BAT DIVERSITY AND HABITAT USE IN NEW JERSEY

by

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ABSTRACT

Bat species around the world are facing declines due to threats such as white-nose syndrome, habitat loss, and climate change. As managers implement conservation strategies it is important to understand bat habitat use and spatially explicit bat diversity. This will allow managers to focus on areas of important habitat and diversity hotspots. Here, I assess how habitat composition impacts bat diversity within the state of New Jersey. I focus on *Eptesicus fuscus, Lasiurus cinereus, Nycticeius humeralis, Lasiurus borealis, Lasionycterus noctivagans, Myotis lucifugus,* and *Myotis sodalis* based on data availability. I use acoustic surveillance data collected from 12 transect routes throughout the state, to assess bat diversity at each transect as well as habitat composition. I then predict the probability of habitat use across New Jersey for each species, and the resultant spatially explicit predicted species diversity. The response to each habitat covariate varied by species, with forest habitat having the most significant positive associations with species. *Eptesicus fuscus* exhibited the most consistently high predicted presence, and *N. humeralis, M. lucifugus* and *M. sodalis,* and *L. noctivagans* were largely constricted to the southern, more evergreen region of the state. Predicted bat diversity was highest in the inner coastal plains of the southern region, as well as the Appalachian region of the north. Diversity was low in the center of the state, near areas of higher urban cover.

Chapter 1

INTRODUCTION

Wildlife management and conservation heavily relies on contemporary basic knowledge of species trends and distribution. Research on the status of a state's species allows informed management to better protect those species. As bat populations around the world face declines, there is an increasing need for research on bat ecology and distribution.

There are approximately 51 species of bats native to the United States (Morgan et al, 2019). These fall into the families Molossidae (free-tailed bats), Mormoopidae (ghost-faced or leaf-chinned bats), Phyllostomidae (leaf-nosed bats), and Vespertilionidae (vesper or evening bats). In the eastern United States, the native species all belong to Vespertilionidae, the largest of the aforementioned families (Voigt et al, 2011).

New Jersey has 10 native bat species, 7 of which are hibernating species and 3 of which are migratory (Maslo and Leu, 2013). The year-round species are the little brown bat (*Myotis lucifugus),* the big brown bat (*Eptesicus fuscus),* the northern long-eared bat (*Myotis septentrionalis),* the Indiana bat (*Myotis sodalis),* the eastern small-footed bat (*Myotis leibii),* the evening bat (*Nycticeius humeralis),* and the tri-colored bat (*Perimyotis subflavus).* The red bat (*Lasiurus borealis*), the hoary bat (*Lasiurus cinereus*), and the silver-haired bat (*Lasionycterus noctivagans*) are all migratory species (Hall, 2021). In this thesis I will focus on *E. fuscus, L. cinereus, N. humeralis, L. borealis, L. noctivagans, M. lucifugus,* and *M. sodalis*, due to a lack of sufficient data on the remaining species.

Vespertilionidae bats are entirely insectivorous. This aspect of their diet provides valuable ecosystem services, acting as a control for insect populations such as mosquitoes and agriculture pests (Medellin et al, 2017). Considering their value to ecosystems, the population declines faced by bat species should be particularly alarming. Bats are vulnerable to threats such as white-nose syndrome and wind energy development, as well as climate change and habitat loss due to development (Hall, 2020). White-nose syndrome (WNS), a fungal infection first detected between 2006 and 2007 across the United States, has depleted bat populations by as much as 94% at certain sites in New Jersey (Conserve Wildlife Foundation of New Jersey, n.d.). The Indiana bat (federally endangered) and the northern long-eared bat (federally threatened) have both seen significant declines compared to their populations at the beginning of the decade, as has the little brown bat (under review for listing) (FWS.gov, n.d.). Little brown bats, once thought to be the most widely distributed species in the United States, have faced declines as high as 99% since the introduction of the fungus (O'Keefe et al, 2019). Climate change is also posing a significant risk to the order, especially in North America where the climate is getting warmer and drier (Adams, 2010). Climate change is causing disruptions in the food chain, migration patterns, and hibernation cycles (Sherwin et al, 2013).

Despite the need to monitor and conserve their populations, there are difficulties in collecting data on bats. They are a relatively elusive order due to their nocturnal nature and remote roosting habits, making it difficult to thoroughly study and understand their habitat use and requirements. Due to this difficulty in collecting data on bats, acoustic surveillance methods are often utilized for population estimates, in place of trapping or capture methods (Rodhouse et al, 2011; O'Farrell and Gannon, 1999). Acoustic detection is a non-invasive approach to identifying bats, allowing researchers to discover information about habitat use, foraging habits, and migration patterns (Russo and Jones, 2003; Reynolds 2006).

Bats utilize a variety of habitats for roosts and foraging, and they typically travel limited distances from their roosts, in what is referred to as a home range (Frajford, 2013). This selection of foraging habitat is known as second order resource selection (Johnson et al, 2006). *E. fuscus* typically utilize hardwood or evergreen forests, travelling about 5 kilometers from their roost for foraging (Menzel et al, 2001). *N. humeralis* similarly utilizes hardwood and evergreen forests, but they have a slightly smaller home range of approximately 3 square kilometers (Perry & Thill, 2008). *M. lucifugus* forage in open water and forested riparian areas, with a home range between 2 and 5 square kilometers (Coleman et al, 2014; Bergeson, 2012). *M. sodalis* typically forage in forested riparian areas and in upland woodland patches, occasionally over open water as well (Menzel et al, 2005; Kniowski & Gehrt, 2014). The home range for *M. sodalis* is small, around 2 square kilometers (Menzel et al, 2005). *L. noctivagans* typically forage in open forests away from clutter, moving only small distances from their migratory tree roosts (Owen et al, 2004; Mattson, 1994). *L. cinereus* is a migratory species with similar habitat requirements as *L. noctivagans* (Owen et al, 2004). *L. borealis* also have a small home range, typically less than 2 square kilometers (Walters et al, 2007). They are a tree-roosting migratory species and travel short distances into the surrounding woodlands to forage (Walters et al, 2007).

Here I will use a generalized linear mixed model to assess second order resource selection of a suite of bat species in New Jersey to contribute to the understanding of their ecology and conservation. I will use my findings to predict where bat species may be present and utilizing habitat across the state for foraging, and how bat species diversity changes across habitat types. My results will hopefully provide insight for conservation planning as we seek to protect this valuable order of mammals and the habitats they utilize.

STUDY AREA

I used acoustic recording data from 12 established transect lines located across the state of New Jersey, 6 in northern New Jersey and 6 in southern New Jersey (Figure 1). The northern and southern halves of the state are defined by dramatic changes in landscape. The northern half is mountainous, with part of the Appalachian region cutting into the northern most part of the state (Stansfield, 1998). Gradually moving south, New Jersey has significant amounts of rolling plains and ridges, before eventually crossing into the southern coastal plains (NJ.gov, 2019). The southern region of the state is almost entirely composed of these coastal plains, divided into the inner coastal plain, with gravel, sand, and clay soils, and the outer coastal plain, mainly composed of gravel and sandy soils (Forman, 1998).

The transects vary in their primary land use/land cover (LULC) type, which I assessed using a NLCD land cover dataset from 2019. The three dominant cover types are forest, urban, and wetland (Figure 2). Generally, there is a trend of higher urban cover in the north, and higher wetland cover in the south. The spread of forest cover is relatively even across the transects, although it is at its minimum value in GRTS3072, which is in the southern region. Agriculture was below 10% cover in all but three transects: GRTS9984 in the north, GRTS3072 in the south, and GRTS6144 in the south. The other LULC types, being barren, shrub, open water, and herbaceous, were low across all transects, never exceeding 11% cover.

METHODS

Data Collection: Acoustic Surveys

When it was created in 2015, the North American Bat Monitoring Program (NABat) organized the United States and Canada into a continental grid framework made up of 100 km^2 grid cells for monitoring purposes (North American Bat Monitoring Program, n.d.). New Jersey monitors 12 active grid cells, with 1 acoustic route and 2 stationary points per cell (Hall, pers. comm.). Since the creation of New Jersey's grid cells in 2017, data collection has taken place yearly between July 1 and June 30, with each mobile transect surveyed twice within the same 10-day window of time each year.

Individuals completing the surveys are equipped with Petterson D500x full spectrum acoustic detectors. Surveyors attach the connecting microphones to the driver's side window using clamps and set them facing forward. The acoustic routes are approximately 15 to 25 miles in length and follow low trafficked areas for minimal disturbance. Drivers are not to exceed 20 mph to minimize ambient noise. Bats tend to be more active within the first hour after sunset, with no wind or rain and mild temperatures. With this in mind, surveys only occurred on nights with the following conditions: temperatures above 55 degrees, light to no wind, no rain, and beginning 45 minutes after local sunset time. This resulted in 2 nights of surveying for each transect, every year from 2017 to 2021. Exceptions to this schedule occurred in cases of extreme rain or scheduling conflicts.

