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ESTIMATING THE OCCUPANCY, ABUNDANCE, AND DENSITY OF DUSKY GROUSE: DEVELOPING METHODS OF UNBIASED POPULATION MONITIORING IN MONTANA

FINAL REPORT

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EXECUTIVE SUMMARY

This report summarizes the results of a four-year (2019–2022) research project to develop methods for unbiased population monitoring for dusky grouse (*Dendragapus obscurus*; previously "blue grouse") in Montana. The primary objectives of this study are to 1) generate a predictive model of habitat suitability for dusky grouse throughout their range in Montana, 2) develop and evaluate survey methods that provide unbiased statewide and regional estimates of dusky grouse densities and annual trend monitoring in Montana, and 3) develop methods that facilitate rigorous and cost-effective evaluations of grouse-habitat relationships and the effects of management.

We built and evaluated a statewide habitat model for dusky grouse in Montana using an ensemble approach. We obtained dusky grouse observations collected during the spring (April–June) from 2009–2020 from the Integrated Monitoring in Bird Conservation (IMBCR) program and extracted habitat information for detected/not-detected locations using remotely-sensed geospatial datasets. We evaluated relative habitat use with resource selection functions (RSFs) calibrated using generalized linear mixed models and randomized classification trees (random forest, RF, technique). For the RSFs, candidate models representing hypothesized relationships between grouse detections/non-detections and habitat conditions (e.g., forest type and coverage, average elevation, slope) were compared using multi-model inference based on information theory. We found the following spatially-explicit habitat attributes to have a significant effect on whether or not a dusky grouse was detected at a site: average distance to nearest stream, average distance to nearest road, proportion of foothill conifer wooded steppe, proportion of montane sagebrush steppe, proportion of trees with a height of 1–5 m, and the proportion of trees with a height of 16–20 m. Our RSF model had high predictive accuracy with an ROC value of 0.89 (95% CI: 0.85–0.93), and correctly classified 150/193 of the independently detected grouse locations collected by FWP. For the RF, the top 10 important variables in decreasing order of importance were: proportion of trees with a height of 16–20m, average slope, average elevation, proportion of Douglas fir forest and woodland, proportion of trees with a height of 21–25m, proportion of montane-foothill deciduous shrubland, proportion of montane mixed conifer forest, proportion of area with 30–39% shrub canopy cover, proportion trees with a height of 1–5m, and proportion of area with big sagebrush steppe. The ROC value for the random forest was 0.87 (95% CI: 0.83-0.92), and the model correctly classified 94% (181/193) of the independently detected grouse locations. Given that both models had high predictive accuracy, we created binary maps (habitat & non-habitat) that we then combined to obtain our ensembled prediction. Our ensemble habitat model classified 109,125 km^2 in Montana to be in the two highest relative probability of use categories, with the majority of the dusky grouse habitat predicted to occur in FWP administrative regions 1,2,3, with some habitat in FWP administrative regions 4 and 5.

In 2019 we conducted a pilot season to compare different sampling methods including the timing of the sampling period (spring vs summer) and the use of electronic playback to increase detection. In 2020 and 2021 we expanded our survey effort to all of western Montana and moved transects from off-trail in 2019 to on roads and trails in order to evaluate the impact of route type on abundance and detection. From the pilot season in 2019 we found that spring surveys with electronic playback were most effective for detecting dusky grouse. Comparing route type (off-trail, trail, or road) for spring point count surveys we found that abundance of dusky grouse was

higher off-trail and that probability of detecting a dusky grouse was slightly higher on roads and trails.

We used the expanded survey effort in 2020 and 2021 to obtain empirical estimates of local abundance and detection that we used to inform our different scenarios for simulation datasets. Given that estimates of local abundance were similar when evaluated using hierarchical distance sampling models and single-season N-mixture models, we chose only one model's results to inform our different simulation scenarios. We used an average abundance of 0.18, a high abundance of 0.31, and a low abundance of 0.08. For detection we estimated an average constant detection and detection under ideal survey conditions. We found that for the N-mixture models, the average probability of detection was 0.37, and under ideal conditions, the probability of detection was 0.57. For the hierarchical distance sampling models for point counts, we found that sigma, which is used to estimate the half-normal detection function, was 43 under average conditions and 58 under ideal survey conditions. For hierarchical distance sampling models for line transects, sigma, which was again used to estimate a half-normal detection function, was 42 under average conditions, and 51 under ideal survey conditions. For hierarchical distance sampling with time removal models for point counts, we estimated both the probability that an individual would be available to be detected and the probability of detecting an individual given that it is available. Under average conditions, the probability that an individual was available was 0.65, and under ideal conditions it was 0.89. The probability of detecting an individual given that it is available was estimated using distance sampling. We estimated a half-normal detection function using sigma, which was 43 under average conditions and 48 under ideal conditions.

Based on the empirical estimates of local abundance and detection, we conducted statistical simulations to evaluate the efficacy of different survey protocols and statistical estimators for monitoring dusky grouse. Based on management criteria of FWP, an acceptable monitoring program should produce unbiased estimates of regional abundance with a coefficient of variation of less than 15%. Using simulations, we identified two survey protocols that met our goals. One approach for achieving unbiased (bias = 0.01 grouse; 95% CI: -0.03, 0.04) and precise (CV = 7%) estimates of annual abundance in a monitoring jurisdiction is one where 80 survey points are surveyed 4 times during periods of high detection (e.g. peak breeding period, early morning, and good weather conditions) and abundance is estimated using an N-mixture model. To evaluate whether visits could occur on the same day, we tested the effects of correlation on the probability of detection and local abundance estimates. When the true probability of detection was high (>57%), the proposed protocol produced unbiased estimates of detection and local abundance. The second approach for achieving unbiased (bias = -0.11 grouse; 95% CI: -0.71, 0.57) and precise (CV = 13%) estimates of annual abundance is one where at least 35 transects of ≥ 2.6 km are surveyed in each area of inference also during periods of high detection.

Our recommended protocol derived from the high detection, average abundance scenario (point-counts where 80 sites are visited four times and evaluated using N-mixture models) had high power (≥ 80%) to detect average population declines of 3%, 5%, and 10% over 5–10-year periods, which was lower than expected given precision of annual abundance estimates were < 15%. Nevertheless, we found that the estimated abundance trends were similar to the target trends, and close to the real trends estimated using the true simulated population size, suggesting that while there may be some uncertainty associated with the estimated trends, our protocols may be sufficient for long-term monitoring and able to detect small changes in population size in as little as 3 years. In addition, as the monitoring period increases (> 5 years), the power to detect

small changes increases indicating that our protocols are appropriate for long-term monitoring of dusky grouse populations.

A secondary objective is that our survey protocol and analytical framework can be used with little modification to evaluate the associations between dusky grouse abundance and habitat conditions or management actions (e.g., effects of beetle-kill or timber harvest). We used the two survey protocols that we identified for meeting our goals to evaluate the effects of a hypothetical habitat condition (X) on dusky grouse abundance. An acceptable sampling protocol would yield unbiased estimates of the true regional population size and the effect of the habitat covariate on local dusky grouse abundance. We evaluated scenarios with varying abundance, detection, and effect (strong or weak) of the hypothetical habitat covariate (X) on site-specific abundance. We evaluated a strong negative effect ($\beta = -1.0$) and a weaker negative effect ($\beta = -0.5$). All scenarios examined yield unbiased estimates of total population size and unbiased estimates of effect size of the site covariate, as well as reasonably precise estimates of total population size ($CV < 15\%$). Overall our results suggest that the two survey protocols we identified (80 sites visited 4 times and analyzed by N-mixture model, and 35 line transects visited and evaluated by hierarchical distance sampling) will yield unbiased and reasonably precise estimates of regional dusky grouse populations and allow for evaluation of associations between local dusky grouse abundance and a habitat covariate or management action.

ESTIMATING THE OCCUPANCY, ABUNDANCE, AND DENSITY OF DUSKY GROUSE: DEVELOPING METHODS OF UNBIASED POPULATION MONITIORING IN MONTANA

2022 Annual Progress Report

OBJECTIVES

Objective 1: Generate a predictive model of habitat suitability for dusky grouse throughout their range in Montana

Methods

We used an ensemble approach to develop and evaluate a model to predict habitat of dusky grouse in Montana that can be used to identify appropriate survey sites and to explore relationships between habitat characteristics and relative probability of use. We obtained dusky grouse observation data from the Integrated Monitoring in Bird Conservation Regions monitoring program (IMBCR) administrated by the Bird Conservancy of the Rockies. The IMBCR program conducts avian point count surveys between May and July each year at randomly selected locations that vary among years across Montana and other western states (Pavlacky et al. 2017, Hanni et la 2018). We obtained observation data from spring surveys during 2009–2020 for a total of 25,654 surveys conducted across 6,092 sites in Montana. We reduced observations from the IMBCR point counts to dusky grouse detected/ not detected data that we then used to represent sites that were used (detected) and available (not detected). If a dusky grouse was detected at least once during the 11-year period, a site was classified as used and if a dusky grouse was not detected the site was classified as available. Sites were classified as available instead of unused because it is possible that a dusky grouse was present but not detected. After reducing the data to used and available sites, we classified 132 sites as used and 5,960 sites as available. Given that a dusky grouse call may be difficult to detect depending on call type at distances greater than 50–100m (Zwickel and Bendell 2004, Farnsworth 2020) and potential uncertainty with GPS locations, we assumed that all dusky grouse observed were located within 250-m of the point count location.

We used remotely-sensed geospatial datasets to extract habitat information within a circular 250-m buffer drawn around each point count location. We used digital elevation models (DEMs) from U.S. Geological Survey, ArcGIS Pro (Environmental Systems Research Institute, Redlands, CA) and geospatial modeling environment (GME) to measure average elevation, slope, and proportions of different facing (N, NE, E, etc.) aspects of the 250-m radii area (Beyer 2015, U.S Geological Survey 2017). We calculated the average distance of the 250-m radii area to the nearest stream and to the nearest road using the spatial analyst tools of ArcGIS Pro applied to the Montana Spatial Data Infrastructure (MSDI) Transportation Framework and Hydrography datasets downloaded from the Montana state library and GME (Beyer 2015, Montana Spatial Data Infrastructure 2017, 2018). We downloaded LANDFIRE geospatial data with a 30 × 30 m spatial resolution for existing vegetation type (EVT), existing vegetation cover (EVC), and existing vegetation height (EVH; Landfire 2016a, b, c). EVT is the type of plant community present, of which in Montana there are 121 types; EVC is the vertically projected percent cover by a live canopy layer given in 1% increments; EVH is the average height of the dominant vegetation given in 1m increments (Landfire 2016a, b, c, 2019, 2020). We created a forest layer

based on the vegetation physiognomy (EVT_PHYS) description for the different LANDFIRE vegetation types and vegetation community name (Table 1; LANDFIRE 2016a). We used the spatial analyst tools of ArcGIS Pro and GME to calculate the average distance to the edge of the forest type from within and outside of the forest (Beyer 2015). We used GME to calculate the proportion of vegetation type, canopy cover, and height within 250 meters of the survey location (Beyer 2015). After the vegetation canopy and height information were extracted, we condensed the information from their 1% or 1m increments to larger categories to reduce the number of variables evaluated. We condensed the 1% increments for the canopy vegetation to 10% increments and the 1-m increments for vegetation height to 5-m increments. For both types of habitat information there were also several categories of developed habitat or barren habitat that was grouped into two categories: developed and sparse vegetation. We removed variables from consideration if they occurred at less than 1% of the survey sites or showed no relationship between use and Dusky Grouse. Overall, we extracted geospatial habitat information for a total of 90 potential variables.

We evaluated relative habitat use with two different methods: resource selection functions and random forest (randomized classification trees; McNew et al. 2021). After evaluating the two models we used an ensemble approach to combine their predictions using a frequency histogram approach to create a final more robust model of dusky grouse habitat.

We fitted our resource selection functions (RSFs) using general linear mixed models (GLMMs) with a logit link function, binomial error distribution, and the "bobyqa" optimizer with a maximum of 100,000 iterations for estimating beta coefficients for our RSF using the 'lme4' package in program R (Bates et al. 2015, R Core Team 2017). Our response variable was either a dusky grouse was detected (1) or not detected (0), with our habitat factors as independent variables, and a random intercept term for unique IMBCR transects to account for potential spatial autocorrelation in the observation data due to the survey points being grouped along survey routes (Zurr 2009, Hanni et al 2018).

Before fitting the models with RSFs, we explored the possibility that the behavioral response of dusky grouse to habitat characteristics is nonlinear. Initially we explored potential nonlinear responses by plotting the relationship between the response variable (detected or not detected) and a "smoothed" function for each habitat variable using univariate generalized additive models (GAMs; Guisan and Zimmerman 2000, Guisan et al 2002, McNew et al 2013). We further explored potential linear and nonlinear relationships using linear equations to represent the hypothesized linear and nonlinear forms (Guisan and Zimmerman 2000). We used $[x + x^2]$ for the quadratic form and the natural log of the explanatory variable $\ln[x + 0.001]$ to represent a pseudolinear threshold (Franklin 2000, Dugger et al 2005, McNew et al 2015). We performed the preliminary screenings of the three functional responses using univariate models built using GLMMs with a logit link function and binomial error distribution. We evaluated support for non-linear relationships for each variable by comparing Akaike's Information Criterion for small sample size (AIC_c) for GLMMs with linear and non-linear terms (Burnham and Anderson 2002). While evaluating the potential non-linear and linear relationships with AIC_c, if the change in AIC_c from the 'best' model to was < 2 then the models were considered to have similar support (Burnham and Anderson 2002), and we chose the simplest model (the model with fewest parameters). If the number of parameters was the same, we looked at figure of the plotted GAM function for that variable to determine which potential relationship best fit the variable. In the majority of the cases, the plotted GAM function best resembled the potential relationship with

the lowest AIC_c. If problems with modeling a relationship occurred while attempting to evaluate one of the relationship forms, that relationship was not considered.

After preliminary screenings of the functional responses, we tested for multicollinearity in the remaining 90 habitat predictor variables using Spearman-rank correlations to prevent overfitting the model. If correlations were ($|r| > 0.7$), we considered the variables to be correlated. If variables were correlated, we first used general knowledge of dusky grouse habitat to evaluate which variable was more biologically relevant to dusky grouse. If we had no previous knowledge on whether one variable was more biologically relevant, we evaluated univariate models using AIC_c, and whichever variable had the lower AIC_c value was selected and the other variable was removed from our analysis (Aldridge et al 2012). If the delta AIC_c was < 2, then we selected the most parsimonious (simplest) model (Burnham and Anderson 2002, Arnold 2010). As a variable may be correlated with more than one variable, we evaluated correlations based upon the highest correlation to the lowest, removing the variable we considered to be less relevant from the variable pool as we went.

After exploring the possibility that some of the behavioral responses of dusky grouse to some habitat variables may be nonlinear and accounting for correlation, we had 66 variables remaining. We evaluated the remaining predictors within groups using backwards stepwise selection. The different groups included aspect, other non-vegetation variables (slope, elevation, distance to variables), conifer vegetation type, hardwood vegetation type, grassland vegetation type, shrubland vegetation type, riparian vegetation type, other vegetation type, tree canopy cover, shrub canopy cover, herbaceous canopy cover, other vegetation cover, and vegetation height. Variable removal was based on p-values calculated using the 'lme4' package in program R from asymptotic Wald tests (Hosmer et al 2013, Bates et al 2015, Heinze et al 2018). We removed the variable with the highest p-value > 0.05, continuing backwards selection until there were no more variables with p-values > 0.05 (Heinze et al 2018). The top performing variables from each of categories were then added to the final model set and evaluated using backwards stepwise selection. To obtain 95% confidence intervals for the beta coefficients we used the Wald method, which estimates the fixed-effects confidence intervals, using the 'lme4' package in program R (Bates et al 2015, R Core Team 2017).

In a used versus available study design, we cannot estimate the true probability of use from a logistic regression model, we can only estimate the relative probability of use (Manly et al 2002). Because of this we used the coefficients from the estimated logistic regression for the corresponding slope coefficients (β_i) to estimate the relative probability of use for a site by dusky grouse.

$$w(x) = \exp(\beta_1 X_1 + \beta_2 X_2, \ldots \beta_i X_i)$$

(Manly et al 2002, Boyce and McDonald 1999).

