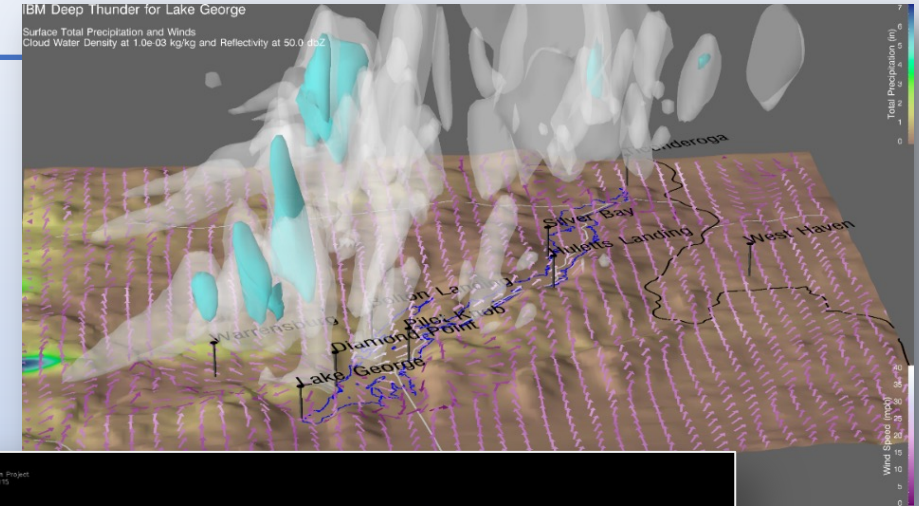
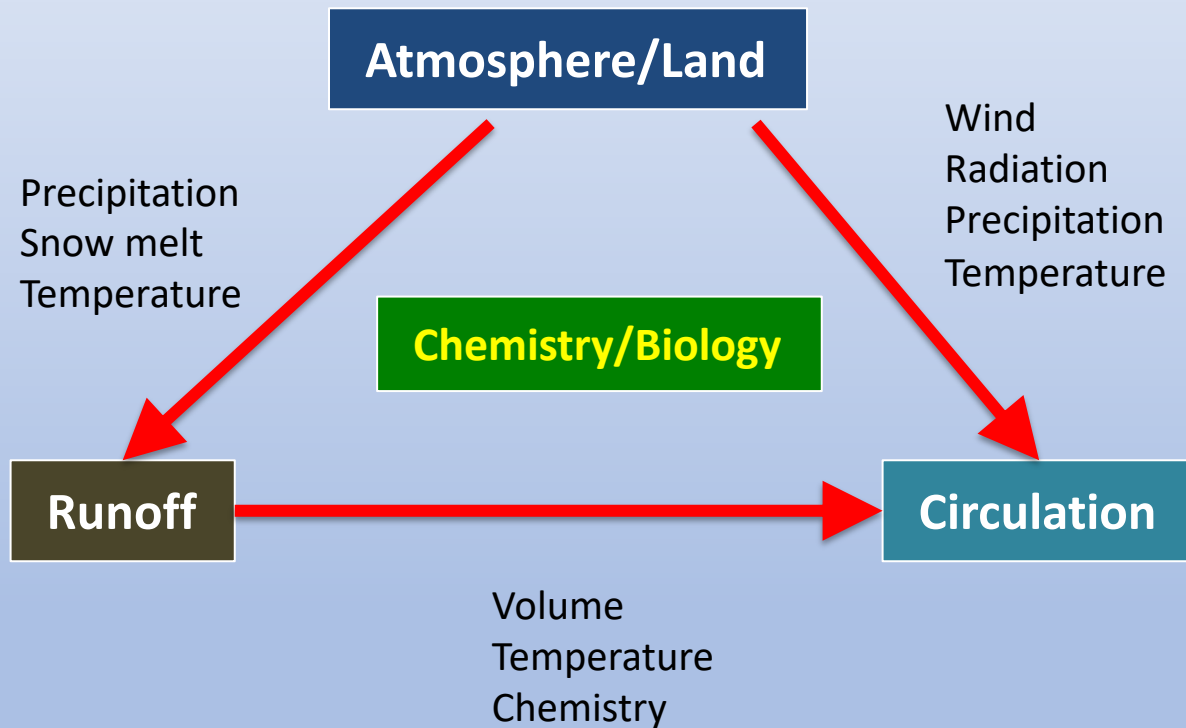