<u>Data Processing</u>

Employees at the New Jersey Division of Fish and Wildlife (NJDFW) analyzed the acoustic recordings using SonoBat© Version 4 North America, a software program used for identifying bat calls by frequency in kilohertz. SonoBat automatically assigns a species code to recordings collected from the surveys based on the frequency, pattern, and length, and NJDFW employees then review and confirm the identifications. The codes used for the species of interest in this study are shown in Table 1. Due to their similar call structure, habitat use, and overall ecology, *M. lucifugus* and *M. sodalis* are combined into one code. An example of a bat call as it is displayed in SonoBat can be found in Figure 3.

I analyzed the acoustic data to determine the number of each species recorded at each transect across the study period. I then used Simpson's diversity index and Shannon's diversity index to calculate the diversity of species in New Jersey at each transect. The equation for Simpson's index is $D = \frac{\sum n_i(n_i-1)}{N(N-1)}$ where D is Simpson's diversity, N is the total of all species present, and n_i is the number of an individual species. Simpson's index results in values ranging from 0-1, with a value of one indicating higher diversity. The equation for Shannon's diversity index is $H' = -\sum(p_i)(\ln p_i)$ where p_i is the proportion of a population contributed by a species. Shannon's index results in a variety of values, with higher values indicating higher diversity and zero indicating only one species in a population. Simpson's index can be sensitive to species dominance, while Shannon's is more sensitive to changes in richness, so both were used to get a more complete idea of the differences between transects (DeJong, 1975). I used the data from all years (2017-2021) where available, as well as individual calculations for the years of 2020 and 2021.

I used the NLCD 2019 Land Cover (CONUS) dataset provided by the Multi-Resolution Land Characteristics Consortium (MRLC) with a 30 m grid cell size in a Geographic Information System (ArcGIS®) to assess landcover/land use (LULC) composition across the state of New Jersey. The original data set included 20 landcover classes within New Jersey, which I condensed to agriculture, barren, deciduous forest, evergreen forest, mixed forest, open water, herbivorous, scrub, urban, or wetland. Using ArcGIS®, I then developed a binary raster dataset for each landcover class and implemented a moving window analysis to determine on a cell-by-cell basis the percent landcover of that class within 2 km^2. I chose 2 km^2 based on the smallest average home range size of my species of interest. This resulted in a new raster for each LULC type with the proportion of that type within 2 km^2 (Figure 4). I next created points along each NABat transect line in New Jersey, with each point spaced 100 meters apart. To these points I extracted the underlying values of each 2 km^2 proportional LULC. These points then represented "available" habitat within my study area. Next, I extracted the percentage of each 2 km^2 proportional LULC to the georeferenced recorded bat calls. This then represented the "used" habitat within my study area.

To assess potential second order resource selection, I implemented a generalized linear mixed model (GLMM) in a Bayesian framework using the program WinBUGS (Spiegelhalter et al, 1999) implemented via R© (R Core Team, 2021). Given my interest in predicting beyond the 12 transects I considered transect as a random effect (random intercept). I used a logit link to account for the binomial distribution of my Bernoulli use = 1 and available = 0 dependent variable (Supplemental Material A). Each model was iterated 80,000 times across two MCMC chains, with the initial 40,000 iterations discarded and the remaining 40,000 iterations thinned to retain every 5th iteration. Across two chains this resulted in 8,000 samples of the posterior distribution.

Next, I used the coefficients from my GLMMs and the associated 2 km^2 proportional LULC to predict probability of use across all of New Jersey for each bat species. I then determined a threshold for probability of use based on the mean probability value for each species and created a new map of predicted bat species diversity.

RESULTS

The acoustic surveys resulted in 2,239 bat calls over the 2020-2021 period. Of those, 1,286 were EPFU, 499 were LABO, 186 were LACI, 155 were LANO, 88 were NYHU, 15 were LUSO, and 9 were PESU. An example of bat recordings collected along one transect can be seen in Figure 5. For all years combined, Shannon's diversity index ranged from 0.81 to 1.45 and Simpson's ranged from 0.23 to 0.58. For individual years, Shannon's index ranged from 0.22 to 1.36 and Simpson's ranged from 0.31 to 0.89. There was no evident relationship between the transect habitat and species diversity, although GRTS3072 had the highest values for Shannon's diversity index in all 5 years combined, as well as in both 2020 and 2021 individually (Table 2).

Response to each habitat covariate varied by species, as determined by the GLMM (Figure 6). Wetland and forest habitat had the most significance across species, with 4 out of 6 species having significant association with wetland, evergreen forest, and deciduous forest, and 3 out of 6 having significant association with mixed forest.

The species-specific predictive maps ranged with values from 2.40e-20 to 1 (Figures 7-12). *E. fuscus* has the most consistent predicted presence with average to high levels predicted across much of the state, while LUSO, NYHU and LANO seem the most restricted to the southern region of the state. The predicted diversity map has higher values in the inner coastal plains of the south as well as in the Appalachian region of the north (Figure 13). Diversity is generally at its minimum along the central region of NJ, within areas of increased urban habitat.

DISCUSSION

This analysis supports the idea that habitat can have an impact on diversity and shows the importance of some habitat types on specialist species (Rocha et al, 2018). Overall, in all 5 years combined as well as in both 2020 and 2021 alone, GRTS3072, in southern NJ, had the highest Shannon's diversity. It also had the joint highest value for Simpson's diversity index in 2021. However, it had the lowest Simpson's diversity value for all years combined. Transect GRTS3072 is primarily agriculture and wetland habitat, the latter of which many bat species often utilize for foraging. This may explain why there is greater diversity according to Shannon's index. The lowest value for Shannon's diversity in 2021 was in GRTS14128, in northern NJ. Transect GRTS14128 is primarily urban and forest habitat, so the high amount of urban habitat may help explain the low reported diversity for that year. The lowest value for Simpson's diversity in 2020 was in transect GRTS12288, in southern NJ. Transect GRTS12288 is primarily wetland and forest habitat. There was a great deal of variation between the Shannon's index values and those from Simpson's index. Shannon's index considers the evenness of a population, whereas Simpson's relies more so on dominance, so the Shannon values may reflect a more accurate measure of diversity considering the potential effect of EPFU's dominance (DeJong, 1975).

Looking at the beta coefficients, there is shared associations with the covariates among some species. For agriculture, there is a significant negative association for EPFU, LABO, and LANO, while there is a significant positive association for LACI. This is not surprising for the former three species, as they utilize forested areas for foraging. Barren habitat only had significant association with LABO and LACI, both of which were negative. That is expected as bats do not typically forage in barren areas, high levels of which are on the coast (Baker et al, 2008; Nelson and Gillam, 2017). There is a positive association with deciduous forest for LUSO, LABO, and NYHU. This association is reflected in the predictive map of species distribution, as they were all highly concentrated in the southern, more forested area of the state. *M. lucifugus* and *M. sodalis* also have a significant positive association with evergreen forests, as does LANO and EPFU. No species have a significant negative relationship with evergreen, indicating that they are not avoidant of that habitat. Only NYHU was significantly associated with herbaceous habitat, in a slightly positive relationship. This is not surprising, as herbaceous habitat is fairly scattered across the state and may not heavily affect many species' abundance. Mixed forest habitat had four significant positive associations, being with LABO, LANO, LUSO, and NYHU. This habitat type had the most positive relationships, indicating it may be a considerable influence in bat presence. Open water habitat was significantly negatively related to EPFU and LACI, while all others were insignificant. This is expected considering the limited amount of open water in New Jersey. *N. humeralis* and LABO were significantly negatively associated with scrub habitat, while LACI was significantly positively associated. The positive association for LACI was surprising, as they typically utilize habitat with high amounts of tree cover (Gruver, 2002). Only EPFU had a significant relationship with urban habitat, being a negative association. This could demonstrate the ability of certain bat species to adapt to urbanization (Jung et al, 2016). Wetlands had a significant positive association with LABO, LUSO, and NYHU, and a significant negative relationship with EPFU. The latter is surprising as they are a generalist species, but as they typically forage in hardwood forests that could help explain the negative association.

The predictive maps for species presence across New Jersey reflects the fact that *E. fuscus* is a generalist and abundant species in New Jersey (Sullivan et. al, 2006). The predictive maps for each species demonstrate how valuable certain habitats and areas are for more specialist species; the less abundant *N. humeralis* was predicted in high levels, but those values were concentrated in southern New Jersey, with limited predicted presence in northern New Jersey. All species had some of their highest values in the southern half of the state, especially LUSO and LANO, which share a positive association with evergreen. This habitat association could be the reason for their predicted presence in southern NJ, as that area has higher density of evergreen forests.

