Trophic Level and Migrational Pattern's Impact on Avian Diversity on a Nassau County Marshland Reserve

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Cold Spring Harbor Laboratory — DNA LEARNING CENTER

Marine Nature Study Area

URBAN BARCODE RESEARCH PROGRAM

SCIENCE SANDBOX

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Abstract

This study was conducted to better understand how trophic levels and migration patterns shape avian diversity at the Marine Nature Study Area (MNSA) in Oceanside, Long Island. The CO1 gene was extracted and sequenced from feathers from the site. 2023 Sequences were combined with data collected by UBRP students in 2022, for a total of 25 data samples, which were compared with an observational data set from eBird for the same periods. We found that our species proportions roughly corresponded to the eBird data and could be partially explained by both trophic level and migratory patterns.

Introduction

The Marine Nature Study Area (MNSA) in Oceanside, Long Island, spans 52 acres and is a hub for avian research due to its diverse ecosystems, including wetlands, beaches, and forests. This biodiversity hotspot has recorded 287 species (eBird 2024). We compared our DNA samples with observed species using the eBird database. With this investigation, we hope to:

- Examine the effectiveness of alternate feather sampling at representing the MNSA's avian populations.
- Analyze how trophic levels impact the size of a population.
- Use knowledge of avian migratory patterns to explain unusual patterns.
- Further document the location's diversity.
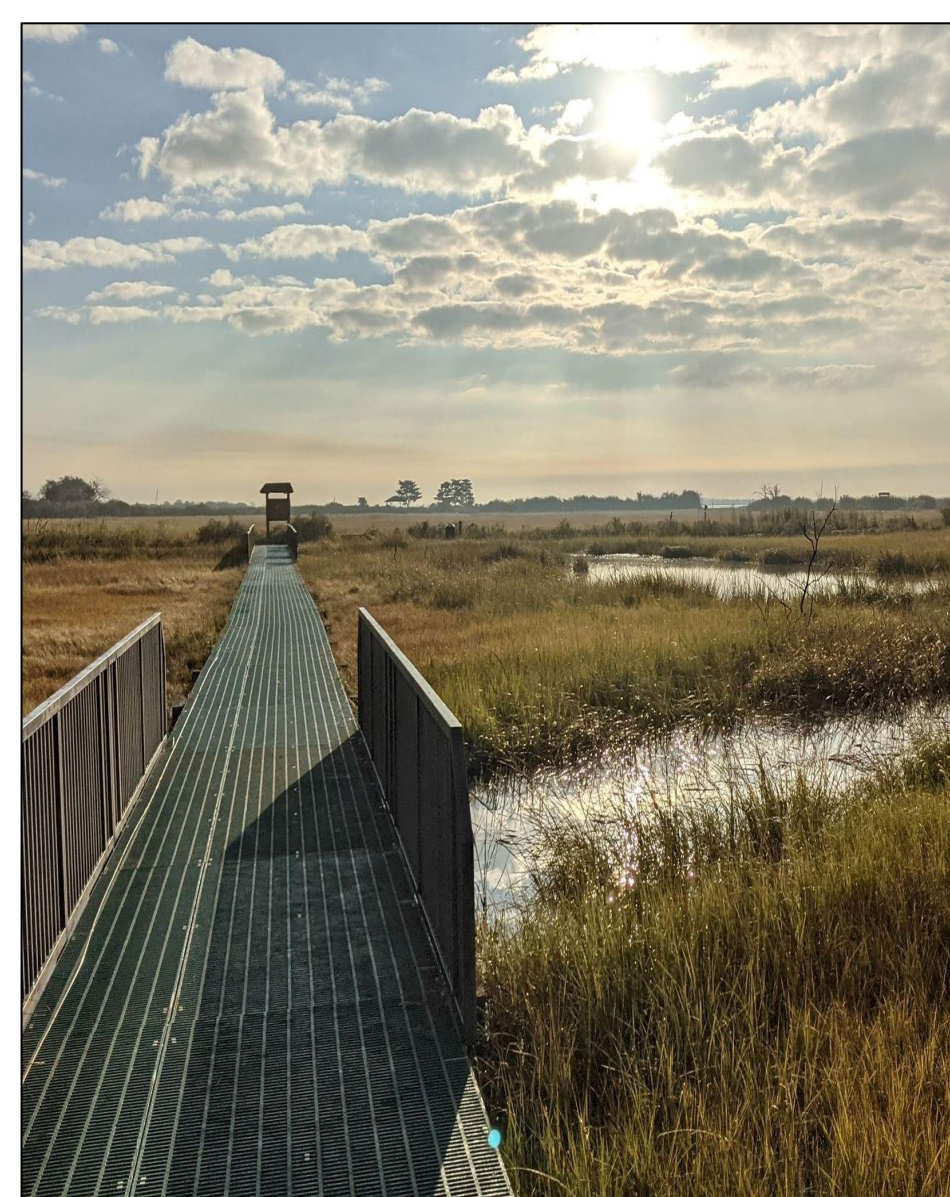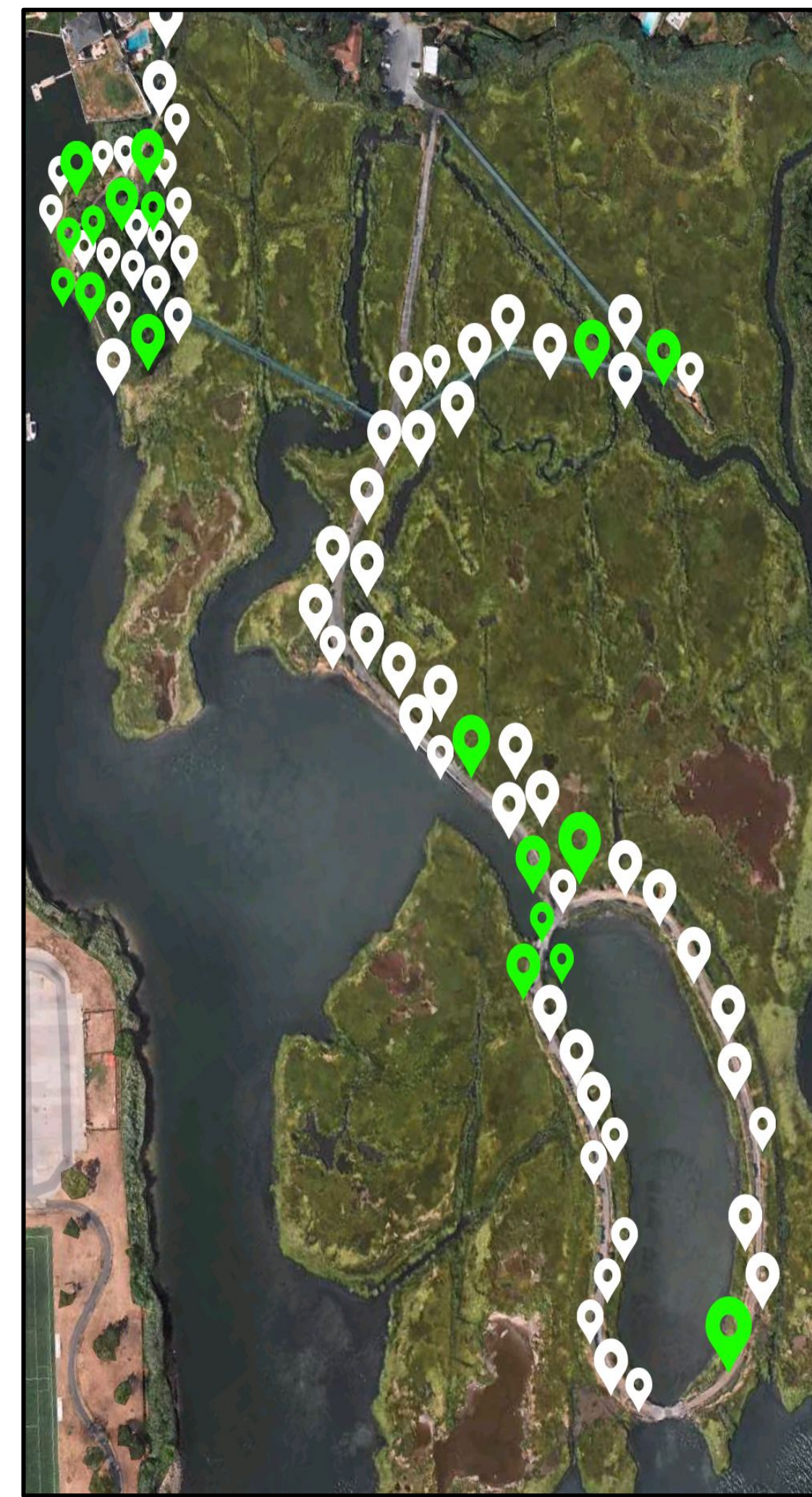
Materials and Methods

Figure 2: Sample sites at MNSA

- Collection of 80 feather samples at the Marine Nature Study Area (500 Slice Dr, Oceanside, NY 11572) on December 10th, 2023. 50 were processed, of which 18 returned avian species through BLASTN.
- DNA extraction using modified Qiagen DNEasy protocol (Lijtmaer D, et al. 2012).
- PCR to amplify CO1 gene.
  - Forward and backward primers BirdF1 and CO1BirdR2
- Sequencing performed by Genewiz (Azenta Life Sciences)
- Sequences trimmed and aligned using DNA Subway
- Sequences identified using BLASTn
- Data graphed using Excel

Results

Figure 3. Map showing the 18 successful samples. we identified 6 through DNA barcoding

Figure 4. Comparison of the –log of the proportions of each species we sampled at MNSA with proportions for the same species listed in eBird's observational data (eBird 2023-4).

