Population estimation, harvest management, and landscape-scale spatial ecology of wild turkeys in Maine

Year 2 Progress Report

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Disclaimer: The findings contained in this report represent preliminary results of ongoing research, and they should be cited as unpublished data until they have undergone peer review and publication. We expect that estimated values and interpretation of results could change as additional years of data are collected. These changes will be incorporated into future reports and final published products.

Summary

1) The reintroduction of wild turkeys to Maine has been extremely successful, with the species now established and breeding in all counties of the state. The Maine Department of Inland Fisheries and Wildlife is now challenged with managing an abundant and popular game species that also lives at the human/wildlife interface.
2) In this report we summarize data collection and preliminary results from two years of research. Our major objectives are to develop tools for wild turkey population and harvest estimation, assess demographic rates and seasonal movements under varying landscape conditions, and evaluate prevalence and ecology of wild turkey diseases in Maine. We have also taken the opportunity to address a number of methodological questions related to wild turkey research in general.
3) Using rocket and drop nets, we captured and banded 124 unique wild turkeys in 2018 and 395 unique wild turkeys in 2019. We fitted 95 females with VHF backpack transmitters, 21 females with VHF necklace transmitters, and 39 females with GPS transmitters. We fitted 33 males with VHF necklace transmitters (Table 2). We collected 3 cloacal swabs each from 92 wild turkeys in 2018 and 2 cloacal swabs each from 126 wild turkeys in 2019. We also collected blood from 89 wild turkeys in 2018 and 266 wild turkeys in 2019.
4) We modeled harvest rates for male turkeys during the spring hunting season using the Seber parameterization of the dead recovery model. We estimated adult male harvest rate to be 0.249 (± 0.122) compared to a harvest rate of 0.106 (± 0.026) for juvenile male turkeys.

5) Using our harvest rate estimates (h) and total harvest numbers (H) provided by MDIFW, we estimated statewide population size (N) using a Lincoln Estimator ($N = \frac{H}{h}$). We estimated Maine's total male turkey population to be 32,696 (± 12,625) prior to the spring 2018 hunting season, and 33,609 (± 13,387) prior to the spring 2019 season.
6) We estimated weekly survival rates for VHF- and GPS-marked wild turkeys using nest survival models. Our top model of weekly survival probability was based on the MDIFW regions in which a turkey was captured (ΔAIC = 0.0; Table 5). Turkeys captured in Region F had the highest weekly survival rate (0.985; 0.979 – 0.989 95% CI) compared to Region A (0.978; 0.963 – 0.987 95% CI) and Region B (0.970; 0.960 – 0.978 95% CI). These correspond to annual survival probabilities of 0.430, 0.288, and 0.182, respectively. We also identified an effect of time of the year on survival (ΔAIC = 0.12; Table 5), with survival being variable throughout the length of the project (Figure 4). Additional support was found for models based on study area, LPDV infection status, WMD, and sex of turkey. No strong support was found for age of turkey, transmitter type, or REV or MG infection status.
7) To assess the potential for mortalities related to capture and handling up to 30 days post capture, we modeled daily survival rate with a log-log link function. Our best performing model was based on transmitter type (ΔAIC = 0.0; Table 6), with birds fit with backpack-style transmitters having greater post-release mortality compared to those fit with necklace-style transmitters. The cumulative survival rate during the first 14 days post-release for birds fit with backpack-style transmitters was 0.786 (0.689–0.854 95% CI), compared to 0.933 (0.780–0.976 95% CI) for birds fit with necklaces. There was

additional support for models based on handling time and age of the bird at capture. We did not find strong support for weather covariates, disease status, sex, or time of the year.

8) We monitored nest success of 69 nests from radio-marked hens. The average dates of initiation for first, second, and third nests (Figure 10) were May 6, June 1, and June 23 (single nest). We estimated daily nest survival rates for these nests and found the top model was based on a linear relationship with age of the nest (ΔAIC = 0.0; Table 8). As nest age increased in days, the probability of daily survival decreased (β = -0.047; -0.078 – -0.017, 85% CI). The probability a nest survived a 38-day exposure period was 0.261 (0.126–0.415, 95% CI; Figure 12). We did not find strong support for models based on transmitter type, disease status, nest initiation date, or nest attempt.
9) We compared hen and nest characteristics to identify sources of variation in clutch size. Average clutch size of VHF-marked hens across both years of the study was 11.210 eggs, with the largest clutch size being 16 and the smallest being 6. Hens that had a positive lymphoproliferative disease virus (LPDV) status at capture had a clutch size that was 1.718 (± 0.736) eggs fewer than those with a negative LPDV status (Figure 13).
10) We used dynamic Brownian Bridge Movement Models to create seasonal home ranges based on shifts in movement behaviors of wild turkey hens. The average area of use (95% UD) for GPS-marked females that survived from capture until August 1 was 2.680 mi^2 (range 1.093 mi^2 – 8.271 mi^2) in 2018 and 2.634 mi^2 (range 0.632 mi^2 – 7.784 mi^2; Table 10, Figure 14, 15) in 2019. The average seasonal movement distance between wintering home range and nesting home range was 2.643 miles in 2018 and 3.267 miles in 2019. Individual female movements between winter and nesting home ranges varied from 0.283

miles to 14.426 miles. Disease status best explained observed variation in seasonal home range size and distance traveled between seasonal home ranges.

11) Molecular methods were used to detect individual infection with LPDV and reticuloendotheliosis virus (REV) while serological methods were used to detect previous exposure to *Mycoplasma gallisepticum* (MG) from blood collected during turkey capture. We found an overall prevalence of 69% (141/203) for LPDV infection, 16% (31/193) for REV infection, and 78% (137/175) for MG exposure.

12) We assessed age, sex, age*sex, study area, and year of collection as risk factors for pathogen infection. Age was the only important variable in predicting LPDV infection (ΔAIC = 0.0), with juveniles less likely to be infected than adults (β = -2.282; -2.994 – -1.612, 95% CI). The best model for probability of infection with REV included year of collection and study area (ΔAIC = 0.0), with a higher prevalence in 2019 than 2018 (β = 1.063; 0.112 – 2.078, 95% CI) and the highest prevalence in the south and lowest in the northeast study areas (β = 0.749; -0.248 – -1.765, 95% CI). Lastly, the predictive model for probability of exposure to MG includes year of collection and the interaction of age and sex (ΔAIC = 0.0), with a lower prevalence in 2019 than 2018 (β = -1.737; -2.722 – -0.872, 95% CI) and lowest prevalence in juvenile males (β = -2.554; -4.777 – -0.699, 95% CI).

13) We examined the relationship between the infection of any two pathogens using a Pearson's chi-squared test. We did not find a correlation between infection with any of the pathogens tested; infection with multiple pathogens did not occur more often than expected by chance.

14) We evaluated the use of cloacal swabs as a minimally invasive detection method for LPDV and found an overall sensitivity (true positives) of 69% (45/65) and specificity of 95% (19/20) (true negatives) compared with the current method of blood collection.
15) We will complete a third year of data collection during 2020, and future reports will contain additional data, updated analyses, and additional conclusions to inform wild turkey management in Maine.

Introduction

The restoration of wild turkeys to Maine has been very successful, as evidenced by a robust population throughout their historical range within the state, and viable populations that now extend into areas that likely lacked turkeys prior to European settlement. Wild turkeys are now established and successfully reproducing in all Maine counties. Over the last 30 years the wild turkey program has grown from one focused on re-establishment and very limited harvest to one that allows for relatively liberal spring and fall hunting seasons. The first spring season in 1986 was limited to 500 hunters resulting in a harvest of 9 birds. Presently both spring and fall seasons are open to all interested participants, and the program supports around 18,000 wild turkey hunters, including an estimated 2,500 youth. In recent years Maine hunters have averaged a spring harvest of 6,000 bearded turkeys, and a fall harvest of 2,000 turkeys of either sex (MDIFW 2017). A recent assessment of wild turkey populations across the country suggests that Maine's wild turkey population is increasing at one of the greatest rates among all states (Erikson et al 2016).

With the success of this reestablished population, MDIFW is now faced with the challenges of managing for a viable turkey population and a successful hunting program, while simultaneously addressing social and ecological issues associated with an abundant wildlife species that often lives at the human/wildlife interface. Maine's wild turkey population continues to increase and expand into nearly all corners of the state. This is an obvious benefit to wild turkey hunters by providing opportunities for quality hunting, and recent surveys suggest that 92% of Maine turkey hunters are satisfied with their wild turkey hunting experience in the state (Responsive Management 2016). However, increases in wild turkey abundance also inherently increase the potential for human-turkey conflicts (Miller et al. 2000), and the same survey

revealed that approximately 30% of Maine residents believe the abundance of wild turkeys should be reduced in the state (Responsive Management 2016). Thus, MDIFW is likely to face societal pressures in coming years to manage Maine turkey populations based on competing objectives.

Greater densities of wildlife are often associated with heightened risk of disease transmission, as well as increased potential for interaction with domestic poultry resulting in a higher risk of pathogen spillover. Information on pathogen prevalence and distribution in Maine wild turkeys is scarce, and little is known about the effects of disease on individual and population health, the potential for disease transmission across the state, or transmission to humans, other wildlife, or domestic animals. In other wild turkey populations, greater than 25% of morbidity or mortality cases have been attributed to infectious diseases (Van Riper III and Forrester 2007). We evaluated the prevalence, risk factors, and coinfection status of three major infectious diseases in Maine wild turkeys: lymphoproliferative disease virus (LPDV), reticuloendotheliosis virus (REV), and the bacterium *Mycoplasma gallisepticum* (MG). Each of these three qualify as pathogens that should be monitored in wild turkeys for several reasons: there are diagnostic tests readily available, they occur at the domestic-wildlife interface, they can infect other wild avian species, they are believed to be immunosuppressive and/or their pathogenicity is increased with stress or secondary infection, and there is a knowledge gap regarding their impact on wild turkeys at the individual and population level.

Our project began in 2018 as a component of MDIFW's implementation of the Big Game Management Plan. In this new management plan, goals and objectives were established through a thorough public input process to guide the Department's wild turkey management over the next 10 to 15 years. In modern wildlife management, a number of toolkits exist for addressing

complex management challenges in the face of uncertainty. Adaptive harvest management and structured decision making are two examples, and these tools clearly have high potential for addressing management questions that are unique to wild turkeys (e.g. Robinson et al. 2017). However, nearly all comprehensive approaches to management require adequate data to inform decisions, and much of the information necessary for informed decisions about wild turkey management is currently lacking in Maine. **The overall goal of our project is to produce rigorous information on a host of biological processes for turkeys in Maine, including population dynamics, survival and harvest rates, habitat use and reproductive success, seasonal movements, and disease prevalence and transmission.** This information can then be used to develop tools that address MDIFW's population and habitat goal to "maintain a healthy turkey population below biological carrying capacity while providing hunting and viewing opportunity." Our specific objectives are to 1) improve MDIFW's ability to monitor wild turkey population trends by exploring population models that incorporate variables such as weather, productivity, harvest, sex, age, natural mortality, pathogen infection and other factors; 2) improve the quality and availability of wild turkey harvest data; 3) inform management that can be used to stabilize wild turkey populations in portions of southern and central Maine and increase the size and distribution of turkey populations in portions of northern, eastern, and western Maine; and 4) identify the prevalence and individual risk factors of LPDV, MG, and REV infection and evaluate if there is a correlation between coinfection of these pathogens within an individual. Given the large amount of data collection required to achieve objectives 1-4, we are also 5) taking every opportunity to address methodological and ecological questions that will improve our ability to study wild turkeys and increase our knowledge of the species in

general. In this report we detail results from our first two years of data collection, which provide preliminary insights to some of these objectives.

Field and Laboratory Methods

Study Areas

In the first year of the project, wild turkey captures took place in 4 study areas located in Wildlife Management Districts (WMD) 17, 18, 21, and 26 (Figure 1). In an effort to increase the sample size of banded individuals during our second year, we expanded banding efforts throughout Maine to sites that were monitored and operated by MDIFW regional staff (pink dots, Figure 1). We banded captured turkey at these sites and collected morphometrics and blood, but transmitters were not deployed.

Our north-western study area (NW) is located in Penobscot County, Maine, USA (44.98912°N, 69.07784°W). NW is within WMD 17 and encompasses the towns of Exeter, Corinth, Charleston, and Bradford. Property within NW is primarily privately owned and its land use is characterized by rural agricultural and pasture fields intermixed with forested areas. Human population density within NW ranges from fewer than 50 up to 100 individuals per sq. mile (USDC 2012) and the landscape has moderate road coverage with both paved, gravel, and dirt roads. NW is in central Maine and experiences moderate winters compared to more Northern regions of the state, but more severe winter weather than more southern regions.

Our north-central study area (NC) is also located in Penobscot County (44.91855°N, 68.66162°W). NC is primarily in the northern part of WMD 26, with some overlap of WMD 17 and 18. Research takes place within the towns of Orono, Old Town, Veazie, Bangor and Hampden. This area is primarily characterized by suburban and urban human residential areas

with population density ranging from 100 to greater than 500 individuals per sq. mile (USDC 2012). Road density and residential development is higher in NC compared to our other study areas; however, forested area and agricultural lands are still present in the study area, albeit far more sparse and isolated compared to the other study areas. NC is in the same climatic zone as NW and experiences comparable weather.

Our north-eastern study area (NE) is located in both Penobscot and Hancock Counties, Maine, USA (45.01749°N, 68.39635°W) within WMD 18 between the towns of Greenfield and Amherst. Human population density in NE is very low with fewer than 50 individuals per sq mile (USDC 2012), and includes large expanses that are completely uninhabited and undeveloped. Despite this, substantial human activity occurs in the form of forestry operations within privately-owned commercial forests that dominate the area. Moderate cover of maintained gravel and dirt roads are also present, although many of these roads become inaccessible in the winter after considerable snowfall. NE is in the same climatic zone as NW and NC, and experiences similar weather patterns.

Our southern study area (S) is in Cumberland County, Maine, USA (43.71543°N, 70.39268°W), and was chosen to represent a distinctly different region of the state than the previous three study areas. S is within WMD 21 and located between the towns of Gorham and Gray. The landscape within S spans a gradient between rural areas and the suburban edge of the greater Portland metropolitan area. This gradient of land use leads to mixed landcover and human activity levels. The landscape is a mix of residential areas, agricultural fields, and fragmented forests. Human population density in this area is greater than 200 individuals per sq. mile (USDC 2012). Being farther south and closer to the coast, S is in a separate climactic zone

compared to the other 3 study areas and experiences generally milder weather compared to NW, NC, and NE.

Wild Turkey Capture and Sample Collection/Storage

Capture of wild turkeys took place from January through March 2018 (Year-1) and December 2018 through March 2019 (Year-2). During this time of year, wild turkeys form large flocks and are more likely to frequent bait sites due to snow obscuring normal food sources. We trapped both male and female wild turkeys using either drop nets (Glazener et al. 1964) or rocket nets (Grubb 1988). Turkeys were weighed (+/- 0.5 lbs) using a spring scale. The sex and age of each bird was assessed based on its plumage and presence of a beard and spurs (Dickson 1992). Each turkey received either a size 22 (female) or 28 (male) butt-end aluminum leg band (National Band and Tag Co., Newport, Kentucky, USA) with an identification number for the bird as well as contact information for reporting the bird if harvested or otherwise discovered dead. During Year-1, each turkey also received an additional mark in the form of an aluminum rivet band, patagial wing tag, or color leg band. During Year-2, only a combination of aluminum and rivet bands was used. Tarsus length was measured for all birds as well as spur and beard length, if present.

Wild turkeys were fitted with a VHF or GPS transmitter, or banded only, based on trap site location, sex and age, and status of deployed transmitters. We deployed transmitters to disperse them within and among the four primary study areas, with a goal of maintaining a 50:50 ratio between adult and juvenile females when possible. We deployed three unique transmitter models; a VHF backpack, a GPS backpack, and a VHF necklace. VHF backpack packages consisted of an 80g transmitter from Advanced Telemetry Systems (Isanti, Minnesota, USA) attached using a backpack-style harness. GPS packages were 90g Litetrack GPS transmitters

with a built in VHF component (Lotek Wireless Fish and Wildlife Monitoring, Newmarket, Ontario, CA), also attached with a similar backpack-style harness. The VHF necklace packages consisted of a 12g transmitter from Advanced Telemetry Systems (Isanti, Minnesota, USA) attached around the neck using wire, crimps, and rubber tubing. We only deployed GPS transmitters in the three northern study areas (NW, NC, NE) as these study areas were located within the same climatic zone and represented the major landcover types (agricultural, suburban-urban, forested) relevant to our objectives on movement and space use of wild turkey hens. Backpack-style transmitters were secured to each bird using paracord tied around the base of both wings. Any transmitters that were recovered and still functioning were reserved so they could be redeployed at a later capture. Transmitters did not exceed 4% body mass, and all capture and handling of wild turkeys was approved by the University of Maine Institutional Animal Care and Use Committee (IACUC Protocol # A2017_11_03).

We collected blood from the brachial vein and cloacal swabs from each wild turkey during capture for pathogen analysis. Within 24-hr post-capture, we processed the blood (see below) and archived additional aliquots in a -80°F freezer. Blood tubes with no anticoagulant (red-top) were centrifuged to separate the serum layer, which was collected and stored to test for MG exposure (see below). Anticoagulant-treated (purple-top) tubes were also centrifuged to enable the collection of the buffy coat layer (concentrated white blood cells), which has been shown to have a high sensitivity (true positive rate) and specificity (true negative rate) for LPDV testing in live birds (Alger et al. 2015). If the buffy coat layer could not be obtained, we used whole blood, which has also been found to be reliable for LPDV diagnostics (Alger et al. 2015). We stored cloacal swabs at -80°F until processing.

GPS Transmitter Programming and Monitoring

GPS transmitters were programmed to take locations every hour during daylight from November through July, along with a single overnight location to document roosting sites. To extend the battery life of the transmitters to collect data over two nesting seasons per bird, the number of daytime points collected were reduced from August through October to only a morning (9am), afternoon (3pm), and roost location. This model of GPS transmitter requires downloading data remotely from the transmitter using a Pin Point Commander unit. We located birds approximately once weekly to download waypoint files from the transmitters as needed to preserve battery life. We uploaded waypoint files to Movebank.org (Wikelski and Kays 2018) to ensure a backup and to easily convert them for viewing and analysis.

Adult Survival Monitoring

At least once a week, we recorded a signal from each bird with a VHF or GPS transmitter using a hand-held three element directional antenna and receiver. When a VHF-marked bird was located, the Live-Dead status was recorded based on the speed of the transmitter signal. Status of GPS-marked birds was determined from downloaded locations where sequential points at the same location indicated a potential death. For two weeks following a trapping event, birds were monitored with increased frequency to more accurately detect any trapping-related mortality. If a bird was suspected dead, the transmitter was approached to determine fate and record a plausible cause of death.

Band Reporting

During the spring and fall wild turkey hunting seasons, an online website and phone line were made available for hunters to report marked birds that were harvested. All wild turkeys harvested by hunters must be reported to a registration station within 18 hours, where band

information is also recorded if a hunter declines to contact us directly. For each bird harvested, we obtained identification codes from all tags that remained on the bird, the date and time of harvest, the town in which the bird was harvested, and whether the bird was seen with any other turkeys.

