

DNA metabarcoding as a tool for assessing nutrient pollution

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(Science speed talks on nutrients-related research)

DNA metabarcoding



Goals

- Characterize diatom- and microbial-environment relationships (periphyton)
- Develop DNA-based indicators
- Explore possible uses for monitoring and assessment programs (e.g., nutrient targets)



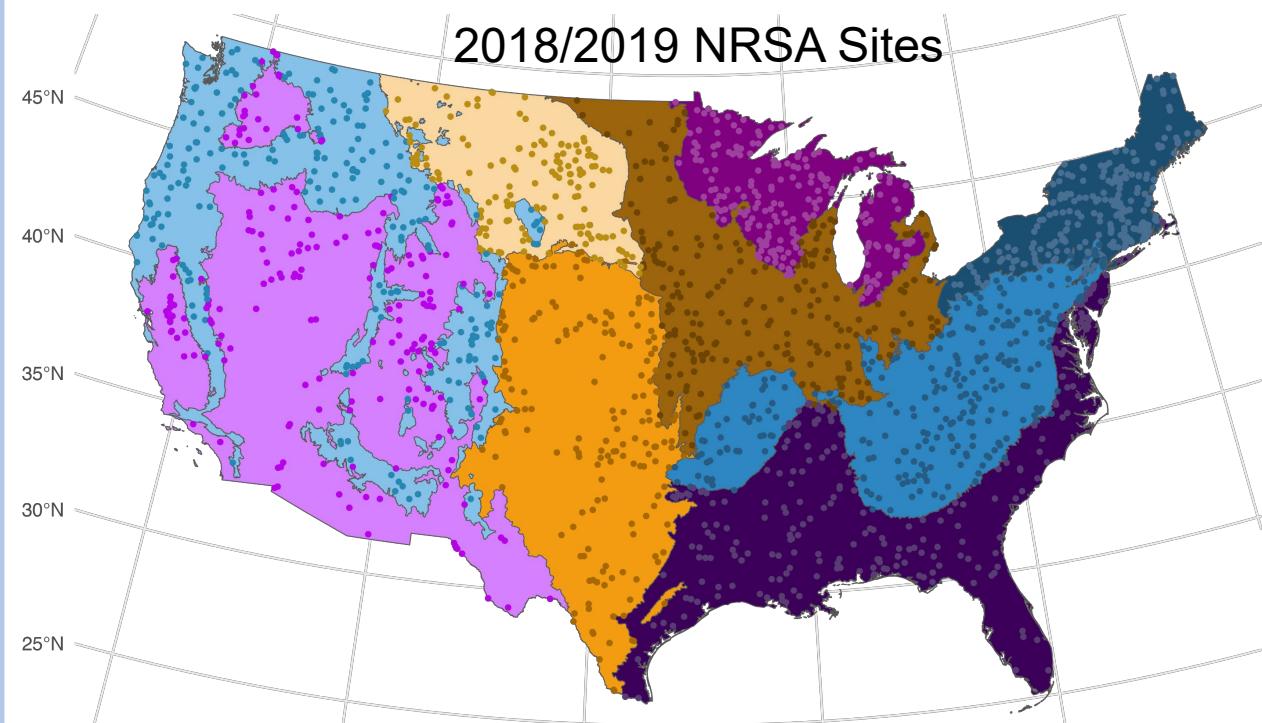
Approach

- National Rivers and Streams Assessment
- Watershed studies and stressor gradients
- Experimental stream mesocosms

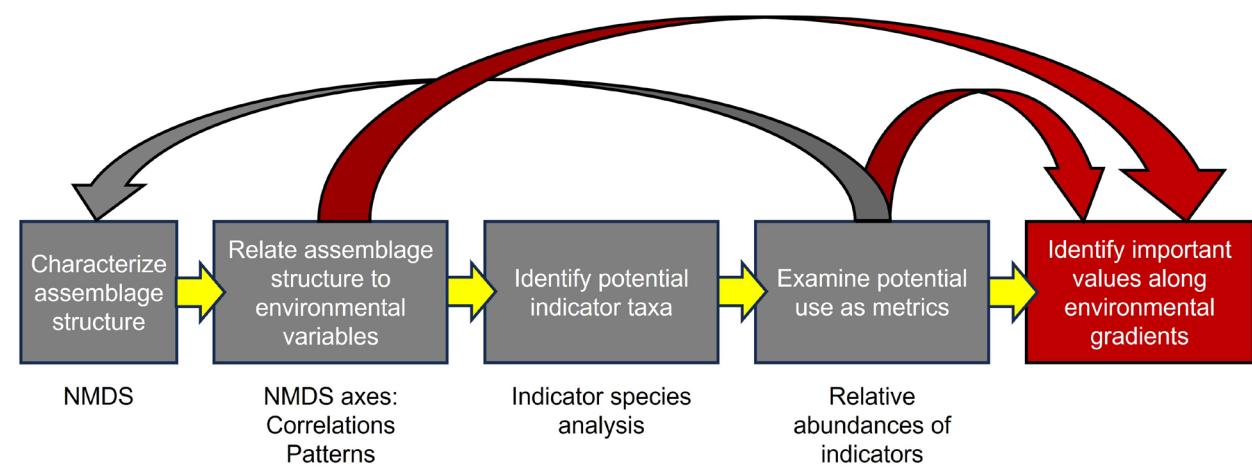


Scope

- National
- State and regional partners
- Washington State Department of Ecology