Discussion

Overall, our results are in line with eBird data, and with what is expected from the MNSA during the time of sampling. Out of 50 samples, 20 were sequenced, with 2 contaminated with human DDA, leaving us with 18 usable samples. Combining our data with 2023's UBRP samples, we compared it against 2023-2024 eBird data. Our proportions closely matched eBird's, especially with the large proportion of Brants, migratory primary consumers. Higher order consumers were rare, as expected. Proportions of 3 species differed slightly from eBird data: Canada Geese were underrepresented, possibly due to migration; Mourning doves were overrepresented, possibly due to permanent residence. A lone Double-crested Cormorant, a secondary consumer, was sampled, a possible product of sampling bias. A short sequence fragment was identified as a Wild Turkey, which we included thoroughness.

Our investigation had limitations, including contamination and sample bias. These were exemplified by two sequences identified as Homo sapiens, the DNA fragment returned as a Wild Turkey, the absence of more abundant seasonal species and slight variations in proportions. Alternate feather sampling studies during different seasons, using a random methodology and at larger scales would offer greater validity to our results. Greater care and use of sterile techniques would limit issues of contamination.
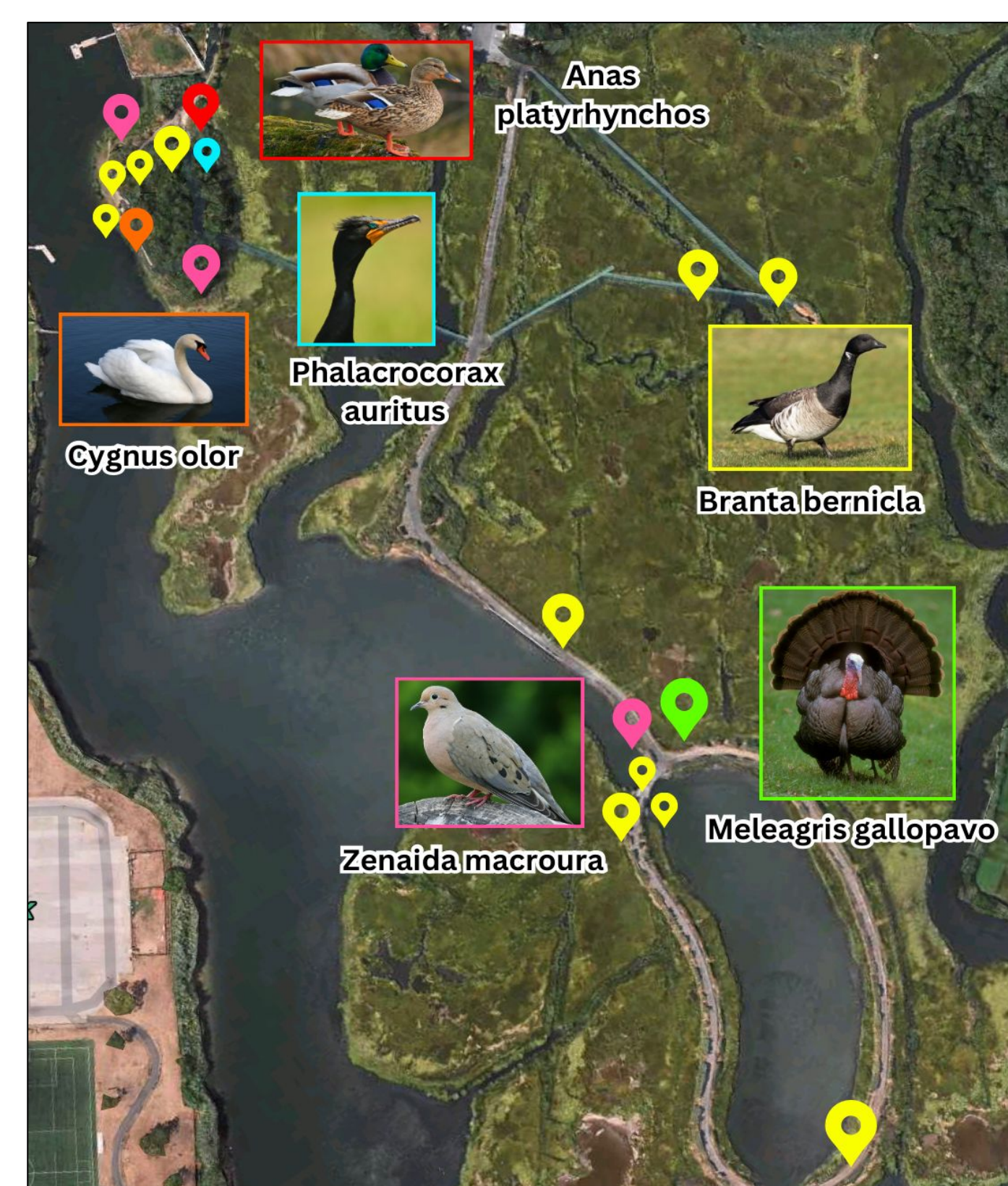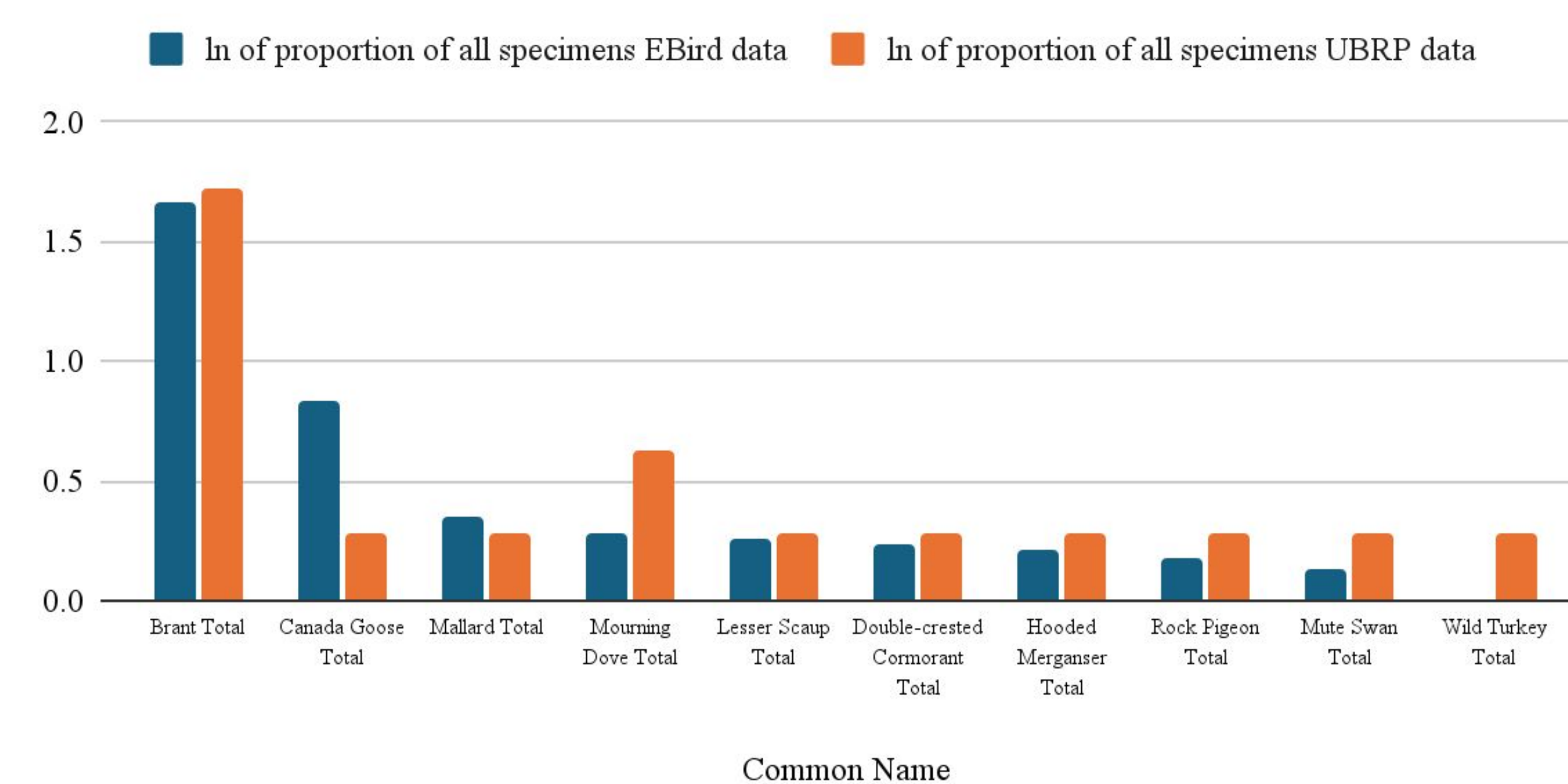
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Acknowledgements