Nest Monitoring

We monitored tagged hens for suspected nesting behavior from April 15 to July 30. Locations of VHF-marked individuals were collected at least twice a week via short-distance triangulation. If a hen was found alive in the same location during two successive visits, she was assumed to be on a nest. After 2 weeks, we approached the hen's location and flushed her to confirm nesting and locate the nest. We then floated 3-4 eggs to determine incubation stage, estimate the initiation date of the nest (Westerskov 1950), and to predict a hatch date. We continued to monitor the nest at least once a week, with a goal of 3 visits per week when possible. We increased visits around suspected hatch date to better determine actual hatch date. Once a hen was suspected to have left the nest, we approached the nest to assess its fate, hatched or failed. If a nest failed, we assessed whether it was abandoned, depredated, or if the hen was killed by a predator.

Location data from GPS-marked hens was downloaded weekly and point locations were reviewed in Google Earth. If we observed that a hen was making repeated visits to a single location around the same time of day, or had settled in a location she had previously visited regularly, we assumed she was nesting. Once the hen began regular movements or discontinued regular daily visits in the case of failure during the laying phase, we visited the suspected nest site to verify the nest and its fate. We did not disturb GPS hens while on nests so that we could

assess the effect of nest monitoring, which was based on comparison between nests of VHF-marked hens (flushed, regularly visited) and GPS-marked hens (never disturbed while nesting).

Molecular Detection of LPDV and REV

We extracted DNA using the Qiagen DNeasy Blood and Tissue Kit (Qiagen, Valencia, CA). Cloacal swabs were allowed to thaw prior to using the TissueLyser LT (Qiagen, Valencia, CA) to dislodge material for DNA extraction. We measured the DNA concentration of each extraction using Nanodrop Technologies or Qubit Fluorometric Quantitation (Thermo Fisher Scientific, Waltham, MA).

A 413 base pair region of the retroviral *gag* gene in LPDV was amplified through PCR using the following primer sequences: LPDV-F 5'-ATGAGGACTTGTTAGATTGGTTAC-3', and LPDV-R 5-TGATGGCGTCAG GGCTATTTG-3 (Allison et al. 2014). PCR reactions were a total volume of 25uL, using the following reagent concentrations: 0.558 ng to 231 ng DNA extract (from blood or cloacal swabs), 0.2 μM primers (Integrated DNA Technologies, Coralville, IA), 1.5 mM $MgCl_2$ (Promega, Madison, WI), 0.2mM dNTPS (Amresco, Solon, OH), 0.625 units of GoTaq¨ Flexi DNA Polymerase and buffer (Promega). The PCR cycling conditions involved an initial denaturation at 95^0C for 3 minutes, followed by 34 cycles of 95^0C for 30 seconds, 54^0C for 30 seconds, and 68^0C for 1 minute, and ended with a final elongation step for 5 minutes at 68^0C.

A 580 base pair region of the retroviral *pol* gene in REV was amplified through PCR using the following primer sequences: LPDV-F 5'- TGCCACCCGAGACTTACTCA-3', and LPDV-R 5- CTGCCCGAAGGTAAGTTTAGAG-3 (Bohls et al. 2006). The PCR protocol for REV was performed using the following previously described methods by Bohls et al. (2006). PCR reactions were a total volume of 50uL, using the following reagent concentrations: 0.558

ng to 231 ng DNA extract (from blood), 0.2 µM primers (Integrated DNA Technologies, Coralville, IA), 1.2 mM $MgCl_2$ (Promega, Madison, WI), 0.2mM dNTPS (Amresco, Solon, OH), 1.25 units of GoTaq¨ Flexi DNA Polymerase and buffer (Promega). The PCR cycling protocol involved an initial denaturation step at 95℃ for 5 minutes, followed by 40 cycles at 95℃ for 30 seconds, 55℃ for 30 seconds and 72℃ for 2 minutes, and a final incubation step at 72℃ for 7 minutes before storing at 4℃.

We confirmed amplification of the proviral DNA target region for both LPDV and REV by electrophoresis, using a 1% agarose gel, and visualized with an Azure c150 Imaging System (Azure Biosystems, Dublin, CA). Both extraction and PCR negative controls were used. In addition, a positive PCR control was included from a previously identified LPDV- and REV-positive wild turkey in Maine, courtesy of Dr. Pete Milligan (University of Maine-Augusta). Exonuclese 1 and Shrimp Alkaline Phosphatase were used to clean-up PCR products prior to sequencing. All positive PCR products were sent to the UMaine Sequencing Facility for genetic sequencing in both forward and reverse directions using the same primers listed above. During future analyses we will use the LPDV sequence data for genetic characterization of the virus and to examine LPDV transmission dynamics.

Serum Diagnostics for Detection of MG Exposure

We performed a plate agglutination test to detect the presence of host MG antibodies by adding one drop of MG antigen (A5969 strain, Charles River Laboratories) to 20uL serum sample. A positive and negative control were included each processing batch (Charles River Laboratories, Wilmington, MA). The plate agglutination protocol involved an initial positive and negative control test, followed by combining 20µl MG blood serum with one drop antigen on a glass plate, and mixing to homogenize. Pathogen exposure was determined by coagulation upon

continuous gentle mixing. A positive serum test indicates previous exposure to the pathogen, not an active infection.

Analytical Methods

Population Estimation

To estimate population size of wild turkeys within Maine, we first modeled harvest rates using the Seber parameterization of the dead recovery model in the RMark package (Laake 2013) in program R (R Core Team 2013). A 'LDLD' encounter history was constructed for each individual turkey, where 'L' corresponded to the year in which the turkeys was captured and 'D' the year in which the turkey was reported as harvested. For the results presented in this report, we limited our analysis to male turkeys harvested during the spring bearded turkey hunting season. Unless otherwise noted, models in this and other analyses were compared using Akaike's Information Criterion (Burnham and Anderson 2003). We identified supporting variables by comparing univariate models against a null. Covariates of models with $\Delta AIC \leq 2.0$ were combined into a best fit model. We evaluated the importance of variables by examining 85% CL of each (Arnold 2010). We only then considered a covariate supported if the CL did not include zero. Covariates of harvest rate included age of the turkey as well as Region or WMD of harvest. The Seber parameterization estimates both the survival probability from one release to the next (S) and the probability of a dead individual being found and recovered (r). Under this parameterization, harvest rate can be calculated as $r * (1 - S)$, yielding the proportion of mortality associated with harvest. We used the delta method (Lyons 1991) to calculate a standard error for the harvest rate. Using harvest rates (h) calculated from RMark and total harvest

numbers (*H*) provided by MDIFW, population size (*N*) for a given management unit *i* (e.g., a wildlife management district) in a given year *j* is estimated as $N_{ij} = \frac{H_{ij}}{h_{ij}}$.

Hen Weekly Survival Rate

We compiled weekly live/dead status for each VHF- and GPS-marked wild turkey hen to create an encounter history which indicated the week the hen was captured (First Found), the last week it was found alive (Last Alive), the last week it was checked (Last Checked), and its final status at the end of the monitoring period for this report (Fate). Turkeys that died within 14 days post capture were censored from this analysis. Following the two-week post-capture period, any deaths were attributed to normal causes and assumed to not be capture-related. We modeled the female weekly survival probability using the nest survival model in the RMark package (Laake 2013) in program R (R Core Team 2013). We chose this approach because it allowed for irregular monitoring of individuals, which best fit our study design where sometimes we were unable to locate hens following extended or irregular movements. Weekly survival probability models considered were based on month of the year, season of the year (determined by movement behavior, see below), age of the turkey, study area, and LPDV infection status.

Post-release Mortality

Wild turkeys are often found to experience elevated mortality following capture and release (Nicholson et al 2000). To assess the potential for mortalities related to capture and handling in the 30 days post capture, we modeled daily survival rate (DSR) with a log-log link function using the RMark package (Laake 2013) in program R (R Core Team 2013). All models included a covariate based on the natural log of the number of days since the capture event, which allows the model to reflect an increase in daily survival probability out to a potential threshold, which presumably reflects the point at which capture-related mortality no longer

persists (Blomberg et al. 2018). One additional covariate related to the trapping event or the individual turkeys was added for each model as an interaction with the ln (days post-capture) term, which allowed us to test whether these factors contributed to post-release mortality. These covariates included age of the turkey, sex, transmitter type (backpack vs necklace mounted), trapping location, disease status, and handling time. Weather covariates related to the trapping event and the following week were compiled using the prism package in program R (Edmund et al 2018). To further define a cut off for trapping mortality, we compared a series of models in which a threshold point was set that allowed daily survival to differ between days before and after the threshold but did not differ within the respective intervals (Blomberg et al 2018). This allowed us to observe shifts in daily survival, define a threshold date for post-release mortality, and evaluate an appropriate censoring period for other survival analyses.

Daily Nest Survival Rate

We modeled nest daily survival rate (DSR) using the RMark package (Laake 2013) in program R (R Core Team 2013). To produce a probability of nest success, we exponentiated the DSR by the average nest exposure period (average length of laying and incubation periods observed during this study; 38 days). We compared models of nest survival to identify important predictors of nest success. Models were based on day of the year, age of the nest in days, nest initiation date, age of the turkey (first nesting season vs second or later nesting season), study area, transmitter type (VHF vs GPS), and LPDV infection status. We compared model sets individually for DSR and parameter coefficients using the same criteria described for our survival analysis above.

Clutch Size

We used linear regression models to identify sources of variation in clutch size between nests. Covariates of interest included date of initiation, turkey age, year, study area, disease status, and whether the nest was a first nest or renest.

Seasonal Home Range and Movements

We fit dynamic Brownian Bridge Movement Models (dBBMM) to the movement track of each GPS-marked hen using the move package (Kranstauber and Smolla 2013) in program R (R Core Team 2013). We *a priori* described expected categories of seasonal movement behavior, which included winter, winter to pre-nesting movement, pre-nesting, and summer. Brownian motion variance (σ_m^2) is a measure of how irregular the path of an animal is between successive locations (Byrne et al 2014) by accounting for changes in movement distance and direction. We delineated seasonal changes in movement behavior by quantifying changes in daily σ_m^2 over time (Kranstauber et al 2012), averaged across all marked hens. Based on patterns of individual changes in σ_m^2, we subset movement tracks into seasonal categories of movement and created individual utilization distributions (UDs) for each category of movement for each hen. If a hen did not survive from capture to August 1, it was censored from estimation of average total range size. 95% UD were estimated for each bird's seasonal home range. Seasonal movements between winter and nesting home ranges were quantified as the distance between the centroids of the winter range and the nesting range. We separately compared regression models of winter home range size, prenesting home range size, and distance traveled between winter and prenesting ranges. Covariates compared included study area, turkey age, and disease status.

Risk Factors for Pathogen Infection

All pathogen data were analyzed using Program R (R Core Team 2013). We used a Generalized Linear Model assuming a binomial distribution with a logit link function to test the effect of the predictor variables (age, sex, age*sex, study area, year of collection) on the probability of pathogen infection. Akaike information criteria (AIC) model selection was used to determine the top model(s). We then assessed the summary statistics on those models to determine which variables were significant ($p<0.05$) and which combination of variables contributed to the explanation of variation using the equation 1-(residual deviance/null deviance). We finally ran a Pearson's chi-squared test with Yates' continuity correction to further validate the inclusion of variables in the selected models.

Pathogen Coinfection

We ran a Pearson's chi-squared test with Yates' continuity correction test on contingency tables to evaluate whether pathogen infection with LPDV, REV, or MG was independent of additional pathogen infection. For this analysis, $p>0.05$ indicates independence of the variables while $p<0.05$ signifies a correlation between variables. This analysis allows us to assess whether two pathogens were more likely to affect a single individual than expected by chance based on the overall prevalence of each pathogen individually.

Cloacal Swabs as an LPDV Detection Method

When assessing cloacal swabs as a minimally invasive detection method for LPDV, we compared PCR results from swab DNA extractions to PCR results from blood DNA extractions for each individual. We quantified both the sensitivity (proportion of correct positives) and specificity (proportion of correct negatives) of the sampling method.

Results

Capture and Sampling

During Year 1, we captured and banded 124 unique wild turkeys between our four primary study areas. During Year 2, we captured and banded 395 unique wild turkeys, 140 of which were in our primary study areas. 108 of those captured were identified as adult males, 126 as juvenile males, 190 as adult females, and 95 as juvenile females. Of turkeys caught outside of the primary study areas, 33 were captured in WMD 12, 2 were captured in WMD 17, 32 were captured in WMD 18, 114 were captured in WMD 23, 29 were captured in WMD 26, 24 were captured in WMD 6, 20 were captured in WMD 27, and 1 was captured in WMD 28 (Table 1). Of turkeys caught in the primary study areas between both years, 96 turkeys were captured at NW, 75 were captured at NC, 36 were captured at NE, and 57 were captured at S. We fitted 95 females with VHF backpack transmitters (71 on adults and 24 on juveniles), 21 females with VHF necklace transmitters (11 on adults and 10 on juveniles), and 39 females with GPS transmitters (25 on adults and 14 on juveniles). We fitted 33 males with VHF necklace transmitters, 14 on adults and 19 on juveniles (Table 2). We also fitted 1 adult male with a used GPS transmitter (Figure 2) which operated from March 14, 2019 to May 3, 2019, when the bird died.

We collected blood from 203 turkeys (89 from 2018, 114 from 2019; 95 adult female, 33 adult male, 40 juvenile female, and 35 juvenile males). The 203 birds sampled spanned 15 towns within the four study areas. Thirty-four birds were sampled from NE, 63 from NC, 55 from NW, and 51 from S. Finally, we collected cloacal swabs from 76 turkeys during the 2018 trapping season.

Harvest Reporting

Five of 39 males banded during 2018 were harvested and reported during the 2018 spring turkey hunting season, while 2 of the 85 females we banded during 2018 were reported during the 2018 fall either sex hunting season. In this later case, one radio-marked hen was shot, recovered, and reported, while a banded-only female was shot and not initially recovered but was found later and reported. Forty one banded males were harvested during the 2019 spring turkey hunting season, 4 of which were banded in Year1 and 37 that were banded in Year2. Five of the 37 were radio-marked in Year 2. Two banded hens and 4 banded males were harvested during the 2019 fall either sex hunting season. One of those banded males was radio-marked. For the three options available for reporting the harvest of a banded turkey, 12 (21.4%) were reported only to the check station, 5 (8.9%) were reported only to the website, 16 (28.6%) were reported only by phone, and 23 (41.1%) were reported to more than one of the three options. One banded turkey harvest was reported outside of these three options (Table 3).

Harvest Rate and Population Size Estimates

Our top band recovery model was based on the age of the turkey at capture (Adult versus Juvenile; ΔAIC = 0.0; Table 4). Using estimates of survival (S) and reporting rate (r) to calculate harvest rates (h), we found that adult male turkeys had a higher h (0.249 ± 0.122) during the spring hunting season than juvenile male turkeys (0.106 ± 0.026). Our second best model (ΔAIC = 1.11; Table 4) sorted capture sites into regions based on MDIFW expected intensity of harvest. Capture sites in WMDs 17, 21, 23, and 26 were considered to have "High" intensity harvest while those in WMDs 6, 12, 18, and 27 were considered "Medium" intensity. In "High" WMDs, adult male harvest rate during the spring hunting season was 0.236 (± 0.047) compared to 0.214 (± 0.077) in low intensity units. For juvenile males during the spring hunting season, harvest

rates were 0.132 (± 0.034) in "High" WMDs compared to 0.047 (± 0.036) in "Medium" WMDs. In WMDs with a large enough sample size, we were able to estimate WMD-specific harvest rates (Figure 3), which varied from 0.119 (+/- 0.069) to 0.228 (+/- 0.054) for adult male turkeys and from 0.046 (+/- 0.051) to 0.178 (+/- 0.066) for juvenile male turkeys.

We used our estimates of adult and juvenile harvest rates in combination with the number of harvested and reported turkeys provided by MDIFW to estimate statewide population size. In the 2018 spring turkey harvest, 4,733 adult males and 1,454 juvenile males were reported, which corresponds to an estimate of 18,932 (± 9,264) adults males and 13,764 (± 3,361) juvenile males. In the 2019 spring turkey harvest, 5,283 adult males and 1,318 juvenile males were reported, which corresponds to an estimate of 21,132 (± 10,341) adults males and 12,477 (± 3,046) juvenile males.

Weekly Adult Survival Rate

Of 189 turkeys fitted with a transmitter, 46 were censored due to death within the first two weeks after release from capture. The majority of censored turkeys appeared to be killed by predators around capture areas, however we cannot rule out death due to other causes (e.g. capture myopathy) followed by scavenging. Of those birds not censored, 86 transmitters were active as of November 22, 2019, when we cut off data collection for our analysis.

Our top model of weekly survival probability was based on the MDIFW regions in which a turkey was captured (ΔAIC = 0.0; Table 5). Turkeys captured in Region F had the highest weekly survival rate (.985; 0.979 – 0.989 95% CI) compared to Region A (.978; 0.963 – 0.987 95% CI) and Region B (.970; 0.960 – 0.978 95% CI). The second best supported model was based on Month of the year (ΔAIC = 0.12; Table 5). Weekly survival rate was variable throughout the length of the project (Figure 4). The lowest weekly survival probability occurred

during the month of May (0.949; 0.925 – 0.965, 95% CI) and the highest was in September (.993; 0.958-0.999, 95% CI). While January had an estimated survival rate of 1.0, this was likely due to low sample size associated with the timing of trapping. Although neither model performed as well as the above models, models based on turkey sex and LPDV status performed better than the null model (Table 5). Females had a greater weekly survival rate (0.980; 0.975 – 0.985 95% CI) compared to males (0967; 0.948 – 0.979 95% CI). Turkeys infected with LPDV had a lower weekly survival probability (β = -0.628; -1.25 – -0.004, 95% CI) compared to uninfected turkeys. The weekly survival probability was 0.987 (0.978–0.992, 95% CI) for uninfected turkeys and 0.975 (0.964–0.983, 95% CI) for LPDV-infected turkeys (Figure 5). When exponentiated across one year (52 weeks), this difference in weekly survival rate translates to a cumulative probability of survival of 0.506 (0.314–0.659 95% CI) for uninfected turkeys compared to 0.268 (0.149–0.410 95% CI) for infected turkeys. We did not find strong support for differences in weekly survival rates between seasons, age classes, or study areas (Table 5).

Post-release Mortality

Our initial model comparisons showed that a relationship between survival and the natural log of days post capture best described the overall trend in daily survival rates. To compare covariates of interest, each model included a covariate for natural log of days post capture ("LN") and an interaction term. Our best performing model from this comparison was based on transmitter type (ΔAIC = 0.0; Table 6), where we compared survival of birds fit with backpack- or necklace-style transmitters. Our model showed that birds with backpack transmitters had a survival rate of 0.950 (0.909–0.973 95% CI) one day post capture compared to a survival rate of 0.994 (0.940–0.999 95% CI) for birds with necklace transmitters (Figure 6). For turkeys fit with a backpack-style transmitter, cumulative survival rate was estimated to be

0.814 (0.728–0.875 95% CI) to 10 days post capture, 0.786 (0.689–0.854 95% CI) to 14 days, and 0.716 (0.588–0.809 95% CI) to 29 days. For turkeys fit with a necklace style transmitter, cumulative survival rate was estimated to be 0.951 (0.813–0.984 95% CI) to 10 days post capture, 0.933 (0.780–0.976 95% CI) to 14 days, and 0.872 (0.642–0.953 95% CI) to 29 days.