The predictive diversity map shows an interesting spread of diversity. While there is not an extreme visual difference between the predicted values for north and south New Jersey, there is a clear band of low values of diversity across the middle of the state. This is mirrored in the figure of urban habitat in New Jersey; the line of low diversity centers around the area with high levels of urban habitat, where Interstate 95 runs.

Predictive modeling and habitat use assessment are important tools for managing populations. They can provide information on species population trends as well as highlight areas and habitats of importance to species of concern (Clement and Castleberry, 2013). This project shows the potential for non-invasive survey techniques which could allow for greater collection of distribution and habitat use data, as well as a deeper understanding of bat ecology and diversity.

I recommend continued research on bat ecology, habitat use, and distribution. As an order that is under ecological stress, it is more important than ever to learn, study, and protect them and their habitat. Understanding species habitat use and species diversity will allow for informed management of bat populations and conservation of their vital habitat.

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TABLES AND FIGURES

Common Name	Species	SonoBat© Code
Big brown bat	*Eptesicus fuscus*	EPFU
Evening bat	*Nycticeius humeralis*	NYHU
Silver-haired bat	*Lasionycterus noctivagans*	LANO
Eastern red bat	*Lasiurus borealis*	LABO
Hoary bat	*Lasuirus cinereus*	LACI
Little brown bat	*Myotis lucifugis*	LUSO
Indiana bat	*Myotis sodalis*	

Table 1. The common name, species name, and associated code for seven species of bat in New Jersey which were surveyed using SonoBat©, an acoustic monitoring system for bat research.

Transect	Shannon's Diversity, 2017-2021	Simpson's Diversity, 2017-2021	Shannon, 2021	Simpson, 2021	Shannon, 2020	Simpson, 2020
GRTS15104	0.81	0.58	0.92	0.51	0.55	0.75
GRTS9984	0.93	0.49	0.73	0.59	0.51	0.77
GRTS19456	0.95	0.53	1.04	0.43	0.99	0.52
GRTS10032	1.02	-	0.83	0.51	0.77	0.55
GRTS14128	1.02	0.48	0.21	0.89	0.61	0.41
GRTS6144	1.03	-	0.93	0.42	0.86	0.53
GRTS7168	1.05	0.46	1.16	0.39	0.54	0.51
GRTS5936	1.12	0.40	1.19	0.35	1.04	0.35
GRTS11264	1.14	0.42	0.90	0.51	1.27	0.36
GRTS12288	1.15	-	0.74	0.58	1.30	0.31
GRTS3840	1.16	0.41	1.13	0.39	1.30	0.32
GRTS3072	1.45	0.23	1.33	0.89	1.36	0.41

Table 2. Shannon and Simpson Diversity indices assessing the diversity of bats across 12 transects in New Jersey. Transects followed the North American Bat Monitoring Program protocol and were implemented between 2017-2021. The two most recent years are included for contemporary evaluation.

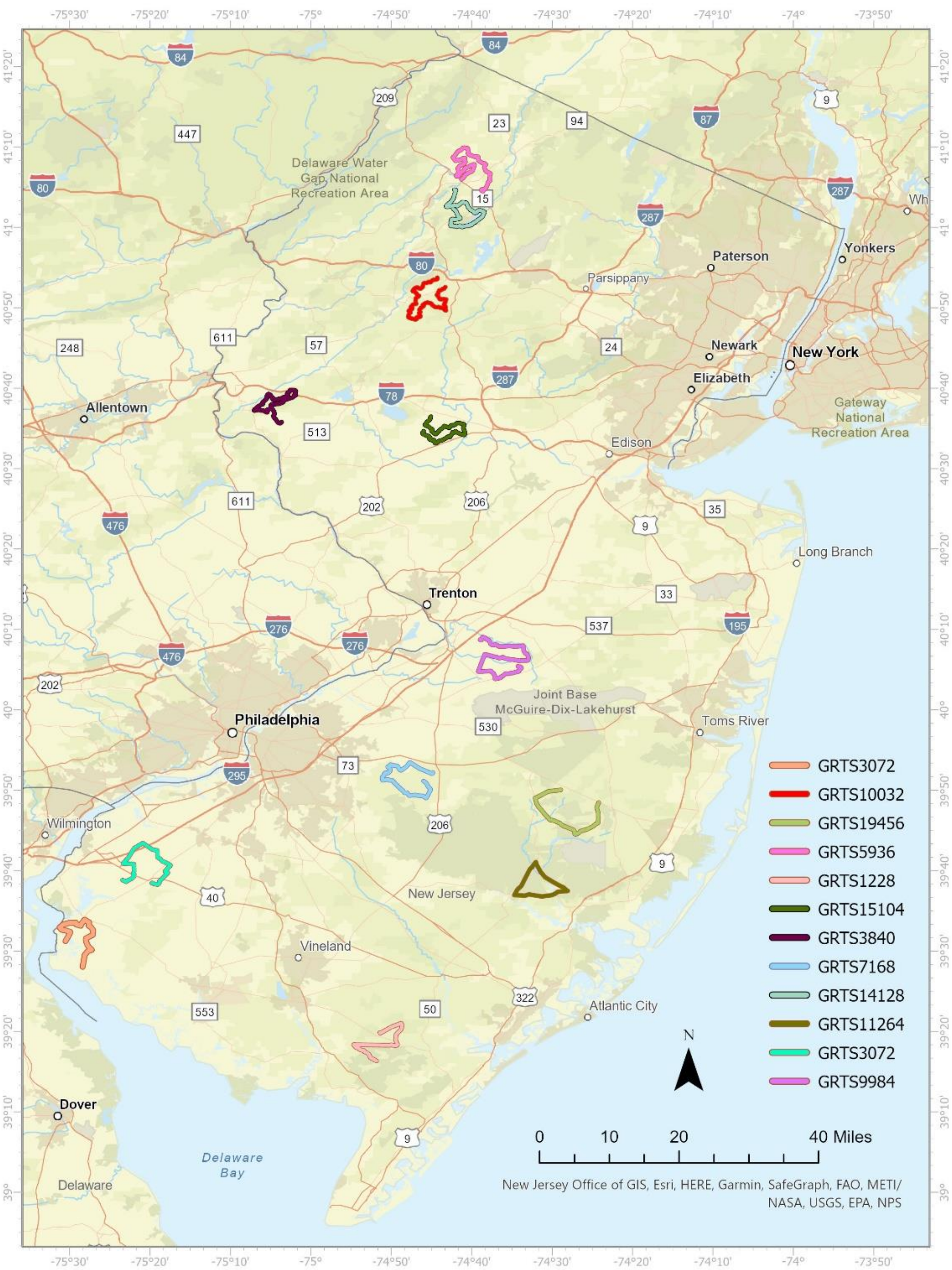

Figure 1. Twelve transects set by the Division of Fish and Wildlife of New Jersey, following the North American Bat Monitoring Program protocol in New Jersey, USA. Surveys are completed yearly along each transect line since 2017.