TITAN / Generalized additive models / Boosted regression trees



The views expressed in this presentation are those of the authors and do not necessarily represent the views or policies of the U.S. Environmental Protection Agency

Selected results

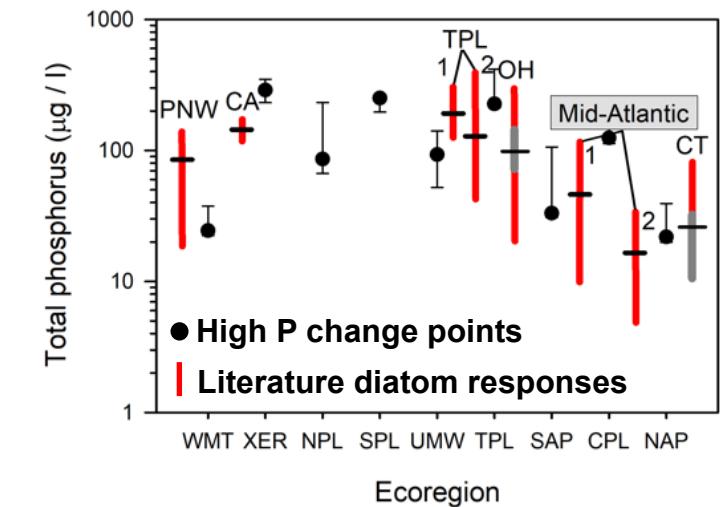
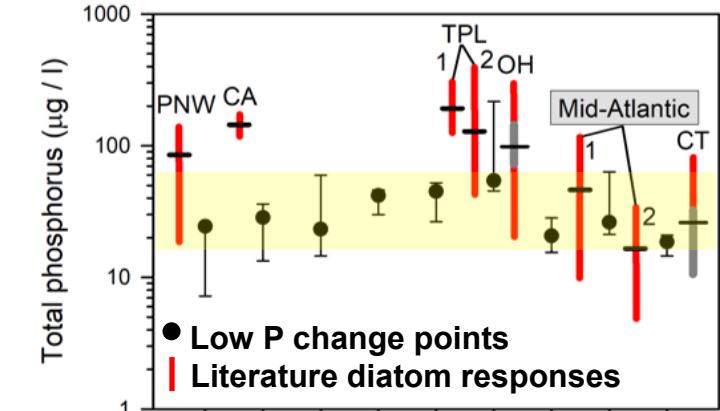
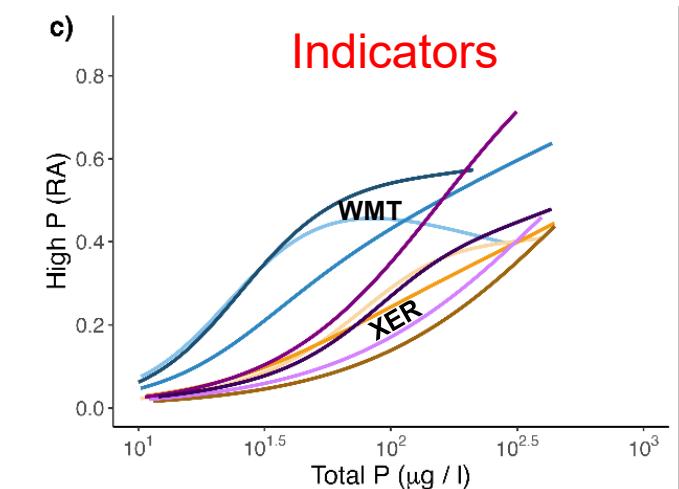
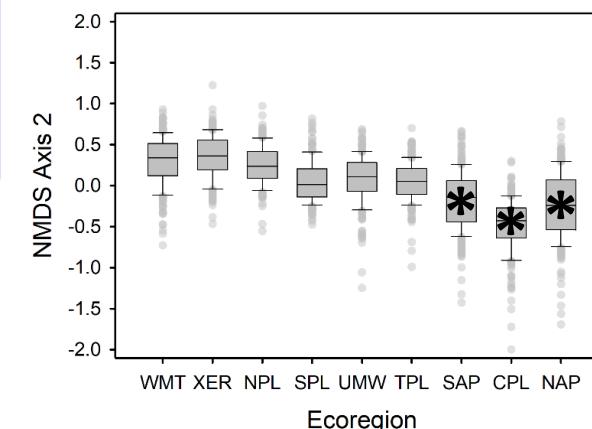
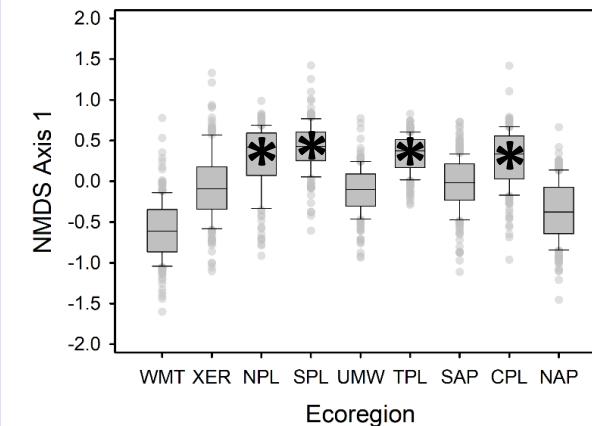
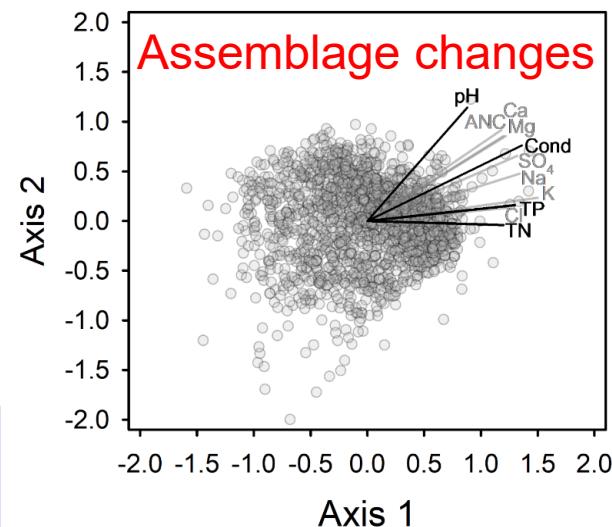
Integrate nutrient effects over time