The second ranked model was based on the total amount of time the bird was held from the trap being triggered to the bird's final release ("HandTime"; ΔAIC = 2.306; Table 6). As handling time increased, there was an observed increase in survival rate in the days following capture (Figure 7). A bird held for the average amount of time for this study (93 minutes) had an initial survival rate of 0.966 (0.936–0.982 95% CI). We also observed a difference in Adult versus Juvenile survival rates post capture (ΔAIC = 2.825; Table 6), where adult initial survival rate was 0.975 (0.939–0.990 95% CI) compared to 0.941 (0.872–0.974 95% CI) for juveniles (Figure 8). We did not find strong support for an effect of weather covariates on post-release survival probability (Table 6). Our AIC comparison for threshold day at which to stop censoring birds for post-release mortality showed that 4 days post capture performed best (ΔAIC = 0.0; Table 7), with days 2-10 falling with 2.0 ΔAIC of the best model. After day 10, there was a gradual decline in model deviance until around day 16, where values began to level off (Figure 9).

Daily Nest Survival Rate

During Spring 2018 and 2019, we located 72 wild turkey nests, 69 belonging to marked hens and 3 belonging to unmarked hens. Of the 69 nests of marked hens, 56 were first attempts, 12 were second attempts, and 1 was a third attempt. 17 of 56 first attempted nests hatched, 4 of 12 second nests hatched, and the single third attempt nest hatched. The average dates of

initiation for first, second, and third nests (Figure 10) were May 6, June 1, and June 23 (single nest), and average predicted hatching dates were June 13, July 8, and July 29 (single nest). The top model for predicting nest DSR was based on a linear relationship with age of the nest (ΔAIC = 0.0; Table 8). As nest age increased in days, the probability of daily survival decreased (β = -0.047; -0.078 – -0.017, 85% CI). Nest DSR was 0.988 (0.975-0.994, 95% CI) on Day 1 compared with 0.936 (0.896-0.62 95% CI) on Day 38, the approximate hatch date for a bird with the average clutch size of 11 (Figure 11). The probability a nest survived a 38-day exposure period was 0.261 (0.126–0.415, 95% CI; Figure 12). We did not find strong support for differences in nest DSR when comparing nest initiation date, disease status, transmitter type, study area, or year (Table 8).

Clutch Size

Average clutch size of VHF marked hens across both years of the study was 11.210, with the largest clutch size being 16 and the smallest being 6. The best model according to AIC was based on LPDV status of the hen (ΔAIC = 0.0; Table 9). Hens that had a positive LPDV status at capture had a clutch size that was 1.718 (± 0.736) eggs fewer than those with a negative LPDV status (Figure 13).

Seasonal Home Range and Movements

Of the 39 hens fitted with GPS transmitters, 9 died within the first two weeks post-capture and were censored from analysis. Three additional females have been categorized as missing despite extensive searches with hand held, truck mounted, and aerial telemetry. Data for these females were included in the analysis until their disappearance. For hens that did not survive the entire year, we included their data in the analysis up until their deaths. 4 hens

captured in 2018 survived the year and their transmitters lasted into the winter of 2019. We included this data in analysis of wintering home ranges.

The average area of use (95% UD) for GPS-marked females that survived from capture until August 1 was 2.680 mi^2 (1.093 mi^2 – 8.271 mi^2) in 2018 and 2.634 mi^2 (0.632 mi^2 – 7.784 mi^2; Table 10, Figure 14, 15) in 2019. The average area of seasonal use (95% UD within each discrete season) for wintering home ranges was 0.496 mi^2 (0.310 mi^2 – 0.941 mi^2) in 2018 and 0.898 mi^2 (0.164 mi^2 – 4.469 mi^2) in 2019. Average area of use for pre-nesting home ranges prior to the first attempt was 0.893 mi^2 (.552 mi^2 – 1.259 mi^2) for 2018 and 1.030 mi^2 (0.193 mi^2 – 3.192 mi^2) for 2019. Average area of use for pre-nesting home ranges prior to a second attempt was 0.508 mi^2 (0.304 mi^2 – 0.701 mi^2) for 2018 and 0.609 mi^2 (0.140 mi^2 – 0.692 mi^2) for 2019. Average area of use for summer home ranges following nesting was 2.844 mi^2 (0.05 mi^2 – 10.607 mi^2) in 2018 and 0.942 mi^2 (0.129 mi^2 – 2.881 mi^2) in 2019. The average seasonal movement distance between wintering home range and nesting home range was 2.643 miles in 2018 and 3.267 miles in 2019. Individual female movements between winter and nesting home ranges varied from 0.283 miles to 14.426 miles. Qualitative observations of hen movement indicated that individual females employed a variety of movement strategies, including among females from within the same study area or winter flock (Figure 16, 17).

Across the 3 analyses, disease status best explained observed variation in home range size and distance traveled between home ranges. Variation in winter home range size was best explained by LPDV infection status (Table 11). Individuals with a positive LPDV status had a winter home range size 0.286 mi^2 (±0.387 mi^2, $p = 0.466$) greater than those with a negative status. Variation in pre-nesting home range size was best explained by MG infection status (Table 12). Individuals with a positive MG status had a pre-nesting home range size 0.890 mi^2

(±0.234 mi^2, p = 0.002) less than those with a negative status. Variation in distance traveled between winter and pre-nesting home ranges was best explained by MG infection status (Table 13). Individuals with a positive MG status traveled 4.110 miles (±1.926 miles, p = 0.049) less than those with a negative status.

Brownian motion variance (σ_m^2) appeared to correspond with changes in seasonal movement behavior throughout the year (Figure 18, 19). Using the average daily σ_m^2 calculated from full dBBMM assessment of home ranges for January through July, we identified 4 periods of distinct movement that appeared to differ between years. The winter period was characterized by steady, low values for σ_m^2 as females made regular movements throughout relatively consistent winter home ranges. Females initiated movements from winter to nesting ranges shortly after the beginning of April, when σ_m^2 values gradually increased for a relatively short period (~3 weeks). Females entered nesting home ranges during the last week of April, which was characterized by the greatest daily average σ_m^2 values as females established nest sites and began laying eggs. Average motion variance then gradually decreased as birds began incubation. In 2018, we observed an increase in σ_m^2 (the second peak in Figure 18) that was not observed in 2019. This second peak in 2018 may be associated with renesting attempts when nests hatched and females moved into their summer brood ranges, or as nests failed and females attempted a second nest. 2018 had a higher proportion of identified renesting attempts by GPS marked hens compared to 2019, which may explain the lack of a pronounced peak in σ_m^2. During July, the beginning of the summer brood rearing season, σ_m^2 values began to level off at values slightly higher than winter but lower than peak movement times during pre-nesting.

Risk Factors for Pathogen Infection

Adult turkeys were found to have a significantly higher LPDV prevalence (87%) than juveniles (40%) and age was the only significant predictor of LPDV infection (β=-2.28; 95% CI = -2.99 to -1.61, $p<0.01$). Pearson's chi-squared analysis also showed an association between LPDV infection and age [X^2 (1, n=203) =46.50, $p<0.01$]. Males sampled had a lower prevalence (57%) than females (76%), however, when combined with age as a main effect or interaction term, sex failed to explain a significant additional portion of the variation. This may be an artifact of high overall prevalence or the distribution of sample size in that adult females more than double any other age/sex class in our sample (see distribution noted above). Study area or year of collection were not predictors of LPDV infection ($p>0.05$). Prevalence varied by study area from 59% in S to 79% in NE and by year from 78% in 2018 to 63% in 2019.

The best model for probability of infection with REV included year of collection (β =1.06; 95% CI = 0.11 to 2.08, p=0.03) and study area. While study area was not significant ($p>0.05$) and the β coefficients were not different than zero (based on the inclusion of zero in the 95% confidence intervals), its inclusion in the model more than doubled the explanation of variation by the model. Pearson's chi-squared analysis showed that there was indeed an association between REV infection and year of collection [X^2 (1, n=193) =5.19, p=0.02] and REV infection and study area [X^2 (3, n=193) =9.35, p=0.02]. The prevalence of REV increased from 8.8% (8/90) in 2018 to 22% (23/104) in 2019. Prevalence varied from 3.0% in NE and 11% in NW to 20% in NC and 25% in S (notably the exact opposite trend for LPDV in these study areas).

The predictive model for probability of exposure to MG included year of collection (β=-1.74; 95% CI = -2.72 to -0.87, p=0.0002) and the interaction of age and sex (age*sex; β=-2.55;

95% CI = -4.78 to -0.70, p=0.02). Pearson's chi-squared test also showed that there was an association between MG exposure and year of collection [X^2 (3, n=175) =16.2, p<0.01] and MG exposure and age*sex [X^2 (3, n=175) =9.48, p=0.02]. The prevalence of MG exposure decreased from 92% (78/85) in 2018 to 66% (59/90) in 2019. The prevalence of MG exposure was relatively high in adult males (93%), juvenile females (82%), and adult females (77%), but was lower in juvenile males (61%; Figure 20).

Pathogen Coinfection

We found an overall prevalence was 69% (141/203) for LPDV infection, 16% (31/193) for REV infection, and 78% (137/175) for MG exposure. With a high prevalence of infection, there is a certain level of co-infection expected by chance within the population. Pearson's chi-squared test was used to analyze whether the rate of infection with any two pathogens was higher in our sample than expected by chance, but we did not find any evidence to support this. Infection with LPDV was not correlated with exposure to MG [X^2 (1, n=175) =1.21.2, p=0.27], with 56% of the total sample positive for both LPDV infection and MG exposure. Infection with LPDV was also not correlated with REV infection [X^2 (1, n=193) =0.003, p=0.95] with only 11% of the total sample infected with both LPDV and REV. And, lastly, exposure to MG was not correlated with REV [X^2 (1, n=175) =0.35, p=0.55], with 12% of the total sample positive for both LPDV infection and MG exposure. Seventeen turkeys (10%, n=175) were infected with all 3 pathogens.

Cloacal Swabs as an LPDV Detection Method

Eighty-five dry cloacal swabs from birds with known LPDV status (confirmed through blood analysis) were tested for LPDV to determine the sensitivity and specificity of using cloacal swabs as a less invasive ante-mortem detection method. Of the 65 known positive wild turkeys,

45 cloacal swabs tested positive for an overall sensitivity of 69%. Of the 20 known negative wild turkeys, 19 cloacal swabs tested negative for an overall specificity of 95%.

Summary and Future Directions

Thanks to increased trapping efforts supported by MDIFW regional offices, our second trapping season saw a more than three-fold increase in the number of turkeys captured. This has also led to an increase in reported harvests of banded individuals, which will improve the precision of harvest rate and population size estimates. Due to low capture success and/or harvest in certain areas, we were unable to generate harvest estimates for all WMDs we captured turkeys in. As we continue to increase sample size and expand trapping efforts into additional areas throughout Maine, we will be able to generate more fine-scale estimates of wild turkey population size.

From the 234 male turkeys we banded and released, we estimated age and WMD specific harvest rates that ranged from 0.046 to 0.228 during the 2018 and 2019 spring bearded turkey hunting seasons. Harvest rates tended to be higher in the southwest and decreased in more northern WMDs. This recovery rate estimate assumes that no mortality occurs between banding and the hunting season. While some researchers have found this assumption to be generally valid (Diefenbach et al. 2012), we plan to incorporate survival information from radio-marked males to evaluate late winter mortality and directly incorporate it into future estimates of harvest. Furthermore, these results only include birds reported directly to us (whether by phone, web, or check station), and does not account unreported harvest or birds that were shot but not recovered. Thus, these are likely underestimates of male harvest during the spring hunting season, and we plan to address the assumptions mentioned above in future work. As we continue to increase our

sample size and expand efforts into additional WMDs across the state, we will be able to incorporate landcover characteristics to increase the precision of harvest rate estimates. We will use this information in our band recovery model (Brownie et al 1985) to produce estimates of harvest rate that accounts for variation in harvest across the state.

We used our estimates of adult and juvenile harvest rates in combination with the number of harvested and reported turkeys provided by MDIFW to estimate statewide population size. We estimated Maine's total male turkey population to be 32,696 (± 12,625) in 2018 and 33,609 (± 13,387) in 2019. As we increase the precision of harvest rate estimates with a third year of banding and the inclusion of landcover information, estimates of population size will also become more precise. Estimates of harvest rates that incorporate landcover information will also allow for more fine scale estimates of abundance by year, WMD, age, and sex.

We found multiple factors had apparent influences on post-release mortality of wild turkeys following capture. The most significant difference in post-release survival was related to style of transmitter, with backpack transmitters showing lower survival than necklaces. Transmitter effects on avian species have been well documented (Barron et al 2010, Bernardo et al 2011), although how an animal is affected and to what degree can be variable depending on transmitter type and species characteristics. Although turkeys primarily walk on the ground, their ability to quickly escape predators and roost at night are reliant on their ability to fly. If there is a period following capture during which flight abilities are decreased, the turkeys will be more susceptible to predation as they acclimate to transmitter. Comparatively, necklace style transmitters are much smaller and less obtrusive to turkeys, which may explain the lower mortalities rates post-release. In our final field season, we will continue deploying both backpack and necklace style transmitters, but we will attempt to more loosely fit backpack transmitters to

identify if transmitter fit can alleviate issues with post-release mortality. We also found that with increased handling time, turkeys experienced lower post-release mortality rates. A previous study of wild turkeys in Oklahoma (Nicholson et al 2000) found an opposite relationship, where decreased handling time lead to lower post-release mortality. While we both followed similar methods for trapping and handling, the differences in climate between Oklahoma and Maine in the winter may have led to differing results. While we did not identify an effect of weather effects on post-release mortality, Nicholson et al (2000) identified humidity and ambient temperature as having an effect on mortality, possibly suggesting that birds are more affected by higher temperatures and humidity rather than lower. We found that adult post-release mortality was lower than that of juveniles, which has been observed in multiple studies of wild turkeys (Nicholson et al 2000, Spraker et al 1987).

We found evidence for variable survival rates throughout the year, with the greatest apparent decrease in survival occurring in May, which corresponded with peak nesting activity for hens based on our Brownian Motion Variance analysis. This decline in survival during the spring nesting season has been observed in other studies of wild turkeys (Kurzejeski et al 1987, Hubbard et al 1999) and likely is caused by increased vulnerability to predation of hens while nesting (Speake 1980). A recent study of ruffed grouse in Maine also found that female survival was substantially reduced during nesting (Mangelinckx et al. in press), and it is likely that ground nesting birds are particularly vulnerable to predation, in general, during this period.

In addition, we found evidence that variation in survival rates can in part be explained by LPDV infection status. LPDV is a neoplastic avian oncogenic retrovirus that was first identified in Arkansas in 2009. A subsequent survey of hunter-harvested wild turkeys from 17 states revealed an overall prevalence of 47%, with variation by state ranging 26–83% (Thomas et al.

2015). While the majority of infected birds appear asymptomatic (Thomas et al. 2015), infection can cause skin lesions and lymphoid tumors in multiple organs (Biggs et al. 1978) and has been linked with mortality of wild turkeys (Allison et al. 2014) and domestic turkeys (Biggs 1997), raising justifiable concern for spillover potential to backyard poultry farms and suggesting the disease could have negative effects on domestic and wild turkey population viability. The observed decrease in survival and clutch size of infected individuals coupled with a large proportion of individuals infected (69%), supports previous claims that LPDV may be a major driver of wild turkey population size. Additionally, LPDV prevalence was found to increase with turkey age, which may impact population demographic structure and have a weighted negative effect at the population level since adults may contribute more to population growth via increased nesting rates, larger clutch sizes, and increased nest success rates (Paisley et al 1998, Norman et al 2001, Thogmartin and Johnson 1999) . The increase in LPDV infection with age has been documented previously (Alger et al. 2017) and may indicate that turkeys are able to survive and harbor chronic pathogen infections, increasing the potential of exposure to others.

REV and MG are both geographically widespread pathogens with a prevalence that varies across studies and geographic regions. REV is another oncogenic retrovirus that can either be asymptomatic or can manifest in non-specific disease syndromes such as anemia, runting, neoplasia, and immunosuppression (Payne and Venugopal 2000). Furthermore, secondary pathogen infection of REV-infected birds can exacerbate the rate of tumor formation in chickens (Mays et al. 2012). Serology tests indicated 63% of apparently healthy wild turkeys had been exposed to REV in southern Georgia (Ingram et al. 2015), while all serum samples were negative (0/70) for REV exposure from wild turkeys in Texas (Peterson et al. 2002). A third pathogen that overlaps in host and geographic range is *Mycoplasma gallisepticum* (MG), a bacterial pathogen

first described in wild turkeys in 1982 as the cause of infectious sinusitis (Davidson et al. 1982), which affects the respiratory system and is easily spread through infectious aerosols and environmental contamination (Brash et al. 2013). It was detected in 28% (200/724) of visibly healthy wild turkeys from 6 western states (Fritz et al. 1992), while all serum samples were negative (0/44) for MG exposure from wild turkeys trapped in Arkansas for relocation (Hopkins et al. 1990).

In our study, the inclusion of year of collection in the best predictive models for REV and MG infection or exposure, respectively, is representative of yearly fluctuations in outbreaks, which may be due to factors driving temporal variation in pathogen transmission (e.g. density, weather), though we did not test these hypotheses. Study area was predictive of REV infection and is also representative of pathogen exposure differences between the study areas, which could be related to land type gradients since the two study areas with highest prevalence of REV are also the most closely associated with residential development. We found that the interaction of age and sex was predictive of MG exposure. Juvenile males have a comparatively reduced prevalence of exposure and it may be reflective of the probability of exposure increasing with age, similar to LPDV. Furthermore, stress or other infectious pathogens have been found to complicate or increase the pathogenicity of MG in poultry (Brash et al. 2013). If this is the case for wild turkeys, hens enduring the energetic responsibilities of nesting and brood-rearing may experience greater stress levels, making them more prone to MG infection.

Disease status best explains variation in home range size and distance traveled between home ranges of captured hens. Individuals with a positive LPDV status had greater winter home range size than their uninfected counterparts (Table 11). While the mechanism of this is currently unknown, it may explain the widespread prevalence of LPDV, since expansion beyond a typical

home range likely increases exposure to other individuals and/or flocks (Nunn et al. 2011). In contrast, individuals with a positive MG status had a smaller pre-nesting home range size and traveled less distance between winter and pre-nesting home ranges than their uninfected counterparts. The bacteria infects a wide host range and frequently results in varying disease symptoms in other wild species, such as conjunctivitis in house finches (Ley et al. 1996). Infected house finches were found to be less mobile and were more likely to be feeding alone than their uninfected counterparts (Dhondt et al. 2005; Hotchkiss et al. 2005). This is a two-way street because host behaviors such as movement and social interaction can drive disease establishment, persistence, and spread, while disease itself can dictate host movement and social interaction. We plan to assess these interactions and their management implications in future analyses.

We observed coinfection between pathogens, but not more than expected by chance. Recent studies have also revealed coinfections between LPDV and other pathogens. In particular, reticuloendotheliosis virus (REV) was detected in 46% (19/41) of clinically ill, LPDV-infected wild turkeys submitted to veterinary diagnostic labs throughout 18 eastern states (Allison et al. 2014). Additionally, MacDonald et al. (2019) found REV in 4% (5/119) of apparently healthy LPDV-infected wild turkeys in Ontario, Canada. We tested for MG exposure, which is indicative of past exposure and not current infection, which could be an explanation for the lack of correlation between MG and the other target pathogens (LPDV and REV). These pathogens are all known to be asymptomatic most or some of the time, suggesting that infected individuals may not be in a constant diseased state throughout infection. Turkeys in a diseased state may be more susceptible to subsequent infection due to their energy reallocation and weakened immune response. This is even more convincing with LPDV and REV because they are retroviruses that,

by nature, insert themselves into the host genome and may have the potential to be either inactive or active at different times (Payne 1993).

