

## USING NULL MODELS TO TEST HYPOTHESES ABOUT THE DRIVERS OF FRESHWATER DIATOM DIVERSITY AND DISTRIBUTION.

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Ecologists have long emphasized that well-designed null models are essential to minimizing the risk of misinterpreting ecological patterns. Consequently, null models are now commonplace in the broader community ecology, biogeography, and biodiversity literature, and ecologists are more cognizant of the pitfalls of interpreting observational data at face value. Has research on diatom ecology, distribution, and diversity witnessed similar advances? Or are important insights potentially being missed owing to an over-reliance on traditional, correlative analyses?

I first provide a brief review of how null models have been used in diatom research, and by drawing parallels with research on macro-organisms, I highlight when and where their application could prove beneficial. Then, using large calibration datasets from North America, I show how null models can reveal intriguing sub-patterns within broader diversity patterns that would otherwise go unnoticed. For example, research on macroorganisms has shown that widespread and rare taxa can contribute to diversity patterns in dramatically different ways, with widespread species accounting for most of the variation in richness. Similar patterns are observed among diatoms: widespread taxa largely account for the observed unimodal relationship between local (lake-scale) taxonomic richness and pH. However, null models of pH tolerance that account for variation in occupancy rate reveal strikingly different patterns, including an intriguing peak in the richness of pH “specialists” that coincides with the pH of the oceans: 8.2. Additional null models show that this pattern is itself highly unlikely to have arisen by chance. Although null models are certainly not a panacea, I argue that their appropriate application could be as beneficial and revolutionary to diatom research as it has been for research in the broader ecology realm.