obtain a competition coefficient, quantifying the parakeets' impact on other species. In Belgium, ring-necked parakeets face invasion ecologists. In Europe, ring-necked parakeets have been widely introduced, and their growing populations are known to compete with native cavity-nesters such as nuthatches. Spatially explicit predictions of potential parakeet and nuthatches. The interaction between parakeets and nuthatches was then quantified, with competition coefficients used to assess the impact of parakeets on other species. In Belgium, ring-necked parakeets were not a threat to native species, but in other areas, they could become one of the dominant species. Understanding species interactions and predicting the impact of invasive species on native species is crucial for conservation efforts.

I address three questions: (1) Can taxa with extensive missing data be used to infer evolutionary history and geographic range overlap in a pan-mictic species? (2) Are there pronounced differences in chromatic populations? (3) Do differences exist among biogeographic regions? A new analysis of clade overlap with node depth into the tree suggests evidence of allopatric speciation, but analyses of geographic range and living taxa entail creating data matrices with huge numbers of species. Invasive species can have significant impacts on native species, and identifying the species most vulnerable to climate change can help in developing strategies for conservation. Understanding the interactions between invasive species and native species is crucial for ecological processes during speciation. We report on the evolution of species in Foundry Cove, a location on the Hudson River about 50 miles north of New York City. We continued this work in the Fall of 2008 and used it as an example of the impacts and success of the clean-up for the last few decades. We found that the microbial community in Foundry Cove is much less diverse than in South Cove, a nearby, un-impacted area. The results suggest improved prospects for assessing patterns of microbial diversity with metagenomics.

The results suggest improved prospects for assessing patterns of microbial diversity with metagenomics. Assessing patterns of microbial diversity with metagenomics is crucial for understanding the role of bacteria in ecosystem processes. The results suggest improved prospects for assessing patterns of microbial diversity with metagenomics. Assessing patterns of microbial diversity with metagenomics is crucial for understanding the role of bacteria in ecosystem processes.