We have blood samples from an additional 162 wild turkeys from trapping efforts in 2019 from within our study areas and from Wildlife Management Districts outside of our study areas that will be tested for LPDV and included in future analysis. We plan to assess genetic sequence data that will enable us to distinguish between LPDV strains and identify transmission pathways and spatial clustering.

Preliminary cloacal swab analysis did not result in a particularly high sensitivity, and we expect this is due to PCR-assay inhibitors commonly present in fecal material. However, we will optimize the cloacal swab LPDV PCR protocol to improve sensitivity, and further evaluate the validity of this method compared with detection of LPDV in blood. While these preliminary findings suggest that the cloacal swab method may not be applicable to the detection of LPDV in an individual, it may be useful in assessing flock infection status and monitoring temporal trends in infection. In particular, it could be used for determining if LPDV is present in wild turkeys at the edges of and beyond its known range in the United States, or for identifying LPDV presence in new hosts, such as other game birds or domestic turkeys.

Using GPS transmitters, we collected data on wild turkey hen locations which showed apparent variability in movement patterns among seasons and individuals. Moving forward, we plan to use this information in two capacities. First, we will incorporate landcover characteristics to identify potential sources of variation in movement throughout the year. We will identify sources of variation in probability of use within each season as well as seasonal movements across the landscape. Second, we will use individual variation in movement behavior to account for individual heterogeneity in nest survival. We will quantify movement variables including

seasonal movement distance, pre-nesting home range size, laying movements, movement phenology, and nesting home range fidelity to identify variation in individual hen nest success.

Our first two years of data collection has afforded us insight into turkey population ecology through the integration of demographic, spatial ecology, harvest, landscape ecology, and disease ecology data to inform Maine Department of Inland Fisheries and Wildlife's goal to "maintain a healthy turkey population below biological carrying capacity while providing hunting and viewing opportunity." Further field sampling through our final year will enable us to better address this goal.

Acknowledgements

We thank R. B. Allen, all the Regional Wildlife Biologists, many other MDIFW staff, and especially B. Currier, B. Peterson, K. Leary, G. LeClaire, K. Overturf, and N. Aielo, who each made significant contributions to field data collection. Student volunteers from the University of Maine and Unity College also contributed to field work. We are grateful to Dr. P. Milligan for providing lab protocols, primers, and positive controls and B. Tweedie and C. Desjardins for their contributions in the lab. We thank American Forest Management and the numerous individual private owners for land access and accommodations. This research was funded by the Maine Department of Inland Fisheries and Wildlife, the National Wild Turkey Federation, the Maine chapter of the National Wild Turkey Federation, the Maine Agricultural and Forest Experiment Station, and the Maine Outdoor Heritage Fund.

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Figures

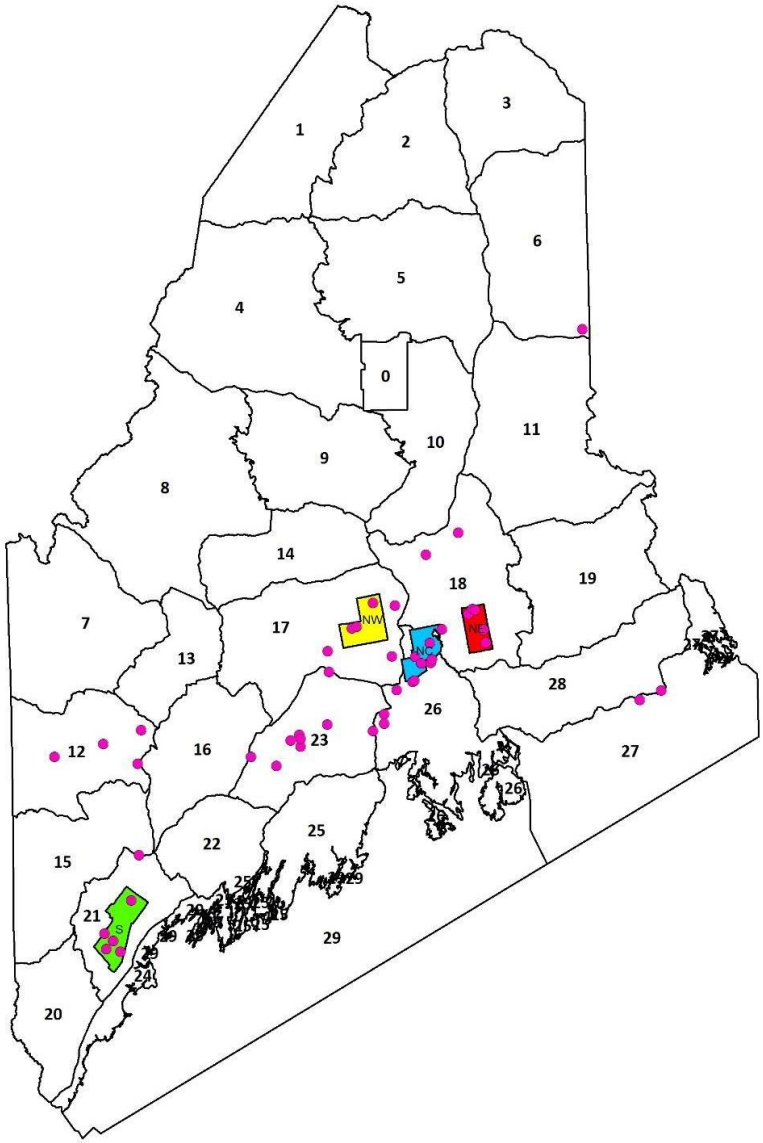

Figure 1. Map of Maine, USA, depicting Wildlife Management District boundaries (numbered) and approximate study area boundaries for Exeter/Corinth (NW, Orange), Orono/Old Town (NC, Blue), Greenfield/Stud Mill Road (NE, Green), Gray/Gorham (S, Purple)). Trapping sites are shown as pink dots.

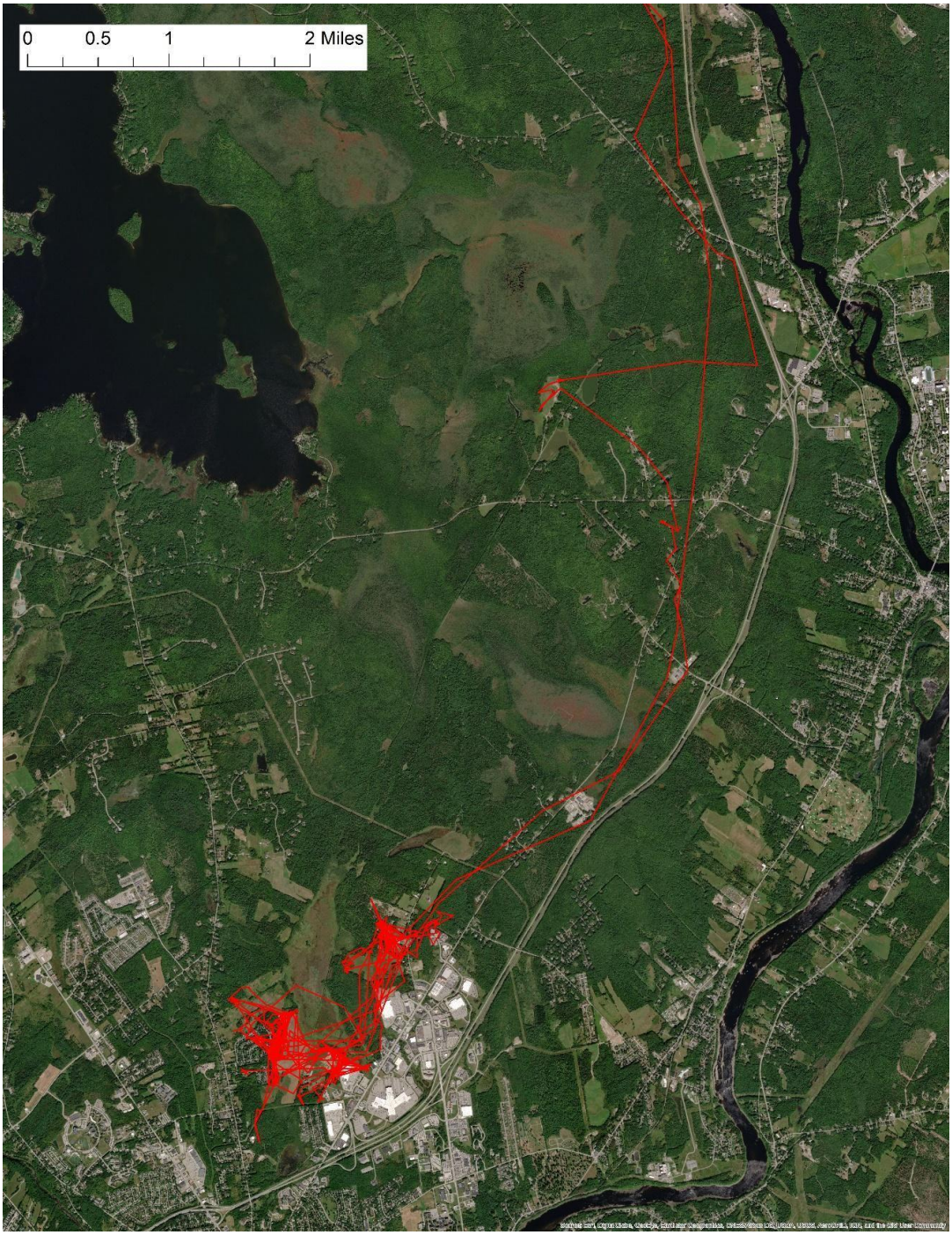

Figure 2. Aerial photography map of Bangor, Maine, USA, with GPS tracks (red line) of the single an adult male wild turkey fit with a GPS transmitter which operated from between March 14, 2019 through May 3, 2019.

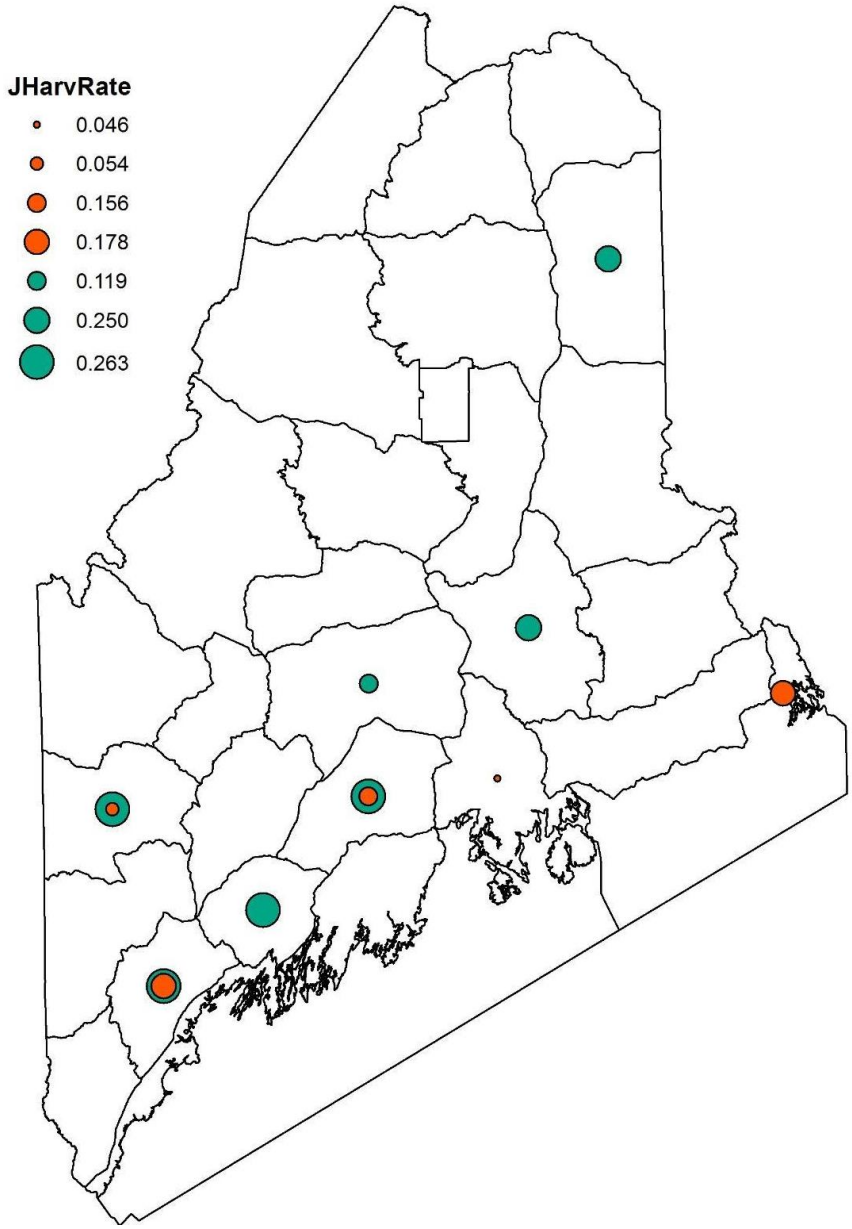

Figure 3. Map of Maine, USA, showing outlines of Maine Department of Inland Fisheries and Wildlife management districts. Where estimates were possible, dots depict harvest rate estimates for adult (blue) and juvenile (orange) male turkeys during the 2018 and 2019 spring hunting season.

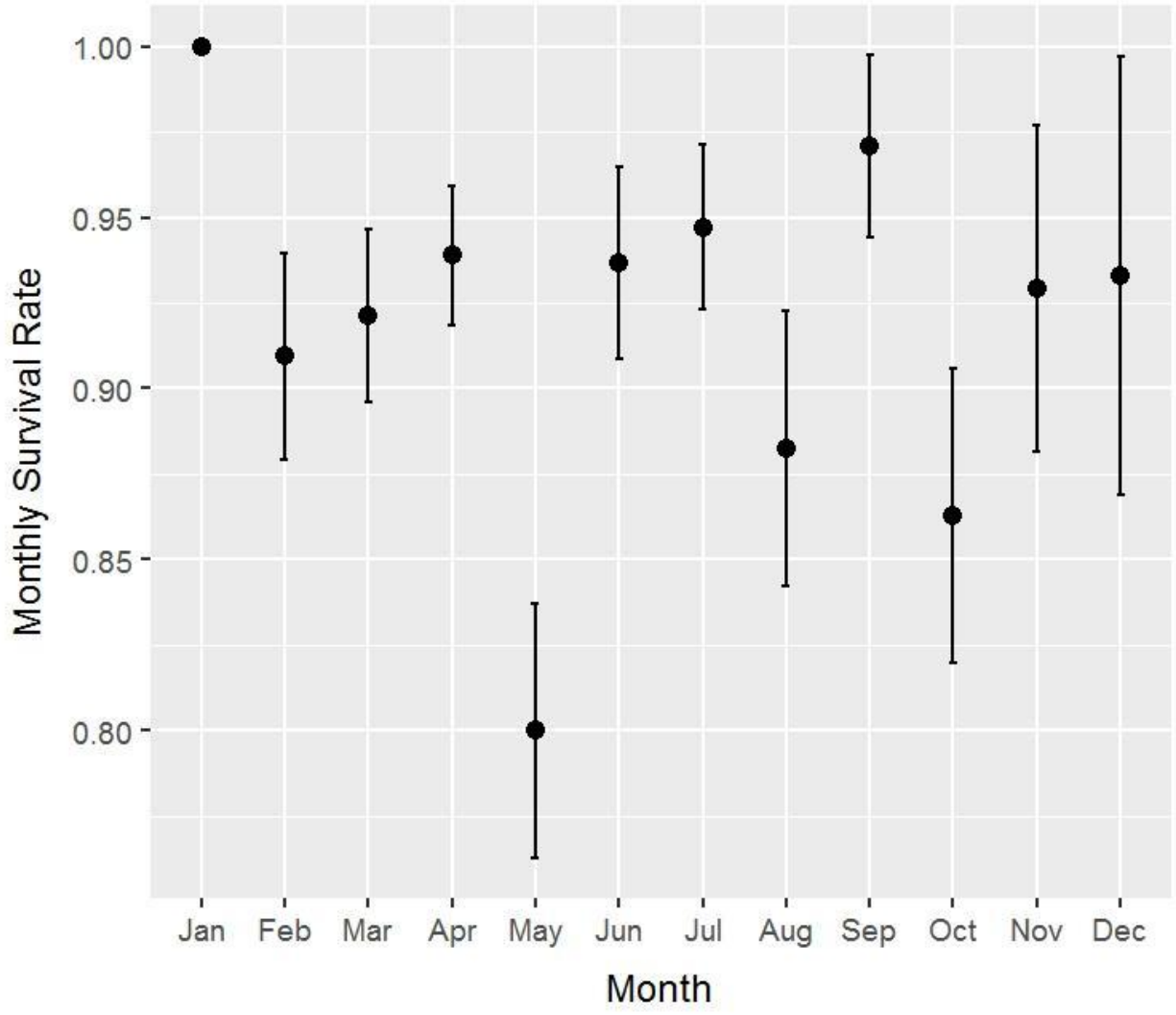

Figure 4. Weekly survival rates, by month, for wild turkey hens in Maine, USA, from January 30, 2018 to November 22, 2019. Estimates were derived from the best performing weekly survival model according to AIC. Estimates are presented with error bars representing 95% confidence intervals.