We developed Random Forest models using the *train* and *trainControl* functions and the 'rf' model from the 'caret' package in R (Kuhn 2008, R Core Team 2017). Random forest models are sensitive to unbalanced datasets, such as the IMBCR dataset where the number of pseudo-absent locations greatly outnumbered the used locations. To account for our dataset being unbalanced, we used the down-sampling function within the caret package to rarify the random sampling data to a 1:1 ratio with the used locations (Evans and Cushman 2009, Evans et al. 2011, Kuhn and Johnson 2013, Kuhn 2019). We tuned our model by varying the number of trees and the number of variables to possibly split at each node (Kuhn 2008, Kuhn and Johnson 2013, R

Core Team 2017). The number of variables to possibly split at each node, "mtry", was tested with the square root of the number of predictors, the square root of the number of predictors divided by 2, and the square root of the number of predictors times 2 (Breiman 2001, Kuhn and Johnson 2013). The number of trees tested were 300, 500, 800, 1000, and 2000. After we tuned the model, we trained it with repeated cross validation, with 5 folds and 500 repeated k-fold cross validation iterations. We used the generated variable importance to evaluate the importance of the different habitat characteristics for fitting the random forest model. For the variables of highest importance, we used partial dependency plots to evaluate the marginal effect a feature had on the model's predictions (Molnar 2022).

We developed separate statewide predictions of relative use from each model. We used a 250-m moving window to create layers for each variable upon which to predict our models. We, first, used slope coefficients from our top GLMM to fit an RSF based on the use-availability design of Manly et al. (2002). Second, to evaluate dusky grouse occurrence across Montana using the random forest model, we used the predict function in R with our 250-m circular moving window layers to construct a predictive map of potential dusky grouse habitat (Kuhn 2008, R Core Team 2017).

We evaluated the performance of our models and their predictive capability using two independent datasets: the training (IMBCR) dataset using k-fold cross-validation, and observations of 193 dusky grouse locations collected April–June from 2017–2019 by Montana Fish, Wildlife, and Parks (MFWP) personnel. We plotted and calculated ROC/AUC using cross validation of the original dataset, where we conducted a simulation with 500 iterations, where for each iteration 80% of the IMBCR data was used to train our model and the other 20% of the IMBCR data was used to test the model. We calculated the average AUC value with a 95% confidence interval.

We extracted the predicted value for habitat suitability from the RSF model, RF model, and ensembled prediction for each independent observation for the IMBCR dataset and the MFWP dataset. We used the IMBCR dataset to categorize the values for each model into 5 quantile bins that represented the relative probability of a point being classified as a site used by dusky grouse (Boyce et al 2002, Johnson et al 2006, McNew et al 2013). The bins represented low, medium-low, medium, medium-high, and high probability of relative use. We then regressed the observed proportion of grouse locations from the MFWP or test dataset in each quantile bin with the observed proportions of grouse locations in each quantile bin from the IMBCR or training dataset. We used linear regression to compare the training and testing datasets, and we considered a good model fit to have a high R^2 value, a slope of 1, and an intercept of 0 (Johnson et al. 2006, McNew et al 2013).

We calculated a threshold for differentiating dusky grouse habitat from non-habitat for the ensembled predictions using the IMBCR data using the 60% quantile bin, which correctly predicted 75% of the used points in the training and test datasets. To evaluate the accuracy of the threshold, we conducted a simulation with 500 iterations for the state-wide MFWP data and MFWP regional data, where we calculated the average percent of correctly predicted locations with a 95% confidence interval for a subset (80%) of the MFWP dataset. Because predictive accuracies of both models were similar (see Results) we added the two binary maps (a frequency histogram approach) to create a final map representing an ensembled prediction of dusky grouse habitat within Montana (Araujo and New 2006, Le Lay et al 2010, Stolgren et al 2010). The final map's pixels consisted of a 0, 1, or 2, where a 1 represented an area where only 1 model

predicted habitat, a 2 represented an area where both models predicted habitat, and a 0 represents an area where neither model predicted habitat. Areas where both models predicted habitat we considered high relative probability of use and areas where only one model predicted habitat we considered to be medium-high relative probability of use.

Using the ensemble model, we calculated the amount of dusky grouse habitat in Montana and within each MFWP administrative region by summing the number of pixels predicted to be medium-high relative probability of use and high relative probability of use and multiplying by pixel size ($0.0009km^2$).

Results

Using the RSF model, we found 7 variables to have significant effects on whether dusky grouse were detected: average distance to nearest stream, distance to nearest road, slope, proportion of foothill conifer wooded steppe, proportion of inter-mountain basins montane sagebrush steppe, proportion of trees with a height of 1–5m, and proportion trees with a height of 16–20m (Table 2). Both average distance to nearest stream ($\beta = 7.40 \pm 2.11$, $\beta = -7.49 \pm 2.70$; Table 3) and proportion of northern rocky mountain foothill conifer wood steppe ($\beta = 216.70 \pm 32.83$, $\beta = -5557.00 \pm 137.60$; Table 3) had a quadratic relationship with relative use (Figure 1). Predicted use was maximized at 0.5 km from a stream. When proportion of northern rocky mountain foothill conifer steppe reached 2%, predicted use was maximized. Proportion of inter-mountain basins montane sagebrush steppe ($\beta = 0.16 \pm 0.06$), and the proportion of trees with a height of 16–20 m ($\beta = 0.32 \pm 0.08$) had positive nonlinear relationships with relative use by dusky grouse (Table 3, Figure 1). Slope had a positive linear relationship with relative probability of use ($\beta = 1.03 \pm$ SE 0.26; Figure 1). Distance to road ($\beta = -0.31 \pm 0.14$) and proportion of trees with a height of 1–5m ($\beta = -0.63 \pm 0.24$) had a negative nonlinear relationship with relative use by dusky grouse (Table 3, Figure 1). Conditional and marginal R^2 for this model were 0.69 and 0.66, respectively, indicating that most of the variation in the response data from our model is described by the fixed effects, with only an additional 3% associated with our points being clustered along survey routes.

Using the random forest model, we examined the variables of importance and the top 10 in decreasing order from most important to least important were: proportion of trees with a height of 16–20 m, average slope, average elevation, proportion of Douglas fir forest and woodland, proportion of trees with a height of 21–25 m, proportion of montane-foothill deciduous shrubland, proportion of montane mixed conifer forest, proportion of area with 30–39% shrub canopy cover, proportion of trees with a height of 1–5 m, and proportion of area with big sagebrush steppe (Figure 2). Partial dependency plots for the variables of importance indicated nonlinear relationships. Trees with a height of 16–20m, average slope, average elevation (km), proportion of Douglas fir forest and woodland, proportion of trees with a height of 21–25m, proportion of montane-foothill deciduous shrubland, proportion of montane mixed conifer forest, canopy shrub cover of 30–39%, and proportion of big sagebrush steppe all had positive nonlinear relationships, while proportion of trees with a height of 1–5m and proportion of 30–39% canopy herb cover have negative nonlinear relationships (Figure 3).

The average AUC values for both the RSF model and RF model were 0.89 (95% CI: 0.85-0.93) and 0.87 (95% CI: 0.83-0.92), respectively, indicated high predictive accuracy (Figure 4). When we evaluated the RSF model with the independent datasets using quantile bins, the model correctly classified 150/193 (78%) of the independently detected grouse locations into the

medium-high and high categories of relative probability of use. Linear regression produced an intercept close to zero (95% CI: -0.40, 0.18), a slope of 1.54 (95% CI: 0.45, 2.65), and a high R^2 value (0.87), indicating high predictive accuracy (Figure 5). The RF model predicted the independent observations of grouse locations with high accuracy; regression produced an intercept close to zero (95% CI: -0.30, 0.23), a slope of 1.17 (95% CI: 0.30, 2.06), and a R^2 value of 0.86 (Figure 5). Because both models had similarly high predictive accuracy, we used the 60% quantile bin as a threshold to convert each map into a binary (habitat, non-habitat) map and added them to obtain ensembled estimates of spatially-explicit habitat suitability for dusky grouse in Montana using a frequency histogram approach. Ensemble predictions also had high predictive accuracy, classifying 97% of the locations correctly (Table 4).

The RSF had more conservative estimates, while the RF model predicted higher amounts of habitat in Regions 1, 2, 4, and 5. In Region 3, the RSF predicted higher amounts of habitat. Despite these differences, across both models, MFWP regions 1, 2, & 3 had the highest amounts of potential dusky grouse habitat (Table 5, Figure 6). Overall, there was high consensus (93%) between the RSF and RF model on whether an area was considered habitat or non-habitat. Using our ensembled map we predict 109,125 km^2 in Montana to be dusky grouse habitat (Table 5) with the majority of the habitat occurring in MFWP regions 1-5 (Figure 6). Of the predicted habitat for the ensembled map, 76% was predicted to have high relative probability of use (representing areas where both models agreed it was habitat) and 24% was predicted to have medium-high relative probability of use (areas where the models disagreed on whether it was habitat; Table 5, Figure 6).

Objective 2: Develop and evaluate unbiased survey methods that provide statewide and regional estimates of dusky grouse densities and annual trend monitoring in Montana

Evaluation of field survey protocols

In 2019 (pilot season), 2020, and 2021 we selected and surveyed transects for grouse. Field biologists and volunteers specifically trained to conduct dusky grouse surveys selected among randomly generated set of potential transects within areas designated as medium-high and high relative probability of use by an initial resource selection function habitat suitability map created in 2018 (McNew et al. 2018). Surveys were conducted from 10 April–21 May in 2019 and 10 April–1 June during 2020 and 2021. In 2019, they also conducted surveys from 17 June–31 July. Using a series of simulations (methods described below) in 2018 and 2019 we developed field protocols determining the number of sites and visits needed for unbiased estimates with the desired level of precision (coefficient of variation, CV, $\leq$ 15%). Simulation results for determining 2019 survey protocols, based off estimates of probability of detection and abundance from Utah, indicated that 100 points surveyed 3 times should be sufficient if analyzed using a single-season N-mixture model. Survey protocols for 2020 and 2021 were determined by a series of simulations with estimates of probability of detection and abundance based on 2019 field data. Through the simulations, we determined that 360 independent points with 4 replicate surveys should, on average, provide unbiased annual estimates of dusky grouse abundance with the desired level of precision using a single-season N-mixture model analysis.

During our pilot season in 2019, surveys only occurred in FWP Region 3 and consisted of off-trail transects with 5 points placed 500-m apart to ensure independence, with the first point located 300-m from a road or trail. Each site was surveyed over 3 mornings within a 2-week

period of closure, with surveys consisting of two four-minute point-counts conducted consecutively, where the first point-count was conducted without playback and the second point-count was conducted with playback (SanDisk 8 GB Clip Jam Mp3 Player, JBL Charge 3 speaker). During the spring, playback consisted of female calls (cantus, whinny, and cackle) to help elicit male responses and in the summer, playback consisted of chick distress calls to help elicit female responses (Stirling and Bendell 1966). Playback recordings consisted of alternating playback of 30 seconds of calling and 30 seconds of silence until the entire four minutes of survey had elapsed. Grouse detections were recorded for all mountain grouse species (dusky grouse, ruffed grouse, and spruce grouse) while walking between points (representing a line transect method) and during each point count. Care was taken to not double count grouse. If a grouse was detected during the line transect and during a point count, it was recorded for each method. The distance to each grouse, vocalization, behavior, and sex (if known) was recorded for each grouse detection. Distance to grouse was measured with a laser rangefinder and placed into four bins: 0–25m, 26–50m, 51–75m, and 76–100m.

In 2020 and 2021, using the results of the simulations based on the 2019 data to inform protocols, we expanded our survey efforts from Region 3 to include Regions 1–5. Surveys consisted of transects located along roads or trails composed of 6 points placed 400-m apart to ensure independence (though the traveled distance along the road/trail may be greater than 400m), with the first point randomly generated within 50–200m from the parking area. Surveys consisted of a total of four four-minute point counts at each point location along the transect, each of which was treated as an independent sample and all grouse observed were recorded during each period. Two of the four independent point counts occurred as the observer traveled from the start to end of the transect, then a 10-minute break occurred, and two additional point counts occurred as observers traveled from end to the beginning of the transect. Each pair of point counts was conducted one right after the other; with ≤ 1 minute between them. This yielded a total of 4 point-counts per point in one morning. In this way, a transect only needed to be visited once, while still achieving 4 replicate surveys at each point. For all point counts, electronic playback of the female call (edited to only include cantus and cackle) was used to increase detection. As before, detections were recorded for both the point counts and while walking the transect. The distance to each observed grouse was measured with a laser rangefinder and recorded into one of 4 bins: 0–25m, 26–50m, 51–75m, 76–100m.

For all surveys in 2019 and the pairs of surveys in 2020 and 2021 we recorded survey conditions for the point counts such as day since the sampling period started, minutes from sunrise, temperature (C), wind speed (km/hr), precipitation, cloud cover, and noise level. Precipitation was classified into four categories: none, rain, snow, and fog. Cloud cover was divided into four categories: 0–15%, 16–50%, 51–80%, and 81–100% of the sky covered. We measured temperature (°C) and wind speed (km/hr) using a hand-held weather meter (Kestrel model 2000, Kestrel Meters, Boothwyn, PA). We used the time of sunrise in Kalispell for Region 1, Missoula for Region 2, Bozeman for Region 3, White Sulphur Springs for Region 4, and Billings for Region 5. After we determined the time of sunrise for each survey day, we subtracted the time of sunrise from the start time for a pair of point-count surveys to determine the minutes since sunrise for each pair of consecutive point-count surveys. Day of the season on which surveys occurred were calculated relative to a start day of 10 April (day 1). Noise level was broken into

four categories: 0 = none, 1 = slight background noise, but no hearing impairment, 2 = moderate background noise and some hearing impairment, 3 = deafening background noise and total hearing impairment.

We addressed four objectives for evaluating sampling designs: 1) we compared spring vs. summer sampling, 2) evaluated the efficacy of playback to increase detection, 3) compared the impacts of route type (off-trail, trail, road) on abundance and detection, and 4) examined the effect of survey conditions on probability of detection in order to identify ideal survey conditions, which would allow us to constrain sampling to periods of high probability of detection. To evaluate the efficacy of spring vs summer sampling for point-count surveys we compared survey effort and the number of detections for the different sampling periods. To evaluate the impact of playback on detection for point-counts, we evaluated single-season N-mixture models using the R package *unmarked*, estimating probability of detection for two models: point-counts without playback and point-counts with playback (Kery and Schaub 2012, Fisk and Chandler 2011, R Core Team 2017). To compare route types for the point-count surveys, we estimated local abundance and probability of detection, again, using single season N-mixture models evaluated using the R package *unmarked* (Fisk and Chandler 2011, R Core Team 2017). To explore the effects of survey conditions on probability of detection using the 2020 and 2021 data, we evaluated single-season N-mixture models, hierarchical distance sampling models, and hierarchical distance sampling with time removal models using the R package *unmarked* estimating the effects of survey conditions on probability of detection for each model type (Fisk and Chandler 2011, R Core 2021).

Impact of playback on probability of detection—We built and evaluated single-season N-mixture and hierarchical distance sampling models using the R package unmarked (Fisk and Chandler 2011, R Core Team 2017) to evaluate whether the use of playback recordings increased detection probability of grouse during both the spring and summer survey periods using the 2019 pilot data. We first evaluated potential overdispersion in our observation data for the N-mixture model by evaluating and comparing constant models with different distributional assumptions: a Poisson distribution, a negative binomial distribution, and a zero-inflated poison distribution. Each set of null models were evaluated using Akaike's Information Criterion (AIC) to assess the most appropriate model for estimating probability of detection (Burnham and Anderson 2002, Kery and Schaub 2012). For the hierarchical distance sampling models we examined two models types: hierarchical distance sampling without temporary emigration and hierarchical distance sampling with temporary emigration. For each model we evaluated a constant model to identify the most appropriate detection function: uniform, half-normal, and hazard-rate.

We then evaluated the effectiveness of playback recordings using two approaches. First, we separately analyzed the data from the point counts without playback and point counts with playback, while specifying constant detection and abundance across survey points. Second, we pooled all point count data to get six repeated visits per transect where three survey visits used playback and three did not. We then evaluated two competing models: one with constant detection and abundance, and one with constant abundance and detection varying by survey type where the two survey types were point counts with electronic playback and point counts without electronic playback.

