

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)



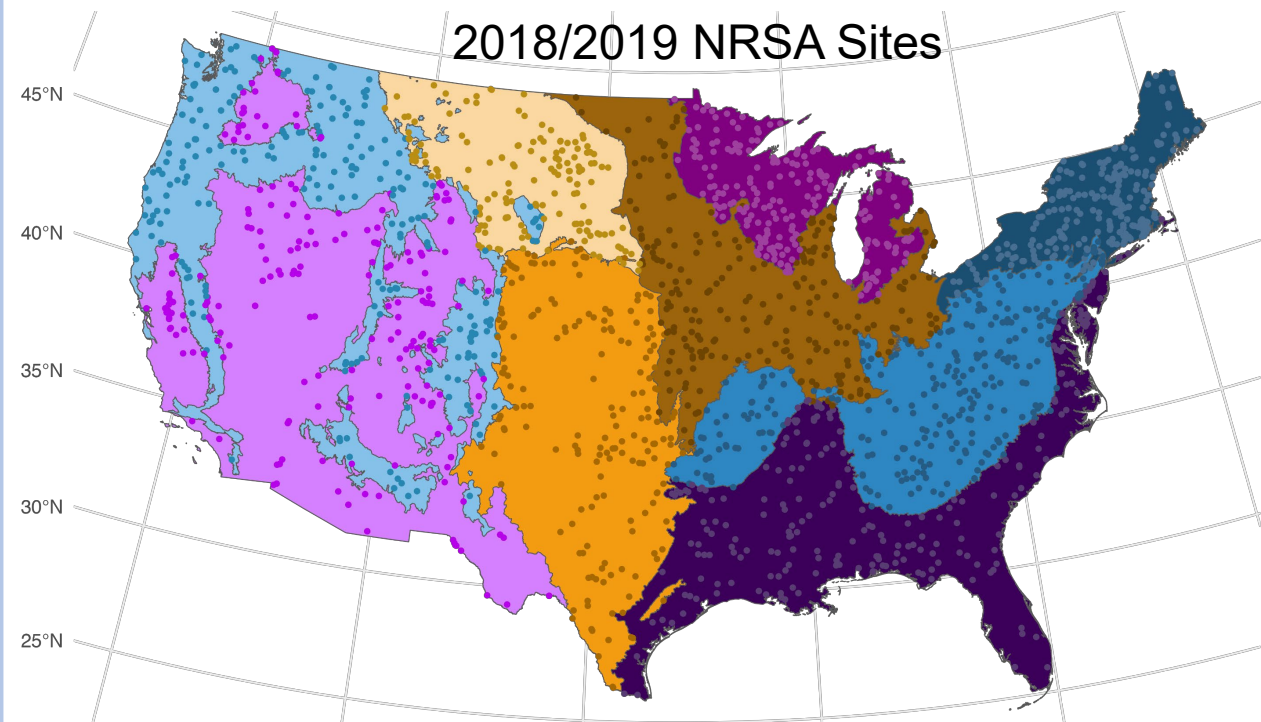
Approach

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

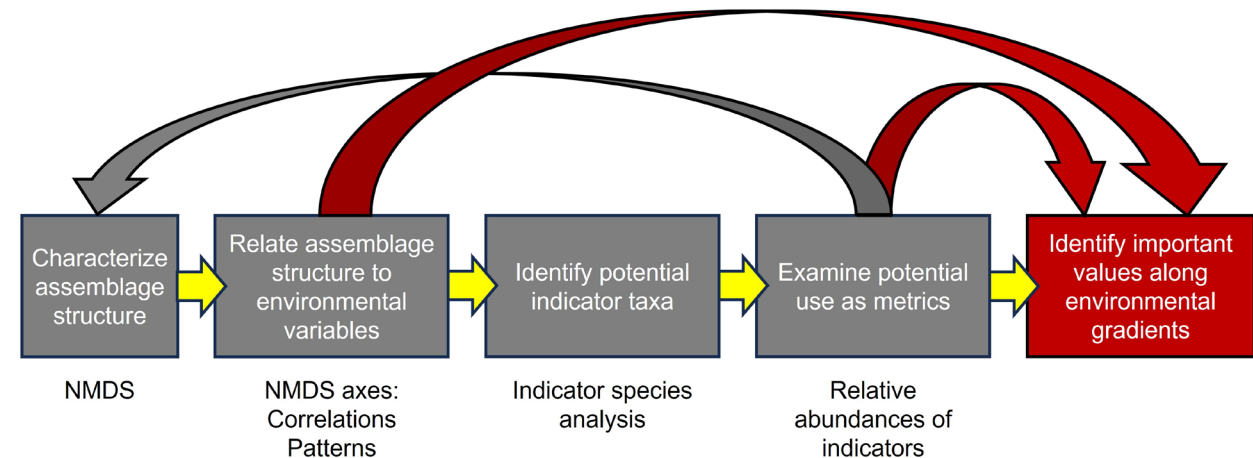


Scope

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

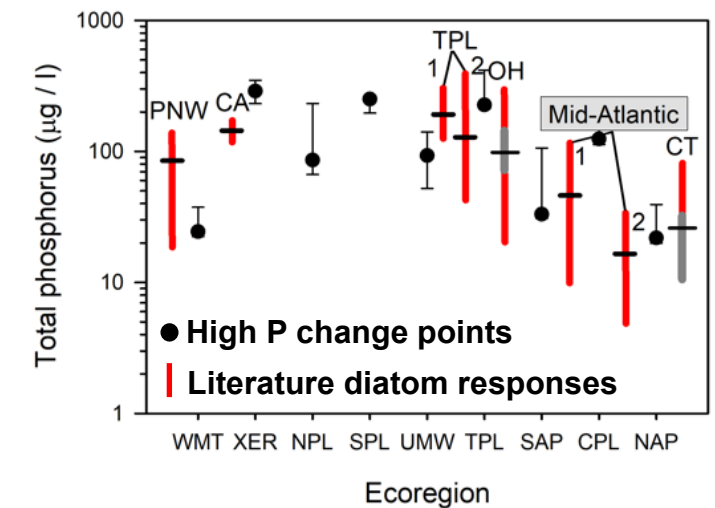
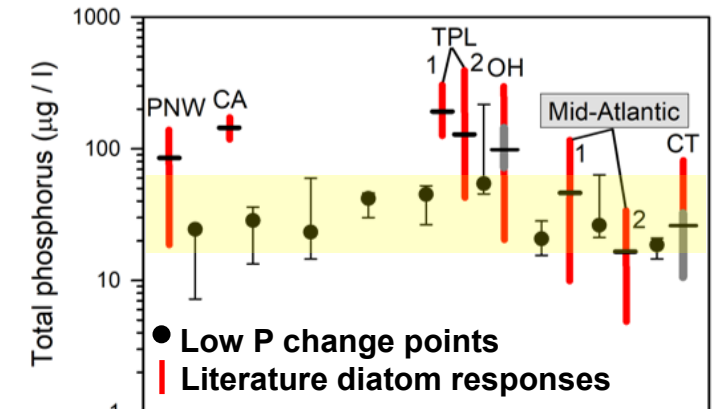
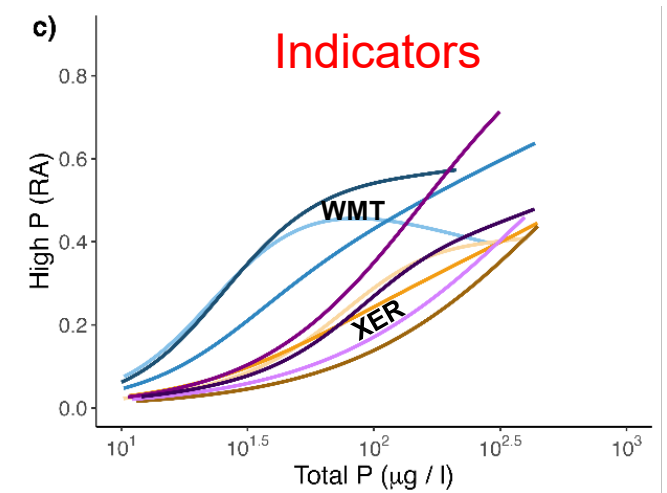