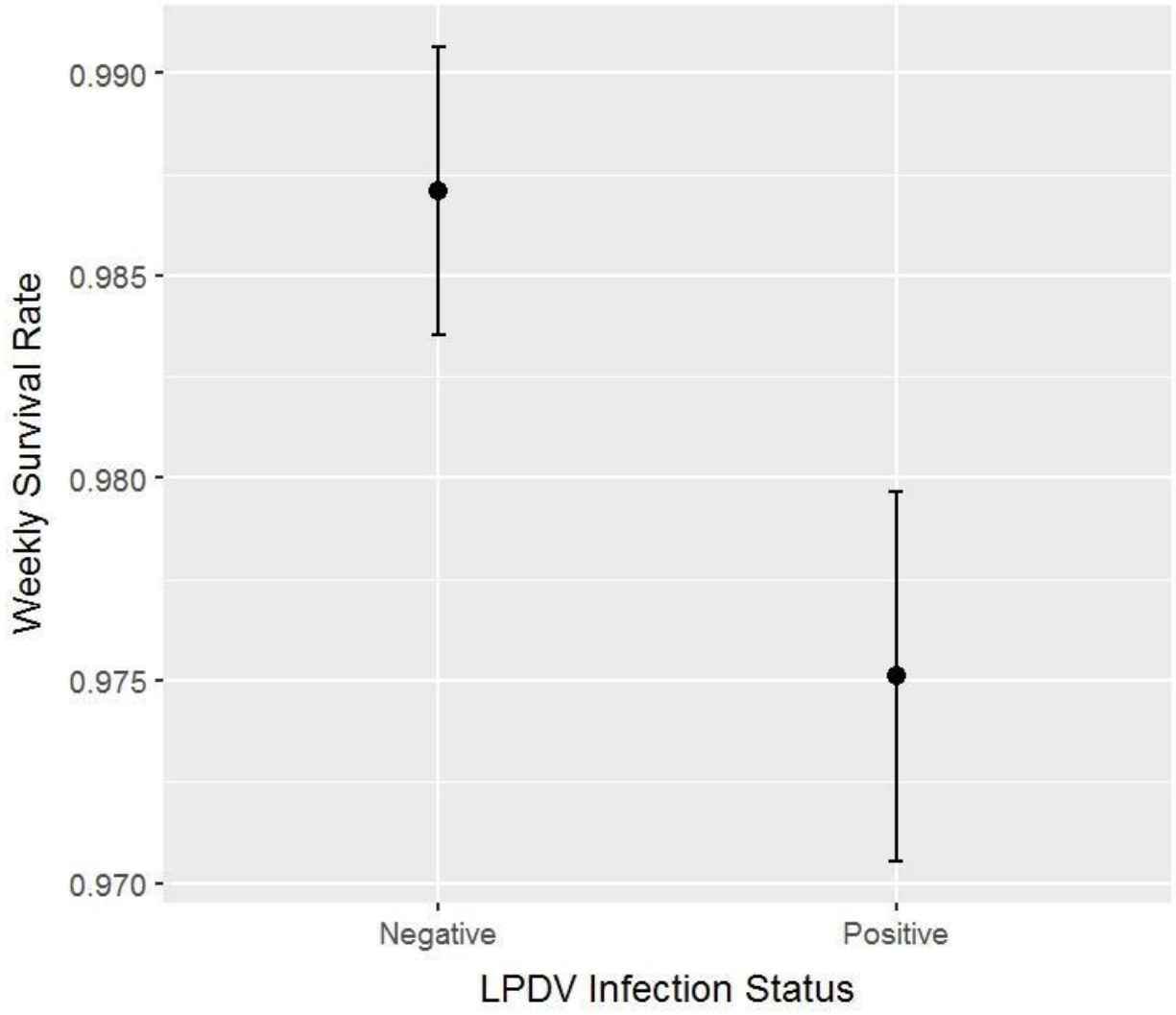

Figure 5. Weekly survival probability, by LPDV infection status, for wild turkey hens in Maine, USA, from January 30, 2018 to November 22, 2019. Estimates were derived from the top performing weekly survival model according to AIC. Estimates are presented with error bars representing 95% confidence intervals.

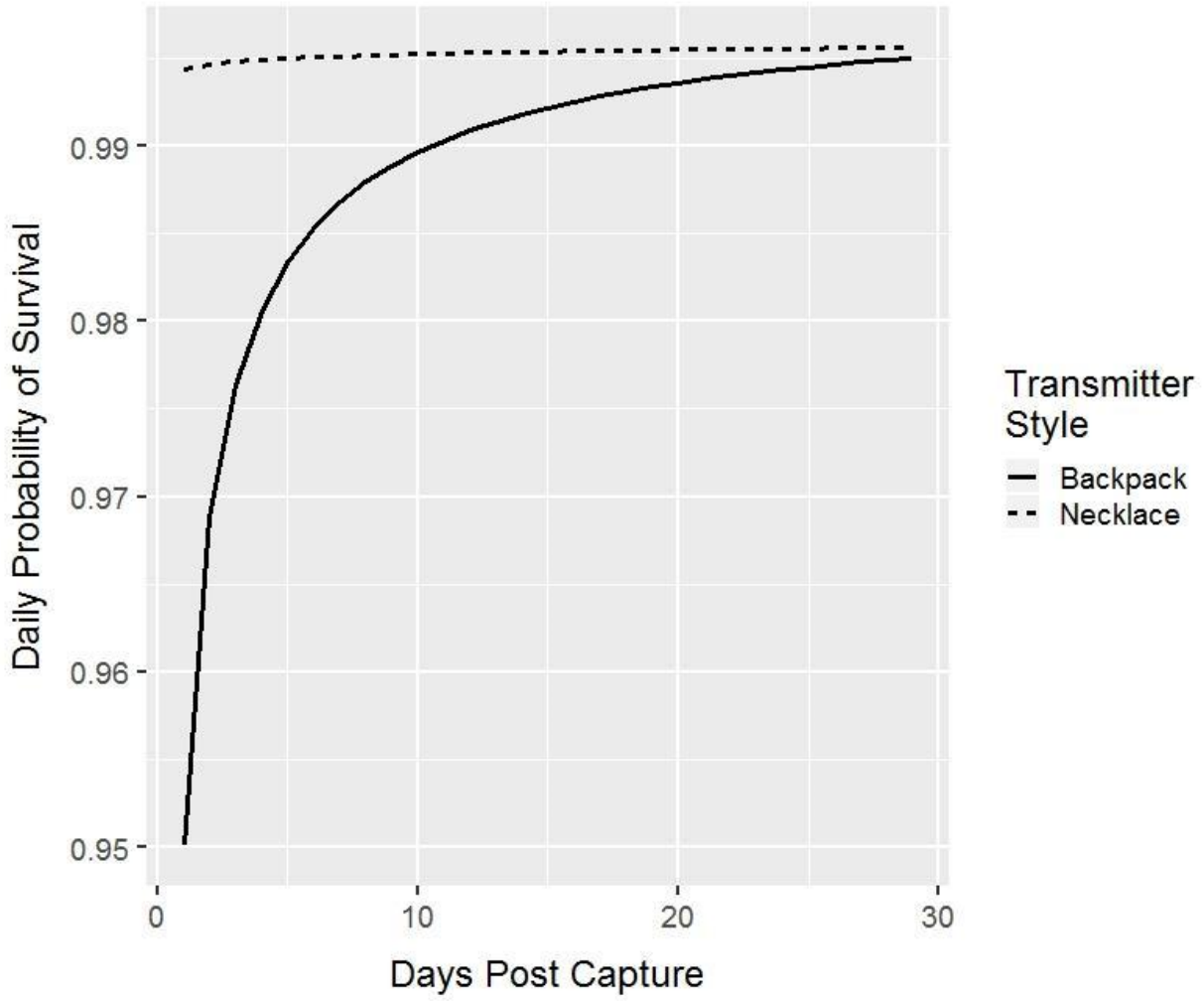

Figure 6. Daily survival probability, by transmitter style, for wild turkeys in Maine, USA, for 30 days post capture. Estimates were derived from the top performing daily survival model according to AIC, where days post-capture (natural log transformation) was allowed to interact with transmitter type.

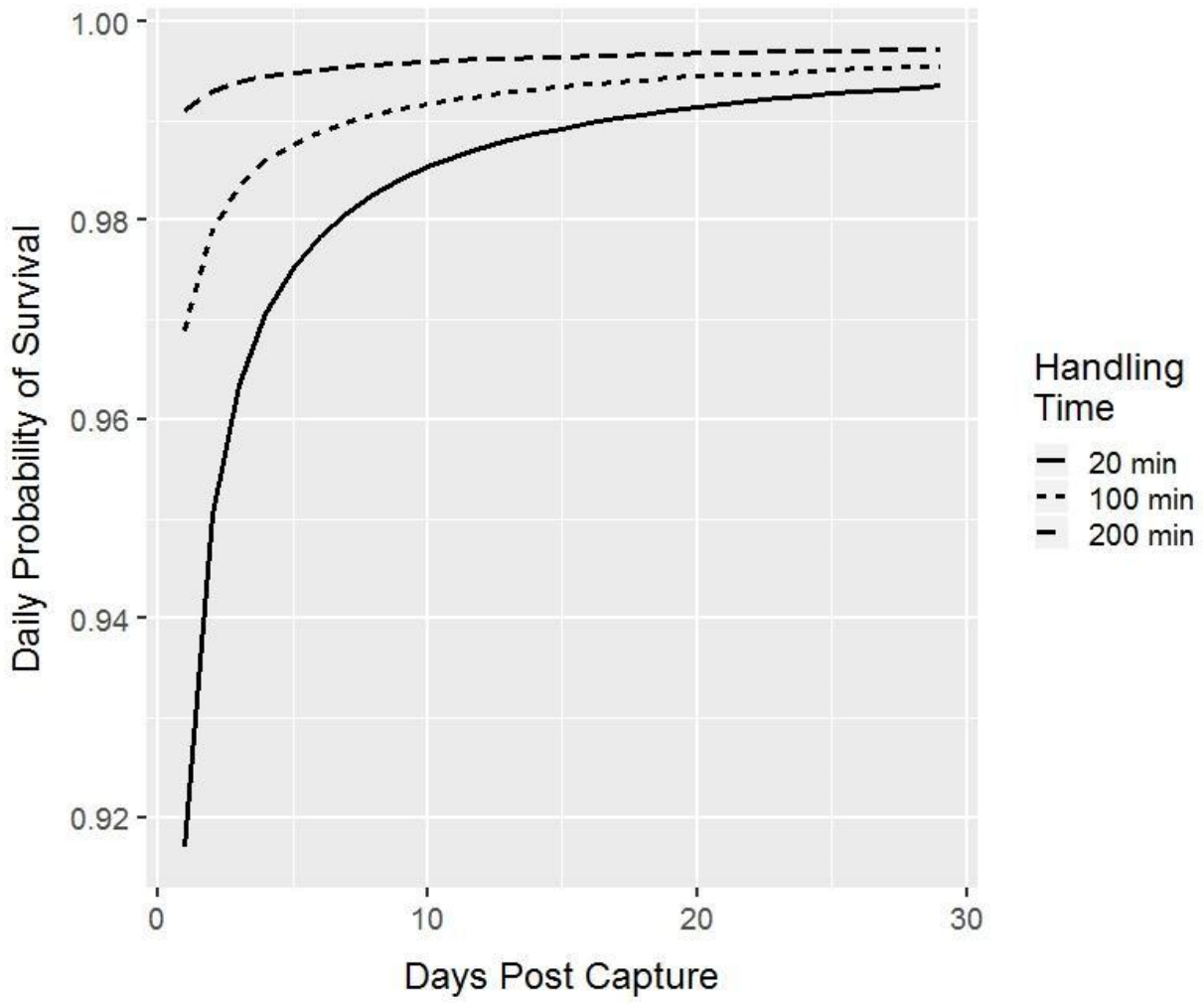

Figure 7. Daily survival probability, by handling time, for wild turkeys in Maine, USA, for 30 days post capture. Estimates for handling times of 20 minutes (solid), 100 minutes (short dashes), and 200 minutes (long dashes) represent approximate minimum, mean, and maximum values for the project.

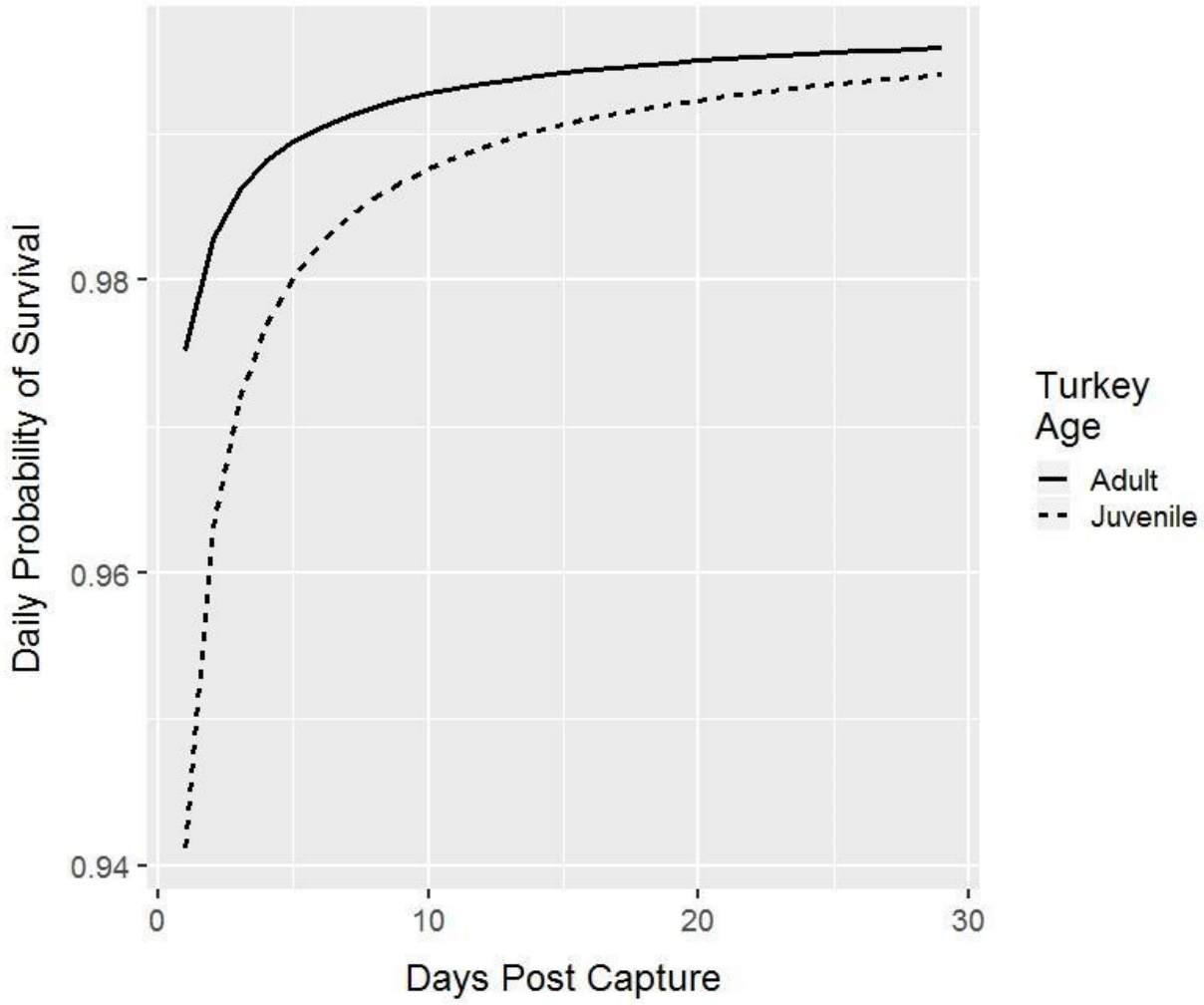

Figure 8. Daily survival probability, by turkey age at capture, for wild turkeys in Maine, USA, for 30 days post capture. Graph compares post capture survival for adults (solid) and juveniles (dashed).

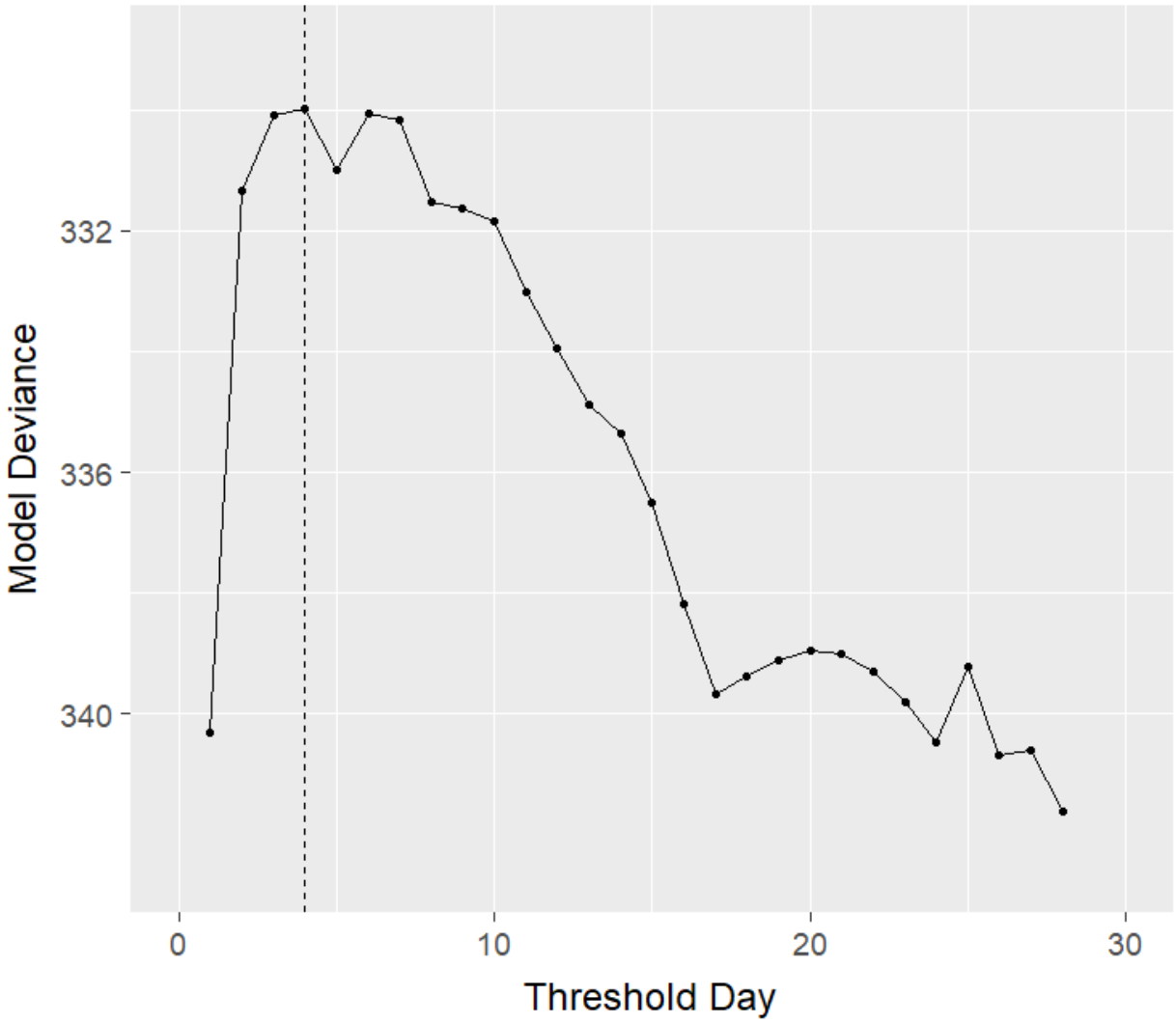

Figure 9. Model deviance among all potential daily thresholds for post-release mortality of wild turkeys captured in Maine, USA, from January through March 2018 and 2019. The y-axis is inverted, and smaller deviance values indicate better fit, where the best-fit model is indicated by the dashed vertical line. All models were run as nest survival analyses, implemented in Program MARK (White and Burnham 1999) using the R package RMark (Laake 2016).