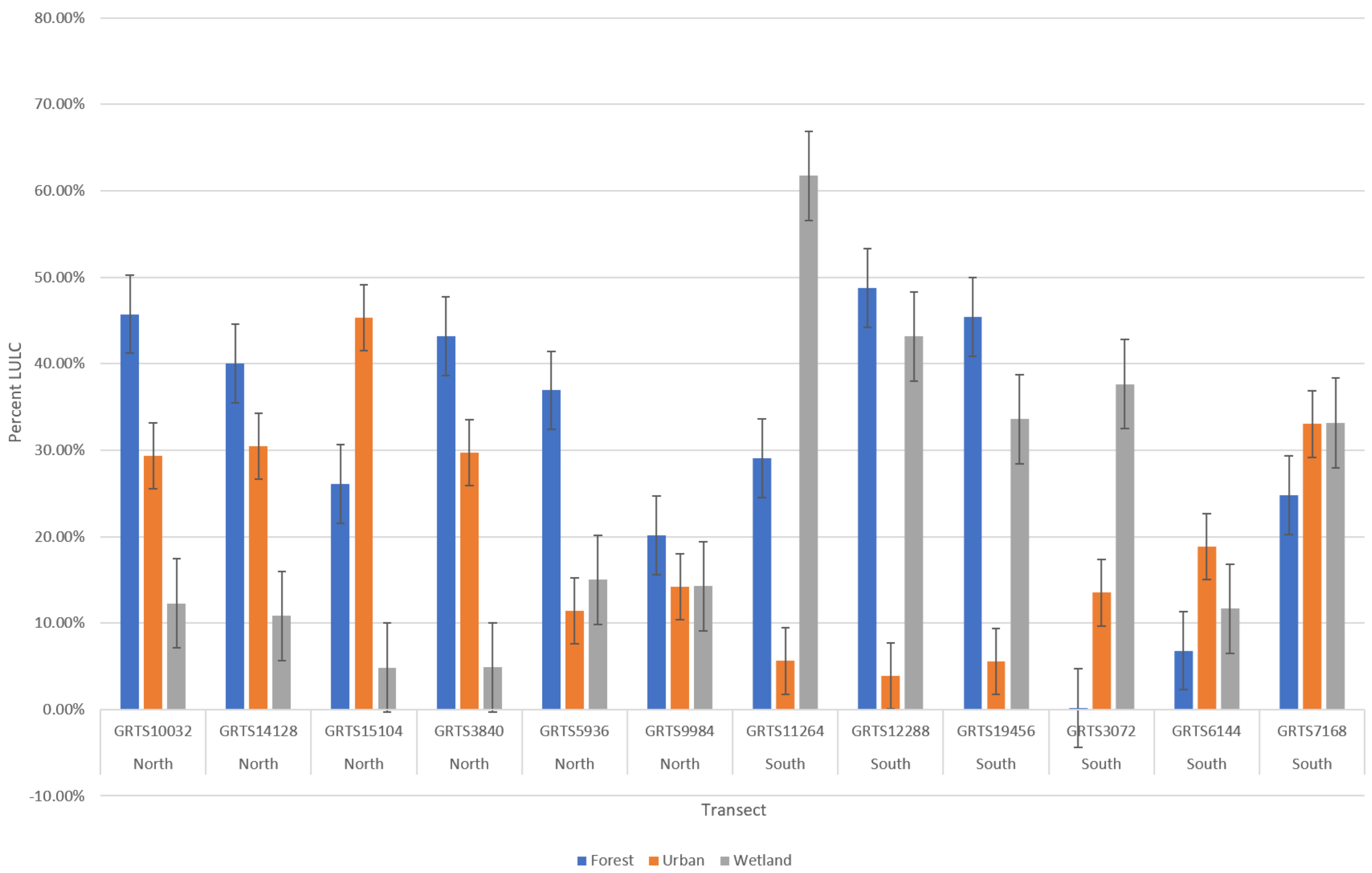

Figure 2. A bar graph displaying the percent cover of Forest, Urban, and Wetland habitat across the 12 North American Bat Monitoring Program transect locations in North and South New Jersey. For the purposes of this graph, Evergreen, Deciduous, and Mixed Forest types are combined to one category of Forest. Landcover data is from the 2019 National Landcover Dataset.

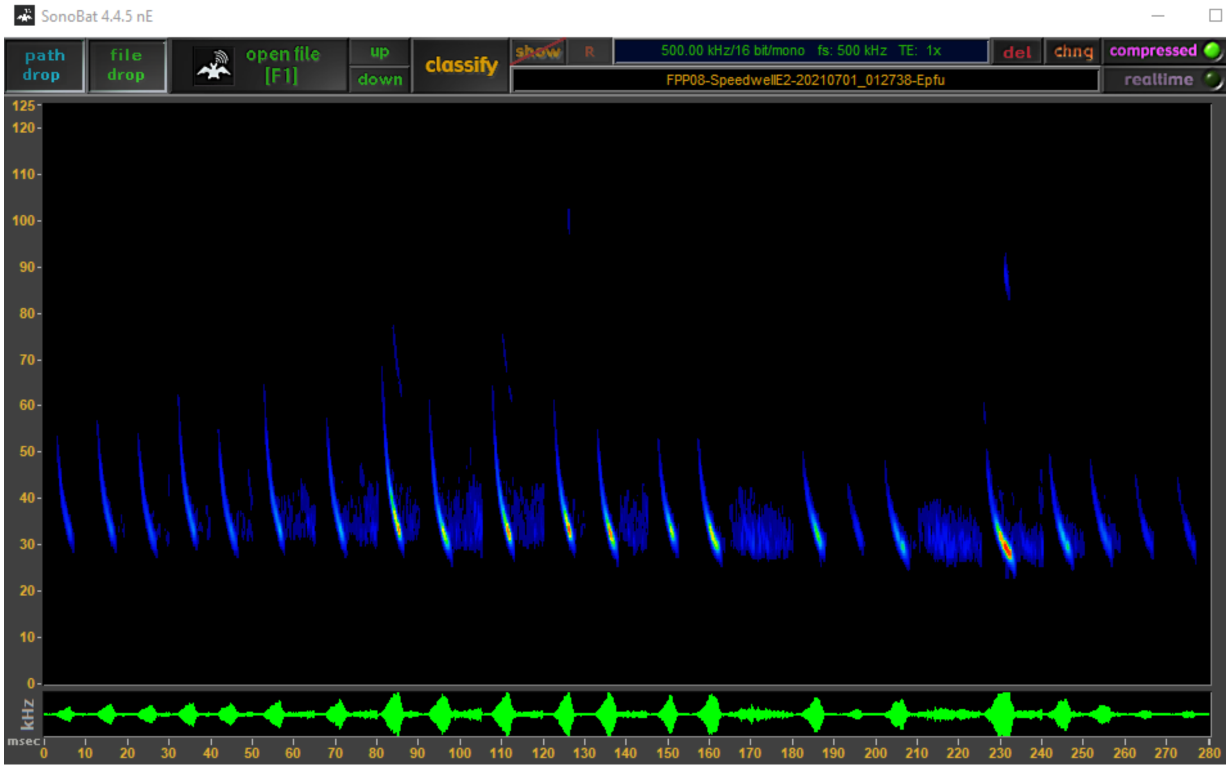

Figure 3. An example recording of a big brown bat call, as displayed in SonoBat© Version 4 North America. Species are automatically classified based on the frequency (kHz), length, and pattern of their calls.

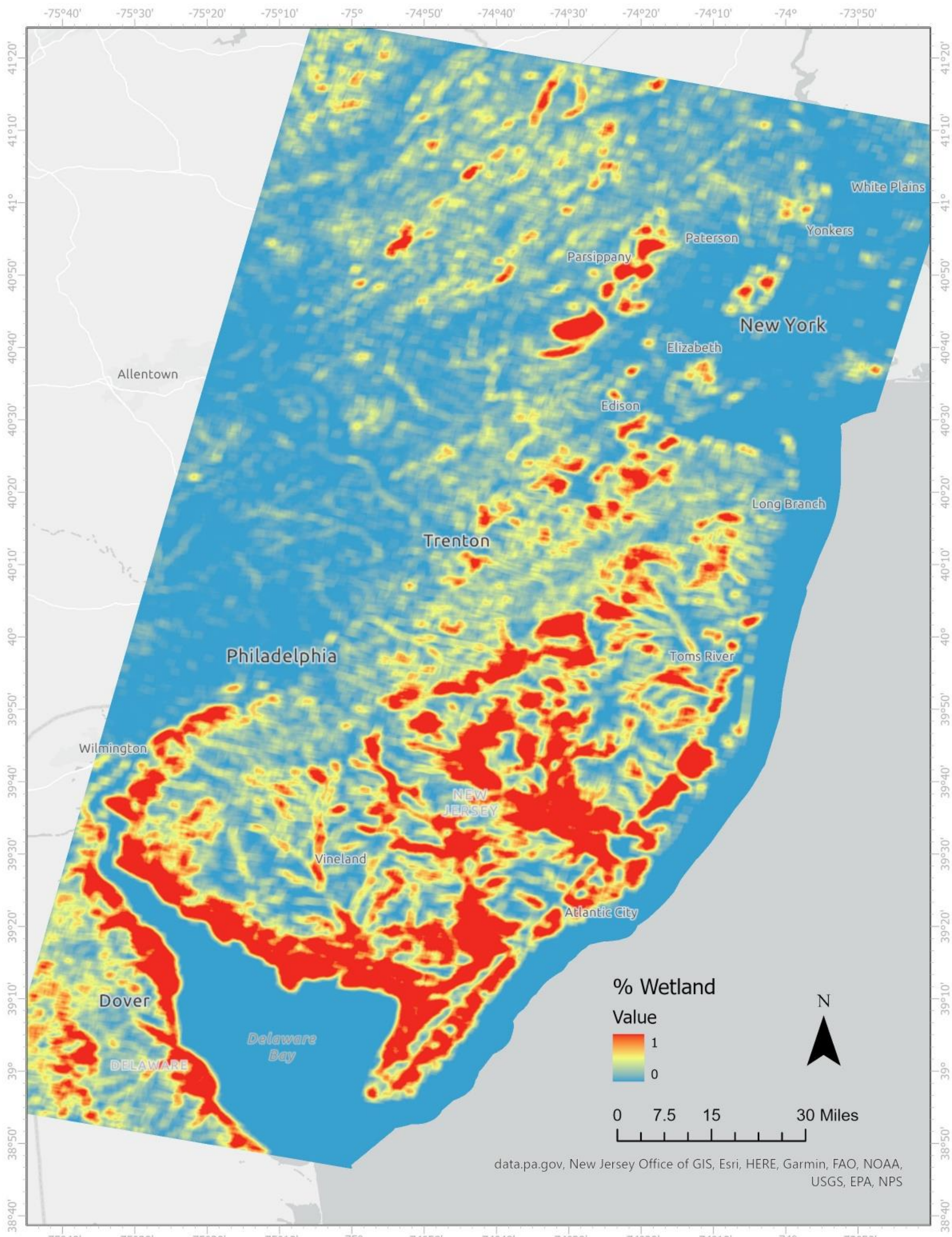

Figure 4. New Jersey's percent wetland landcover in New Jersey, ranging from 0 to 1, wherein each cell represents the proportion of wetland within 2 km^2.