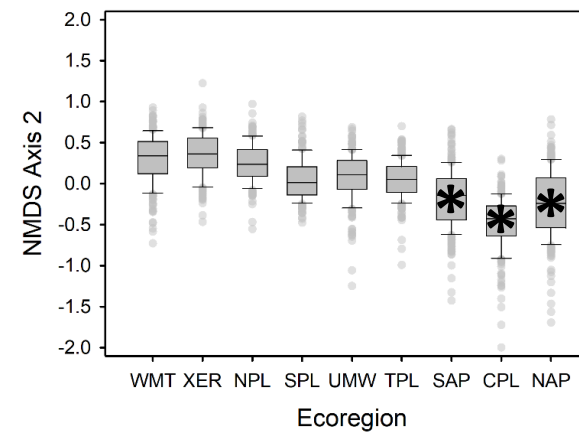
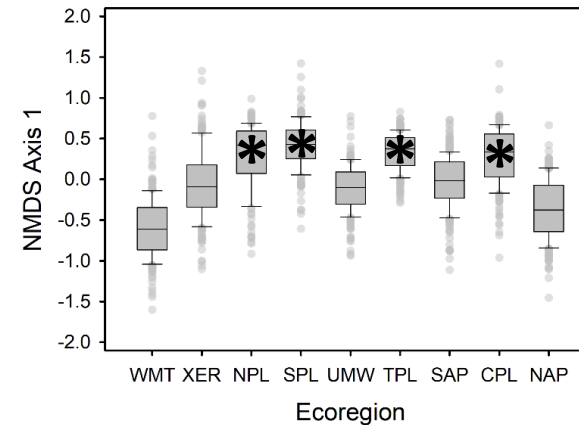
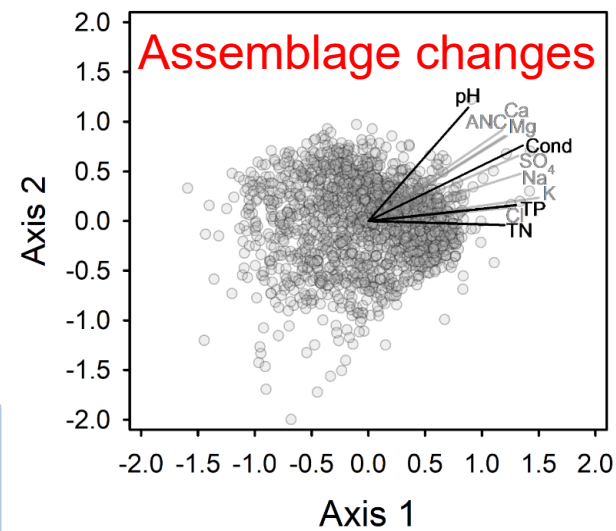
Integrate nutrient effects over time

Ecoregional differences

Differences in variable importance

Environmental relationships

Possible management targets



Next steps and transferability



Test and refine indicators for real-world applications



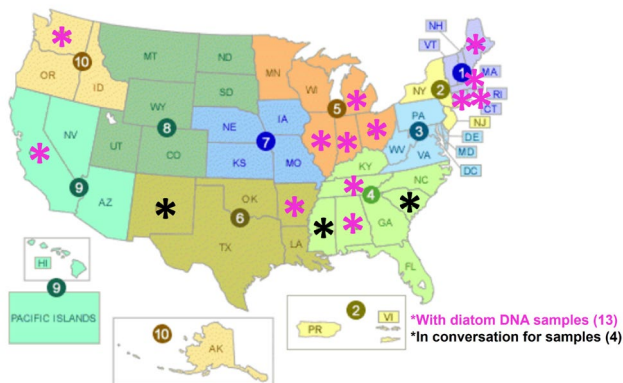
Bridge gaps between watershed and large regional/national scales



Develop efficient R workflow for:

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

Partnerships with states and other EPA offices and locations



- (1) Test and refine indicators for real-world applications
- (2) Fill in gaps between watershed and large regional/national scales