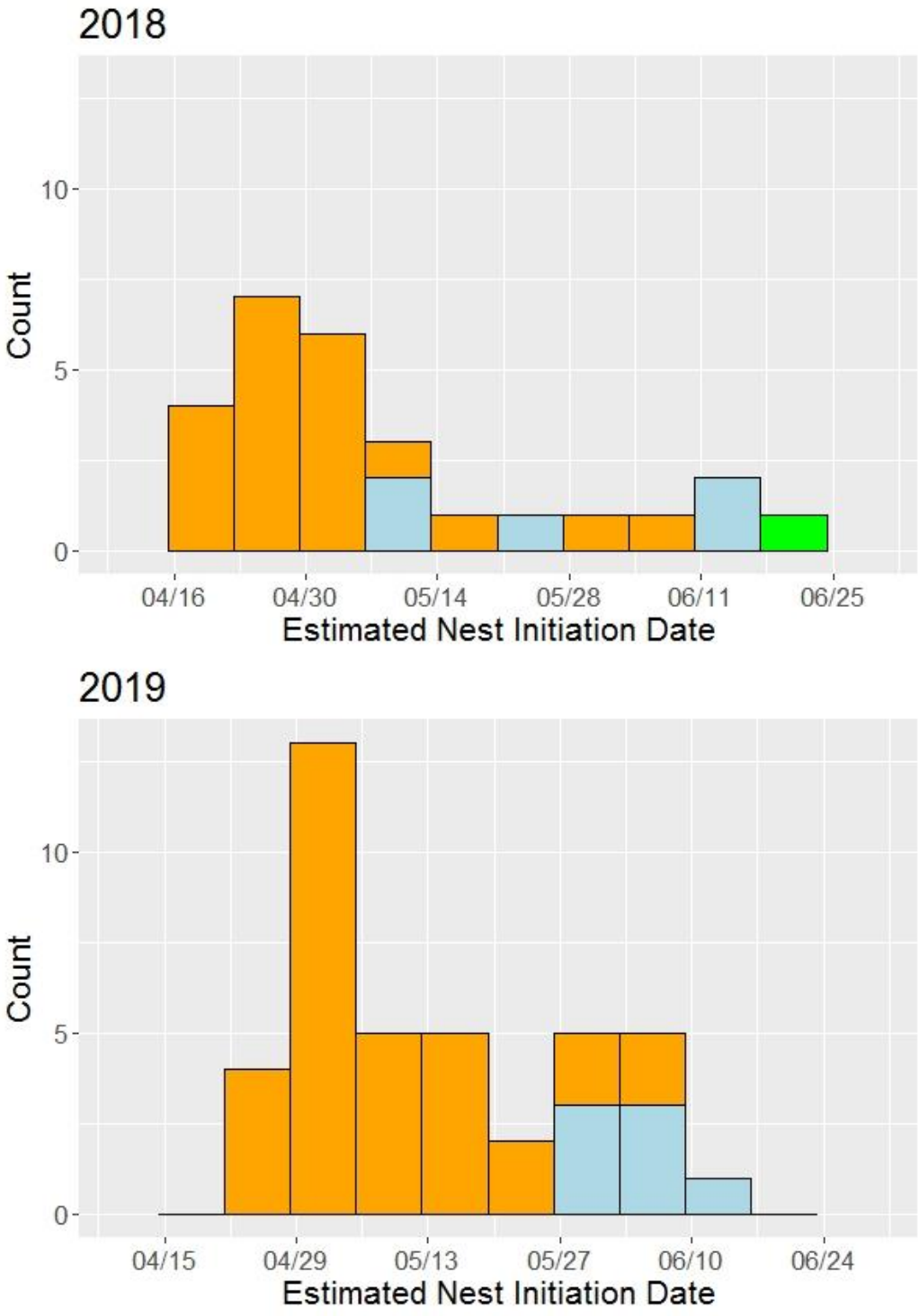

Figure 10. Estimated initiation dates for VHF and GPS marks wild turkey hens in Maine, USA in 2018 and 2019. Dates are grouped by week and by attempt number; first (orange), second(blue), and third (green).

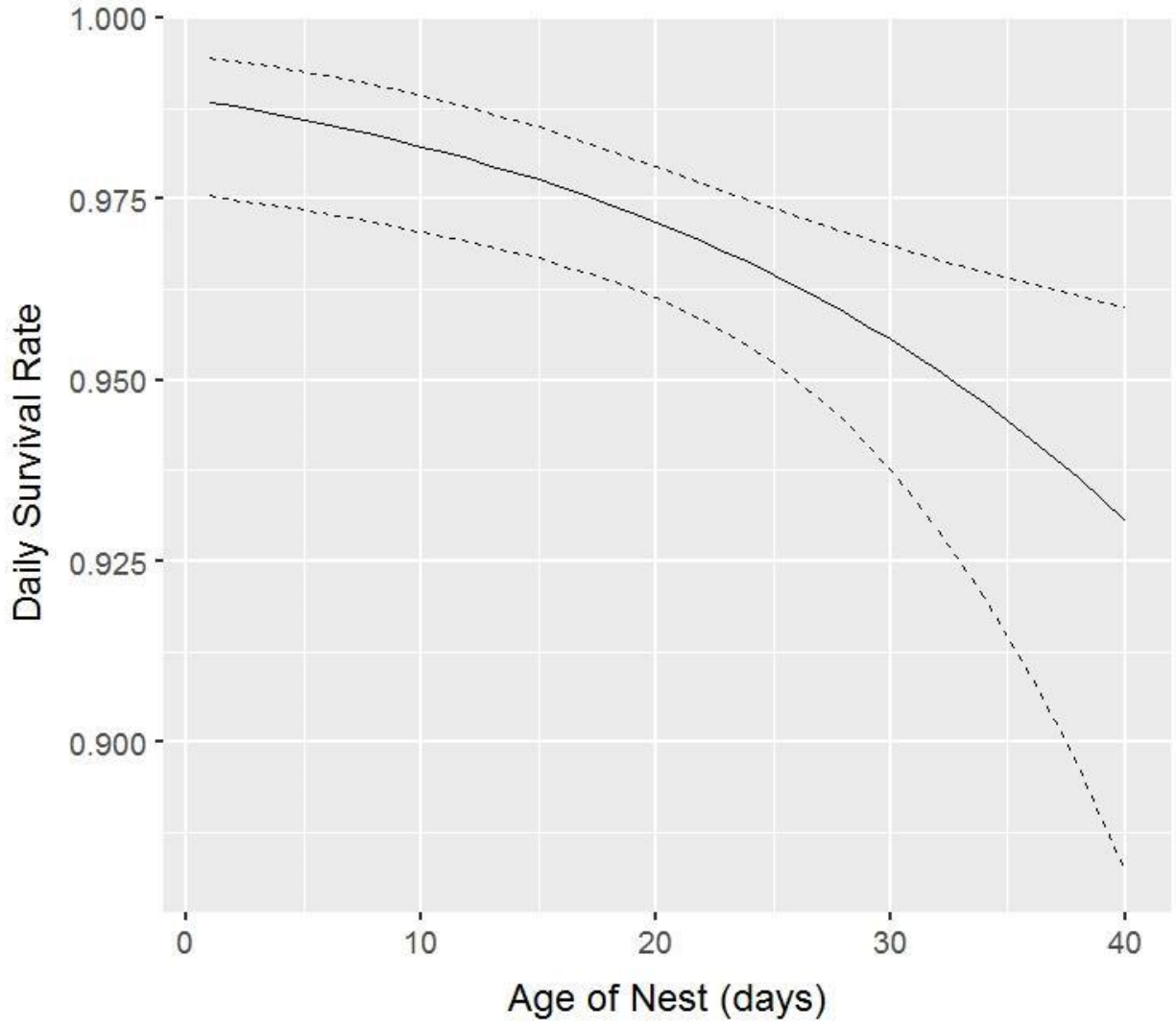

Figure 11. Daily survival rates, by age of nest, for wild turkey nests in Maine, USA, from April to July 2018 and 2019. Estimates were derived from the top performing daily survival rate model according to AIC. Estimates are presented with upper and lower 95% confidence intervals (dotted lines).

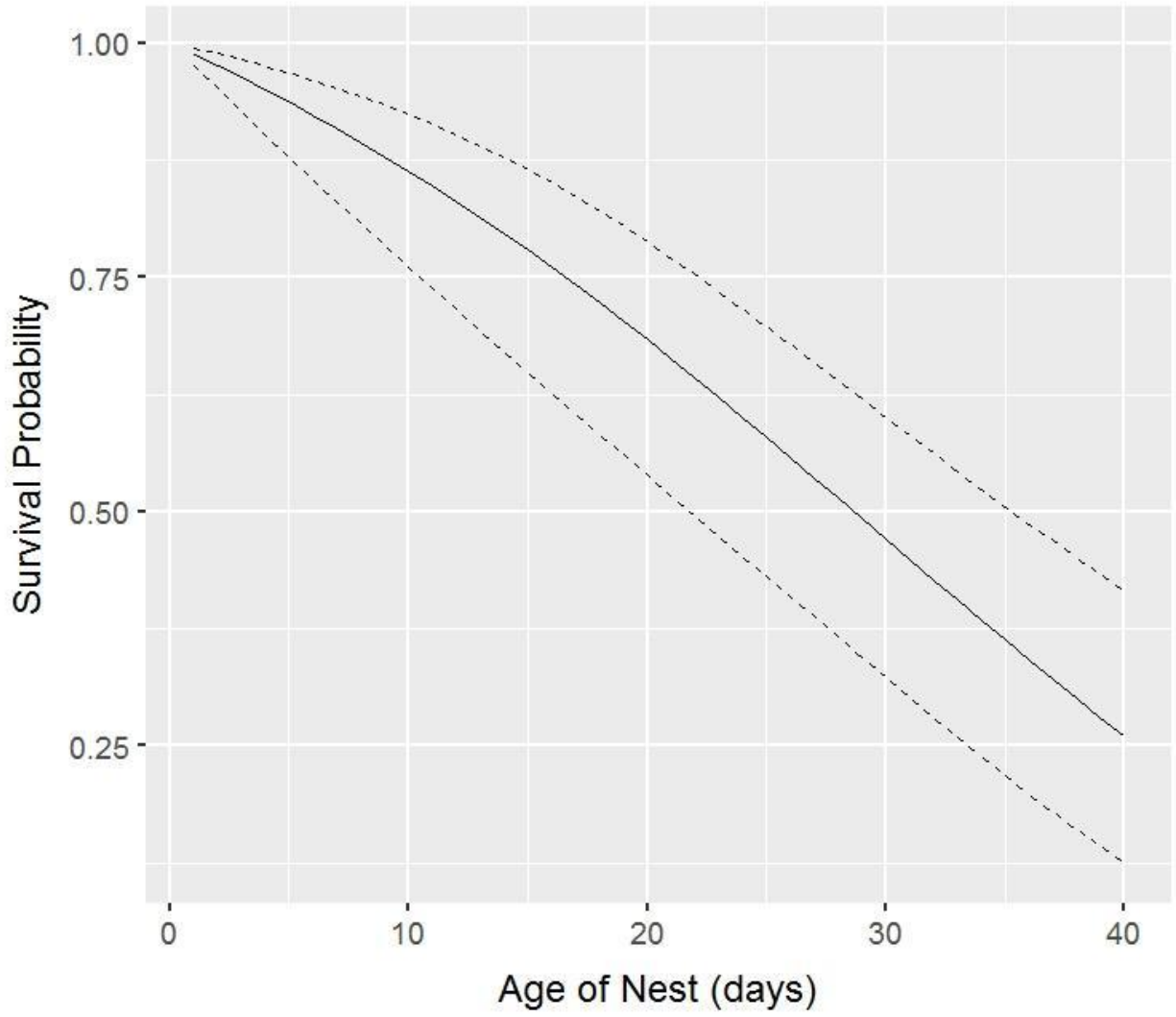

Figure 12. Cumulative probability of nest survival throughout a 40-day exposure period for wild turkey nests in Maine, USA, from April to July 2018 and 2019. Estimates were derived from the top performing daily survival rate model according to AIC. Estimates are presented with upper and lower 95% confidence intervals (dotted lines).

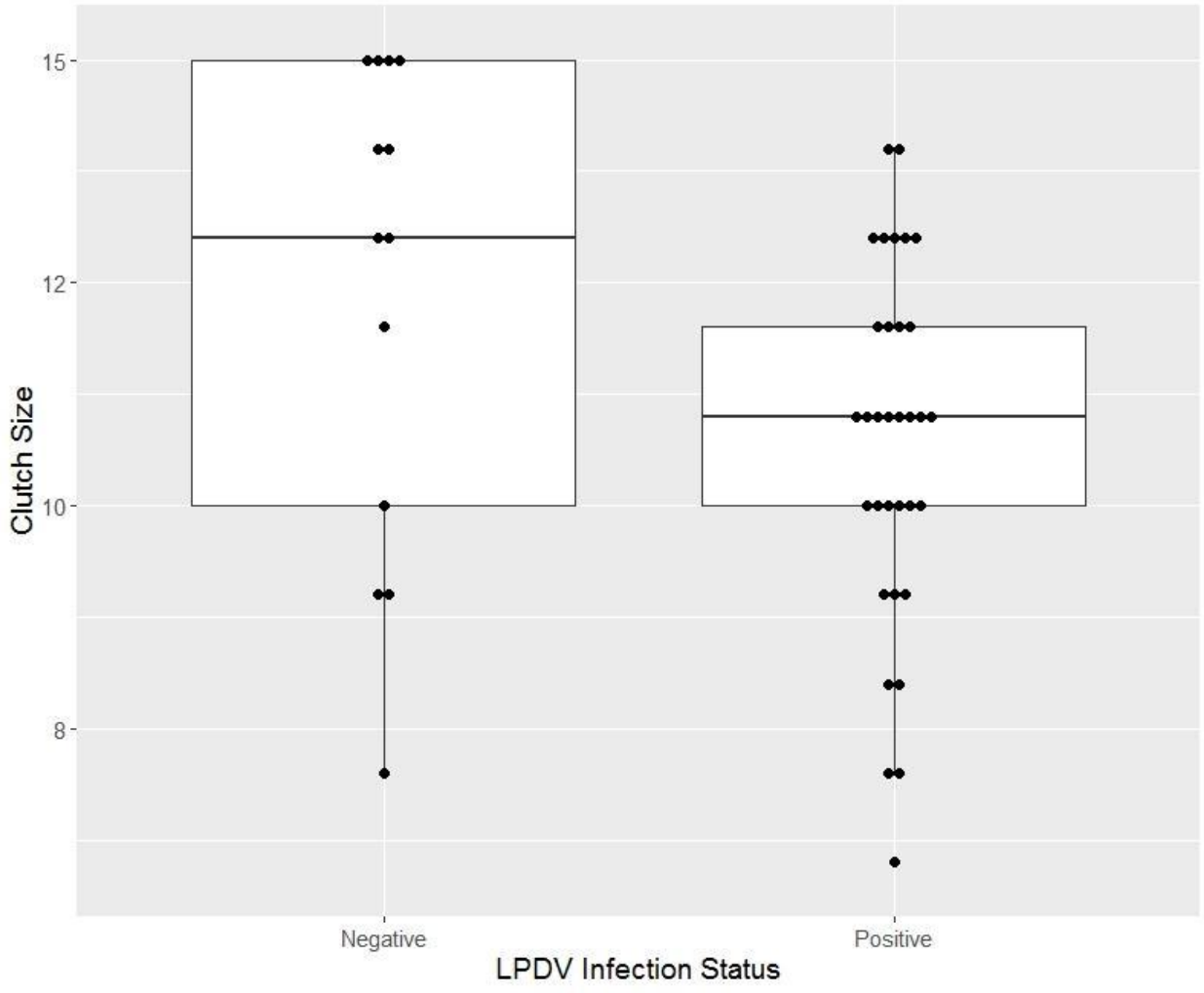

Figure 13. Clutch sizes of wild turkey hens in Maine, USA, from April through July 2018 and 2019. Nests are grouped according to hen LPDV infection status at capture.

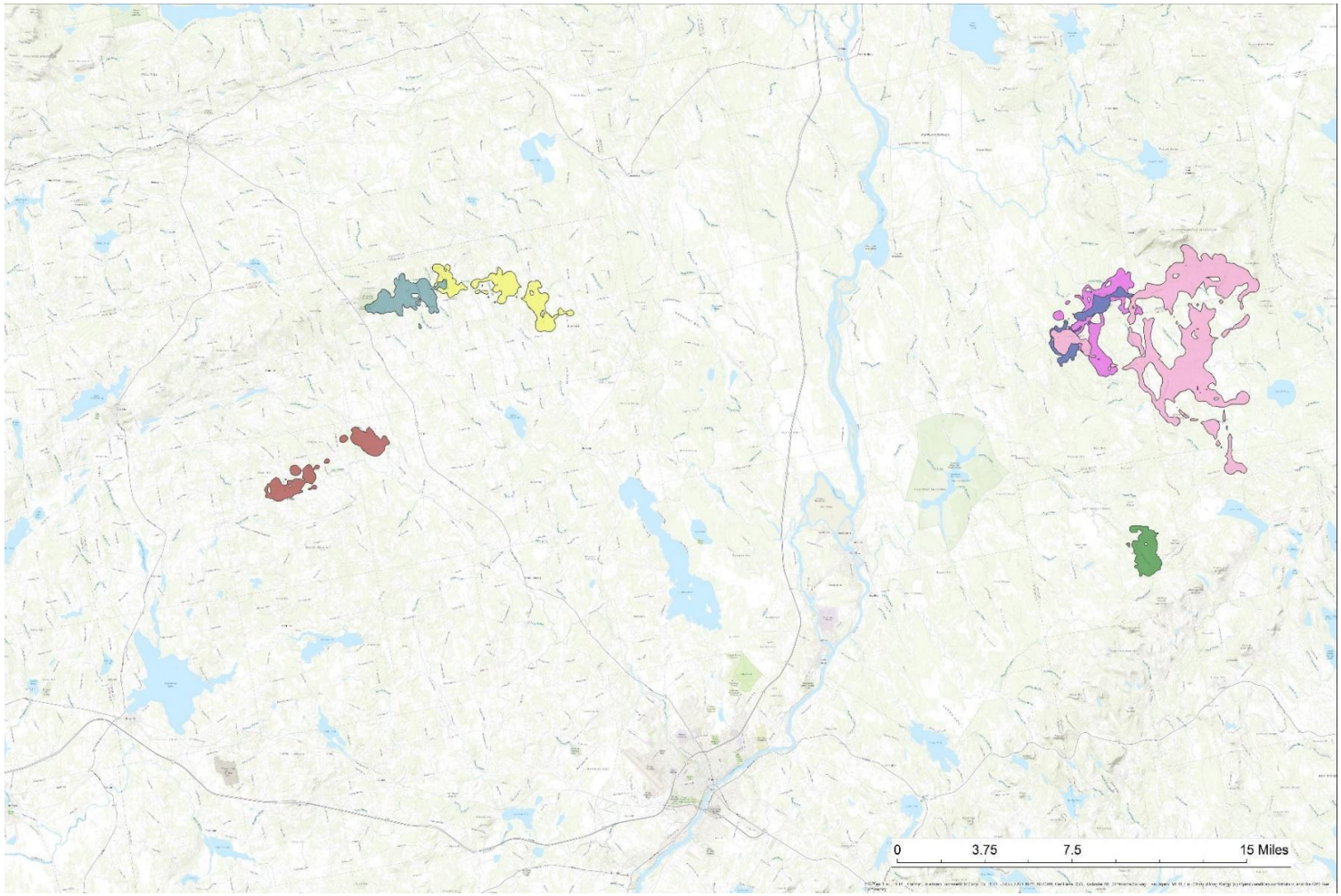

Figure 14. 99% Utilization Distributions (UD) depicting space use of individual wild turkey hens from capture through July 31, 2018 in central Maine, USA. UDs were derived using dynamic Brownian Bridge Movement Models. Individuals are represented by unique colors.