Ecoregional differences

Differences in variable importance

Environmental relationships

Possible management targets

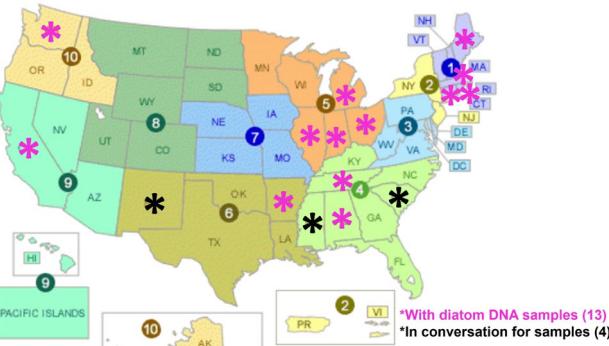


Next steps and transferability

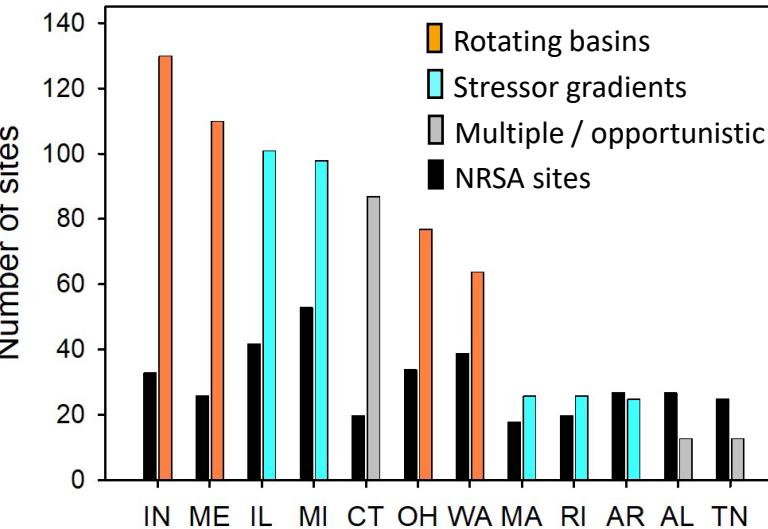


Test and refine indicators for real-world applications

Partnerships with states and other EPA offices and locations



Bridge gaps between watershed and large regional/national scales



Develop efficient R workflow for:

Integrating new DNA metabarcoding datasets
Harmonizing taxa (gene sequences) and traits
Conducting statistical analyses
Producing figures and visualizations