Vertical profiler deployments and tributary monitoring station rollout





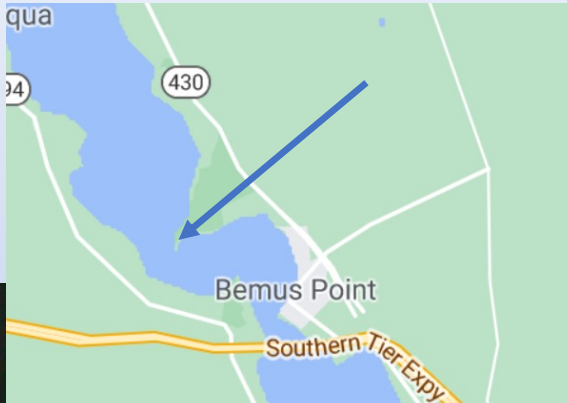
Coupled computer models provide the foundation for prediction



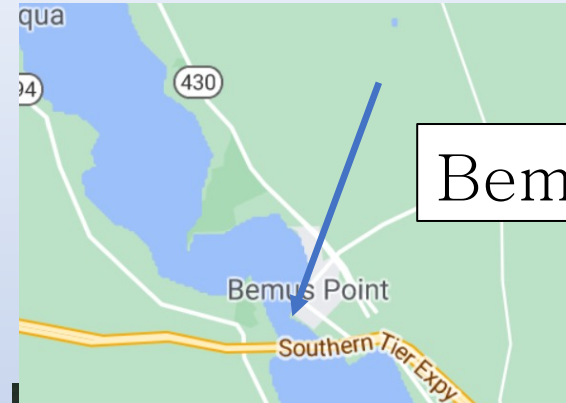
These models are “operational,” running daily and generating huge amounts of data...



Chautauqua Lake circulation studies 2022



Long Point

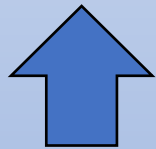


Bemus Point

Low
Frequency



Currents



: upper



: lower

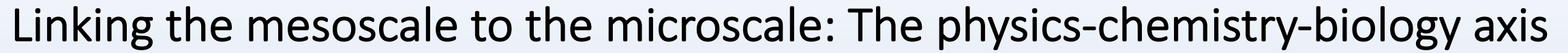
Low
Frequency



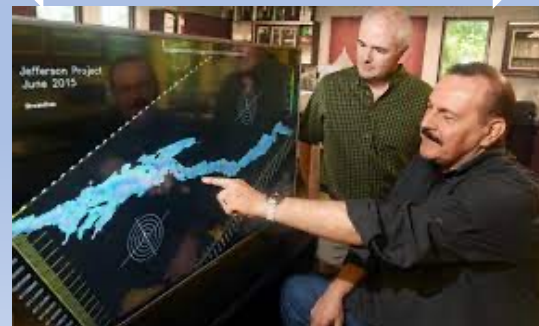
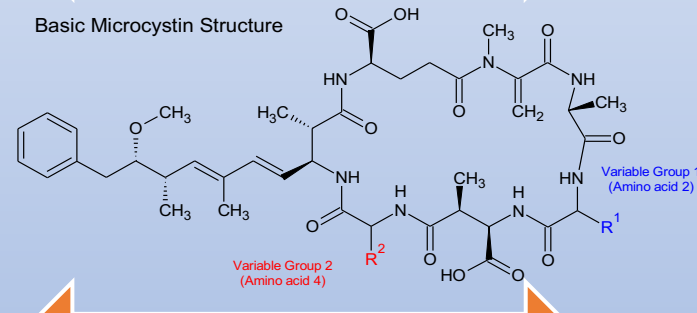
High
Frequency



Genomics



A photograph showing three people standing in front of a large, open server rack in a data center. On the left, a man in a dark suit and patterned tie points towards the server. In the center, a woman in a dark blazer and skirt stands with her hands clasped. On the right, a man in a red t-shirt with 'NASC' and 'NATIONAL ASSOCIATION OF STATE CHIEFS OF POLICE' printed on it, and dark pants, stands with his hands on his hips. The server rack is filled with numerous network cables and components. The background shows other server racks and a tiled floor.



The diagram illustrates two primary methods for analyzing microbial communities: the 16S-based approach and the shotgun metagenomic approach.