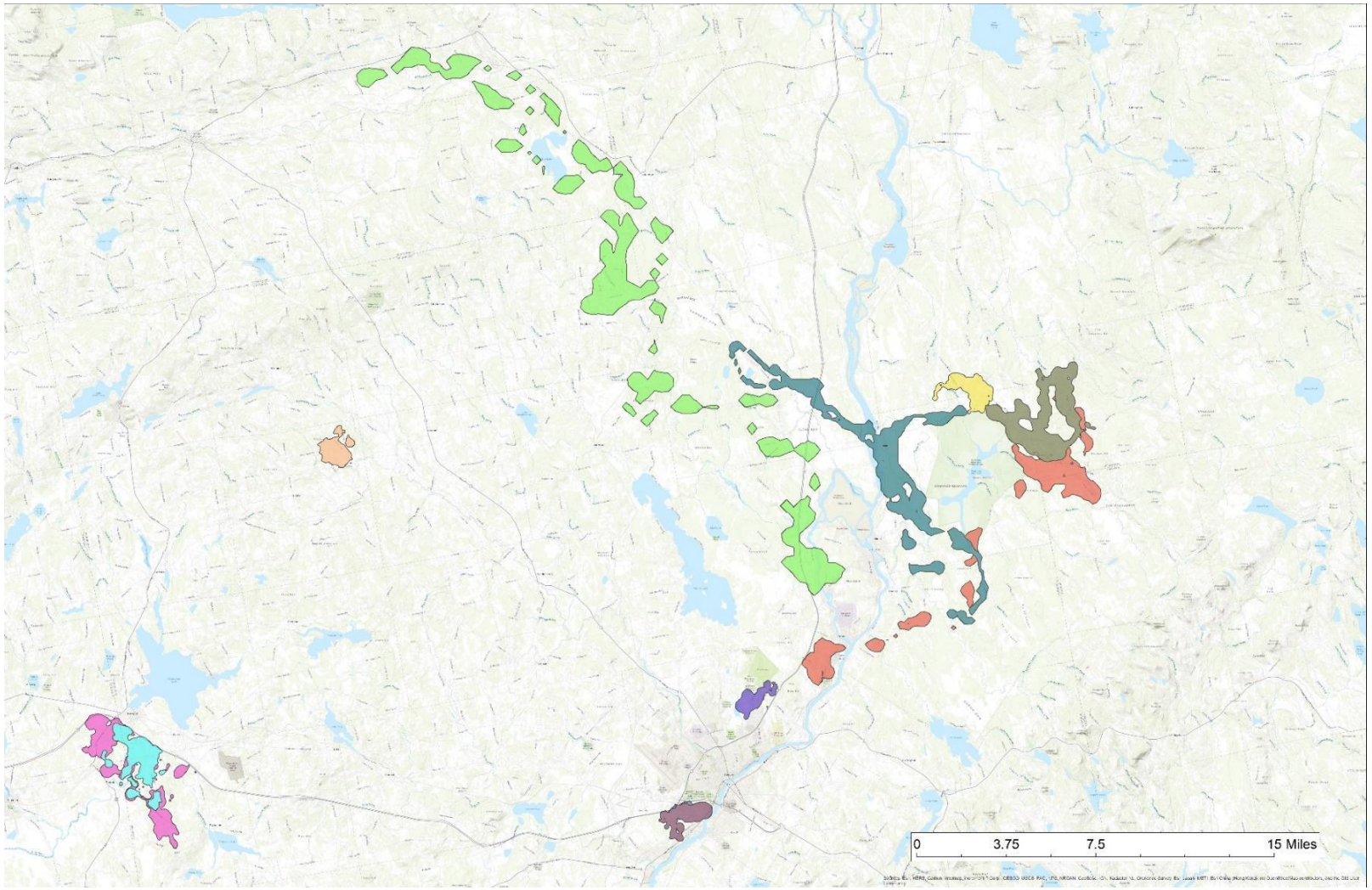

Figure 15. 99% Utilization Distributions (UD) depicting space use of individual wild turkey hens from capture through July 31, 2019 in central Maine, USA. UDs were derived using dynamic Brownian Bridge Movement Models. Individuals are represented by unique colors.

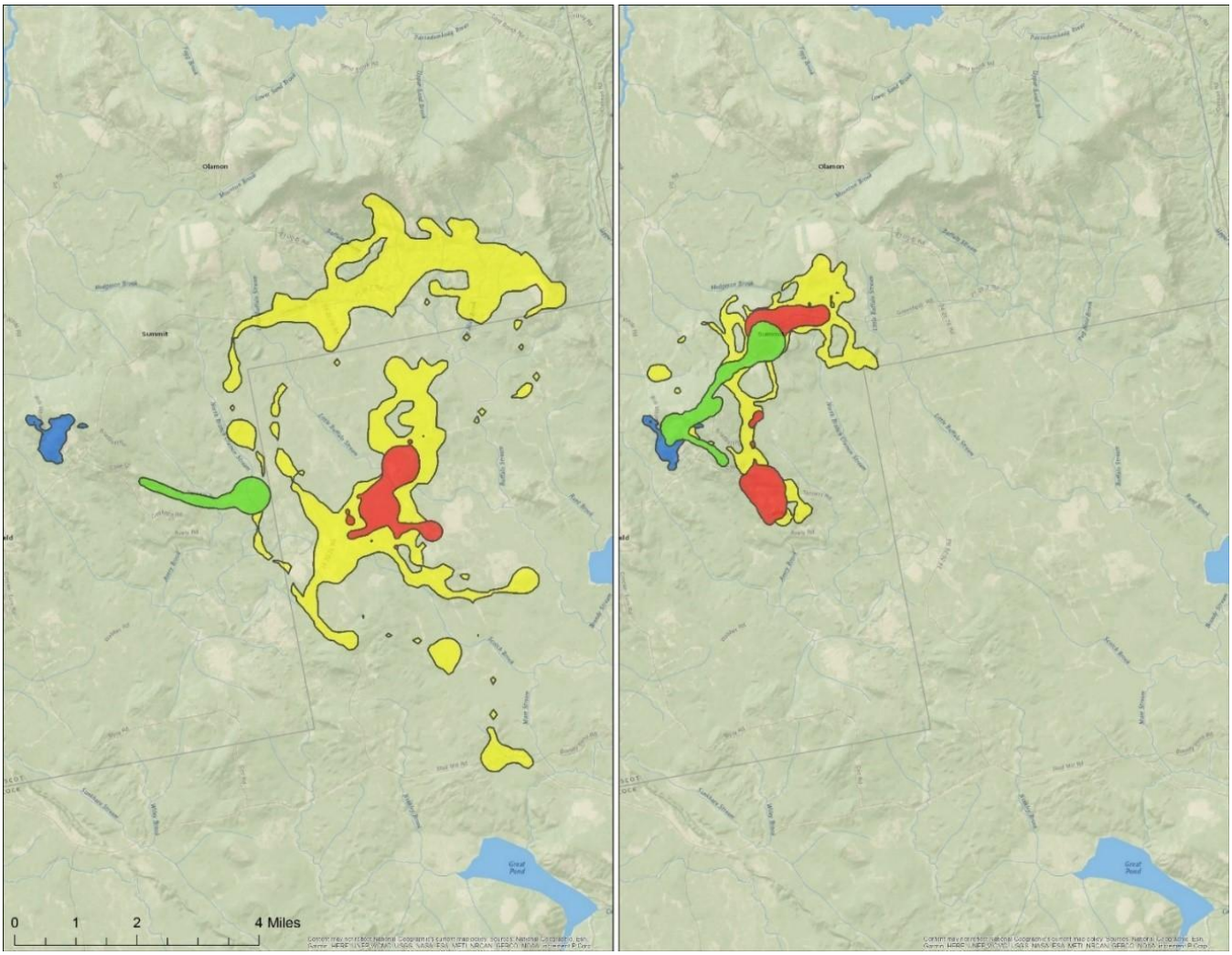

Figure 16. Example of 95% Utilization Distributions for seasonal home ranges of two wild turkey hens (ID 251, left panel, and 361, right panel) from the same flock in the NE study area, Maine, USA. This figure illustrates the potential variation in seasonal movements and home range sizes for female wild turkeys inhabiting the same area. Seasonal ranges were derived using dynamic Brownian Bridge Movement Models. Seasons are Winter (Blue), Winter to Nest Movement (Green), Nesting (Red), and Summer (Yellow). All maps displayed using the same scale and cover the same area.

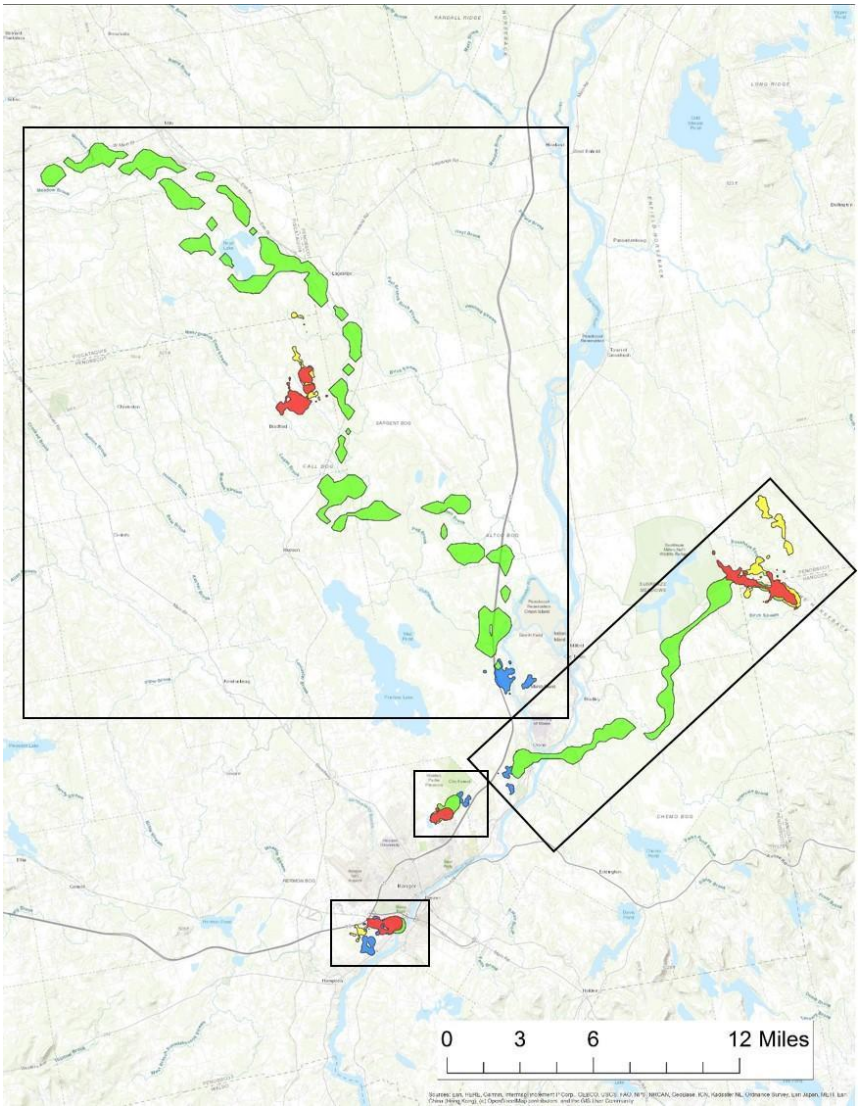

Figure 17. Example of 95% Utilization Distributions for seasonal home ranges of four wild turkey hens capture in the NC study area, Maine, USA. This figure illustrates the potential variation in seasonal movements and home range sizes for female wild turkeys inhabiting the same area. Black boxes individuate individual hen UDs. Seasonal ranges were derived using dynamic Brownian Bridge Movement Models. Seasons are Winter (Blue), Winter to Nest Movement (Green), Nesting (Red), and Summer (Yellow). All maps displayed using the same scale and cover the same area.

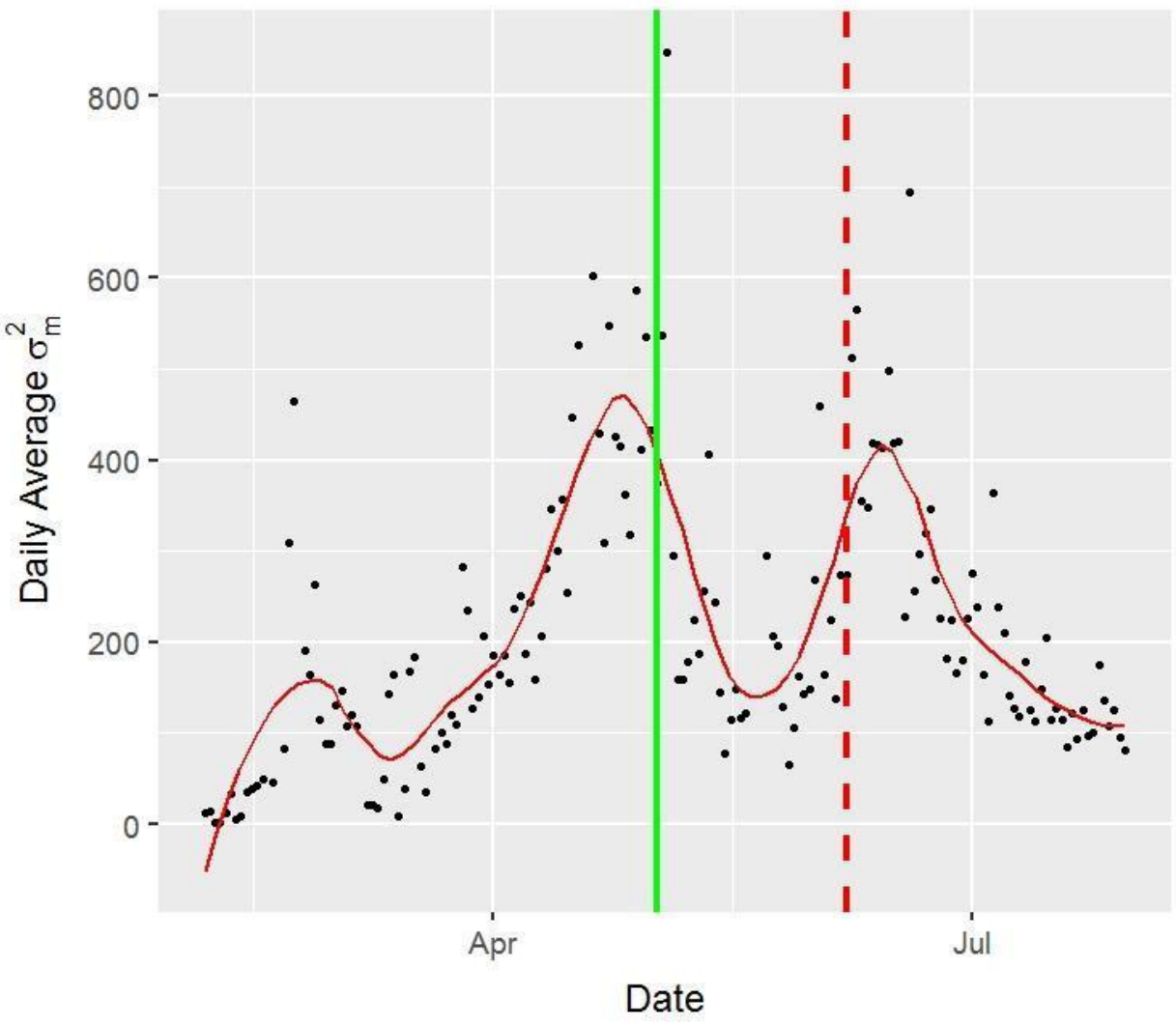

Figure 18. Daily average Brownian Motion Variance (σ_m^2), by date, for wild turkey hens in Maine, USA, from February 2 through July 31, 2018. σ_m^2 was derived using dynamic Brownian Bridge Movement Models. σ_m^2 are presented with a spline trend line, and vertical lines indicate mean nest initiation (solid green) and mean estimated hatch (dashed red) dates.

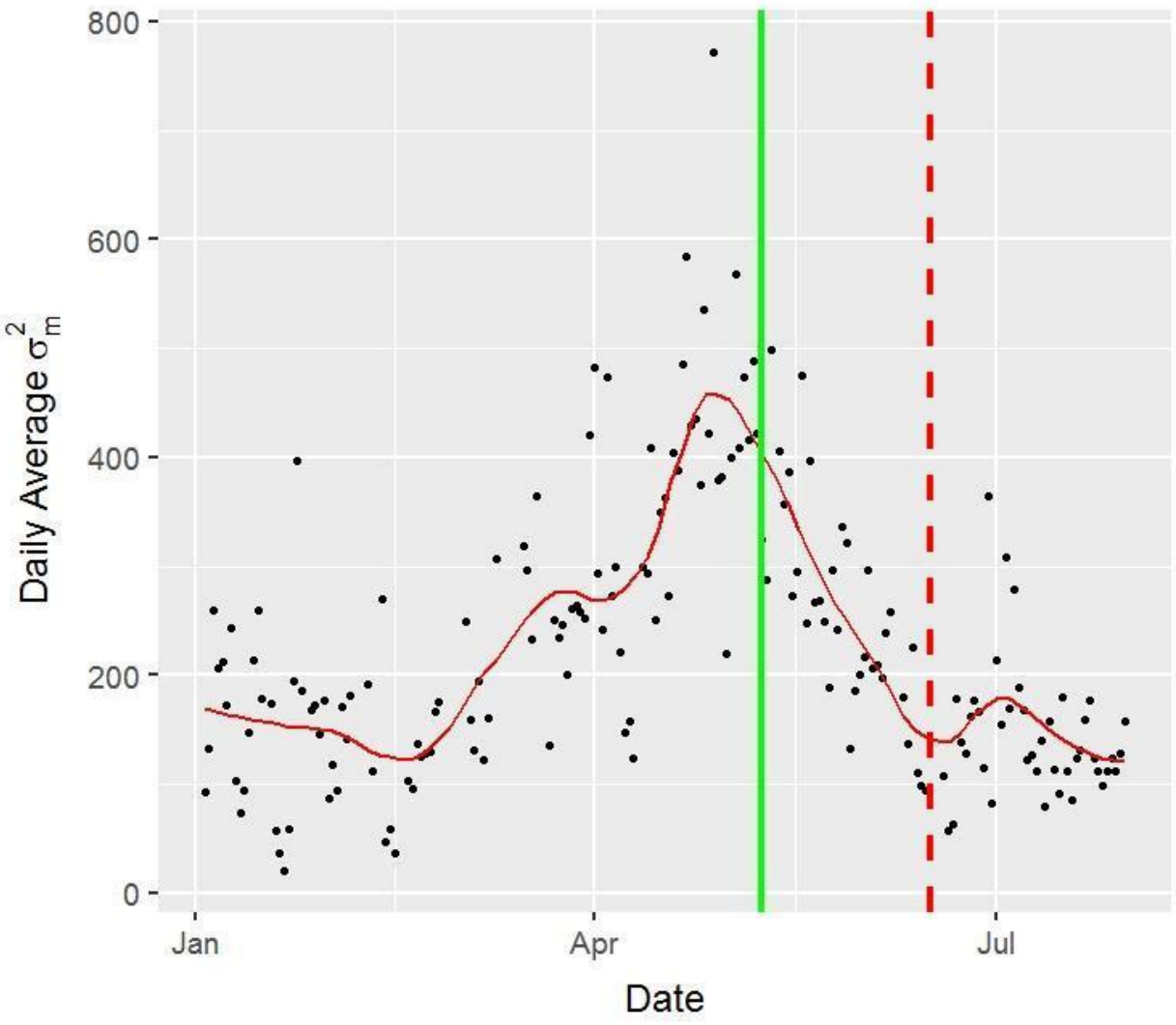

Figure 19. Daily average Brownian Motion Variance (σ_m^2), by date, for wild turkey hens in Maine, USA, from January 1 through July 31, 2019. σ_m^2 was derived using dynamic Brownian Bridge Movement Models. σ_m^2 are presented with a spline trend line, and vertical lines indicate mean nest initiation (solid green) and mean estimated hatch (dashed red) dates.

