

# HARMFUL ALGAL BLOOM SURVEILLANCE VIA SEQUENCING OF ENVIRONMENTAL DNA

## CASE STUDY

Elder Research partnered with Signature Science and JMU to develop an Environmental DNA Sequencing and Bioinformatics analysis pipeline to predict harmful algal blooms (HABs) to protect human life, the environmental, and commercial interests. This technology was designed to be a portable and affordable solution for governmental agencies and commercial co-ops to leverage.

## THE CHALLENGE

Toxic HABs of many different species represent a direct risk of injury or death to humans, but even algal blooms that are not directly toxic can cause significant damage by leading to hypoxia/anoxia in the water column, shading critical submerged aquatic vegetation, and degrading ecosystem function.

Harmful algal blooms (HABs) represent a significant problem for the Blue Economy, adversely affecting drinking water, commercial fisheries, water recreation, and tourism costing hundreds of millions of dollars in management and mitigation efforts. As the global climate continues to warm, the number and severity of HABs is expected to increase, along with their incumbent deleterious health and economic effects.

Early detection of HABs is crucial in mitigating their effects. To date, there has been little characterization of water ways and the current make up of the water at any given point in time to assess conditions before, during, and following a HAB due to previous costs and complexity.

## THE SOLUTION

The HABSSSED pipeline is a novel, rapid, inexpensive surveillance technique for detecting HABs by leveraging abundance of microbial taxa in the environment, measured through eDNA sequencing using 3rd generation sequencing technology, specifically Oxford Nanopore's MinION device. The pipeline will be simple enough to democratize the process, such that citizen scientists and labs with limited funding can benefit from it.

HABSSSED is designed to be field-portable, incorporating 'omics tools and workflows that can be run on a well-powered laptop or using Amazon Web Services (AWS) or other similar cloud instance to rapidly obtain an estimate of aquatic microbial species abundance for HAB-related organisms from a raw water sample.

## PARTNERS



## INDUSTRY

- Aquaculture & Ecotourism
- Maritime Transportation
- Federal, State, and Local Government
- Environmental Advocacy

## NEED

- Harmful algal blooms (HABs) represent a significant challenge to the health of the world's waters
- Early detection of HABs by monitoring of affected waters is critical to mitigation efforts

## SOLUTION

- HABSSSED is an Environmental DNA Sequencing and Bioinformatics analysis pipeline to predict harmful algal blooms (HABs)

## BENEFIT

- Implement mitigations before people, animals, and industry are impacted
- Powered by the same laptop used for data analysis

## FUNDING AGENCY

- National Oceanic and Atmospheric Administration (NOAA)

### OFFICE LOCATIONS

Charlottesville, VA | Baltimore, MD  
Raleigh, NC | Washington, DC



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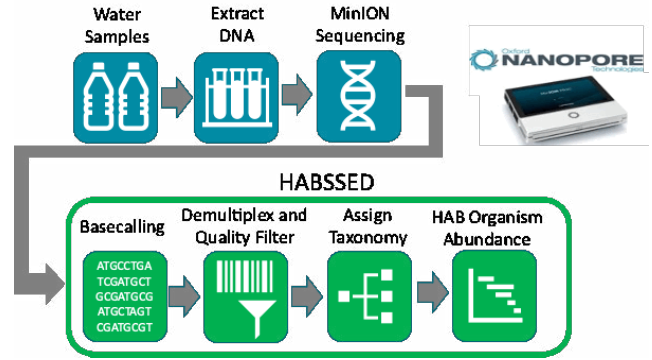
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## THE SOLUTION *(continued)*

Satellite-based approaches (e.g. Sentinel-3) and other approaches relying on biomass can only detect blooms already in progress. PCR-based approaches require either the deployment of large instruments or expensive and complicated microfluidic chips, or a return of samples to a non-field laboratory and can miss rare taxa.

Currently, we are the only provider who offers the combination of the technologies for the purpose of field-forward, early-detection and analysis of HABs. HABSSED provides the needed data infrastructure and storage to enable the development of quantitatively rigorous forecasts for HAB initiation, duration, and severity.



## RESULTS

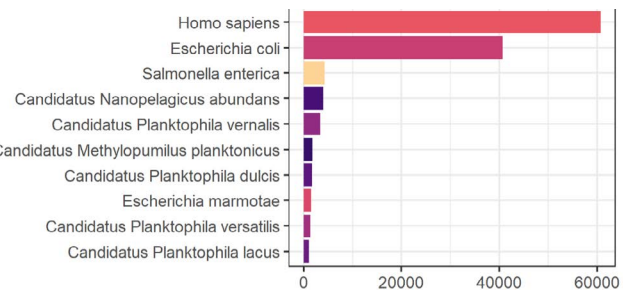
We have successfully demonstrated the feasibility of our approach, by sequencing water samples drawn from Lake Erie GLERLs before and during Microcystic blooms that took place in 2019, and showing differential abundance of Microcystis species between bloom-drawn and pre-bloom samples.

We sequenced the prepared sample libraries using the Oxford Nanopore MinION hand-held sequencer over a 48-hour run, working in close consultation with the MinION sequencing experts at Signature Science.

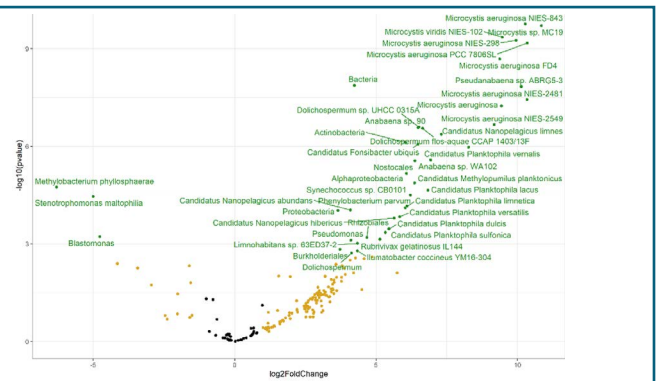
We found that the relative abundance of Microcystis and the qualitative distribution of taxa stabilized between 16 and 24 hours into the 48-hour run. This suggested that multiplexing two to three samples per flow cell would be effective for detecting Microcystis at pre-bloom abundance levels.

We performed differential abundance analysis to determine which taxa significantly differ in their abundance between bloom and non-bloom conditions. Confirming that Microcystis spp. are among the differentially abundant organisms was a key sanity check that this method can effectively detect blooms. The taxa more abundant in pre-bloom conditions are useful indicators of a pending bloom and form the basis for our predictive model.

**Top 10 Most Abundant Species In Pre-Bloom Full Run Samples**



Panel plot showing species abundance for pre-bloom samples showing evidence of Homo s. and E. coli contamination.



Volcano plot displaying results of differential abundance estimates. Significance level (y-axis) and fold change between bloom and pre-bloom (x-axis) are displayed.

## ABOUT ELDER RESEARCH

Elder Research is an internationally recognized data analytics solution provider with over 28 years of expertise in data strategy, data science, data engineering, and training. We have operationalized innovative solutions for hundreds of organizations across diverse industries. Our handcrafted AI and machine learning solutions inform decisions, deliver business value, and transform organizations.

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