

Factors Affecting Bird Diversity in a Long Island Saltmarsh

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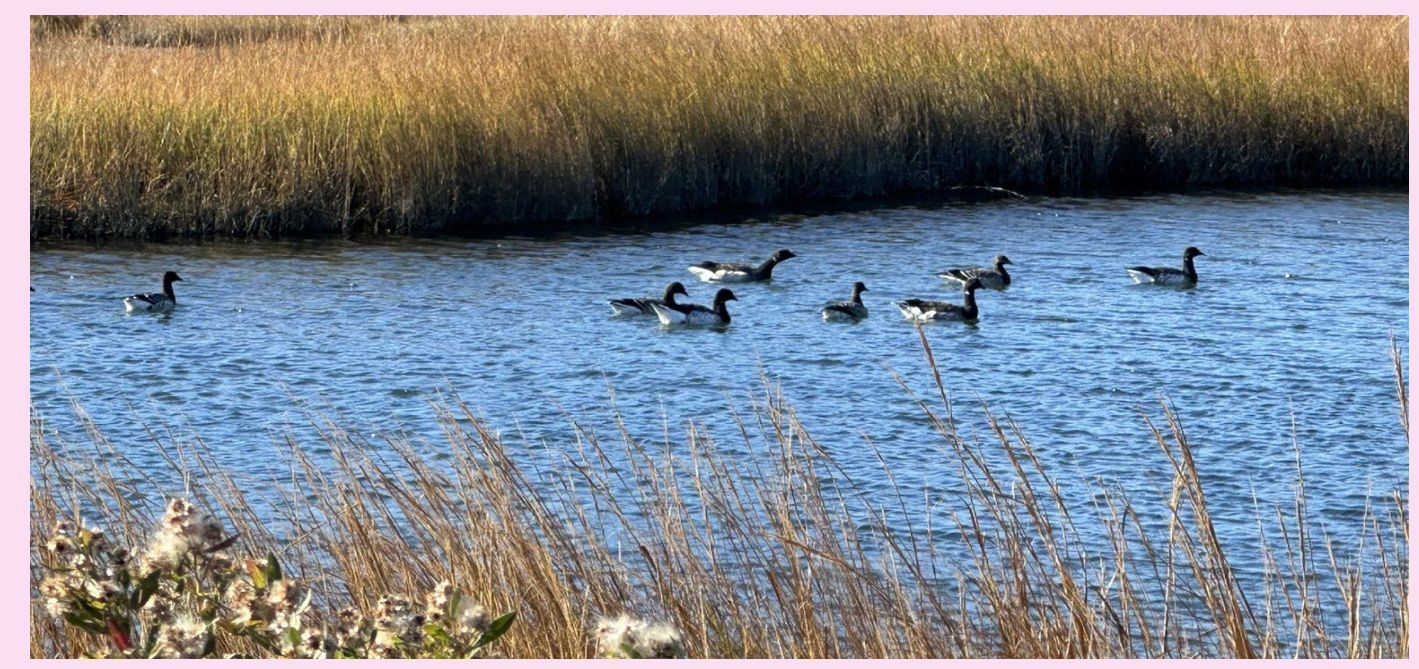
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Abstract

This study aimed to analyze factors impacting **bird species** causing annual changes within salt marshes using **E-Bird data** and **DNA barcoding** to understand species adaptations, identify trends, and inform conservation strategies for maintaining the ecological balance of these vital ecosystems. The sampling for this study was conducted at **Marine Nature Study Area**, a salt marsh in Oceanside, New York. The sampling was a sterile procedure which involved **non-invasive recovery of feathers** and a **modified quadrat approach**. For the DNA extraction process, we used a **Modified DNEasy procedure** (Lijtmaer, 2012) with additional **Proteinase K** and **Dinitrothreitol**. A total of 50 feathers collected from the Marine Nature Study Area were utilized for this research. While the small sample size collected is inconclusive to the effects of climate change on the biodiversity of birds in the Marine Nature Study Area, it does provide insight to the predictions of the effects such that the **temperature** and **sea level rising** will cause for the **food supply**, **displacement of nesting birds**, and **displacement of birds** to other zones of the salt marsh as their lands get eroded and their habitats are causing them to forcefully travel up.



Introduction

Salt marshes are homes to a wide variety of species of plants and animals despite their harsh intertidal conditions such as high salinity, low oxygen content in soil, and acute heat (Silliman, 2014). Marine Nature Study Area (MNSA) is a 52-acre saltmarsh preserve in Oceanside, New York that is split into four distinct zones based on soil's salinity and water content. Along with many plant species present, there is an abundant variety of bird species. At MNSA, birds such as brants, Canada geese, mallards, piping plovers, and more can be spotted in appropriate seasons. Rising sea levels, habitat loss, salinity increase, and altered plant communities from climate change are expected to negatively impact salt marsh bird biodiversity, causing species decline without conservation. We would like to examine how climate change may affect the biodiversity of birds in the Marine Nature Study Area.