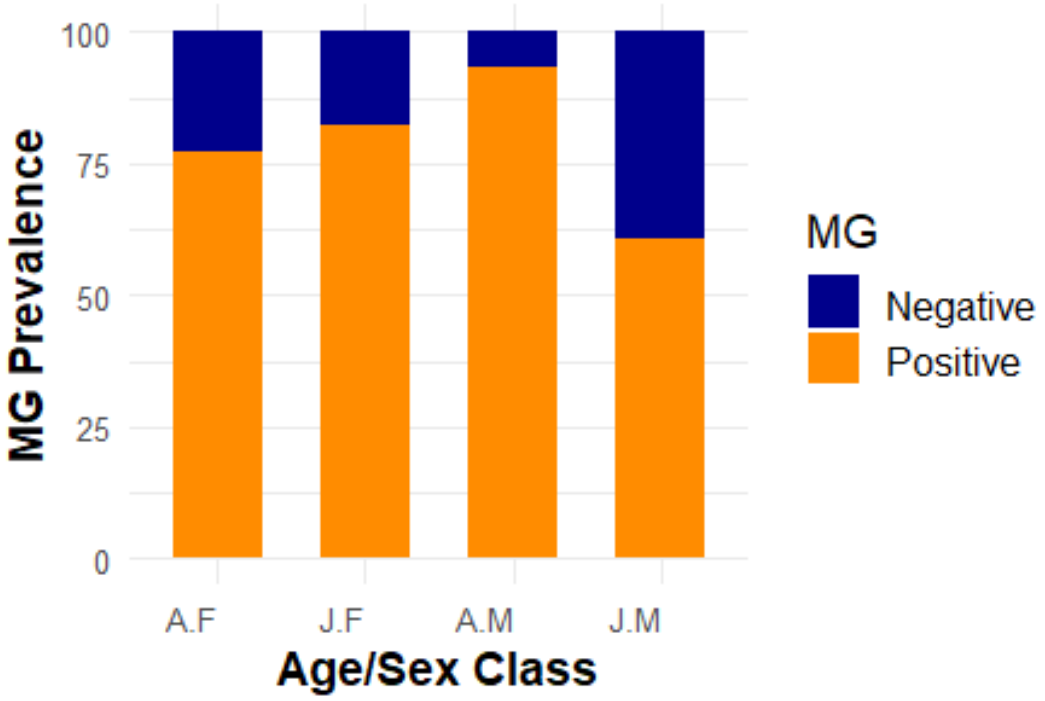

Figure 20. Prevalence of MG by age/sex class justifying the inclusion of the age*sex interaction term in the model predicting MG infection.

Tables

Table 1. Unique wild turkey captures, by year, sex, and age in Maine, USA during January through March of 2018 and 2019. Birds were captured in the areas of Exeter/Corinth (NW), Orono/Bangor (NC), Stud Mill Rd./Greenfield (NE), Gorham/Gray (S), and WMDs 6, 12, 17, 18, 23, 26, 27, and 28.

	2018				2019				
	Female		Male		Female		Male		
	Adult	Juv	Adult	Juv	Adult	Juv	Adult	Juv	**Total**
NC	-	-	-	4	34	17	8	12	**75**
NE	12	-	7	1	11	5	-	-	**36**
NW	34	20	18	-	9	8	3	4	**96**
S	17	2	1	8	8	5	4	12	**57**
WMD 6	-	-	-	-	6	2	8	8	**24**
WMD 12	-	-	-	-	5	5	8	15	**33**
WMD 17	-	-	-	-	-	-	2	-	**2**
WMD 18	-	-	-	-	13	3	9	7	**32**
WMD 23	-	-	-	-	24	11	34	45	**114**
WMD 26	-	-	-	-	12	8	5	4	**29**
WMD 27	-	-	-	-	5	9	-	6	**20**
WMD 28	-	-	-	-	-	-	1	-	**1**
Total	**63**	**22**	**26**	**13**	**127**	**73**	**82**	**113**	**519**

Table 2. Summary of transmitter deployments in Maine, USA during January through March of 2018 and 2019. Transmitters were deployed in the areas of Exeter/Corinth (NW), Orono/Bangor (NC), Stud Mill Rd./Greenfield (NE), and Gorham/Gray (S).

	Female		Male		
	Adult	Juv	Adult	Juv	**Total**
GPS Backpack	25	14	1	-	**40**
VHF Backpack	71	24	-	-	**95**
VHF Necklace	11	10	14	19	**54**
Band Only	83	47	93	107	**330**
Grand Total	**190**	**95**	**108**	**126**	**519**

Table 3. Summary of methods for reporting of harvested banded turkeys during Maine's spring or fall wild turkey hunting seasons in 2018 and 2019.

Check Station	Online	Phone	Total	Percent
Y	-	-	12	21.4%
-	Y	-	5	8.9%
-	-	Y	16	28.6%
Y	Y	-	5	8.9%
Y	-	Y	11	19.6%
-	Y	Y	2	3.6%
Y	Y	Y	4	7.1%
-	-	-	1	1.8%

Table 4. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect survival probability (S) and band recovery probability (r) of wild turkey males during the spring 2018 and 2019 hunting seasons in Maine, USA. We modeled S and r as functions of turkey age, WMD of capture, Region of Capture, and Time using a band recovery rate approach (Laake 2013). All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
S(~TurkAge) r(~TurkAge)	248.698	0.000	0.537	4	39.906
S(~TurkAge) r(~Expert_Region + TurkAge)	249.809	1.111	0.308	5	38.929
S(~TurkAge) r(~Region + TurkAge)	252.995	4.297	0.063	9	33.575
S(~1) r(~1)	253.815	5.117	0.042	2	49.146
S(~TurkAge) r(~WMD + TurkAge)	254.828	6.130	0.025	12	28.800
S(~time) r(~time)	255.697	6.999	0.016	4	46.905
S(~Expert_Region) r(~Kelsey_Region)	256.808	8.110	0.009	4	48.016
S(~Region) r(~Region)	269.094	20.396	0.000	12	43.065
S(~WMD) r(~WMD)	278.965	30.267	0.000	18	39.167

[a] Turk.Age: Adult, Juvenile; Expert_Region: expected harvest based on expert opinion - Medium, High; Region: A, B, F; WMD: 6, 17, 18, 21, 23, 26, 27, 28
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 5. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect weekly survival probability (S) of wild turkey hens in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Gorham/Gray study areas in Maine, USA. We modeled S as a function of Region of capture, WMD of capture, transmitter type, age, sex, study area, disease infection status (LPDV, MD, REV), and Month of the year using a daily survival rate approach (Laake 2013). All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
S(~IFWReg)	751.013	0	0.314	3	745.007
S(~Month)	751.14	0.127	0.295	12	727.061
S(~Study.Area)	752.565	1.552	0.145	7	738.537
S(~Sex)	754.02	3.007	0.07	2	750.017
S(~LPDV)	754.557	3.544	0.053	3	748.551
S(~WMD)	755.141	4.128	0.04	5	745.126
S(~1)	755.772	4.759	0.029	1	753.771
S(~Adult)	756.758	5.745	0.018	2	752.754
S(~REV)	757.111	6.098	0.015	3	751.105
S(~Trans.Type)	757.261	6.248	0.014	2	753.258
S(~MG)	758.463	7.45	0.008	3	752.457

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; MG: Infected, Uninfected, Unkown; Month: January-December; Adult: 1, 0; Study.Area: NC, NW, S, NE, WMD; IFWReg: A, B, F; Sex: Male, Female; WMD: 17, 18, 21, 23, 26; Trans.Type: Back, Neck
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 6. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect post capture survival probability (S) of wild turkeys in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Gorham/Gray study areas in Maine, USA. All models include natural log of days post capture (LN) and interaction term. We modeled S as a function of transmitter type, age, sex, study area, disease infection status (LPDV, MD, REV), time of the year, precipitation the day of capture (pcpCDy) and through the week (avgpcpWk), minimum temperature the day of capture (mtCDy) and through the week (avgmtWk), and trap site location using a daily survival rate approach (Laake 2013). All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
S(~Trans.Type * LN)	347.613	0.000	0.390	4	339.604
S(~HandTime * LN)	349.919	2.306	0.123	4	341.910
S(~TurkAge * LN)	350.438	2.825	0.095	4	342.429
S(~LN)	350.659	3.045	0.085	2	346.656
S(~Time)	351.851	4.238	0.047	2	347.849
S(~Time + I(Time^2))	352.235	4.621	0.039	3	346.229
S(~pcpCDy * LN)	352.391	4.778	0.036	4	344.382
S(~mtCDy * LN)	352.485	4.872	0.034	4	344.476
S(~Sex * LN)	353.065	5.452	0.026	4	345.056
S(~Hematoma * LN)	353.158	5.544	0.024	4	345.149
S(~YearDay * LN)	353.203	5.590	0.024	4	345.194
S(~avgmtWk * LN)	353.244	5.630	0.023	4	345.235
S(~Pat.Tag * LN)	353.889	6.276	0.017	4	345.880
S(~avgpcpWk * LN)	353.982	6.369	0.016	4	345.973
S(~MG * LN)	355.019	7.405	0.010	6	342.999
S(~REV * LN)	355.783	8.169	0.007	6	343.763
S(~LPDV * LN)	357.052	9.438	0.003	6	345.032
S(~Study.Area * LN)	361.296	13.683	0.000	14	333.198
S(~1)	363.277	15.663	0.000	1	361.276
S(~Location * LN)	394.497	46.883	0.000	56	280.997

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; MG: Infected, Uninfected, Unkown; Trans.Type: Back, Neck; HandTime: time in minutes; TurkAge: Adult, Juvenile; LN: natural log of day post capture; Time: day post capture; pcpCDy: precipitation day of capture; mtCDy: minimum temperature day of capture; Sex: Male, Female; Hematoma: 1, 0; YearDay: Julian day of the year for capture; avgmtWk: average minimum temperature for week post capture; Pat.Tag: 1, 0; avgpcpWk: average precipitation for week post capture; Study.Area: NC, NW, NE, S, WMD; Location: categorical for trapping location.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameter
[e]Model Deviance

Table 7. Model selection results for daily survival rate analyses that describe post capture survival probability of Wild Turkey for 30 days following release and radiomarking. Models were implemented in Program MARK using the R package RMark (Laake 2016). Models represent discrete threshold points of postrelease mortality.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
S(~Days4 + Trans.Type + TurkAge + HandTime)	339.987	0.000	0.146	5	329.973
S(~Days6 + Trans.Type + TurkAge + HandTime)	340.079	0.092	0.139	5	330.065
S(~Days3 + Trans.Type + TurkAge + HandTime)	340.109	0.122	0.137	5	330.095
S(~Days7 + Trans.Type + TurkAge + HandTime)	340.185	0.198	0.132	5	330.171
S(~Days5 + Trans.Type + TurkAge + HandTime)	341.016	1.029	0.087	5	331.002
S(~Days2 + Trans.Type + TurkAge + HandTime)	341.343	1.356	0.074	5	331.329
S(~Days8 + Trans.Type + TurkAge + HandTime)	341.545	1.558	0.067	5	331.531
S(~Days9 + Trans.Type + TurkAge + HandTime)	341.656	1.669	0.063	5	331.642
S(~Days10 + Trans.Type + TurkAge + HandTime)	341.849	1.863	0.057	5	331.836
S(~Days11 + Trans.Type + TurkAge + HandTime)	343.023	3.037	0.032	5	333.009
S(~Days12 + Trans.Type + TurkAge + HandTime)	343.952	3.965	0.020	5	333.938
S(~Days13 + Trans.Type + TurkAge + HandTime)	344.888	4.901	0.013	5	334.874
S(~Days14 + Trans.Type + TurkAge + HandTime)	345.366	5.379	0.010	5	335.352
S(~Days15 + Trans.Type + TurkAge + HandTime)	346.518	6.531	0.006	5	336.504
S(~Days16 + Trans.Type + TurkAge + HandTime)	348.205	8.218	0.002	5	338.191
S(~Days20 + Trans.Type + TurkAge + HandTime)	348.975	8.989	0.002	5	338.961
S(~Days21 + Trans.Type + TurkAge + HandTime)	349.016	9.029	0.002	5	339.002
S(~Days19 + Trans.Type + TurkAge + HandTime)	349.126	9.140	0.002	5	339.112
S(~Days25 + Trans.Type + TurkAge + HandTime)	349.247	9.261	0.001	5	339.233
S(~Days22 + Trans.Type + TurkAge + HandTime)	349.309	9.322	0.001	5	339.295
S(~Days18 + Trans.Type + TurkAge + HandTime)	349.393	9.406	0.001	5	339.379
S(~Days17 + Trans.Type + TurkAge + HandTime)	349.677	9.690	0.001	5	339.663
S(~Days23 + Trans.Type + TurkAge + HandTime)	349.821	9.834	0.001	5	339.807
S(~Days1 + Trans.Type + TurkAge + HandTime)	350.321	10.334	0.001	5	340.307
S(~Days24 + Trans.Type + TurkAge + HandTime)	350.475	10.488	0.001	5	340.461
S(~Days27 + Trans.Type + TurkAge + HandTime)	350.619	10.632	0.001	5	340.605
S(~Days26 + Trans.Type + TurkAge + HandTime)	350.700	10.713	0.001	5	340.686
S(~Days28 + Trans.Type + TurkAge + HandTime)	351.623	11.636	0.000	5	341.609

[a]Trans.Type: Back, Neck; TurkAge: Adult, Juvenile; HandTime: time in minutes; Day#: Threshold Day
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 8. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect daily survival rate (S) of wild turkey nests in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Gorham/Gray study areas in Maine, USA. We modeled S as a function of day of the year, age of the nest, initiation date, age of the turkey, study area, transmitter type, and disease infection status (LPDV, REV, and MG) using a daily survival rate approach (Laake 2013). All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
S(~NestAge)	332.794	0.000	0.896	2	328.785
S(~Turk.Age)	340.246	7.452	0.022	2	336.238
S(~1)	340.376	7.582	0.020	1	338.373
S(~Time)	340.991	8.197	0.015	2	336.982
S(~LPDV)	341.409	8.615	0.012	3	335.392
S(~Nest.Attempt)	341.978	9.184	0.009	3	335.961
S(~Nest.Init)	342.081	9.287	0.009	2	338.072
S(~NestYear)	342.379	9.585	0.007	2	338.370
S(~Trans.Type)	343.641	10.847	0.004	3	337.624
S(~REV)	344.181	11.387	0.003	3	338.164
S(~MG)	344.195	11.401	0.003	3	338.178
S(~Study.Area)	347.383	14.590	0.001	6	335.323

[a]NestAge: number of days since nest established; Nest.Init: Date nest established; LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; MG: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Trans.Type: Neck, Back; Study.Area: NW, S, NE, time: days since first nest found
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 9. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect clutch size (CS) of wild turkey nests in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Gorham/Gray study areas in Maine, USA. We modeled CS as a function of initiation date, age of the turkey, study area, year, whether the nest was a renest, and disease infection status (LPDV, REV, and MG) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
CS(~LPDV)	209.604	0.000	0.871	3	101.516
CS(~REV)	214.694	5.090	0.068	3	104.061
CS(~MG)	214.944	5.340	0.060	3	104.186
CS(~Init)	262.750	53.146	0.000	3	128.168
CS(~Init2)	263.442	53.838	0.000	4	127.370
CS(~Renest)	282.920	73.315	0.000	3	138.253
CS(~1)	290.279	80.675	0.000	2	143.038
CS(~TurkAge)	291.544	81.939	0.000	3	142.565
CS(~Year)	292.451	82.846	0.000	3	143.018
CS(~StudyArea)	293.603	83.999	0.000	7	138.765

[a]; LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; MG: Infected, Uninfected, Unkown; Init: Julian day of nest initiation; Init2: quadratic term for julian day of nest initiation; Renest: 1, 0; TurkAge: Adult, Juvenile; Year: 2018, 2019; StudyArea: NC, NE, NW, S, WMD
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 10. Average area estimates for 95% Utilization Distributions (UD) by season for wild turkey hens at NW and NE study areas, Maine, USA, from January through July 2018 and 2019. Estimates are presented in mi^2 and were derived using dynamic Brownian Bridge Movement Models. Estimates are presented with the number of individuals sampled (n), the maximum value recorded during a given season (Max.), the minimum value recorded during a given season (Min.).

	n	Average	Max.	Min.
Capture-to-August 1				
2018	7	2.680	8.271	1.095
2019	11	2.634	7.784	0.632
Winter				
2018	10	0.496	0.942	0.311
2019	22	0.898	4.469	0.164
Winter-to-Nest				
2018	8	1.107	2.441	0.266
2019	13	3.083	20.509	0.092
Nesting (1st Attempt)				
2018	8	0.893	1.259	0.553
2019	12	1.030	3.192	0.194
Nesting (2ndAttempt)				
2018	3	0.508	0.701	0.304
2019	2	0.609	0.692	0.526
Nesting (3rd Attempt)				
2018	1	0.379	0.379	0.379
2019	-	-	-	-
Summer				
2018	6	2.844	10.607	0.052
2019	11	0.942	2.881	0.129

Table 11. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect winter home range size (WHR) of wild turkey hens in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Bangor/Orono study areas in Maine, USA. We modeled WHR as a function of age of the turkey, study area, and disease infection status (LPDV, REV, and MG) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
WHR(~LPDV)	133.277	0.000	0.356	3	63.138
WHR(~REV)	133.447	0.170	0.327	3	63.223
WHR(~MG)	133.520	0.243	0.315	3	63.260
WHR(~1)	145.503	12.226	0.001	2	70.545
WHR(~TurkAge)	147.844	14.568	0.000	3	70.494
WHR(~StudyArea)	148.751	15.474	0.000	4	69.635

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; MG: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Study.Area: NW, S, NE, NC, WMD.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 12. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect pre-nesting home range size (PNHR) of wild turkey hens in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Bangor/Orono study areas in Maine, USA. We modeled PNHR as a function of age of the turkey, study area, and disease infection status (LPDV, REV, and MG) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
PNHR(~MG)	80.763	0.000	0.972	3	36.715
PNHR(~LPDV)	89.289	8.527	0.014	3	40.978
PNHR(~REV)	90.183	9.420	0.009	3	41.425
PNHR(~StudyArea)	91.385	10.622	0.005	4	40.693
PNHR(~1)	96.048	15.285	0.000	2	45.751
PNHR(~TurkAge)	97.686	16.923	0.000	3	45.272

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; MG: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Study.Area: NW, S, NE, NC, WMD.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 13. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect distance between winter and pre-nesting home ranges (SD) of wild turkey hens in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Bangor/Orono study areas in Maine, USA. We modeled SD as a function of age of the turkey, study area, and disease infection status (LPDV, REV, and MG) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
SD(~MG)	107.448	0.000	0.495	3	49.801
SD(~LPDV)	108.566	1.118	0.283	3	50.360
SD(~REV)	109.050	1.603	0.222	3	50.602
SD(~1)	122.520	15.072	0.000	2	58.907
SD(~TurkAge)	124.851	17.403	0.000	3	58.675
SD(~StudyArea)	128.187	20.739	0.000	4	58.760

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; MG: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Study.Area: NW, S, NE, NC, WMD.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance