



# Using DNA Barcoding to Analyze the Biodiversity of Spiders Throughout



## Mastic Beach

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## Abstract

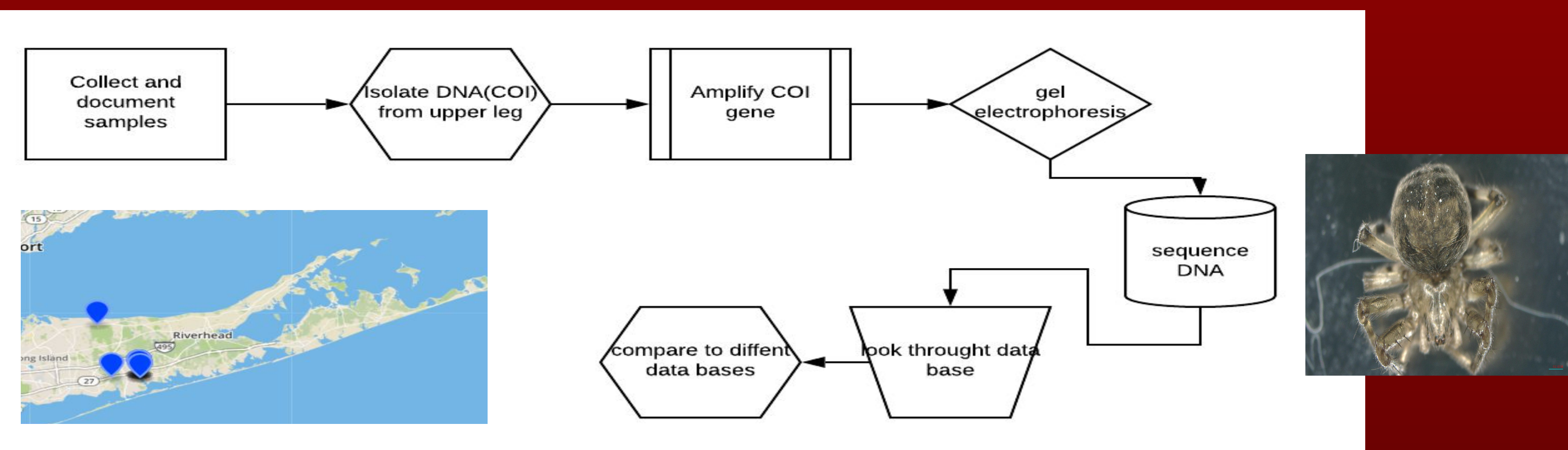
The Forge River is a highly polluted area due to historical duck farming (Swanson et al., 2010). Spiders are important to study because they are biological controls for vectors (Riechert & Lockley 1984). If spiders decrease than other levels of the trophic pyramid may fluctuate with the spider population(Liu,s,2015). A process called DNA barcoding will be used to identify spider species and evaluate regional biodiversity. Specifically, the gene Cytochrome oxidase subunit 1 (COI ) will be used for DNA isolation. A study conducted in 2017-2018 concluded species present varied by location. However, only 8 at of the 20 barcodes were successfully barcoded. The aims of this research is to observe biodiversity of spiders year to year and to increase sample size of the species.

## Introduction

Predatory arachnids are biological controls and consume vectors, such as mosquitoes (Riechert & Lockley 1984). Currently, biodiversity, or the variation of species within the biosphere, is decreasing as a whole due to industrialization (Vörösmarty et al .,2010). Evaluating trends of predatory arachnids is crucial because if one population is decreasing, a trophic cascade may occur. A trophic cascade occurs when a population change in one trophic level influences the surrounding or proceeding trophic levels. When there is a decrease in biological controls, there is potential for vectors populations to increase and spread diseases (Levine & Miller, 1991). The study aims to analyze the biodiversity of predatory arachnids throughout the Forge River regions and compare soil quality to species present.