Figure 5. An example of a North American Bat Monitoring Program transect line GRTS19456, in New Jersey, USA, with recorded bat calls of *L. noctivagans* (n = 4), *L. borealis* (n = 32), *E. fuscus* (n = 78), *L. cinereus* (n = 9) *M. lucifugus and M. sodalis* (n = 9), and *N. humeralis* (n = 19) from 2020 and 2021.

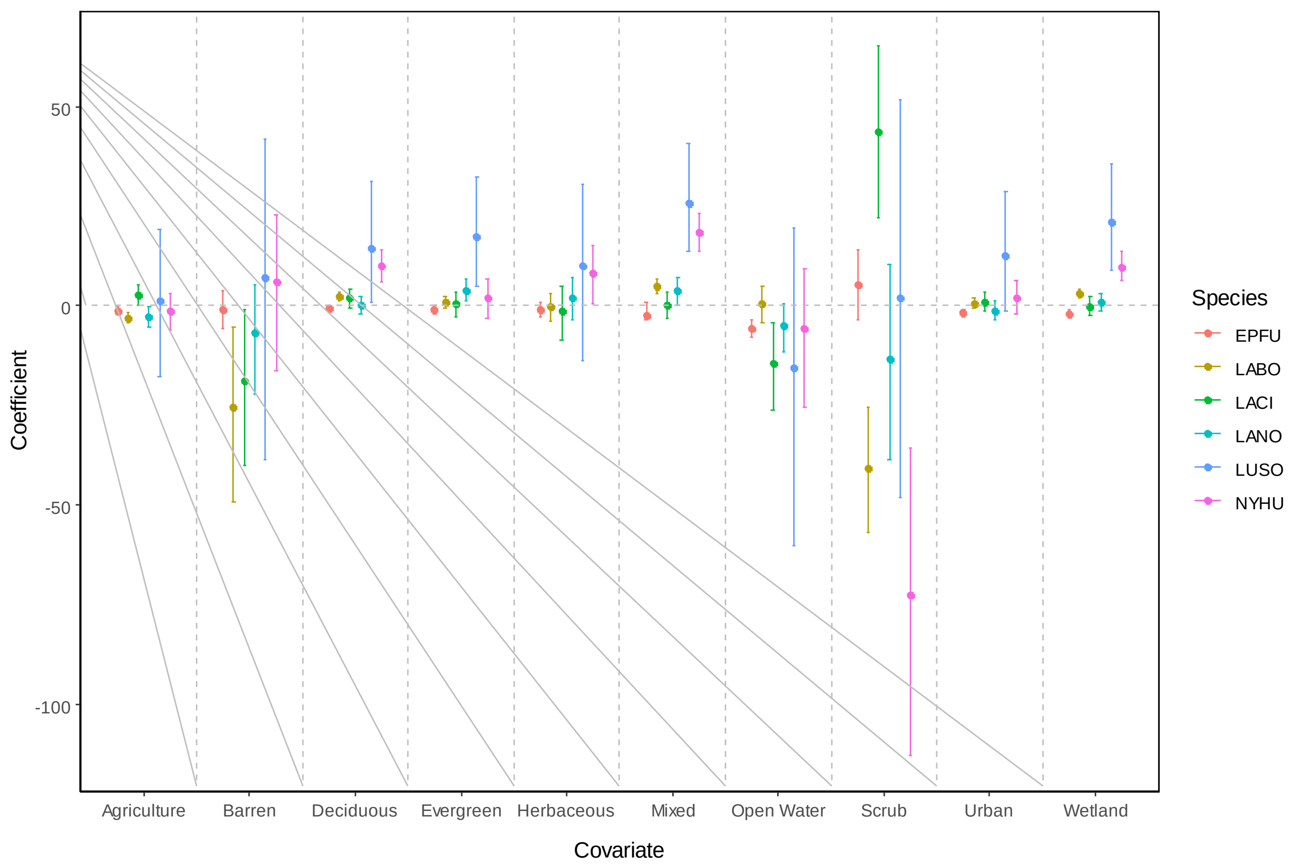

Figure 6. Habitat coefficients and 95% credible intervals from 2nd order resource selection models of *E. fuscus, L. cinereus, N. humeralis, L. borealis, L. noctivagans, M. lucifugus,* and *M. sodalis*. Models were based on bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database.

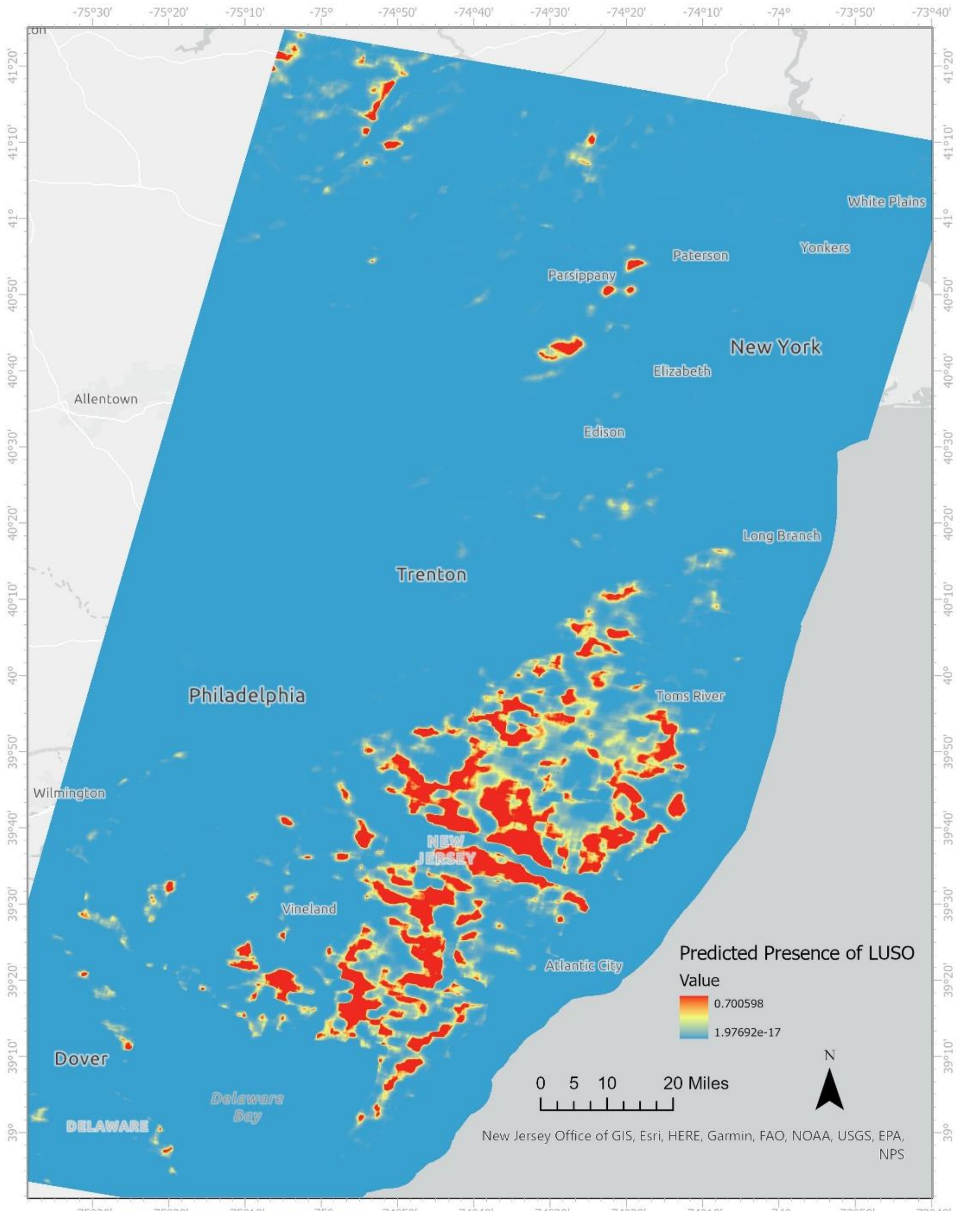

Figure 7. Species-specific predicted presence of *M. lucifugus* and *M. sodalis* across New Jersey, USA. Predictions are based on 2nd order resource selection models using bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database.