Methods

- Collection of a total of 67 feathers using a modified quadrat sampling method to limit bias
- Randomizer used to eliminate bias (50/67 samples) (Urbaniak et al., 2013)
- DNA Extraction using Modified DNEasy procedure (Lijtmaer, 2012)
- Two sets of Forward and Backwards nested primers for the CO1 mitochondrial gene used: BirdF1 and COIBirdR2, AvMiR1 and AvMiF1
- Positive Control (successful sample from prior set of collected data), Negative Control (distilled water)
- Sequencing performed by Genewiz (Azenta Life Sciences)
- Sequences analyzed, trimmed, and aligned using DNA Subway & identified using BLASTN

Results

Due to our rigorous sampling procedure, many samples contained degraded DNA due to prolonged feather immersion in mud and water. Of the 38 out of 50 samples sequenced, 33 required nested primer pairs, while 5 were sequenced using standard CO1 primers. Of these, 10 specimens were identifiable using BLAST. 14 sequences returned dubious BLAST results due to low sequence length or contamination resulting in corresponding low bit scores.

Figure 1. The chart above showcases the Ebird data from October to December 2024 with the most abundant 25 species noted. The arrows and numbers above indicate the number of the same species that our data identified.

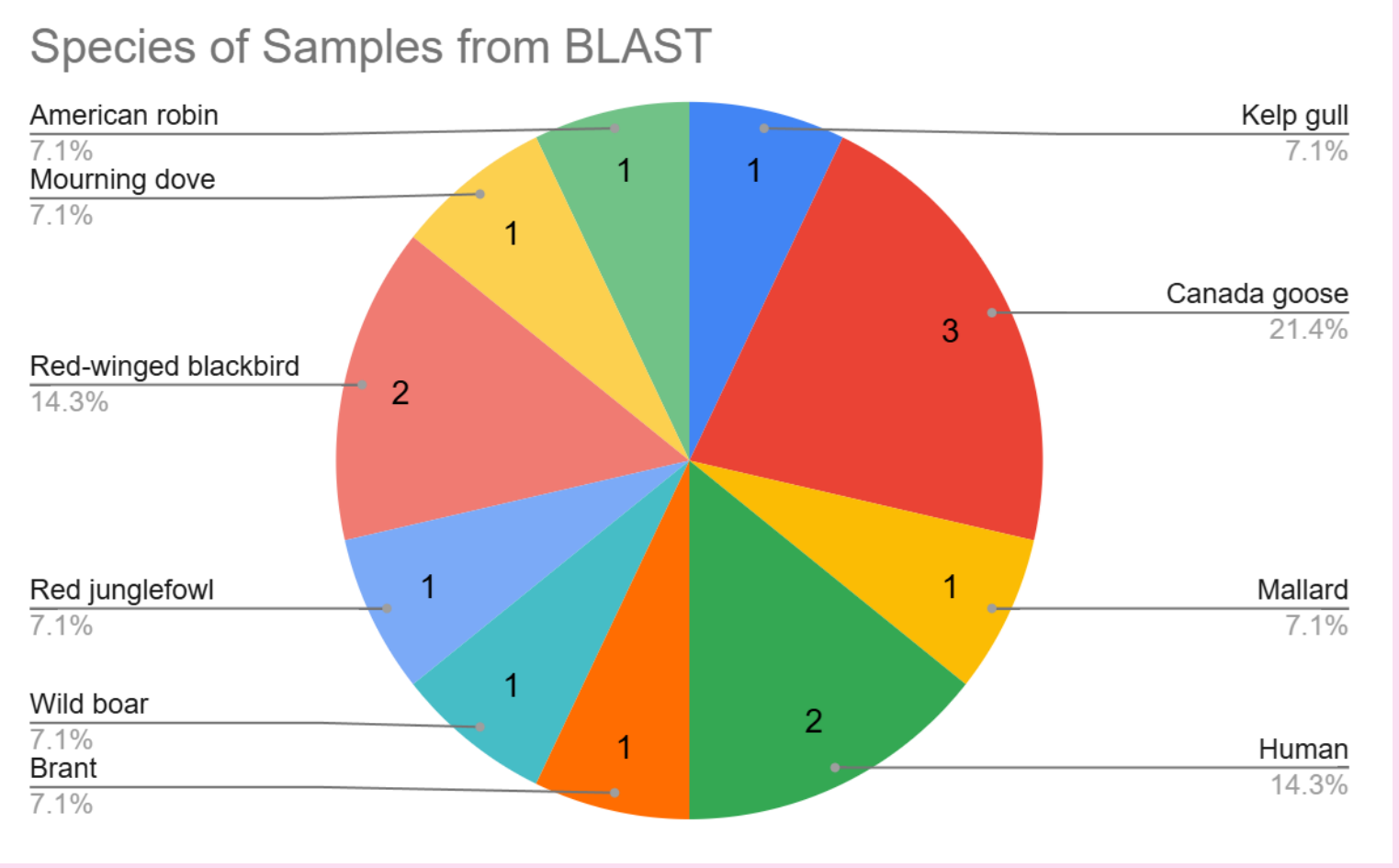
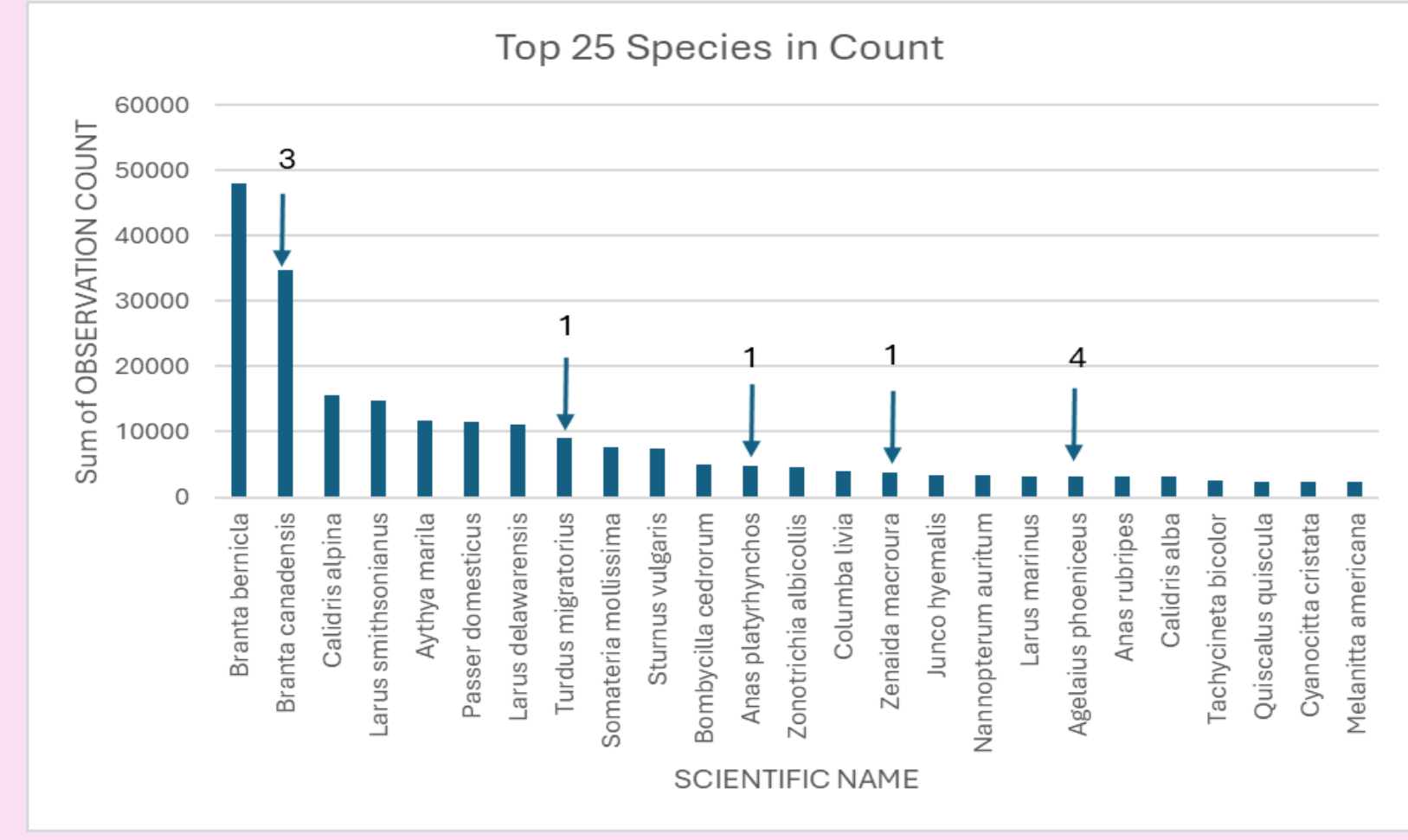


Figure 2. The pie chart shows the breakdown of species identified via BLAST.

Discussion

While our sampling technique led to a high proportion of degraded DNA, it limited bias that was present in previous studies. Low sample size and lack of baseline data prevented hypothesis testing. While our results are inconclusive, it is worth noting that climate-change impacts have been noted and or predicted for salt-marsh species, including Canada Geese, Mallards and Red-winged Blackbirds (National Audubon Society, n.d.) For example, anecdotal evidence (Farina 2024) indicates that increasingly resident Canada Geese have displaced Mallards nesting at MNSA. Many of the species we identified are also at risk if the temperature increases by just 1.5 degrees Celsius. The birds we identified all fell within the 25 most abundant species and all were year-round resident species. This distribution may reflect the timing of our sampling, after fall terrestrial bird migration and early in waterfowl migration. All of our feathers were recovered from Zone 4, the high tide zone, which may reflect both habitat and duration of immersion. For future efforts, we recommend continuation of quadrat sampling, use of avian-specific extraction protocols and PCR protocols for degraded DNA. We recommend taking additional steps to prevent contamination.

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