Identifying ideal survey conditions.—Before fitting a model to explore the relationships between survey conditions and probability of detection, we first examined the possibility of nonlinear relationships between probability of detection and a survey condition. We hypothesized probability of detection could exhibit a nonlinear response to temperature, minutes from sunrise, and day since the sampling period started due to known temporal display behaviors of grouse (Bendell and Elliot 1967, Zwickel and Bendell 2004, Farnsworth 2020). We explored nonlinear responses by using linear equations to represent our hypothesized relationship. We used $[x + x^2]$ to represent the quadratic form. We evaluated support for non-linear relationships using AIC to evaluate univariate models for the two different functional responses for the N-mixture, hierarchical distance sampling, and hierarchical distance sampling with time removal for point count surveys and hierarchical distance sampling for transect surveys. After preliminary screenings of the different potential functional responses, we evaluated the relationship between survey conditions and detection by placing all survey conditions in one model. For the hierarchical distance sampling with time removal model we predicted all survey conditions except noise level to affect availability (the probability that an individual is available to be detected), and predicted noise level to affect detection (probability that an individual is detected given that it is available; Amundson et al 2014).

Analytical methods

Single season N-mixture models— N-mixture models are hierarchical models that use repeated visits to a site within a period of closure to estimate detection probability and local abundance (Kery and Schaub 2012). Local abundance is the estimated average number of grouse occurring within a survey area, which based upon recorded distances to dusky grouse was generally within 100-m of a point. N-mixture models are composed of two linked processes where the variation in local abundance is described with a Poisson distribution (ecological process), and the variation in detection was described by a binomial random process (observation process) as described by Kery and Schaub (2012) and Kery and Royle (2016) where N_i is the true abundance at site i, $(y_{i,j})$ is the observed counts at site i during replicate survey j and p is the probability of detecting a grouse during a survey (Royle 2004):

$$N_i \sim Poisson(\lambda)$$

$$y_{i,j}|N_i \sim Binomial(N_i, p)$$

Other distributions can be specified besides a Poisson distribution such as a negative binomial or a zero-inflated Poisson, which separates sites into suitable sites and non-suitable sites and assumes a Poisson distribution only for suitable sites. Two downsides to N-mixture models is that the spatial domain is undefined and repeated visits are required. N-mixture models have five main assumptions: 1) counts occur within a period of closure, 2) no false positives, 3) detection probability (p_{ij}) is constant for all individuals (N_i) within a site (i) during survey j, 4) individuals are detected independently of other individuals, and 5) the distribution of abundance and detection are adequately described by their chosen parametric form (Kery and Schaub 2012, Kery and Royle 2016).

Hierarchical distance sampling models—There are two types of hierarchical distance sampling models examined: one without temporary emigration (hereafter hierarchical distance sampling) and one with temporary emigration (hereafter hierarchical distance sampling with temporary emigration). We only used the hierarchical distance sampling model that incorporated temporary emigration to evaluate abundance and detection of the pilot (2019) season data because it

requires multiple visits, while the other hierarchical distance sampling model does not (Kery and Royle 2016). Only requiring one visit is one of the benefits of distance sampling that can make it more logistically feasible than other model types such as the N-mixture model which needs repeated visits. For the hierarchical distance sampling model we use a three-part multinomial, binomial, Poisson mixture model as described by Kery and Royle (2016):

$$y_s|n_s \sim Multinomial\ (n_s, \pi_s^c)$$

Where $\pi_k^c = \pi_k/(1-\pi_0)$, the index k here representing the kth element of the vector π_s^c,

$$n_s|N_s \sim Binomial(N_s, 1-\pi_0)$$

$$N_s \sim Poisson\ (\lambda_s)$$

The first part of the model with the multinomial distribution describes the distance class of n_s individuals (Kery and Royle 2016). The second part of the model is used to describe the variation in detection or imperfect detection of N_s individuals that leads to the count data or n_s (Kery and Royle 2016). The third part of the model is similar to the N-mixture model where local abundance (N_s) is estimated as a Poisson random variable with a mean λ (Kery and Royle 2016). The main assumptions of distance sampling are that animals are distributed uniformly in space, probability of detection is a function of distance and at a distance of 0, probability of detection is 1, individuals are detected at their original locations, and that distances are measured without error (Buckland et al. 2011, Kery and Royle 2016).

Hierarchical distance sample with time-removal models—Imperfect detection can be the result of multiple processes that include availability and perceptibility. Availability represents the probability of an individual being present and producing a signal that allows it to be detected (Amundson et al. 2014). Perceptibility is the probability that an observer will detect an individual given that it is available (Amundson et al. 2014). Like hierarchical distance sampling, hierarchical distance sampling with time removal only requires one visit. For the hierarchical distance sampling model with time removal, we use a four part hierarchical model as described by Kery and Royle (2016) and Amundson et al (2014):

$$M_s \sim Poisson\ (\lambda_s)$$

$$N_s \sim Binomial\ (M_s, \phi)$$

$$n_s \sim Binomial(N_s, \bar{p}_s)$$

In the first part of the model, M_s represents the local population size at a sample unit (s) where local population size is again estimated with a Poisson random variable with a mean λ (Kery and Royle 2016). The number of individuals available to be detected (N_s) is the result of a binomial draw with parameters probability of availability (ϕ) and M_s. The probability of availability (ϕ) is related to the per-interval probability of availability (p_a; probability that an individual is available to be detected in any interval, j), where $\phi = 1-(1-p_a)^j$ and, p_a is estimated from the interval an individual was first detected in, using the data. The number of individuals detected at site s, n_s, is the result of a binomial draw based on the number available to be detected (N_s) and the net probability of an individual being detected, $\bar{p}_s$. Last, conditional on n, the distributions for two categorical individual covariates for distance class (*dclass*) and time interval (*tint*) are specified. Cell probabilities for *dclass* depend on the distance based probability of detection model, while cell probabilities for *tint* are dependent on p_a. Assumptions for the hierarchical distance sampling model with time removal are similar to the assumptions for distance sampling and include: 1)

random placement of points with respect to the distribution of individuals, 2) individuals are detected at their original locations, 3) individuals are identified correctly in reference to species and double counting, 4) distances are measured without error, 5) availability and perceptibility are independent, 6) survey occurs within a period of closure, and 7) all individuals within the population are present during the survey so that probability of presence equals 1 (Amundson et al. 2014).

Naïve Models— In our case, the naïve models represented a model that did not take imperfect detection into account. We hypothesize that this model will result in biased estimates of local abundance.

For the naïve models we only used the best model and protocol derived from analyzing the other three methods, N-mixture model, hierarchical distance sampling, and hierarchical distance sampling with time removal, as our protocol for each scenario. For example, the best protocol for the N-mixture model for average abundance, high probability of detection was 80 sites visited 4 times, so for the naïve model we simulated data for 80 sites visited once. For the naive model we described the count data with a Poisson distribution, where N_i was the count at each site, and detection was not taken into account.

$$N_i \sim Poisson(\lambda)$$

Simulations

We conducted several series of simulations to evaluate the efficacy of potential survey protocols for monitoring dusky grouse. The first series of simulations occurred in 2018 and were used to inform protocols for the 2019 field season. The second series of simulations were conducted in 2019 and were used to determine protocols for the 2020 and 2021 field seasons. The last series of simulations evaluated and compared four analytical methods for estimating local abundance under different scenarios to inform protocols and analysis for a monitoring program. Based on discussions with FWP Region 3 personnel, an acceptable monitoring program would produce an unbiased index of annual population in each administrative region. In addition, the annual estimate or index should have a coefficient of variation (CV) of less than 15% in order to be adequately precise for management.

To quantify bias of estimates for each survey protocol scenario, we ran 400-500 iterations of each data simulation and subsequent analysis and calculated the difference between the estimated local abundance ($\widehat{N}_i$) and the true abundance known for the simulated site (N_i). Similarly, we quantified bias in the total estimated population size by calculating the difference between Total $\widehat{N}$ estimated as $\sum \widehat{N}_i$ and the true known total abundance for all sites ($\sum N_i$). We compared the posterior distributions of the mean differences between each estimate and the true values across all 400-500 simulations to evaluate the bias of each estimate. We considered an estimate to be clearly biased if the 95% credible interval (CrI) of the differences did not include 0. In addition, at each of the iterations, we estimated the precision of each estimate by calculating the coefficient of variation ($CV = \frac{estimated\ standard\ error}{mean\ parameter\ estimate}$). We evaluated the posterior distributions of the 400-500 derived CV estimates to determine whether survey protocols yielded acceptable levels of precision for average local abundance and total population size. We estimated probability that the average coefficient of variation would meet the manager-determined threshold of 15% by calculating the proportion of the total posterior distribution density greater than 0.15.

Simulations to inform 2019 survey protocols.—Our simulation approach was to use the same model to build and analyze simulated observational data sets representing varying scenarios of survey effort. We simulated sixteen data sets and analyses of dusky grouse abundance across various survey protocols, including 2–3 replicated surveys within a period of population closure at 50, 100, 200, and 500 independent survey sites. Each simulation was parameterized with a unique combination of number of survey sites and number of replicate surveys (2 or 3), under two specifications of mean local abundance per site ($\lambda = 0.625$ grouse per survey site and 1.25 grouse per survey site). Preliminary work in northeastern Utah has indicated that average dusky grouse abundance in good to excellent habitat in Utah ranges from 0.625 to 1.25 grouse per survey site (Dahlgren et al. 2018). All simulations assumed that detection probability of dusky grouse during a survey was similar across sites and averaged 0.5 (D. Dahlgren, Utah State University, personal communication). Stochasticity in local abundance was included by sampling abundance from a Poisson distribution; site specific abundance N_i was determined by $N_i \sim Poisson(0.625)$ and $N_i \sim Poisson(1.25)$ for scenarios designed to represent medium and high grouse densities. Observations of grouse at each site *i* during survey *j* was simulated by drawing randomly from a binomial distribution $y_{i,j} \sim Binomial(\widehat{N}_i, p)$ where the probability of detecting a grouse (p) = 0.5.

We used WinBUGS to analyze our sixteen simulated datasets using the single-season N-mixture models in a Bayesian framework (Lunn et al. 2000) and used vague priors for all hyper-parameters that provided little or no information about the estimated parameters (see S1 for a general description of the simulations and model in the BUGS language). We estimated the total number of individuals across all sites by summing the estimated number of individuals at each survey site. We ran three chains of length 40,000 after a burn-in period of 10,000 and thinned the posterior chains by 100 to ensure independence. We assessed convergence using the Gelman-Rubin ($\hat{R}$) statistic, which examines the variance ratio of the Markov chain Monte Carlo (MCMC) algorithm within and between chains across iterations (Gelman and Rubin 1992). We accepted parameter estimates when they came from Markov chains with $\hat{R}$ between 1.0 and 1.01. All simulations and analyses were conducted in R computing software (R Core Team 2017).

Simulations to inform 2020 and 2021 protocols.—Survey results from the pilot season in 2019 were analyzed using two different statistical methods that accounted for imperfect detection (probability of detection < 1): N-mixture models and distance sampling (Kery and Schaub 2012, Buckland et al. 2001). We built and evaluated single-season N-mixture models and hierarchical distance sampling models with and without incorporating temporary emigration to estimate local abundance and detection (Fish and Chandler 2011, R Core Team 2017).

For the N-mixture models we evaluated potential overdispersion in our observation data by evaluating and comparing constant models with different distributions: a Poisson distribution, a negative binomial distribution, and a zero-inflated poison distribution. We evaluated the null models using Akaike's Information Criterion (AIC) to determine the model with the most support, which we then used for estimating local abundance and probability of detection (Burnham and Anderson 2002, Kery and Schaub 2012). We estimated local abundance and probability of detection for point counts with playback and point counts without playback for both spring and summer surveys separately specifying constant detection and abundance. We also pooled all six repeated visits per transect and compared models varying by survey type (with and without playback) and estimated local abundance.

We built and evaluated distance sampling models to estimate grouse densities per km^2 and local abundance. We used two different types of hierarchical distance sampling models to analyze survey point-count and transect-level survey data, one that incorporated temporary emigration (hierarchical distance sampling with temporary emigration) and one that did not (hierarchical distance sampling; Buckland et al. 2011, Kery and Royle 2016). For the purpose of estimating density and local abundance from the pilot study for the hierarchical distance sampling model, we treated each visit to a transect as an independent transect in order to have a larger sample size; 3 visits to one transect = 3 independent transects. We evaluated this approach using the *distsamp* function within the R package *unmarked* (Fisk and Chandler 2011, Kery and Royle 2016, R Core Team 2017). For the second type of hierarchical distance sampling, repeat visits to a site allowed us to evaluate temporary emigration or availability of an individual to be detected (Kery and Royle 2016). We fit these models using the *gdistamp* function in the R package *unmarked* (Fisk and Chandler 2011, Kery and Royle 2016, R Core Team 2017). For both types of distance sampling, we evaluated constant models (i.e., models that constrain density and detection probability to be constant across survey sites).

Similar to the N-mixture models, we again analyzed the data based on survey method: point counts with electronic playback, point counts without electronic playback, and line transects. We also pooled the point count surveys from the two survey types (with and without electronic playback). For the line transects, we determined the length of transect by the GPS tracks collected during the summer surveys. Spring transect length was determined by either the average length of its summer survey route, or if the transect was not completed in both spring and summer, then the average of all transect lengths was used. We evaluated each constant model with three different realistic detection functions: the half-normal, hazard-rate, and uniform (Buckland et al. 2001). Each model set was evaluated using AIC to assess the best model for estimating density or local abundance (Burnham and Anderson 2002).

The models with the most support from each model set from the spring pilot season data were then used to estimate detection and local abundance. We assessed a low and high estimate for abundance, and an estimate for abundance when point count surveys were conducted with electronic playback. The purpose of this was to evaluate the efficacy of our current survey methods given a low estimate of abundance, a high estimate of abundance, and an estimate using the most effective survey method for point counts. We then used combinations of these estimates in a series of simulations to evaluate the efficacy of the pilot season survey protocols analyzed using N-mixture models, and then given the inadequacy of the pilot season protocols for the desired level of precision, to evaluate the efficacy of other potential survey protocols.

Initial simulation sets examined estimates for abundance and detection based upon the 2019 survey protocol: 3 replicated visits at 100 independent survey sites located off trail. We simulated data using a "best case" scenario using an estimate of detection probability, 0.28 ± 0.10 SE, produced from the N-mixture model for spring point-counts conducted with the use of electronic playback, and our high estimate 0.48 ± 0.20 for abundance. After examining the results of simulations using the 2019 survey protocol, we then evaluated whether estimator precision could be increased by 1) increasing the number of replicate survey visits per point, and 2) increasing numbers of independent survey points.

We evaluated simulated model sets based on varying number of visits and varying number of independent points. For our first set of simulations, we evaluated simulated datasets based on 100 independent survey points per region with increasing numbers of replicate visits under the

"best case" scenario for estimates of detection and abundance. Next, we varied the number of visits between 3–9, and the number of survey points from 100–360. For these simulations, abundance and detection were based on empirical estimates from the 2019 spring survey effort achieved using the estimates from the electronic playback survey methodology; an estimate of detection probability of 0.28 ± 0.10 SE, and an estimate of abundance of 0.36 ± 0.13.

Our simulation approach was like that described for the 2018 simulations. The main difference was that these simulations and analyses were conducted in R using the function jags from the *jagsUI* package (Kellner 2019, R Core Team 2017). We used vague priors that provided little information about the estimated parameters. We used a standard vague prior (0.005, 0.005) for lambda, and a uniform distribution with a minimum of 0 and a maximum of 10 for p (Kery and Schaub 2012). We ran three chains of length 40,000 after a burn-in period of 10,000 and thinned the posterior chains by 100 to ensure independence. We assessed convergence using the Gelman-Rubin ($\hat{R}$) statistic and accepted parameter estimates when they came from Markov chains with $\hat{R}$ between 1.0 and 1.1 (Gelman and Rubin 1992, R Core Team 2017).

Simulations for comparing different protocols and analytical methods.—Using empirical data from 2020 and 2021 surveys, we evaluated single-season N-mixture models (Kery and Schaub 2012) and hierarchical distance sampling models (Kery and Royle 2016) to obtain baseline estimates of local abundance and detection within MFWP regions 1–5 for informing different scenarios for our simulations. For the N-mixture models we used a Poisson distribution like before and examined c-hat from a goodness of fitness test to evaluate for overdispersion. For hierarchical distance sampling, we used the first visit to each site, and then evaluated a constant model with three different detection functions: half-normal, hazard rate, and uniform (Buckland et al. 2001). We used AIC to rank and select the most appropriate detection function for estimating local abundance (Burnham and Anderson 2002). We then compared regional estimates of local abundance for the two statistical estimators; estimated local abundance was similar (see Results) and we used estimated local abundance and detection probability from the N-mixture model to inform our simulation scenarios (e.g., low abundance, average abundance, and high abundance).

Based on discussions that occurred in 2018, an acceptable monitoring program should produce unbiased estimates of regional abundance with a coefficient of variation of less than 15%. To evaluate survey effort required to achieve annual estimates of dusky grouse abundance with a coefficient of variation of less than 15%, from point-count and transect survey protocols, we developed and modeled simulated datasets based on empirical estimates of abundance and detection probabilities from our 2020 and 2021 spring survey effort. We defined average, high, and low abundances based on estimates of state-wide abundance, the region with the lowest estimated abundance, and the region with the highest estimated abundance. We defined average probability of detection as the average state-wide constant detection and high probability of detection as the probability of detection under ideal survey conditions. We developed and modeled simulated datasets based on six scenarios:

1. average abundance with average detection,
2. high abundance with average detection,
3. low abundance with average detection,
4. average abundance with high detection,
5. high abundance with high detection, and
6. low abundance with high detection.

We analyzed our simulated data sets using N-mixture models, hierarchical distance sampling, hierarchical distance sampling with time removal models, and naïve models with constant detection and abundance. For our N-mixture models we varied the number of visits to a site, evaluating survey protocols with 2, 3, or 4 visits. For the N-mixture models, hierarchical distance sampling and hierarchical distance sampling with time removal we evaluated whether estimator precision could be increased by increasing the number of independent survey sites. For our simulated survey protocols for point counts, we increased the number of sites visited each time by 100 until we achieved unbiased and relatively precise (<15% CV, 90% of the time) estimates of population abundance. Once we identified the required number of sites for the desired level of precision, we then decreased the number of sites by 20, evaluating the different protocols until we no longer had the desired level of precision, after which we increased the number of sites by 10 to evaluate the midpoint between the thresholds to determine a more precise requisite number of sites. For line transects we started with 100 sites, and then as 100 sites was more than sufficient for reaching our desired level of precision, we decreased the number of sites from 100 by 20 until the coefficient of variation was not < 15%, 90% of the time. At that point we then increased the number of sites by 10 and then decreased by 5 in order to further narrow down the number of sites that need to be visited. We evaluated naïve models using the protocols identified to be most effective and logistically feasible. We conducted analyses of our simulated datasets using the Bayesian framework. All simulations were conducted in R using the function *jags* from the *jagsUI* package (Kellner 2019, R Core Team 2021). We assessed convergence using the Gelman-Rubin ($\hat{R}$) statistic and accepted parameter estimates when they came from Markov chains with $\hat{R}$ between 1.0 and 1.1 (Gelman and Rubin 1992, R Core Team 2021).

For the N-mixture models (S1), the variation in local abundance was described with a Poisson distribution, and the variation in detection was described by a binomial random process (Kery and Schaub 2012). In addition, to evaluate whether visits could occur on the same day, we tested the effects of correlation on the probability of detection and local abundance (S2), with the correlation matrix estimated from the 2020 and 2021 point count data. For the simulations, we used vague priors that provided little information about the estimated parameters. We used a standard vague prior (gamma 0.005, 0.005) for lambda, and a uniform distribution with a minimum of 0 and a maximum of 1 for p (Kery and Schaub 2012, Kery and Royle 2016). For the non-correlated simulations, we ran three chains of length 5,000 after a burn-in period of 1,000 and thinned the posterior chains by 1. For the correlated simulations, we ran three chains of 30,000 after a burn-in period of 100 and thinned the posterior chains by 1.

For the hierarchical distance sampling models, we used a three-part multinomial, binomial, Poisson mixture model as described by Kery and Royle (2016). We evaluated hierarchical distance sampling models for both point counts (Appendix 3) and line transect surveys (Appendix 4). For the line transect surveys we conducted simulations for transect lengths of 2,681m (the average transect length) and 5,000m transects. For both the line transect and point count simulations we used a uniform prior with a minimum of 0 and a maximum of 100 for sigma and a standard vague prior (gamma 0.001, 0.001) for lambda (Kery and Royle 2016). We ran three chains of length 5,000 after a burn-in period of 1,000 and thinned the posterior chains by 1.

For the hierarchical distance sampling model with time removal (S5), we use a four part hierarchical model as described by Kery and Royle (2016) and Amundson et al (2014). Because of the time it took to run these simulations and the logistically unfeasible number of point counts

needed (> 6,000) for the high abundance, average detection scenario, we chose to only simulate and evaluate data under two scenarios: high abundance and average detection, and high abundance, high detection. Given previous patterns, the scenarios with high abundance often required the lower amounts of survey effort, and we believed that this pattern would hold true for this analysis as well. If the needed number of point counts for achieving relative precise estimates of population size was already logistically unfeasible with the high abundance scenarios, then logically, we assumed that scenarios with average or low abundance would require even higher and more logistically unfeasible number of point counts, making hierarchical distance sampling with time removal unlikely to be recommended for the creation of a population monitoring program. For the simulations we used a standard vague prior (gamma 0.001, 0.001) for lambda, a uniform prior with a minimum of 0 and a maximum of 100 for sigma, and a uniform distribution with a minimum of 0 and a maximum of 1 for p_a, which is the probability of an individual being detected during any time interval (Kery and Schaub 2012, Amundson et al. 2014, Kery and Royle 2016). We ran three chains of length 20,000 after a burn-in period of 1,000 and thinned the posterior chains by 1.

We evaluated naïve models (S6) for point counts using only 1 visit and basing the number of sites visited on the 'best' survey protocol out of the other three model types. For the simulations, we used a vague prior for lambda (gamma 0.005, 0.005). We ran three chains of length 3,000 after a burn-in period of 100 and thinned the posterior chains by 1.

We quantified bias and coefficient of variation the same way we did before, except this time we ran 500 iterations of each data simulation and subsequent analysis from those iterations. We calculated the difference between the estimated local abundance ($\widehat{N}_i$) and the true abundance known for the simulated site (N_i). Similarly, we quantified bias in the total estimated population size by calculating the difference between Total $\widehat{N}$ estimated as $\sum \widehat{N}_i$ and the true known total abundance for all sites ($\sum N_i$). We quantified bias in detection probability using N-mixture models by calculating the difference between the estimated probability of detection and the true probability of detection defined for each simulation. For the hierarchical distance sampling models, we quantified bias in sigma by calculating the difference between the estimated sigma and the true sigma defined for each simulation. For the hierarchical distance sampling with time removal, we quantified bias for availability by calculating the difference between the estimated availability parameter, *PHImean* (mean availability across sites), and the true availability defined for each simulation. We compared the posterior distributions of the mean differences between each estimate and the true values across all 500 simulations to evaluate the bias of each estimate. We considered an estimate to be clearly biased if the 95% credible interval (CrI) of the differences (truth-estimates) did not include 0. In addition, at each of the 500 iterations, we estimated the precision of the total estimated population size estimate by calculating the coefficient of variation ($\mathrm{CV} = \frac{\text{estimated standard error}}{\text{mean parameter estimate}}$). We evaluated the posterior distributions of the 500 derived CV estimates to determine whether survey protocols yielded acceptable levels of precision for average local abundance and total population size. We estimated probability that the average coefficient of variation would meet the manager-determined threshold of 15% by calculating the proportion of the total posterior distribution density greater than 0.15, with a goal of meeting that threshold ≥ 90% of the time.

Results

Evaluation of field survey protocols.—We surveyed 90 and 110 sites in the spring and summer of the pilot season in 2019, respectively. Most (98%) sites during each sampling period were surveyed three times. Survey effort during the spring sampling period was concentrated at the end of the sampling period when accessibility was highest versus in the summer when sampling was more evenly spread out across the sampling period (Figure 7). In total (including point count and transect data), we had 108 and 36 total dusky grouse detections during the spring and summer sampling periods, respectively (Table 6). Estimates of local abundance for both the N-mixture and distance sampling models had much lower precision for summer surveys than spring surveys suggesting low utility of summer point-count surveys (Tables 8, 9).

For point counts for both spring and summer data for 2019 for the N-mixture models, models with Poisson distributions were most supported, indicating no overdispersion (Tables 10, 11). Estimated probability of detection was greater when electronic playback during the spring was used (0.28; 95% CI: 0.13, 0.50) versus when not used (0.09; 95% CI: 0.01, 0.48; Figure 8). During the summer when the point count data was pooled for surveys with and without playback calls, a constant model for detection was supported, suggesting that the use of electronic playback during the summer surveys did not improve the probability of detecting dusky grouse (Table 11). Similar results were found for both hierarchical distance sampling methods where playback had an effect during the spring and did not have an effect during summer surveys (Tables 12, 13, 14, 15). For both hierarchical distance sampling methods a half-normal detection function was most supported (Tables 12, 13, 14, 15).

Over 2020 and 2021 we conducted 3,292 sets of points counts (each set varying between 1-4 repeat visits) across 2,372 sites with some sites surveyed in both 2020 and 2021 for a total 12,492 point counts. We used point count sets with complete data (4 visits, complete covariates) for the N-mixture models resulting 3,123 point count sets across 2,286 sites. For the hierarchical distance sampling models we also used complete datasets, which is this case referred to complete covariates for visit 1 and distance data, resulting in 3,234 point counts across 2,349 sites. For the line transects we walked 551 transects, surveying each transect twice. We again only used transects that we had complete information for, which in this case was transect length, and totaled 514 transects.

We used N-mixture models to estimate probability of detection and local abundance for different route types. Spring 2019 data was used to estimate off-trail abundance and 2020 and 2021 were used to estimate trail and road local abundance and detection. Local abundance was higher off-trail than on trails or roads, with abundances for 2020 and 2021 not significantly different from each other (Table 16, Figure 9). Detection was not significantly different most likely due a small sample size for off-trail point-counts across off-trail, road, and trail transects, though there was a slight trend where detection was higher on roads and trails versus off-trail transects (Table 17, Figure 10).

Identifying ideal survey conditions.—For N-mixture models, we found model support was highest for a quadratic relationship between probability of detection and day of the survey season and minutes from sunrise, but not for temperature (Table 18). We found support for the effects of noise level, minutes from sunrise, day since sampling period started, and cloud cover on the probability of detection of dusky grouse, as well as slight potential impacts from wind, temperature, and precipitation (Figure 11). Detection was highest on clear days and lowest when it was raining (Table 19, Figure 11, 12). Higher detection of dusky grouse was slightly positively associated with temperature ($\beta = 0.12$, 95% CI: -0.02, 0.25) and slightly negatively associated

with wind speed (β = -0.07, 95% CI: -0.18, 0.04). Probability of detecting a dusky grouse had a nonlinear quadratic relationship with both minutes since sunrise (β = 0.41, 95% CI: 0.02, 0.81, β = -0.73, 95% CI: -1.14, -0.31) and day since the sampling period started (β = 1.29, 95% CI: 0.56, 2.02, β = -1.25, 95% CI: -1.97, -0.54; Table 19). Probability of detection was highest at 86 minutes post-sunrise and on day 34 (May 13th) during the sampling period (Figure 13).

The relationships between survey conditions and detection (sigma and availability) were similar for the hierarchical distance sampling model for point counts and the hierarchical distance sampling model with time removal. Unlike the N-mixture models, while evaluating the effects of survey conditions on sigma we only found strong support for day since sampling period started to have a nonlinear quadratic relationship with sigma for both models (Tables 20, 21). Both minutes from sunrise and temperature had similar support for quadratic and linear relationships, and we choose to use the relationship from the most parsimonious model (Tables 20, 21). The change in response for minutes from sunrise from that found when evaluating the N-mixture models could be an impact of only using the first visit out of four in the hierarchical distance sampling models, and that the first visit generally occurred earlier in the day than the later visits also incorporated into the N-mixture model. For hierarchical distance sampling, we found support for the effects of cloud cover, noise level, and day since sampling period started on sigma (Figure 14). We found that for hierarchical distance sampling higher sigma was associated with days with less cloud cover, and a quadratic relationship with days since the sampling period started (β = 0.57, 95% CI: 0.20, 0.95, β = -0.62, 95% CI: -0.99, -0.24; Table 22, Figure 14). For hierarchical distance sampling with time removal, availability was most strongly associated with a quadratic relationship with days since the sampling period started (β = 2.62, 95% CI: 1.18, 4.07, β = -2.65, 95% CI: -4.05, -1.26) and sigma was associated with decreased noise level (Table 23, Figures 15, 16). We did not record transect-level survey conditions and so we did not evaluate the impact of survey conditions with the exception of day during the sampling period for hierarchical distance sampling for line transects. We found that similar to the other hierarchical distance sampling models, we found support for day since sampling period started to have a nonlinear quadratic relationship with sigma (β = 1.04, 95% CI: 0.47, 1.61, β = -1.13, 95% CI: -1.71, -0.56; Table 25). For the hierarchical distance sampling model for point counts, sigma was highest on day 31 (May 10th), for hierarchical distance sampling for line transects, sigma was highest on day 30 (May 9th), and for hierarchical distance sampling with time removal, availability was highest on day 33 (May 12th; Figure 13).

Simulations

Simulations to inform 2019 survey protocols.—Results of our simulations revealed that 3 replicate surveys at each of 100 independent survey sites yielded unbiased and relatively precise (≤15% CV) indices of regional population abundance when site-specific abundance was at least 0.625 grouse (Table 26). For example, the mean difference between true and estimated local abundance was 0.02 (95% CrI: -0.13 – 0.19) when 100 independent sites were each surveyed 3 times and the average local abundance was 0.625 grouse. The N-mixture model yielded unbiased estimates of total abundance for all other scenarios as well (Table 26). Precision associated with estimates of local abundance and total population size (summed site-specific estimated abundance;$\sum \widehat{N}_i$) increased with the number of sites surveyed as well as the number of replicate visits per site (Table 26). For example, the CV from 400 simulation runs averaged 0.09 (95% CrI: 0.6–0.14) when 100 sites were each surveyed 3 times (when λ = 1.25, p = 0.5); the probability that the CV ≥ 0.15 was 0.02. When average local abundance was half as high (λ =

0.625), the average CV of the total population size estimate was 0.13 (95% CrI: 0.07–0.16) and the probability that CV ≥ 0.15 was 0.09 under the same survey protocols (100 sites, 3 visits). As expected, reducing the number of replicate survey visits per site from 3 to 2 reduced precision. An average CV ≤ 0.15 was only achieved when the number of survey sites was increased from 100 to 500 (Table 26). From this we concluded that for our pilot season, a survey design where 100 sites were each surveyed 3 times during a period of population closure was the most efficient protocol for meeting management objectives relative to annual monitoring region-specific dusky grouse populations.

Simulations to inform 2020 and 2021 protocols.—For the N-mixture models, we found little evidence that observation data from point-count surveys were overdispersed (Table 10) and used Poisson distributions for all subsequent N-mixture models based on point counts. However, we did find support for the use of negative binominal distributions when using counts pooled across transects, suggesting potential overdispersion at the transect level (Table 10). We estimated local abundance during the spring season while holding the estimated probability of detection constant. For spring point counts where electronic playback was used, estimated mean local abundance was 0.36 (95% CI: 0.18–0.73) grouse (Table 8). Estimates from summer point counts had low precision as a result of a few grouse observations.

For the hierarchical distance sampling models (with and without temporary emigration) we found the half-normal detection to be most supported (Tables 12, 13). We then used the top models to estimate the number of dusky grouse per km^2 and the local abundance of dusky grouse in the area surveyed (~ 0.03 km^2 ; Table 8). For the spring, using hierarchical distance sampling methods that did not incorporate temporary emigration, estimates of local abundance from point count data varied from 0.13 (95% CI: 0.05–0.31) when electronic playback was not used to 0.20 (95% CI: 0.10–0.38) when electronic playback was used to 0.22 (95% CI: 0.09, 0.56) when all point count data was pooled (Table 8). Using hierarchical distance sampling methods where temporary emigration was incorporated, estimates of local abundance from point count data varied from 0.40 (95% CI: 0.18, 0.86) for point counts conducted with electronic playback to 0.48 (95% CI: 0.21, 1.07) when all point count data was pooled (Table 8). Estimates from point counts where electronic playback was not used had low precision (Table 8).

We used empirical estimates for detection and abundance from the spring 2019 survey data to evaluate the efficacy of a variety of survey protocols. For the all simulations, we used an estimate of detection probability, 0.28 (95% CI: 0.13, 0.50), produced from the N-mixture model for point counts conducted with the use of electronic playback. For the first set of simulations for our estimates of abundance we used a low estimate of 0.17 (95% CI: 0.06, 0.48) and a high estimate of 0.48 (95% CI: 0.21, 1.07) from when the point count data was pooled, and an estimate of 0.36 (95% CI: 0.18, 0.73) which was from the N-mixture model where point counts were conducted with electronic playback. Results from the simulations evaluating the efficacy of 2019's survey effort yielded relatively imprecise estimates where the probability that >15 % CV was around 1 (Table 27). Using the high abundance estimate we then evaluated many sites would need to be visited if we kept the number of visits at 3 and how many visits would be needed if we kept the number of sites at 100. Our simulations indicated that replicate surveys at each of 500 independent sites would yield unbiased and relatively precise (<15% CV) indices of regional population abundance if site specific abundance is closer to our high estimate of 0.48 birds per survey point (Table 27). If only 100 independent sites are surveyed, a minimum of 8 replicate

visits would be needed to yield unbiased and relatively precise (< 15%) indices of regional population abundance (Table 27).

For our second set of simulations we used an estimate of detection, 0.28 (95% CI: 0.13, 0.50), and an estimate of abundance, 0.36 (95% CI: 0.18, 0.73), produced from the N-mixture model for point counts conducted with electronic playback. We varied the number of independent sites from 100 to 360, and the number of replicate visits from 3 to 9. The models for many of these potential protocols produced convergence errors for site-level abundance estimates. Protocols that yielded unbiased and relatively precise (<15% CV) indices of regional population abundance while having relatively few convergence errors were 200 independent sites with 6 replicate visits, 300 independent sites with 4 replicate visits, and 360 independent sites with 4 replicate visits (Table 28).

To examine the feasibility of each of these potential protocols that yielded relatively precise results, we calculated how many survey mornings would be needed if we had 5 or 6 points per transect, and 3 or 4 replicates occurring in one morning. We calculated that if we conducted surveys at 200 independent sites with 6 replicate visits, we would need 68–80 mornings to reach our survey goals. If we conducted surveys at 300 independent sites with 4 replicate visits, we would need 50–60 mornings, and if we conducted surveys at 360 independent sites with 4 replicate visits, we would need 60–72 mornings. From this, we recommended a survey protocol of 360 independent sites with 6 survey points per transect and 4 replicate visits for the Spring 2020 and 2021 field seasons for each FWP region with dusky grouse habitat.

Simulations for comparing different protocols and analytical methods.—For the hierarchical distance sampling for point-counts we found that the half-normal detection function best fit our data (Table 29). We evaluated models where detection was constant and local abundance was constant to obtain average state-wide estimates of abundance. For the N-mixture models we used a Poisson distribution as the data did not appear overdispersed (c-hat = 1.4). Average local abundance was 0.18 (95% CI: 0.17, 0.20) dusky grouse for the N-mixture model and for the hierarchical distance models average abundance was 0.20 (95% CI: 0.16, 0.24). To obtain regional local abundance estimates we evaluated models where detection was constant and abundance varied by MFWP administrative region for the hierarchical distance sampling and N-mixture models. Local abundance estimates were similar across the N-mixture and distance sampling models (Figure 17). Estimated abundance estimates were lowest for FWP Region 4, where the N-mixture model estimated a local abundance of 0.08 (95% CI: 0.06, 0.11) and the hierarchical distance sampling model estimated a local abundance of 0.07 (95% CI: 0.04, 0.12; Tables 30, 31). Estimated abundance was greatest in MFWP Region 2, where the N-mixture model estimated a local abundance of 0.31 (95% CI: 0.27, 0.37) and the hierarchical distance sampling model estimated a local abundance of 0.36 (95% CI: 0.27, 0.47; Tables 30, 31). Because the N-mixture models on average produced more precise estimates of local abundance, we chose to use the estimates from the N-mixture models to inform our simulation scenarios; we used a low local abundance of 0.08, an average local abundance of 0.18, and a high local abundance of 0.31 (Table 32).

We evaluated three different detection functions for the transect data, both for visit 1 and for visit 2. For visit 1, both the hazard-rate and half-normal had support and had similar abundance estimates (Table 33, Figure 18). For visit 2, the half-normal was most supported because the hazard-rate model was unable to converge and produced unrealistically high abundance estimates (for average abundance estimated 43 dusky grouse per transect; Table 34). For these

reasons, we chose to use a half-normal detection function to generate our simulated data and to analyze it. To inform our abundance estimates, we extrapolated the estimated abundance per transect from the abundance estimates from the N-mixture models for the point counts. Those estimates were higher than the estimates extrapolated from the line transect data itself.

To examine the probability of detection estimated using N-mixture models under ideal conditions, we held cloud cover at 0-15%, precipitation at none, noise level at 0, wind at 0, temperature at 7.0ºC (the average temperature), and minutes from sunrise at 86 (max detection). We examined how probability of detection varied across days and found that probability of detection was highest at 34 days (0. 57 (95% CI: 0.52, 0.62, Figure 13). We concluded that under ideal conditions, to inform our scenarios, probability of detection was 0.57 (95% CI: 0.52, 0.62) for our simulated data evaluated using N-mixture models (Table 32).

To estimate sigma using hierarchical distance models for point counts under ideal survey conditions, we held cloud cover at 0-15%, precipitation at none, wind speed at 0, noise level at 0, temperature at 7.0ºC (average temp), and at 297 minutes post sunrise (max detection). Like before, we examined how sigma varied across day under ideal survey conditions and found that sigma was highest at 31 days with a sigma of 58 (Figure 13). Therefore, we used $\sigma = 58$ (95% CI: 38.40, 86.39) to inform our simulated scenarios (Table 32).

For the hierarchical distance sampling model for transects, average sigma was estimated to be 42 (Table 32). As we didn't have transect level covariates for weather conditions, for high detection we examined the effects of day since sampling period started on sigma. Sigma was highest on day 30 with a sigma of 51 (95% CI: 41.87, 61.30; Table 32).

For the hierarchical distance sampling with time removal model, average sigma (for a half-normal detection function) was estimated to be 43 and availability was estimated to be 0.65. We examined the effects of day since sampling period started, minutes from sunrise, cloud cover, precipitation, temperature, and wind on probability of availability and the effect of noise level on sigma (the detection function). To estimate sigma and availability under ideal conditions, for availability we held cloud cover at 0-15%, precipitation at none, temperature at 7°C, wind at 0, minutes since sunrise at max (297 minutes), and varied across day, and for sigma we held noise level at 0. We found that availability was highest at 33 days with a probability of availability of 0.89, and sigma was 48, and we therefore used those values in our high detection scenarios (Table 32).

Hierarchical distance sampling with time removal required a logistically unfeasible number of point counts for the high abundance average detection scenario (> 6,000) which suggests low utility for this method (Table S7, Figure 19). Even with high detection, hierarchical distance sampling with time removal still required the most amount of sites visited out of all the methods for that scenario (Figure 20). For example 1,390 sites vs 800 for hierarchical distance sampling or 60 for N-mixture models for the high abundance, high detection scenario (Tables S7, S8, S9).

The survey protocols that allowed us to obtain our desired level of precision (≤15% CV) were unbiased across the hierarchical distance sampling (point count and transect), N-mixture models, and hierarchical distance sampling with time removal models, but not for the naïve models (Figures 21, 22, 23). This highlights the importance of using an unbiased estimator that takes imperfect detection into account to estimate abundance.

For point counts, a general trend existed where protocols for hierarchical distance sampling and hierarchical distance sampling with time removal required the most number of sites visited, while protocols for N-mixture models with four visits required the least (Table 35, Figure 19, Figure 20). Under simulated conditions of high abundance ($\bar{N}$ = 0.31 grouse per survey point) and average detection ($\bar{p}$ = 0.37, σ = 43, availability = 0.65 and σ = 43), 170 survey sites would need to be surveyed 4 times to obtain acceptably precise estimates of population size evaluated using an N-mixture model, 1,090 sites using hierarchical distance sampling or > 6,000 sites for hierarchical distance sampling with time removal (Table 35). This same trend of N-mixture models where sites were visited 4 times requiring less survey effort than the other point count methods holds true over all six scenarios (Figure 19, Figure 20). The least amount of survey effort required to obtain the desired level of precision for population size estimates under average abundance ($\bar{N}$ = 0.18 grouse per survey point) and average detection ($\bar{p}$ = 0.31) is 240 sites visited 4 times for a total of 960 point-counts (Table 35). Under low abundance ($\bar{N}$ = 0.08 grouse per survey point) and average detection ($\bar{p}$ = 0.31) it is 490 sites, visited 4 times for a total of 1,960 point-counts (Table 35). Under periods of high probability of detection, the requisite number of point counts greatly decreased. Under high abundance ($\bar{N}$ = 0.37 grouse per survey point), high detection ($\bar{p}$ = 0.59) it is 60 sites, visited 4 times for 240 total point-counts (Table 35). Under average abundance ($\bar{N}$ = 0.18 grouse per survey point), high detection ($\bar{p}$ = 0.59) it is 80 sites visited 4 times for a total of 320 point-counts, and under low abundance ($\bar{N}$ = 0.08 grouse per survey point), high detection ($\bar{p}$ = 0.59) it is 140 sites visited 4 times for a total of 560 point-counts (Table 35).

If the four visits for each site required by the N-mixture models are able to be completed in one day, it reduces the time and effort for completing the surveys by making it so a site only has to be visited over one morning. When point counts are conducted back-to-back or on the same day, there can be correlation between the counts. To evaluate whether visits could occur on the same day, we tested the effects of correlation on the probability of detection and abundance estimates. We evaluated correlation between the counts for the 2020 and 2021 surveys. On average the back-to-back point counts were 67% correlated, while the other point counts were ~44% correlated (Table 35). We used this correlation matrix to simulate correlated data to evaluate the impacts of bias on the abundance estimates. When the true probability of detection was >57%, the proposed sampling effort and protocol produced unbiased estimates of detection and local abundance (Table 36, Figure 24). However, we found modest upward (high) bias in detection probability (+ 10%) and low bias in local abundance (-0.04 birds per survey area) when detection rates are below 37% (Table 36, Figure 24). In short, conducting 4 replicated surveys on the same survey route in the same day will not result in meaningful bias on estimated abundance if surveys are conducted during periods of high detection.

We simulated data for transects that were 2,681m (the average transect length) and 5,000m. We found that under high abundance, average detection 25 transects needed to be surveyed for 2,681m transects and 15 for 5,000m transects (Tables S10, S11). Under average abundance and average detection 40 transects need to be surveyed for the 2,681m transect and 25 for the 5,000m transect (Tables S10, S11). This pattern where the 5,000m transect requires less transects than the 2,681m holds true across all the scenarios (Figure 25). Under high detection high abundance, the 2,681m transect only requires 20 transects to be visited, while the 5,000m transect requires 15 (Tables S10, S11). Under high detection, average abundance, the 2,681m transect requires 35 transects and the 5,000m transect requires 20 (Tables S10, S11).

Walking a transect and using hierarchical distance sampling requires similar amounts of effort compared to point counts analyzed using N-mixture models with point counts analyzed using N-mixture models requiring fewer transects but more visits (which can occur on the same day) and walking transects requiring 2-3x more transects but only 1 visit. Overall, both types of surveys can occur in a single morning, but the point counts take a longer time than walking a transect. Both methods require feasible amounts of effort if surveys occur during periods of high detection. To increase the probability of detecting dusky grouse we recommend surveying during times of peak breeding activity and under ideal weather conditions. Peak breeding activity occurs approximately May 5–May 25 and from sunrise to approximately 9:30am. Ideal weather conditions are days with little to no wind, little to no cloud cover, no precipitation (including fog), and slighter warmer temperatures, though temperature is less important than cloud cover or wind. We also recommend surveying on transects with limited background noise from either artificial or natural (rivers) sources. Overall we recommend conducting point count surveys using electronic playback to increase detection and analyzing the data using N-mixture models.

Power Analysis

Survey protocols that yielded ≤ 15% CV in annual estimates of abundance did not have power to detect a 1% annual decline in abundance over 10 years but did have power (≥ 80%) to detect a 3% and 5% annual decline (Table 37). Over 5 years, we had power (≥ 80%) to detect a 10% annual decline (Table 37). The average slope was close (within 0.08–1.08) to the target trend for each combination of year and annual decline (Table 38). A negative trend was predicted over 70% of the time for all combinations of 3%, 5%, and 10% annual declines, and after 5 years for a 1% annual decline (Tables 39). On average across the different scenarios the difference between the annual trends estimated using the estimated abundance and the true abundance was small (Table 40).

Objective 3: Develop methods that facilitate rigorous and cost-effective evaluations of grouse-habitat relationships and the effects of management (e.g. timber harvest)

Methods

We conducted a series of statistical simulations to evaluate the efficacy of potential survey protocols to evaluate the associations between dusky grouse abundance and habitat conditions or management actions (e.g. effects of timber harvest or beetle-kill, S12, S13). Simulation scenarios were the same as those in Objective 2 and included: high abundance with average detection, average abundance with average detection, low abundance with average detection, high abundance with high detection, average abundance with high detection, and low abundance with high detection. For each scenario, we tested the top protocol as a result of the previous simulations in objective 2 for the N-mixture models for point counts and the hierarchical distance sampling models for line transects with a length of 2,681m, both of which had protocols that did not require unrealistic levels of survey effort.

The simulated habitat covariate (X) was distributed as a uniform random variable ranging from -1 to 1. The first set of scenarios included a relatively strong effect of the habitat covariate (X) on local abundance ($\lambda = \exp^{(\log(original\ \lambda) - 1 * X)}$) where original λ is the high (0.31), average (0.18), or low (0.08) local abundances estimated using 2020 and 2021 field data. In the second set of scenarios we included a weaker, but still negative effect of the habitat covariate on local abundance ($\lambda = \exp^{(\log(original\ \lambda) - 0.5 * X)}$). Within each set of scenarios, we had average probability of detection (0.37) and high probability of detection (0.57). We evaluated bias and

CV of total population size (as described in Objective 2), as well as bias in the model parameters related to the habitat covariate. We considered a sampling protocol to provide unbiased estimates if the 95% credible interval overlapped 0.

We ran 500 iterations of each data simulation. We used jags and R to analyze the N-mixture and hierarchical distance sampling model in a Bayesian framework. We used vague priors for all parameters that provided little to no information about the estimated parameters. We ran three chains of length 5,000 after a burn-in period of 1,000, and thinned the posterior chains by 1. We assessed convergence using the Gelman-Rubin ($\widehat{R}$) statistic and accepted parameter estimates when they came from Markov chains with $\widehat{R}$ between 1.0 and 1.1.

Results

All scenarios yielded unbiased estimates of total population size and unbiased estimates of effect size of the site covariate (Tables 41, 42, Figure 26). The different sampling protocols also yielded acceptable levels of precision for total population size estimates (CV < 15%; Tables 41, 42)). This indicates that the protocols (number of sites and visits) recommended in objective 2 are sufficient for evaluating the effect of habitat conditions or management actions on the abundance of dusky grouse.

Table 1. Description of variables used to create a forest layer for Montana. Information taken from EVT_descriptions table LANDFIRE 2021). The vegetation lifeform for all variables is Tree.

EVT code (ecological systems)	Existing Vegetation Type (ecological systems name)	Vegetation Physiognomy	Collapsed Vegetation Type Name
7010	Northern Rocky Mountain Western Larch Savanna	Conifer	Western Larch Forest and Woodland
7045	Northern Rocky Mountain Dry-Mesic Montane Mixed Conifer Forest	Conifer	Douglas-fir-Ponderosa Pine-Lodgepole Pine Forest and Woodland
7046	Northern Rocky Mountain Subalpine Woodland and Parkland	Conifer	Subalpine Woodland and Parkland
7047	Northern Rocky Mountain Mesic Montane Mixed Conifer Forest	Conifer	Douglas-fir-Grand Fir-White Fir Forest and Woodland
7049	Rocky Mountain Foothill Limber Pine-Juniper Woodland	Conifer	Limber Pine Woodland
7050	Rocky Mountain Lodgepole Pine Forest	Conifer	Lodgepole Pine Forest and Woodland
7053	Northern Rocky Mountain Ponderosa Pine Woodland and Savanna	Conifer	Ponderosa Pine Forest, Woodland and Savanna
7055	Rocky Mountain Subalpine Dry-Mesic Spruce-Fir Forest and Woodland	Conifer	Spruce-Fir Forest and Woodland
7056	Rocky Mountain Subalpine Mesic-Wet Spruce-Fir Forest and Woodland	Conifer	Spruce-Fir Forest and Woodland
7057	Rocky Mountain Subalpine-Montane Limber-Bristlecone Pine Woodland	Conifer	Limber Pine Woodland
7062	Inter-Mountain Basins Curl-leaf Mountain Mahogany Woodland	Conifer	Mountain Mahogany Woodland and Shrubland
7165	Northern Rocky Mountain Foothill Conifer Wooded Steppe	Conifer	Douglas-fir Forest and Woodland
7166	Middle Rocky Mountain Montane Douglas-fir Forest and Woodland	Conifer	Douglas-fir Forest and Woodland
7167	Rocky Mountain Poor-Site Lodgepole Pine Forest	Conifer	Lodgepole Pine Forest and Woodland
7179	Northwestern Great Plains-Black Hills Ponderosa Pine Woodland and Savanna	Conifer	Ponderosa Pine Forest, Woodland and Savanna
7193	Recently Logged-Tree Cover	Conifer	Transitional Forest Vegetation
7197	Recently Burned-Tree Cover	Conifer	Transitional Forest Vegetation
7200	Recently Disturbed Other-Tree Cover	Conifer	Transitional Forest Vegetation
7061	Inter-Mountain Basins Aspen-Mixed Conifer Forest and Woodland	Conifer-Hardwood	Aspen-Mixed Conifer Forest and Woodland
7009	Northwestern Great Plains Aspen Forest and Parkland	Hardwood	Aspen Forest, Woodland, and Parkland
7011	Rocky Mountain Aspen Forest and Woodland	Hardwood	Aspen Forest, Woodland, and Parkland
7161	Northern Rocky Mountain Conifer Swamp	Riparian	Spruce-Fir Forest and Woodland
9019	Rocky Mountain Lower Montane-Foothill Riparian Woodland	Riparian	Western Riparian Woodland and Shrubland
9022	Rocky Mountain Subalpine-Montane Riparian Woodland	Riparian	Western Riparian Woodland and Shrubland

Table 2. Definitions for variables in final model for predicting dusky grouse occurrence.

Variable	EVT code	Definition	Vegetation Physiognomy	Relationship Form	Direction
Distance to Road	N/A	Average distance to nearest road (km) within a circle with a 250m radii	N/A	linear	Negative
Slope	N/A	Average slope within a circle with a 250m radii	N/A	linear	positive
Distance to stream	N/A	Average distance to nearest stream (km) within a circle with a 250m radii	N/A	nonlinear: quadratic	positive, then negative
Foothill Conifer Wooded Steppe	EVT 7165	Proportion of northern rocky mountain foothill conifer wooded steppe within a circle with a 250m radii	Conifer	nonlinear: quadratic	positive, then negative
Montane Sagebrush Steppe	EVT 7126	Proportion of inter-mountain basins montane sagebrush steppe within a circle with a 250m radii	Shrubland	nonlinear: pseudo-linear threshold	positive
Tree Height 1–5m	N/A	Proportion of trees with a height of 1–5m within a circle with a 250m radii	N/A	nonlinear: pseudo-linear threshold	negative
Tree Height 16–20m	N/A	Proportion of trees with a height of 16–20m within a circle with a 250m radii	N/A	nonlinear: pseudo-linear threshold	positive

Table 3. Slope estimates for all terms in the final habitat model.

Variable	Estimated slope (β_i)	95% Confidence Interval
Distance to Road	-0.31	-0.58– -0.03
Distance to Stream	7.40	3.26–11.53
Distance to Stream^2	-7.49	-12.79– -2.19
Foothill Conifer Wooded Steppe	216.70	152.32–281.03
Foothill Conifer Wooded Steppe^2	-5557.00	-5826.86– -5287.36
ln(Slope + 0.001)	1.03	0.52–1.54
ln(Montane Sagebrush Steppe + 0.001)	0.16	0.05–0.27
ln(Tree Height 1–5m + 0.001)	-0.68	-1.14– -0.22
ln(Tree Height 16–20m + 0.001)	0.32	0.15–0.48

Table 4. Percent of simulated data correctly classified for all of Montana and each MFWP region for the independent dataset. Percent correctly classified is calculated with 95% confidence intervals for the three models: resource selection function model (RSF), random forest model (RF), and the ensemble model.

Area	RSF Model	RF Model	Ensemble Model
Montana	77.7 (95% CI: 74.7, 81.2)	93.8 (95% CI: 92.2, 95.5)	96.9 (95% CI: 96.1, 98.1)
Region 1	96.2 (95% CI: 95.0, 100)	100 (95% CI: 100, 100)	100 (95% CI: 100, 100)
Region 2	85.6 (95% CI: 81.3, 93.8)	100 (95% CI: 100, 100)	100 (95% CI: 100, 100)
Region 3	87.2 (95% CI: 83.8, 91.2)	94.3 (95% CI: 92.6, 97.1)	96.5 (95% CI: 95.6, 98.5)
Region 4	83.6 (95% CI: 77.8, 100)	100 (95% CI: 100, 100)	100 (95% CI: 100, 100)
Region 5	45.9 (95% CI: 37.8, 51.4)	87.3 (95% CI: 83.8, 91.9)	93.7 (95% CI: 91.9, 97.3)

Table 5. Estimated area (km^2) of potential Dusky Grouse habitat for Montana FWP administrative regions for the 3 predictive maps. The RSF and RF models are divided into a binary map of habitat and non-habitat based on the 60% quantile, while the ensemble map is based on an ensemble frequency histogram where consensus between the models on predicted habitat resulted in high relative probability of use and areas of unagreed upon predicted habitat between the RSF and RF models resulted in medium-high relative probability of use, and consensus between the models on predicted non-habitat resulted in non-habitat.

Region	RSF: Non-Habitat	RSF: Habitat	RF: Non-Habitat	RF: Habitat	E: Non-Habitat	E: Med. High	E.: High	E: Total Habitat
Region 1	9489	25045	5402	29133	4714	5463	24357	29821
Region 2	7112	20195	4498	22809	4073	3464	19770	23234
Region 3	22589	27509	22669	27429	19077	7104	23917	31021
Region 4	60602	10725	55435	15892	54751	6535	10041	16576
Region 5	40171	5456	39471	6157	38538	2566	4524	7089
Region 6	71873	581	71590	865	71459	544	451	995
Region 7	78732	351	78944	139	78694	289	100	390
Total	290570	89862	278008	102423	271306	25966	83160	109125

Table 6. Total dusky grouse detections during the 2019 pilot season when playback calls were and were not used. Transect refers to all grouse detections that occurred while walking the transect that did not occur during a point count.

Period Detected	Spring	Summer
Without playback	15	4
With playback	27	4
Transect	66	28
Total Detected	108	36

Table 8. Parameter estimates for local abundance (lambda) and probability of detection (*p*) for spring 2019 pilot season dusky grouse survey data for point counts with and without electronic playback and when point count data was pooled. Poisson distribution is used for all N-mixture models. A half-normal detection was used for the distanced sampling models when the data was not pooled and a hazard-rate detection function when the data was pooled. For models for the pooled data local abundance was held constant and detection varied by survey method (with or without electronic playback).

Model	**Local abundance**	**95 % CI**	***p***	**95 % CI**
Point counts without electronic playback: 3 visits per site				
N-mixture model	0.60	(0.08, 4.29)	0.09	(0.01, 0.48)
Hierarchical distance sampling	0.13	(0.05, 0.31)	-	-
Hierarchical distance sampling with temporary emigration	2.19	(0, 1235)	-	-
Point counts with electronic playback: 3 visits per site				
N-mixture model	0.36	(0.18, 0.73)	0.28	(0.13, 0.50)
Hierarchical distance sampling	0.20	(0.10, 0.38)	-	-
Hierarchical distance sampling with temporary emigration	0.40	(0.18, 0.86)	-	-
Point count data pooled: 6 visits per site				
N-mixture model	0.40	(0.21, 0.77)	-	-
Hierarchical distance sampling	0.22	(0.09, 0.56)	-	-
Hierarchical distance sampling with temporary emigration	0.48	(0.21, 1.07)	-	-

Table 9. Parameter estimates for local abundance (lambda) and probability of detection (*p*) for summer 2019 pilot season dusky grouse survey data for point counts with and without electronic playback and when point count data was pooled. Poisson distribution is used for all N-mixture models. A half-normal detection was used for the distanced sampling models when the data was not pooled and a hazard-rate detection function when the data was pooled. For models for the pooled data local abundance and detection were held constant.

Model	**Local abundance**	**95 % CI**	***p***	**95 % CI**
Point counts without electronic playback: 3 visits per site				
N-mixture model	52.6	(0, 3.00e+28)	0.00	(0, 1)
Hierarchical distance sampling	0.22	(0.06, 1.29)	-	-
Hierarchical distance sampling with temporary emigration	27.6	(0, 3.12e+24)	-	-
Point counts with electronic playback: 3 visits per site				
N-mixture model	55.9	(0, 1.02e+13)	0.00	(0, 1)
Hierarchical distance sampling	0.12	(0.03, 0.51)	-	-
Hierarchical distance sampling with temporary emigration	56.5	(0, 5.89e+10)	-	-
Point count data pooled: 6 visits per site				
N-mixture model	57.9	(0.01, 556,296)	-	-
Hierarchical distance sampling	0.17	(0.06, 0.48)	-	-
Hierarchical distance sampling with temporary emigration	58.6	(0.05, 72,382)	-	-

Table 10. Support for candidate models predicting abundance and probability of detection estimates using N-mixture models for different dusky grouse survey methods for spring 2019 pilot season. Three different abundance distributions are examined: Poisson distribution, negative binomial distribution, and zero-inflated Poisson distribution. ~ 1 ~ 1 indicates that models were fitted with constant probability of detection and local abundance, respectively. The number of parameters (K), AIC_c values, Δ AIC_c values, and model weights (w_i) are reported.

Model	K	AICc	Δ AICc	w_i
Point counts without electronic playback – 3 visits per site				
~ 1 ~ 1; Poisson distribution	2	120.08	0.00	0.47
~ 1 ~ 1; Zero-inflated Poisson distribution	3	121	0.91	0.3
~ 1 ~ 1; Negative binomial distribution	3	121.53	1.45	0.23
Point counts with electronic playback – 3 visits per site				
~ 1 ~ 1; Poisson distribution	2	171.72	0.00	0.47
~ 1 ~ 1; Zero-inflated Poisson distribution	3	172.59	0.87	0.3
~ 1 ~ 1; Negative Binomial distribution	3	173.19	1.47	0.23
Point count data pooled – 6 visits per site				
~ Survey type ~ 1; zero-inflated Poisson distribution	4	290.09	0.00	0.228
~ Survey type ~ 1; Poisson distribution	3	290.11	0.016	0.226
~ 1 ~ 1; zero-inflated Poisson distribution	3	290.65	0.559	0.172
~ 1 ~ 1; Poisson distribution	2	291.05	0.96	0.141
~ Survey type ~ 1; negative binomial distribution	4	291.16	1.066	0.134
~ 1 ~ 1; negative binomial distribution	3	291.75	1.658	0.099
Transect surveys				
~ 1 ~ 1; negative binomial distribution	3	135.5	0.00	1.00
~ 1 ~ 1; zero-inflated Poisson distribution	3	148.24	12.73	0.00
~ 1 ~ 1; Poisson distribution	2	178.95	43.44	0.00

Table 11. Support for candidate models predicting abundance and probability of detection estimates using N-mixture models for different dusky grouse survey methods for summer 2019. Three different abundance distributions are examined: Poisson distribution, negative binomial distribution, and zero-inflated Poisson distribution. ~ 1 ~ 1 indicates that models were fitted with constant probability of detection and local abundance, respectively. The number of parameters, AIC_c values, Δ AIC_c values, and model weights (w_i) are reported.

Model	K	AICc	Δ AICc	w_i
Point counts without electronic playback – 3 visits per site				
~ 1 ~ 1; Poisson distribution	2	47.18	0.00	0.58
~ 1 ~ 1; Zero-inflated Poisson distribution	3	49.18	2.00	0.21
~ 1 ~ 1; Negative binomial distribution	3	49.18	2.00	0.21
Point counts with electronic playback – 3 visits per site				
~ 1 ~ 1; Poisson distribution	2	47.18	0.00	0.58
~ 1 ~ 1; Negative Binomial distribution	3	49.18	2.00	0.21
~ 1 ~ 1; Zero-inflated Poisson distribution	3	49.18	2.00	0.21
Point count data pooled – 6 visits per site				
~ 1 ~ 1; Poisson distribution	2	90.36	0.00	0.42
~ Survey type ~ 1; Poisson distribution	3	92.36	2.00	0.16
~ 1 ~ 1; zero-inflated Poisson distribution	3	92.36	2.00	0.16
~ 1 ~ 1; negative binomial distribution	3	92.37	2.00	0.16
~ Survey type ~ 1; zero-inflated Poisson distribution	4	94.36	4.00	0.06
~ Survey type ~ 1; negative binomial distribution	4	94.37	4.00	0.06
Transect surveys				
~ 1 ~ 1; zero-inflated Poisson distribution	3	117.06	0.00	0.38
~ 1 ~ 1; Poisson distribution	2	117.28	0.22	0.34
~ 1 ~ 1; negative binomial	3	117.6	0.54	0.29

Table 12. Support for candidate models predicting density and abundance estimates using hierarchical distance sampling for different dusky grouse survey methods for spring 2019. Three different detection functions were examined: half-normal, hazard-rate, and uniform. ~ 1 ~ 1 indicates that models were fitted with constant probability of detection and local density, respectively. The number of parameters (K), AIC_c values, Δ AIC_c values, and model weights (w_i) are reported.

Model	K	AICc	Δ AICc	w_i
Point counts without electronic playback				
~ 1 ~ 1; half-normal detection function	2	156.24	0.00	0.54
~ 1 ~ 1; hazard-rate detection function	3	156.81	0.57	0.41
~ 1 ~ 1; uniform detection function	1	160.89	4.65	0.05
Point counts with electronic playback				
~ 1 ~ 1; half-normal detection function	2	247.8	0.00	0.62
~ 1 ~ 1; hazard-rate detection function	3	249.04	1.25	0.33
~ 1 ~ 1; uniform detection function	1	252.67	4.88	0.05
Point count data pooled				
~ Survey type ~ 1; hazard-rate detection function	4	401.88	0.00	0.41
~ Survey type ~ 1; half-normal detection function	3	402.58	0.70	0.29
~ 1 ~ 1; half-normal detection function	2	403.89	2.01	0.15
~ 1 ~ 1; hazard-rate detection function	3	404.04	2.16	0.14
~ 1 ~ 1; uniform detection function	1	413.22	11.34	0.00
~ Survey type ~ 1; uniform detection function	1	415.22	13.34	0.00
Transect surveys				
~ 1 ~ 1; half-normal detection function	3	196.68	0.00	0.72
~ 1 ~ 1; hazard-rate detection function	4	198.58	1.90	0.28
~ 1 ~ 1; uniform detection function	2	239.51	42.83	0.00

Table 13. Support for candidate models predicting density and abundance estimates using hierarchical distance sampling with temporary emigration for different dusky grouse survey methods for spring 2019. Repeat visits are used to estimate the availability of an individual to be surveyed (phi). Model parameters are ~ abundance ~ phi ~ detection, with a constant parameter being represented by a 1. Three different detection functions were examined: half-normal, hazard-rate, and uniform. The number of parameters (K), AIC_c values, Δ AIC_c values, and model weights (w_i) are reported.

Model	K	AICc	Δ AICc	w_i
Point counts without electronic playback				
~ 1 ~ 1 ~ 1; half-normal detection function	3	156.74	0.00	0.768
~ 1 ~ 1 ~ 1; uniform detection function	2	159.39	2.65	0.204
~ 1 ~ 1 ~ 1; hazard-rate detection function	4	163.39	6.65	0.028
Point counts with electronic playback				
~ 1 ~ 1 ~ 1; half-normal detection function	3	239.79	0.00	0.788
~ 1 ~ 1 ~ 1; uniform detection function	2	242.67	2.88	0.187
~ 1 ~ 1 ~ 1; hazard-rate detection function	4	246.67	6.88	0.025
Point count data pooled				
~ 1 ~ 1 ~ Survey type; hazard-rate detection function	4	401.88	0.00	0.41
~ 1 ~ 1 ~ Survey type; half-normal detection function	3	402.58	0.70	0.29
~ 1 ~ 1 ~ 1; half-normal detection function	2	403.89	2.01	0.15
~ 1 ~ 1 ~ 1; hazard-rate detection function	3	404.04	2.16	0.14
~ 1 ~ 1 ~ Survey type; uniform detection function	1	413.22	11.34	0.00
~ 1 ~ 1 ~ 1; uniform detection function	1	415.22	13.34	0.00
Transect surveys				
~ 1 ~ 1 ~ 1; half-normal detection function	3	196.68	0.00	0.72
~ 1 ~ 1 ~ 1; hazard-rate detection function	4	198.58	1.90	0.28
~ 1 ~ 1 ~ 1; uniform detection function	2	239.51	42.83	0.00

Table 14. Support for candidate models predicting density and abundance estimates using hierarchical distance sampling for different dusky grouse survey methods for summer 2019. Three different detection functions were examined: half-normal, hazard-rate, and uniform. ~ 1 ~ 1 indicates that models were fitted with constant probability of detection and local density, respectively. The number of parameters (K), AIC_c values, Δ AIC_c values, and model weights (w_i) are reported.

Model	K	AICc	Δ AICc	w_i
Point counts without electronic playback				
~ 1 ~ 1; half-normal detection function	2	51.71	0.00	0.73
~ 1 ~ 1; hazard-rate detection function	3	53.68	1.97	0.27
~ 1 ~ 1; uniform detection function	1	67.16	15.45	0.00
Point counts with electronic playback				
~ 1 ~ 1; half-normal detection function	2	53.46	0.00	0.53
~ 1 ~ 1; hazard-rate detection function	3	53.68	0.22	0.47
~ 1 ~ 1; uniform detection function	1	62.77	9.31	0.01
Point count data pooled				
~ 1 ~ 1; half-normal detection function	2	102.27	0.00	0.42
~ 1 ~ 1; hazard-rate detection function	3	103.45	1.18	0.23
~ Survey type ~ 1; half-normal detection function	3	103.80	1.53	0.20
~ Survey type ~ 1; hazard-rate detection function	4	104.40	2.13	0.15
~ 1 ~ 1; uniform detection function	1	125.93	23.66	0.00
~ Survey type ~ 1; uniform detection function	1	127.93	25.66	0.00
Transect surveys				
~ 1 ~ 1; hazard-rate detection function	3	132.09	0.00	1.00
~ 1 ~ 1; half-normal detection function	2	143.92	11.83	0.00
~ 1 ~ 1; uniform detection function	1	188.75	56.66	0.00

Table 15. Support for candidate models predicting density and abundance estimates using hierarchical distance sampling for different dusky grouse survey methods for summer 2019. Repeat visits are used to estimate availability of an individual to be surveyed (phi). Model parameters are ~ abundance ~ phi ~ detection, with a constant parameter being represented by a 1. Three different detection functions were examined: half-normal, hazard-rate, and uniform. For point counts with electronic playback and for pooled point count data where survey type affected detection, hazard-rate detection functions could not be fit to the data. The number of parameters (K), AIC_c values, Δ AIC_c values, and model weights (w_i) are reported.

Model	**K**	**AICc**	**Δ AICc**	w_i
Point counts without electronic playback				
~ 1 ~ 1 ~ 1; half-normal detection function	3	53.71	0.00	0.73
~ 1 ~ 1 ~ 1; hazard-rate detection function	4	55.68	1.97	0.27
~ 1 ~ 1 ~ 1; uniform detection function	2	67.17	13.45	0.00
Point counts with electronic playback				
~ 1 ~ 1 ~ 1; half-normal detection function	3	55.46	0.00	0.975
~ 1 ~ 1 ~ 1; uniform detection function	2	62.77	7.31	0.025
Point count data pooled				
~ 1 ~ 1 ~ 1; half-normal detection function	3	104.27	0.00	0.49
~ 1 ~ 1 ~ 1; hazard-rate detection function	4	105.45	1.18	0.27
~ 1 ~ 1 ~ Survey type; half-normal detection function	4	105.8	1.53	0.23
~ 1 ~ 1 ~ 1; uniform detection function	2	125.94	21.66	0.00
~ 1 ~ 1 ~ Survey type; uniform detection function	2	125.94	21.66	0.00
Transect surveys				
~ 1 ~ 1 ~ 1; hazard-rate detection function	4	126.44	0.00	1.00
~ 1 ~ 1 ~ 1; half-normal detection function	3	137.7	11.26	0.00
~ 1 ~ 1 ~ 1; uniform detection function	2	180.53	54.09	0.00

Table 16. Estimates of local abundance with 95% confidence intervals (per 0.03 km^2) for point counts conducted along different transect types: off trail (2019 data, n = 90), on roads (2020-2021 data, n = 1589), and trails (2020-2021 data, n = 1534).

Route Type	Year	Estimate	SE	95% Confidence Interval
Road	2020	0.17	0.02	0.14–0.20
Road	2021	0.14	0.01	0.12–0.17
Trail	2020	0.19	0.16	0.16–0.23
Trail	2021	0.23	0.02	0.20–0.27
Off-trail	2019	0.36	0.13	0.18–0.73

Table 17. Estimates of probability of detection with 95% confidence intervals for point counts conducted along different transect types: off trail (2019 data, n = 90), on roads (2020-2021 data, n = 1589), and trails (2020-2021 data, n = 1534).

Route Type	Year	Estimate	SE	95% Confidence Interval
Road	2020	0.32	0.03	0.27–0.38
Road	2021	0.38	0.03	0.33–0.43
Trail	2020	0.42	0.03	0.37–0.48
Trail	2021	0.36	0.02	0.32–0.41
Off-trail	2019	0.28	0.10	0.13–0.50

Table 18. Model support for candidate models evaluating linear and nonlinear relationships between detection and temperature (temp), day during the survey season (day), and minutes since sunrise (minute) evaluated using single-season N-mixture models.

Model	# Parameters	AIC	Delta AIC	Model Weight
Temp	3	5114.6	0	0.71
$Temp^2$	4	5116.4	1.8	0.29
Day^2	4	5096.6	0.0	0.99
Day	3	5110.1	13.5	<0.01
$Minutes^2$	4	5086.5	0.0	0.98
Minutes	3	5094.6	8.1	0.02

Table 19. Estimates of coefficients for standardized covariates from N-mixture model with constant abundance and a global model for detection that includes cloud cover, precipitation, noise level, temperature, minutes since sunrise, day during the sampling period. Reference level for precipitation (precip) is none, for cloud cover is 0-15%, and for noise level is level 0.

Parameter	Estimate	SE	95% Confidence Interval
Intercept	-0.22	0.09	-0.41– -0.04
Precip: Fog	0.76	0.39	-0.01–1.53
Precip: Rain	-0.10	0.37	-0.82–0.63
Precip: Snow	0.01	0.32	-0.62–0.64
Cloud Cover: 16-50	-0.82	0.19	-1.19– -0.46
Cloud Cover: 51-80	-0.86	0.20	-1.25– -0.47
Cloud Cover: 81-100	-0.53	0.15	-0.83– -0.24
Temperature	0.12	0.07	-0.02–0.25
Wind	-0.07	0.05	-0.18–0.04
Noise Level: 1	-0.38	0.12	-0.61– -0.15
Noise Level: 2	-1.54	0.20	-1.93– -1.15
Noise Level: 3	-3.03	0.63	-4.26– -1.80
Minutes	0.41	0.20	0.02–0.81
$Minutes^2$	-0.73	0.21	-1.14– -0.31
Day	1.29	0.37	0.56–2.02
Day^2	-1.25	0.36	-1.97– -0.54

Table 20. Model support for candidate models evaluating linear and nonlinear relationships between sigma for the half-normal detection function and temperature, day during the survey season, and minute since sunrise evaluated using hierarchical distance sampling models.

Model	# Parameters	AIC	Delta AIC	Model Weight
Temp	3	2221.4	0.0	0.68
$Temp^2$	4	2223.0	1.6	0.32
Day^2	4	2219.5	0.0	0.99
Day	3	2228.8	9.3	0.01
Minutes	3	2228.1	0.0	0.62
$Minutes^2$	4	2229.1	1.0	0.38

Table 21. Model support for candidate models evaluating linear and nonlinear relationships between availability and temperature, day during the survey season, and minute since sunrise evaluated using hierarchical distance sampling with time removal models.

Model	# Parameters	AIC	Delta AIC	Model Weight
Temp	3	2792.75	0.0	0.58
$Temp^2$	4	2793.43	0.68	0.42
Day^2	4	2784.25	0.0	1.00
Day	3	2797.80	13.55	0.00
$Minutes^2$	4	2797.02	0.0	0.56
Minutes	3	2797.50	0.48	0.44

Table 22. Estimates of coefficients for standardized covariates from hierarchical distance sampling model with constant abundance and a global model for detection that includes cloud cover, precipitation, noise level, temperature, minutes since sunrise, day during the sampling period. Reference level for precipitation is none, for cloud cover is 0-15%, and for noise level is level 0.

Parameter	Estimate	SE	95% Confidence Interval
Intercept	3.94	0.08	3.78–4.11
Precip: Fog	-0.23	0.23	-0.67–0.22
Precip: Rain	-0.46	0.21	-0.88– -0.05
Precip: Snow	-0.11	0.22	-0.54–0.33
Cloud Cover: 16-50	-0.48	0.13	-0.73– -0.23
Cloud Cover: 51-80	-0.32	0.12	-0.55– -0.09
Cloud Cover: 81-100	-0.18	0.09	-0.36– 0.005
Temperature	0.08	0.04	-0.002–0.17
Wind	0.02	0.04	-0.05–0.10
Noise Level: 1	-0.11	0.07	-0.25– 0.04
Noise Level: 2	-0.49	0.11	-0.69– -0.28
Noise Level: 3	-6.26	76.10	-155.40–142.89
Minutes	0.00	0.04	-0.08–0.08
Day	0.57	0.19	0.20–0.95
Day^2	-0.62	0.19	-0.99– -0.24

Table 23. Estimates of coefficients for standardized covariates from hierarchical distance sampling with time removal model with constant abundance and a global model for availability that includes cloud cover, precipitation, temperature, minutes since sunrise, day during the sampling period. Reference level for precipitation (precip) is fog, for cloud cover is 0-15%, and for noise level is level 0.

Parameter	Estimate	SE	95% Confidence Interval
Intercept	-3.84	1.19	-6.17– -1.51
Precip: None	2.59	1.25	0.14–5.03
Precip: Rain	1.68	1.33	-0.92–4.29
Precip: Snow	2.19	1.33	-0.41–4.79
Cloud Cover: 16-50	-0.14	0.79	-1.69–1.42
Cloud Cover: 51-80	-0.35	0.71	-1.76–1.05
Cloud Cover: 81-100	-0.31	0.49	-1.26–0.65
Temperature	0.06	0.16	-0.26–0.38
Wind	0.10	0.09	-0.09–0.30
Minutes	0.12	0.14	-0.16–0.40
Day	2.62	0.19	1.18–4.07
Day^2	-2.65	0.71	-4.05– -1.26

Table 24. Estimates of coefficients for standardized covariates from hierarchical distance sampling model with constant abundance and a global model for detection that includes cloud cover, precipitation, noise level, temperature, minutes since sunrise, day during the sampling period.

Parameter	Estimate	SE	95% Confidence Interval
Intercept	3.87	0.07	3.72–4.01
Noise Level: 1	-0.14	0.07	-0.29–0.004
Noise Level: 2	-0.51	0.10	-0.71– -0.31
Noise Level: 3	-1.34	0.53	-2.38– -0.29

Table 25. Model support for candidate models evaluating linear and nonlinear relationships between sigma and day during the survey season using hierarchical distance sampling for line transects.

Model	# Parameters	AIC	Delta AIC	Model Weight
Day^2	4	1201.94	0.0	1.00
Day	3	1214.62	12.68	0.00

Table 26. Mean (95% credible interval) for bias and coefficient of variation from 400 simulation runs for each suite of parameters. R = number of sites, J = number of replicate visits, λ = mean abundance per site, p = mean detection probability, CV = coefficient of variation for total population size (Total N), and N.site = estimated number of dusky grouse per survey site.

Simulation Parameters				Bias in λ	Bias in *p*	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	CV λ	Probability that CV λ > 0.15	Protocol meets Management Requirements
R	J	λ	*p*									
50	3	1.25	0.5	0.08 (-0.28 – 0.51)	-0.01 (-0.14 – 0.11)	4.0 (-8.9 – 21.8)	0.08 (-0.17 – 0.43)	0.16 (0.09 – 0.27)	0.48	0.21 (0.15 – 0.28)	0.98	No
100	3	1.25	0.5	0.05 (-0.21 – 0.36)	-0.01 (-0.09 – 0.08)	4.8 (-14.3 – 25.7)	0.05 (-0.14 – 0.26)	0.09 (0.06 – 0.14)	0.02	0.13 (0.11 – 0.16)	0.12	Yes
200	3	1.25	0.5	0.01 (-0.18 – 0.20)	-0.004 (-0.06 – 0.05)	4.0 (-18.1 – 31.4)	0.02 (-0.09 – 0.15)	0.06 (0.05 – 0.08)	0.00	0.09 (0.08 – 0.10)	0.00	Yes
500	3	1.25	0.5	0.008 (-0.11 – 0.11)	-0.002 (-0.04 – 0.04)	5.0 (-35.2 – 46.3)	0.01 (-0.07 – 0.09)	0.04 (0.03 – 0.05)	0.00	0.055 (0.05 – 0.06)	0.00	Yes
50	2	1.25	0.5	0.35 (-0.30 – 1.87)	-0.02 (-0.22 – 0.13)	17.2 (-12.5 – 90.1)	0.34 (-0.25 – 1.80)	0.39 (0.15 – 0.92)	0.94	0.41 (0.20 – 0.93)	1.00	No
100	2	1.25	0.5	0.11 (-0.26 – 0.59)	-0.01 (-0.14 – 0.10)	12.8 (-18.0 – 57.3)	0.13 (-0.18 – 0.57)	0.19 (0.11 – 0.34)	0.70	0.21 (0.14 – 0.36)	0.92	No
200	2	1.25	0.5	0.06 (-0.19 – 0.31)	-0.01 (-0.09 – 0.08)	12.3 (-31.5 – 61.7)	0.06 (-0.16 – 0.31)	0.11 (0.08 – 0.16)	0.14	0.13 (0.10 – 0.17)	0.23	Yes-ish
500	2	1.25	0.5	0.02 (-0.12 – 0.21)	-0.003 (-0.06 – 0.05)	10.0 (-53.1 – 88.9)	0.02 (-0.11 – 0.18)	0.07 (0.05 – 008)	0.00	0.08 (0.07 – 0.09)	0.00	Yes
50	3	0.625	0.5	0.07 (-0.19 – 0.39)	-0.02 (-0.16 – 0.11)	3.1 (-4.5 – 15.3)	0.06 (-0.09 – 0.31)	0.19 (0.09 – 0.39)	0.59	0.27 (0.20 – 0.42)	1.00	No
100	3	0.625	0.5	0.02 (-0.13 – 0.19)	-0.01 (-0.11 – 0.08)	2.3 (-6.1 – 13.7)	0.02 (-0.06 – 0.14)	0.13 (0.07 – 0.16)	0.09	0.16 (0.14 – 0.21)	0.86	Yes-ish
200	3	0.625	0.5	0.008 (-0.11 – 0.14)	-0.004 (-0.08 – 0.06)	2.3 (-10.4 – 17.8)	0.01 (-0.05 – 0.09)	0.07 (0.05 – 0.09)	0.00	0.11 (0.10 – 0.13)	0.00	Yes
500	3	0.625	0.5	0.008 (-0.08 – 0.10)	-0.003 (-0.07 – 0.06)	5.1 (-29.7 – 48.5)	0.01 (-0.06 – 0.09)	0.08 (0.06 – 0.10)	0.00	0.10 (0.09 – 0.11)	0.00	Yes
50	2	0.625	0.5	0.24 (-0.17 – 1.02)	-0.03 (-0.25 – 0.17)	11.9 (-6.5 – 53.4)	0.24 (-0.13 – 1.06)	0.51 (0.16 – 1.10)	0.96	0.55 (0.25 – 1.12)	1.00	No
100	2	0.625	0.5	0.09 (-0.15 – 0.47)	-0.02 (-0.19 – 0.12)	9.1 (-10.9 – 45.4)	0.09 (-0.11 –0.45)	0.25 (0.11 – 0.47)	0.81	0.29 (0.18 – 0.49)	1.00	No
200	2	0.625	0.5	0.04 (-0.12 – 0.23)	-0.01 (-0.13 – 0.09)	8.2 (-17.9 – 44.3)	0.04 (-0.09 – 0.22)	0.14 (0.09 – 0.23)	0.34	0.17 (0.13 – 0.24)	0.63	No
500	2	0.625	0.5	0.02 (-0.08 – 0.12)	-0.008 (-0.07 – 0.06)	8.5 (-31.5 – 49.1	0.02 (-0.06 – 0.10)	0.08 (006 – 0.10)	0.00	0.10 (0.08 – 0.11)	0.00	Yes

*Table printed as image here to fit the page; a spreadsheet of this table is available in provided supplemental materials

Table 27. Results of simulations evaluating the efficacy of survey protocols using parameters estimated from the 2019 spring pilot study. Simulations 1, 2, and 3 evaluated current survey protocols. Simulations 4, 5, and 6 evaluated survey protocols where the number of sites surveyed was increased. Simulations 7, 8, and 9 evaluated survey protocols where the number of visits was increased. Mean (95% credible interval) for bias and coefficient of variation from 400 simulation runs for each suite of parameters. R = number of survey sites, J = number of replicate visits, λ = mean abundance per site, p = mean detection probability; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site.