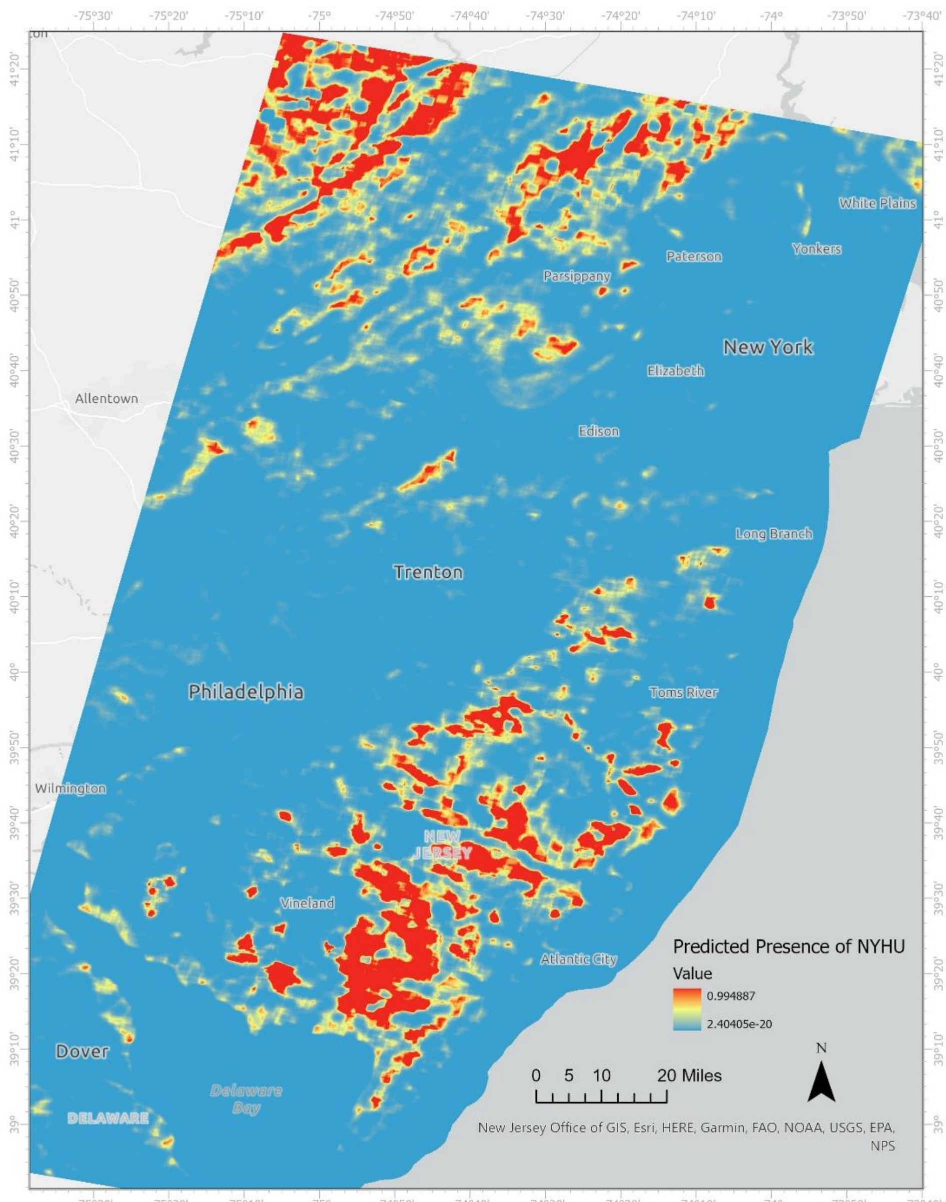

Figure 8. Species-specific predicted presence *N. humeralis* across New Jersey, USA. Predictions are based on 2nd order resource selection models using bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database.

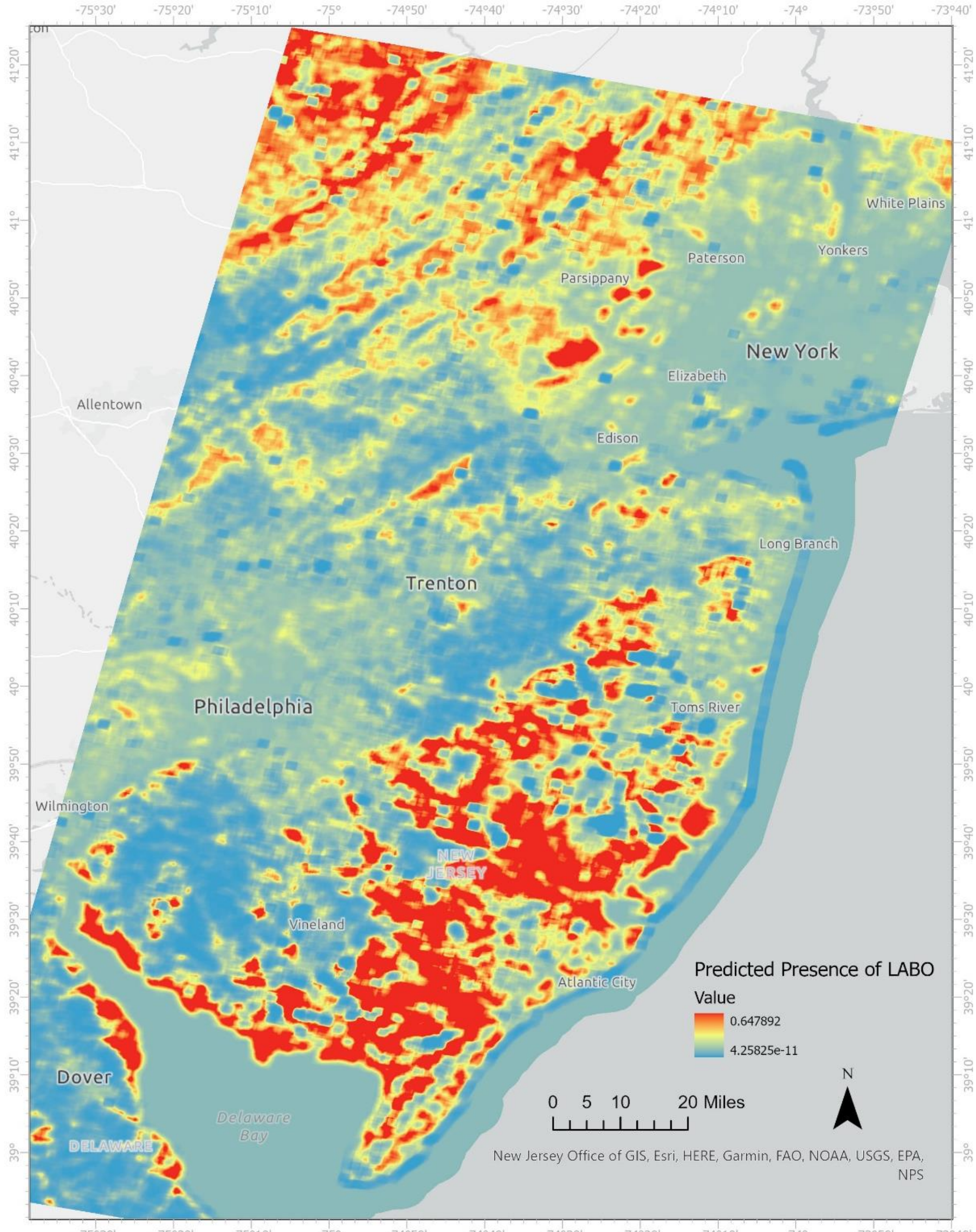

Figure 9. Species-specific predicted presence of *L. borealis* across New Jersey, USA. Predictions are based on 2nd order resource selection models using bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database.