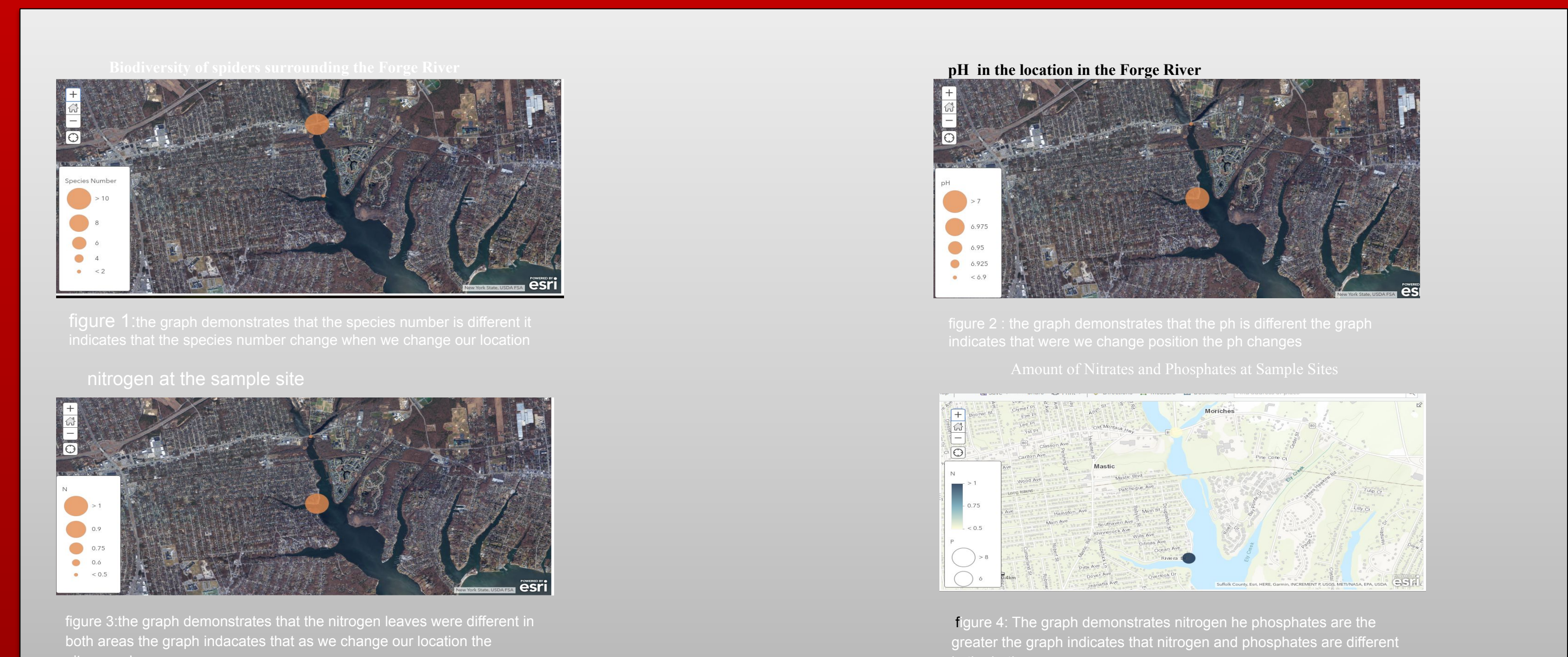
The Forge River is a polluted ecosystem in the Mastic Shirley region. The pollution in Forge River has increased since 1960 due to industrial agriculture and duck farming. The nitrogen levels were at its peak in 1992 then decreases in 1996 and fluctuates throughout the next decade (Swanson et al., 2010). Soil quality affects the way the predatory arachnids success rate of reproducing (Hendrickx et al.,2003).

## Methodology



## References

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## Discussion

### Prey Availability and Arachnid Biodiversity

The head of the river contained the highest biodiversity of predator arachnids. Although, it cannot be confirmed it is believed that this is due to increased prey availability. One reason for this is that the head of the river is forested and contains higher habitat complexity this is associated with increased prey to hide (Halaj et al., 1998). In addition to habitat complexity, the historical duck farms that were located at the head of the river, increased the nitrogen and phosphates within these ecosystems. These nutrients are associated with increased plants growth which then increases food availability for primary consumers. This increase in primary consumers can also attribute to the increased spider presence as they are often the food source for these organisms.

### Human Health Impact

Spiders are bioindicators for the presence of contaminants as they are often the invertebrate apex predators of an ecosystem, feeding on the primary consumers. Studies analyzing the biodiversity of predatory arachnids are important as they can serve as canary species of potential pollutants present. One study published in 2014, suggested that when there are harmful contaminants present, the spiders migrate elsewhere. Therefore, truly polluted regions contain low arachnid diversity (Zommers, 2015). This is alarming as the biodiversity of spiders collected overall within this riverine ecosystem was, with the lowest region containing less than two species of spiders and low populations of both of those species, as seen in figure 4.

### Future Implications and Limitations:

This study had a sample size limited to 20. A future study should increase the sample size to increase the validity of the project. Additionally, using DNA barcoding to identify spiders would increase the accuracy of a biodiversity analysis. Barcoding of the COI gene was attempted however, the COI was not successfully isolated.

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