The 16S-based approach

This method focuses on the 16S rRNA gene, which is present in all bacteria and archaea. The process involves:

- Extract DNA**: DNA is extracted from the microbial community sample.
- Amplify and sequence 16S rRNA**: The 16S rRNA gene is amplified and sequenced.
- Group similar sequences into OTUs**: Sequences are grouped into Operational Taxonomic Units (OTUs) based on similarity. The diagram shows four OTUs (OTU1, OTU2, OTU3, OTU4) with their corresponding 16S rRNA sequences.
- Use database to identify OTUs**: The OTUs are identified using a database like GreenGenes, myRDP, or Silva. The NCBI logo is also present.

Community composition: Which organisms are present?

From the 16S-based approach, two types of data are derived:

- Abundance of OTUs in community**: Represented by a bar chart showing the relative abundance of each OTU.
- OTU phylogeny**: Represented by a circular phylogenetic tree showing the evolutionary relationships between the OTUs.

Variant sequences and SNPs: The diagram shows several variant sequences and single nucleotide polymorphisms (SNPs) for the GATTACA sequence:

- GATTACA
- GATTACA
- GATTACA
- GATTACA
- GATTACA

The shotgun metagenomic approach

This method involves sequencing all the DNA in a sample, providing a more comprehensive view of the community. The process involves:

- Extract DNA**: DNA is extracted from the microbial community sample.
- Sequence community DNA**: The entire community DNA is sequenced.
- Compare sequences to reference genomes**: The sequenced DNA is compared to reference genomes in a database like NCBI.
- Use database to identify sequences**: The sequences are identified using a database like KEGG, SEED, or BLAST.

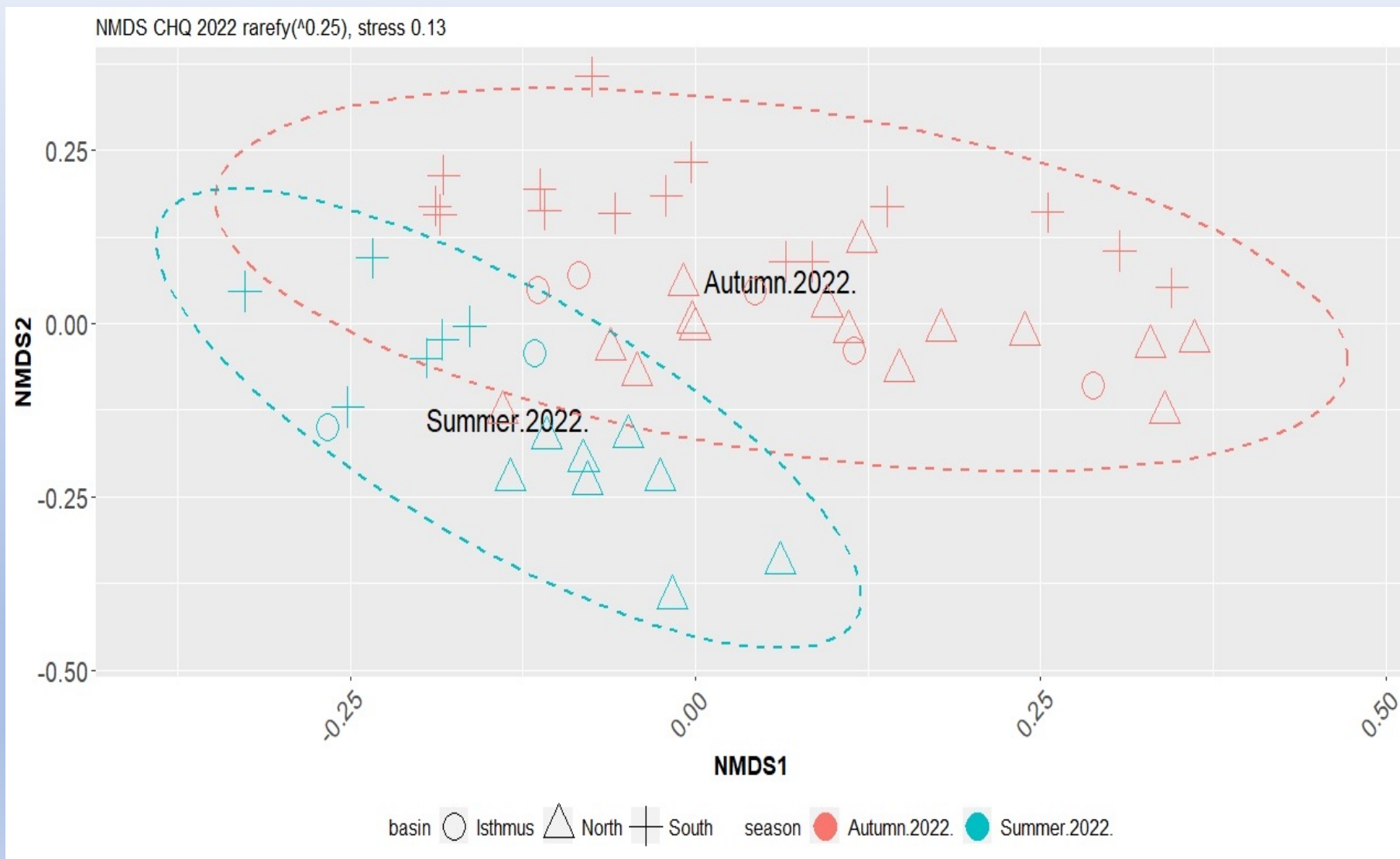
Community function: What can the community do?

From the shotgun metagenomic approach, two types of data are derived:

- Relative abundance of gene pathways in community**: Represented by a bar chart showing the relative abundance of different gene pathways.
- Functions**: The diagram shows a bar chart with the label "Functions" on the x-axis and "Abundance" on the y-axis.

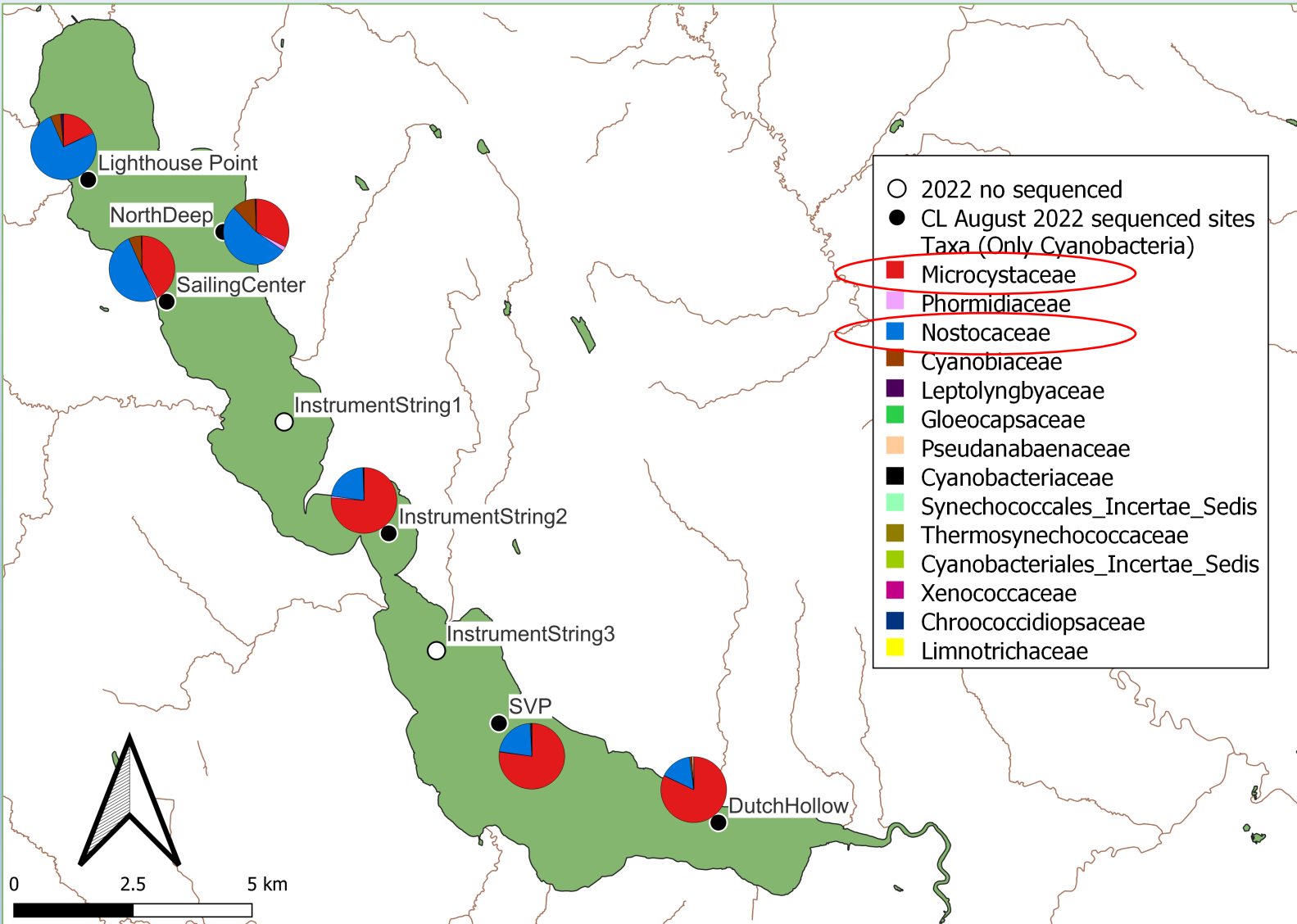


Microbial community structure – Chautauqua Lake



At a large time scale (entire season) the community structure is separated by season and basin, most likely explained by the many differences between basins

Spatial distribution of 16S cyanobacteria abundances in Chautauqua Lake blooms (Aug. 2022)



- Cyanobacteria in Chautauqua Lake are represented by a few families.
- Most abundant: Microcystaceae (red) & Nostocaceae (blue).
- Very different bloom composition than Lake George.
- Cyanobiaceae (brown) (*Synechoccus*) is more abundant in the less eutrophic Northern basin.



What is next?

- Continue to obtain samples and obtain high-quality sequences
- Perform transcriptomics (RT-PCR) of cyanobacteria focusing on known toxin pathway genes. Correlate bloom vs. no bloom and toxin formation vs. no toxin formation.
- Perform mass spectrometry analysis to identify and quantify toxin production from lake samples.
- Develop models that link the physical and chemical features of the lakes with the microbial populations.

Goal: Curate the data and develop predictive machine learning models.