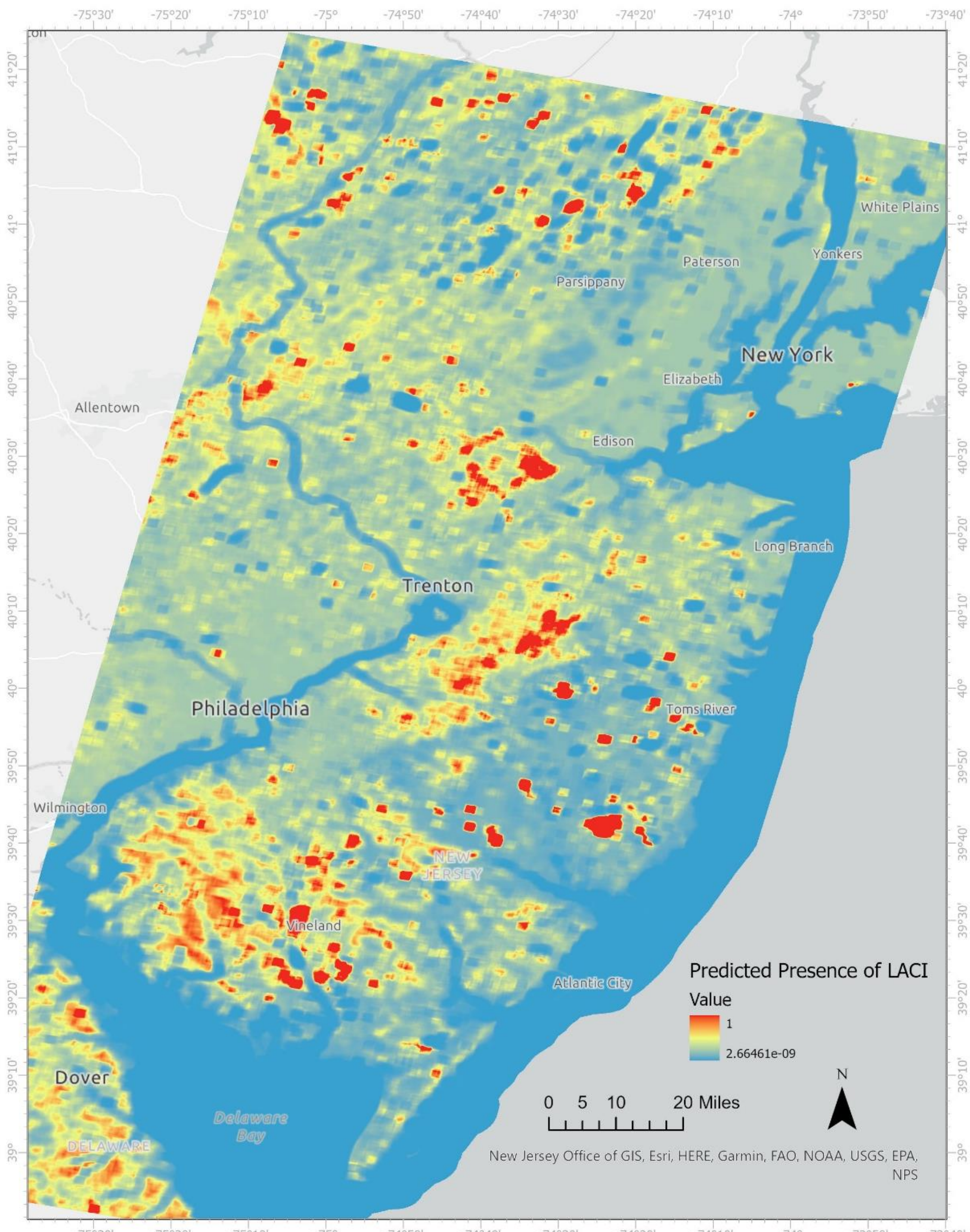

Figure 10. Species-specific predicted presence of *L. cinereus* across New Jersey, USA. Predictions are based on 2nd order resource selection models using bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database.

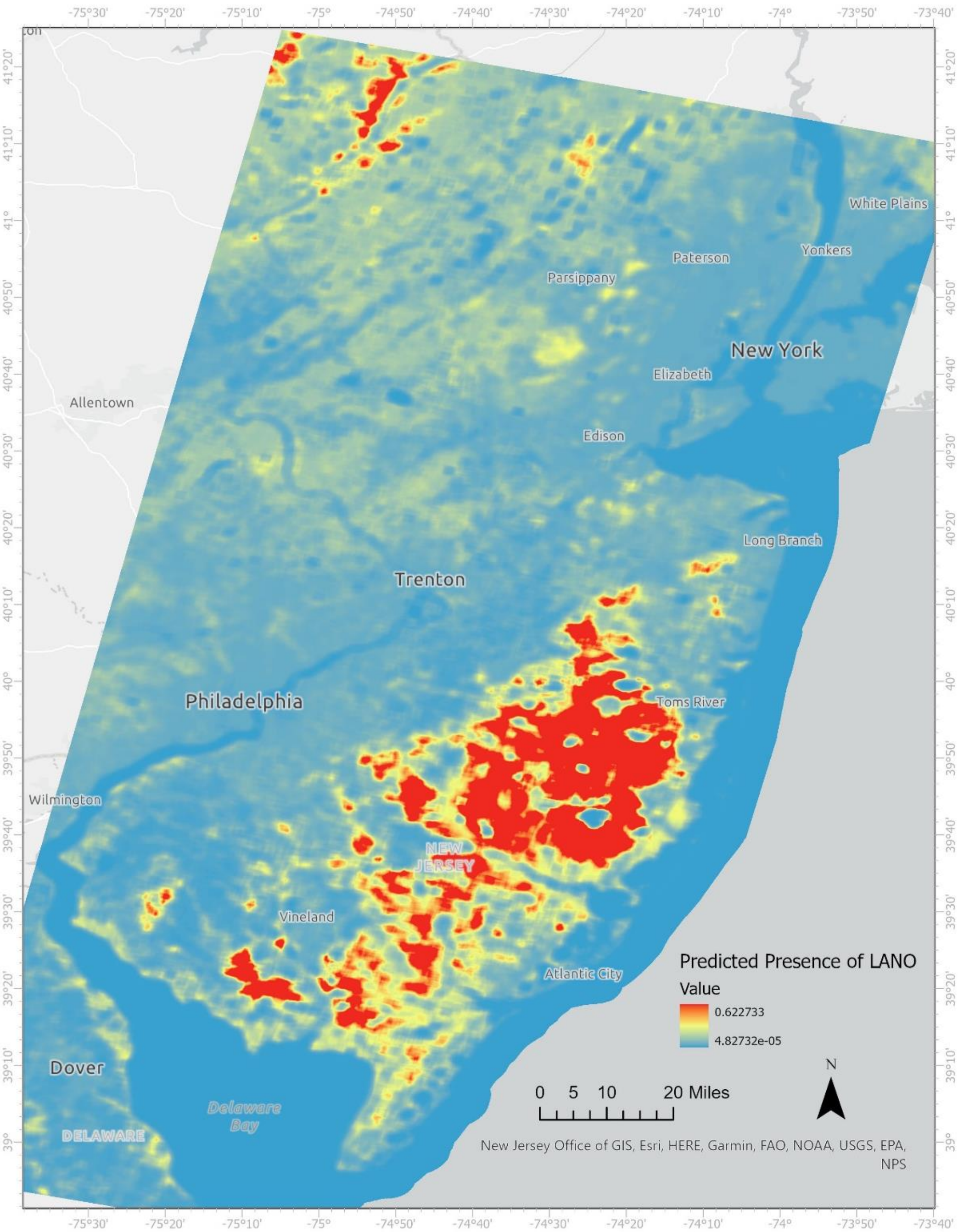

Figure 11. Species-specific predicted presence of *L. noctivagans* across New Jersey, USA. Predictions are based on 2^{nd} order resource selection models using bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database.

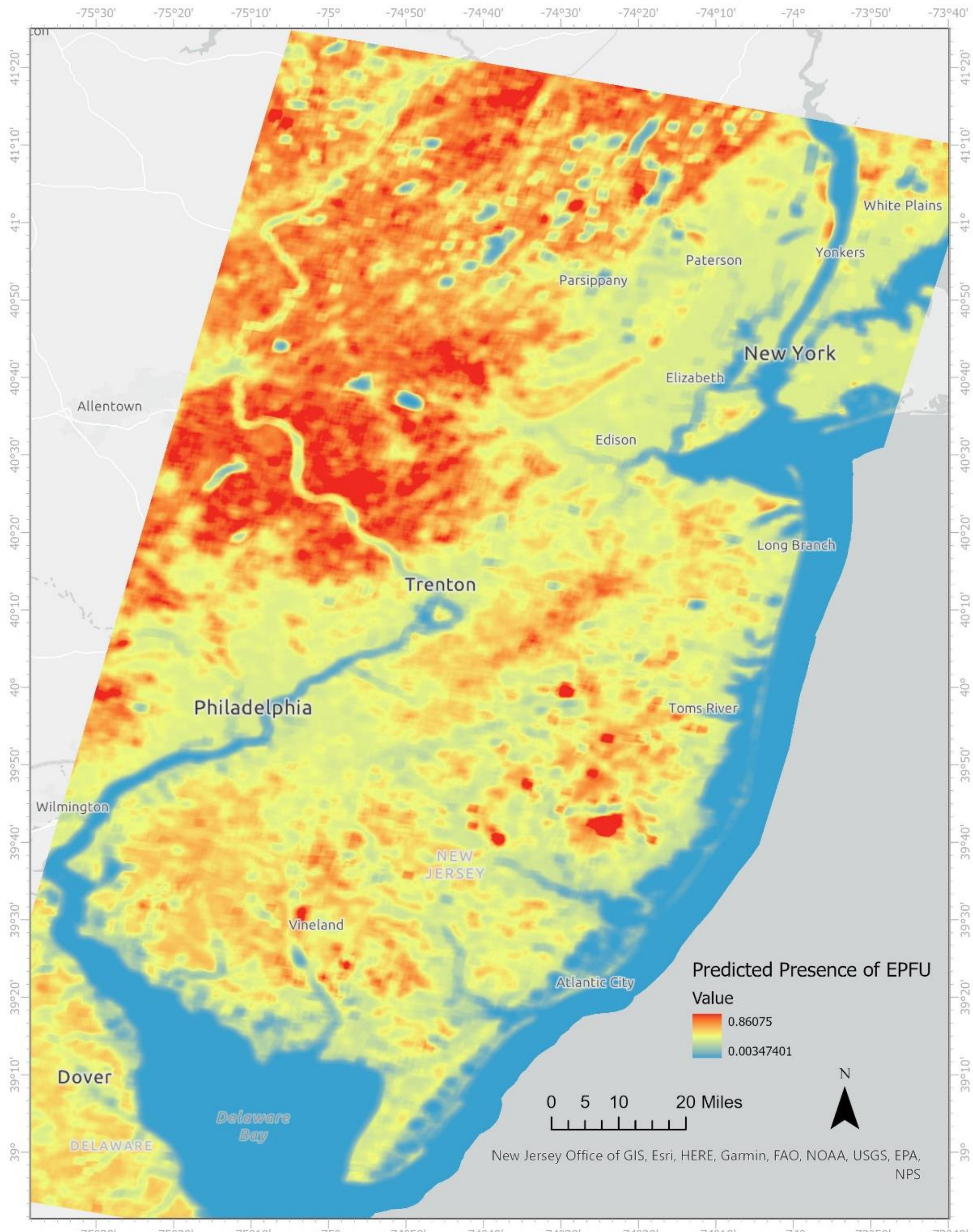

Figure 12. Species-specific predicted presence of *E. fuscus* across New Jersey, USA. Predictions are based on 2nd order resource selection models using bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database.

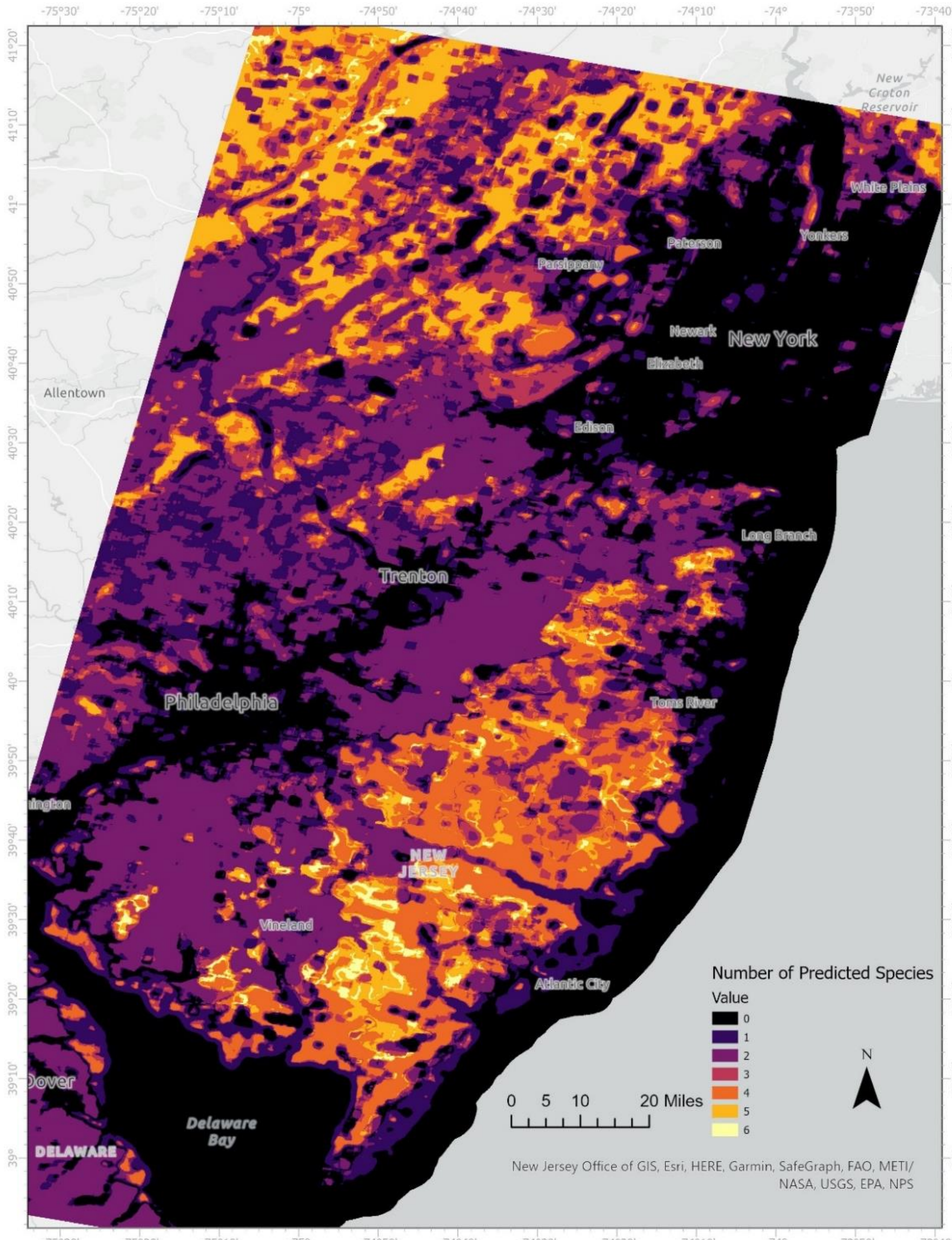

Figure 13. A map of the predicted diversity of *E. fuscus*, *L. cinereus*, *N. humeralis*, *L. borealis*, *L. noctivagans*, and *M. lucifugus* and *M. sodalis* across New Jersey. Predictions are based on 2nd order resource selection models using bat location data from the North American Bat Monitoring Program in New Jersey, USA, between the years of 2020 and 2021, and landcover data from the 2019 National Landcover Database. To denote presence a threshold of the mean probability of use for each species was applied.

SUPPLEMENTAL MATERIALS

```
model{
    a1 ~ dnorm(0,.001)
    b1 ~ dnorm(0,.001)
    b2 ~ dnorm(0,.001)
    b3 ~ dnorm(0,.001)
    b4 ~ dnorm(0,.001)
    b5 ~ dnorm(0,.001)
    b6 ~ dnorm(0,.001)
    b7 ~ dnorm(0,.001)
    b8 ~ dnorm(0,.001)
    b9 ~ dnorm(0,.001)
    b10 ~ dnorm(0,.001)

    tau.transect ~ dgamma(.01,.01)
    sd.transect <- 1/sqrt(tau.transect)

  for(r in 1:ntransect){
      transect.effect[r] ~ dnorm(0, tau.transect)
    }

    for(i in 1:n){
      y[i] ~ dbern(rUSE[i])
      logit(rUSE[i]) <-

    a1 +
    b1 * ag[i] +
    b2 * barren[i] +
    b3 * decid[i] +
    b4 * ever[i] +
    b5 * herb[i] +
    b6 * mixed[i] +
    b7 * openWater[i] +
    b8 * scrub[i] +
    b9 * urban[i] +
    b10 * wetland[i] +

       transect.effect[transect[i]]

    }

    }
```

A. Example of a logit link code for *E. fuscus*, used to account for the binomial distribution of Bernoulli use = 1 and available = 0 dependent variable, created using WinBUGS and implemented via R©. Each model was iterated 80,000 times across two MCMC chains then thinned to retain every 5th iteration.