(Optionally: Perform highly controlled mesocosm studies to test models)



2023 Plans: the way forward

Sampling

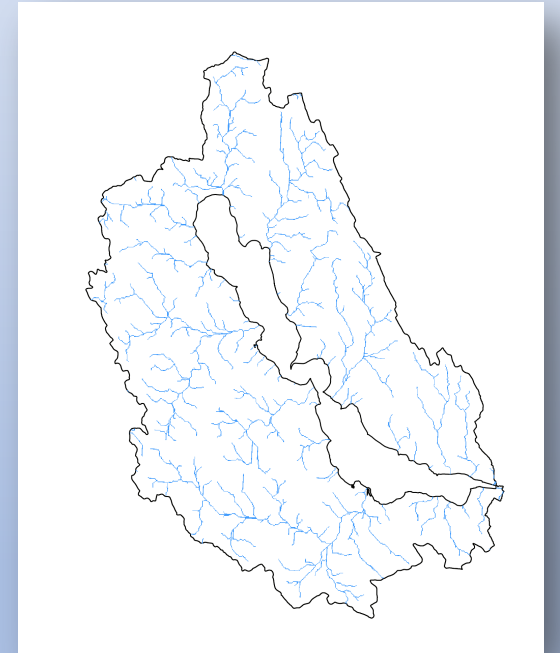
- Continue biweekly lake sampling program
 - Focus on toxins via transcriptomics

Observations/measurements

- Redeploy next generation vertical profilers in N and S basins
- Complete the tributary station and outlet (Chadakoin River) rollout

Modeling

- Validate and refine the hydrological (runoff) model
- Characterize stream runoff effects
- Determine water residency times for Bemus Bay
 - water from the north basin
 - water from the south basin
 - during both stratified and unstratified seasons
- Continue building the lake nutrient model





Summary

- We continue to make significant progress in the understanding of the multiple components contributing to the development of HABs. These include physical, chemical, and biological elements.
- The investment in research and technology development in conjunction with research spanning multiple lakes has been instrumental to this progress.
- Our recent advances in the application of genomics have shown great promise and suggest important findings for the near future.
- Due to the complexities of the possible multiple mechanisms involved with HABs, our near-term focus is on characterization, detection, and prediction.
- HABs remediation/prevention is likely to be complicated and expensive. Nutrient reduction will be very important and actions on this front should remain a priority.