	Simulation Parameters				Bias in λ	Bias in *p*	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	Protocol meets Management
	R	J	λ	*p*							
Sim 1	100	3	0.17	0.28	0.07 (-0.08, 0.30)	0.01 (-0.15, 0.18)	6.89 (-5.25, 30.45)	0.07 (-0.05, 0.30)	0.68 (0.23, 1.35)	1	no
Sim 2	100	3	0.36	0.28	0.08 (-0.13, 0.41)	0.00 (-0.12, 0.14)	8.13 (-10.49, 41.42)	0.08 (-0.10, 0.41)	0.45 (0.21, 0.94)	0.99	no
Sim 3	100	3	0.48	0.28	0.1 (-0.17, 0.47)	0.00 (-0.11, 0.13)	9.48 (-13.34, 45.66)	0.09 (-0.13, 0.46)	0.39 (0.18, 0.78)	0.99	no
Sim 4	300	3	0.48	0.28	0.02 (-0.10, 0.18)	0.00 (-0.06, 0.07)	5.24 (-25.79, 45.50)	0.02 (-0.09, 0.15)	0.16 (0.12, 0.22)	0.59	no
Sim 5	400	3	0.48	0.28	0.02 (-0.09, 0.17)	0.00 (-0.06, 0.07)	6.70 (-31.02, 58.30)	0.02 (-0.08, 0.15)	0.13 (0.10, 0.18)	0.27	no
Sim 6	500	3	0.48	0.28	0.01 (-0.09, 0.13)	-0.00 (-0.06, 0.06)	7.73 (-36.82, 62.82)	0.02 (-0.07, 0.13)	0.12 (0.09, 0.16)	0.09	yes
Sim 7	100	6	0.48	0.28	0.02 (-0.12, 0.17)	-0.00 (-0.07, 0.07)	1.96 (-7.05, 13.97)	0.02 (-0.07, 0.14)	0.13 (0.09, 0.18)	0.20	no
Sim 8	100	8	0.48	0.28	0.01 (-0.11, 0.16)	0.00 (-0.05, 0.06)	0.79 (-5.80, 7.80)	0.01 (-0.06, 0.08)	0.09 (0.06, 0.11)	0.00	yes
Sim 9	100	9	0.48	0.28	0.01 (-0.11, 0.14)	-0.00 (-0.05, 0.04)	0.90 (-4.75, 6.78)	0.01 (-0.05, 0.07)	0.08 (0.06, 0.10)	0.00	yes

* Table is printed here as an image in order to fit the page; a spreadsheet of this table is available in the provided supplemental materials

Table 28. Results of simulations evaluating the efficacy of survey protocols using parameters from the 2019 spring pilot study. Mean (95% credible interval) for bias and coefficient of variation from 400 simulation runs for each suite of parameters. Simulations evaluated survey protocols with an estimate of abundance and probability of detection from spring 2019 surveys using electronic playback. R = number of survey sites, J = number of replicate visits, λ = mean abundance per site, p = mean detection probability; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site. Convergence errors = model convergence errors for estimated number of dusky grouse per survey site despite running 3 chains of length 40,000. The number of convergence errors was not initially recorded and thus is not available for all simulations; the current classification of yes – many or few is based on personal observation.

	Simulation Parameters				**Bias in λ**	**Bias in *p***	**Bias in Total N**	**Bias in N.site**	**CV Total N**	**Probability CV N.total > 0.15**	**Protocol meets Management Requirements**	**Convergence Errors**
	R	**J**	**λ**	***p***								
Sim 1	100	8	0.36	0.28	0.01 (-0.10, 0.11)	-0.00 (0.05, 0.05)	0.85 (-3.96, 6.47)	0.01 (-0.04, 0.06)	0.09 (0.07, 0.13)	0.02	yes	yes - many
Sim 2	100	9	0.36	0.28	0.01 (-0.10, 0.13)	-0.00 (-0.06, 0.05)	0.8 (-3.70, 5.70)	0.01 (-0.04, 0.06)	0.08 (0.06, 0.11)	0	yes	yes - many
Sim 3	150	6	0.36	0.28	0.02 (-0.09, 0.12)	-0.00 (-0.06, 0.06)	2.01 (-7.18, 12.75)	0.01 (-0.05, 0.09)	0.11 (0.08, 0.14)	0.04	yes	yes - many
Sim 4	150	8	0.36	0.28	0.01 (-0.08, 0.10)	-0.00 (-0.05, 0.05)	0.76 (-4.14, 7.47)	0.01 (-0.03, 0.05)	0.07 (0.05, 0.09)	0	yes	yes - many
Sim 5	180	6	0.36	0.28	0.01 (-0.09, 0.10)	0.00 (-0.05, 0.06)	0.86 (-8.28, 11.59)	0.00 (-0.05, 0.06)	0.09 (0.07, 0.12)	0.01	yes	yes - many
Sim 6	300	4	0.36	0.28	0.00 (-0.08, 0.10)	0.00 (-0.06, 0.07)	1.92 (-17.13, 24.09)	0.01 (-0.06, 0.08)	0.12 (0.09, 0.16)	0.08	yes-ish	few
Sim 7	360	4	0.36	0.28	0.01 (-0.06, 0.09)	0.00 (-0.05, 0.06)	2.84 (-17.50, 26.25)	0.01 (-0.05, 0.08)	0.11 (0.08, 0.14)	0.02	yes	few
Sim 8	200	6	0.36	0.28	0.01 (-0.07, 0.11)	-0.00 (-0.06, 0.05)	1.78 (-7.85, 12.14)	0.01 (-0.04, 0.06)	0.09 (0.07, 0.12)	0.01	yes	few
Sim 9	200	8	0.36	0.28	0.01 (-0.06, 0.09)	-0.00 (-0.05, 0.04)	1.49 (-5.96, 10.08)	0.01 (-0.03, 0.05)	0.06 (0.05, 0.08)	0	yes	yes - many
Sim 10	200	9	0.36	0.28	0.00 (-0.07, 0.09)	0.00 (-0.04, 0.04)	0.66 (-5.98, 6.99)	0.00 (-0.03, 0.03)	0.05 (0.04, 0.07)	0	yes	yes - many

* Table is printed here as an image in order to fit the page; a spreadsheet of this table is available in the provided supplemental materials

Table 29. Support for candidate models examining three different detection functions, half-normal, hazard-rate, and uniform, for hierarchical distance sampling models for point counts fitted with constant probability of detection and local density/abundance.

Model	**K**	**AICc**	**Δ AICc**	w_i
Null model, Half-normal detection function	2	2226.8	0.0	1.00
Null model, Uniform detection function	1	2332.4	105.7	0.00
Null model, Hazard-rate detection function	3	2334.4	107.7	0.00

Table 30. Estimates for MFWP regional local abundance (grouse per survey site) evaluated using single season N-mixture models. Average lambda/local abundance was estimated using a model where abundance and detection were both held constant. FWP regional local abundances were estimated using a model where local abundance was varied by region and detection was held constant.

Parameter	Estimate	SE	95% confidence interval
Region 1 λ	0.13	0.02	0.10–0.17
Region 2 λ	0.31	0.03	0.27–0.37
Region 3 λ	0.19	0.02	0.16–0.23
Region 4 λ	0.08	0.01	0.06–0.11
Region 5 λ	0.21	0.02	0.17–0.26
Average λ	0.18	0.01	0.17–0.20

Table 31. Estimates for FWP regional local abundance evaluated using hierarchical distance sampling models. Average lambda/local abundance was estimated using a model where abundance and detection were both held constant. FWP regional local abundances were estimated using a model where local abundance was varied by region and detection was held constant.

Parameter	Estimate	SE	95% confidence interval
Region 1 λ	0.12	0.03	0.08–0.19
Region 2 λ	0.36	0.05	0.27–0.47
Region 3 λ	0.21	0.03	0.15–0.29
Region 4 λ	0.07	0.02	0.04–0.12
Region 5 λ	0.23	0.04	0.16–0.33
Average λ	0.20	0.02	0.16–0.24

Table 32. Parameter estimates used to inform simulation scenarios. Abundance estimates were used to inform scenarios for both single-season N-mixture and hierarchical distance sampling models. Sigma was used to inform the detection function for the hierarchical distance sampling models and detection was used to inform the probability of detection for the single-season N-mixture models.

Parameter	Survey Type	Model	Estimate
Low abundance	-	-	0.09
Average abundance	-	-	0.18
High abundance	-	-	0.31
Average detection	PC	N-mixture	0.37
High detection	PC	N-mixture	0.57
Average sigma	PC	Hierarchical distance sampling	43
High sigma	PC	Hierarchical distance sampling	58
Average sigma	PC	Hierarchical distance sampling with time removal	43
High sigma	PC	Hierarchical distance sampling with time removal	48
Average availability	PC	Hierarchical distance sampling with time removal	0.65
High availability	PC	Hierarchical distance sampling with time removal	0.89
Average sigma	Line	Hierarchical distance sampling	42
High sigma	Line	Hierarchical distance sampling	51

Table 33. Support for candidate models examining three different detection functions, half-normal, hazard-rate, and uniform, for hierarchical distance sampling models for transects for visit 1 fitted with constant probability of detection and local density/abundance.

Model	K	AICc	Δ AICc	w_i
Null model, Hazard-rate detection function	3	1211.34	0.00	0.82
Null model, Half-normal detection function	2	1214.43	3.09	0.18
Null model, Uniform detection function	1	1286.29	74.95	0.00

Table 34. Support for candidate models examining three different detection functions, half-normal, hazard-rate, and uniform, for hierarchical distance sampling models for transects for visit 2 fitted with constant probability of detection and local density/abundance.

Model	K	AICc	Δ AICc	w_i
Null model, Half-normal detection function	2	743.96	0.00	0.99
Null model, Uniform detection function	1	753.55	9.59	0.01

Table 35. From the simulation results, the number of visits, sites to be surveyed, total number of point counts to be conducted, and the potential number of transects (if there are 6 points on each transect) for providing robust population estimates using N-mixture models (point counts), hierarchical distance sampling (point counts and transects), and hierarchical distance sampling with time removal under 6 different scenarios. HA = high abundance, average detection, AA = average abundance, average detection, LA = low abundance, average detection, HH = high abundance, high detection, AH = average abundance, high detection, LH = low abundance, high detection. Simulations were only conducted under 2 scenarios for the hierarchical distance sampling with time removal. The transect length evaluated was 2,681m (the average transect length for 2020 and 2021).

Scenario	Model	# of Visits	# of Sites	# of Point Counts	Transect (6pts)
HA	N-mixture point count	4	170	680	29
	HDS point count	1	1,090	1,090	182
	HDS with time removal point count	1	> 6,000	> 6,000	> 1,000
	HDS transect	1	25	NA	25
AA	N-mixture point count	4	240	960	40
	HDS point count	1	1870	1870	312
	HDS with time removal point count	1	NA	NA	NA
	HDS transect	1	40	NA	40
LA	N-mixture point count	4	490	1960	82
	HDS point count	1	4230	4230	705
	HDS with time removal point count	1	NA	NA	NA
	HDS transect	1	90	NA	90
HH	N-mixture point count	4	60	240	10
	HDS point count	1	800	800	134
	HDS with time removal point count	1	1390	1390	232
	HDS transect	1	20	NA	20
AH	N-mixture point count	4	80	320	14
	HDS point count	1	1360	1360	227
	HDS with time removal point count	1	NA	NA	NA
	HDS transect	1	35	NA	35
LH	N-mixture point count	4	140	560	24
	HDS point count	1	3110	3110	519
	HDS with time removal point count	1	NA	NA	NA
	HDS transect	1	70	NA	70

Table 35. Correlation matrix for correlation between point counts for combined 2020 and 2021 data. Point counts 1 and 2, and point counts 3 and 4 are conducted back-to-back. All point counts occurred on the same day.

	Point Count 1	Point Count 2	Point Count 3	Point Count 4
Point Count 1	1.00	0.67	0.41	0.44
Point Count 2	-	1.00	0.48	0.47
Point Count 3	-	-	1.00	0.67
Point Count 4	-	-	-	1.00

Table 36. Results of simulations evaluating the effects of correlation between point counts for the recommended protocols for the N-mixture models under 6 different scenarios. Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of survey sites, λ = mean abundance per site, sigma = mean sigma, p.avail = mean probability of availability; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site.

Simulation Parameters				Bias in λ	Bias in *p*	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	Protocol meets Management Requirements
R	J	λ	*p*							
170	4	0.31	0.37	-0.04 (-0.11, 0.03)	0.10 (0.05, 0.16)	-6.80 (-13.46, -0.91)	-0.04 (-0.08, -0.01)	0.07 (0.05, 0.09)	0.00	yes
240	4	0.18	0.37	-0.02 (-0.07, 0.02)	0.10 (0.05, 0.15)	-5.69 (-11.41, -0.49)	-0.02 (-0.05, 0.00)	0.07 (0.05, 0.09)	0.00	yes
490	4	0.08	0.37	-0.01 (-0.03, 0.01)	0.11 (0.06, 0.16)	-4.73 (-9.50, -0.05)	-0.01 (-0.02, 0.00)	0.07 (0.05, 0.09)	0.00	yes
60	4	0.31	0.57	0.00 (-0.13, 0.13)	-0.04 (-0.13, 0.04)	0.41 (-2.22, 2.62)	0.01 (-0.04, 0.04)	0.10 (0.06, 0.15)	0.05	yes
80	4	0.18	0.57	0.01 (-0.06, 0.09)	-0.04 (-0.13, 0.03)	0.33 (-1.68, 1.99)	0.00 (-0.02, 0.02)	0.10 (0.07, 0.16)	0.07	yes
140	4	0.08	0.57	0.00 (-0.03, 0.04)	-0.05 (-0.13, 0.02)	0.26 (-1.40, 1.48)	0.00 (-0.01, 0.01)	0.11 (0.07, 0.17)	0.16	yes-ish

*Table printed as image here to fit the page; a spreadsheet of this table is available in provided supplemental materials

Table 37. Predicted power for a protocol where 80 sites are visited 4 times and abundances are estimated using an N-mixture model. Power was examined for a 1, 3, 5, and 10% annual decline over a period of 3, 5, and 10 years. A 10% decline over 10 years was not evaluated as sufficient power was reached after a period of 5 years..

Annual Decline	3 years	5 years	10 years
1%	8.2	14.4	39.2
3%	19	40.6	80.8
5%	26.8	61	94.6
10%	49.6	87.2	NA

Table 38. Mean estimated slopes for predicted annual trend for a protocol where 80 sites are visited 4 times and abundances are estimated using an N-mixture model. Trend were examined for 1, 3, 5, and 10% annual declines over a period of 3, 5, and 10 years. 95% confidence intervals are calculated using a quantile of 0.025 and 0.975. A 10% decline over 10 years was not evaluated.

Annual Decline	3 years	5 years	10 years
1%	-1.13 (-8.29, 5.94)	-1.18 (-6.13, 2.78)	-1.08 (-3.75, 0.84)
3%	-3.58 (-12.82, 4.38)	-3.17 (-9.32, 1.63)	-3.21 (-7.81, -0.1)
5%	-5.3 (-16.25, 3.68)	-5.39 (-13.89, -0.08)	-5.24 (-11.1, -1.16)
10%	-11.08 (-26.6, -0.11)	-10.73 (-21.34, -0.07)	NA

Table 39. Percent of estimated slopes < 0 for predicted annual trend for a protocol where 80 sites are visited 4 times and abundances are estimated using an N-mixture model. Trends were examined for 1, 3, 5, and 10% annual declines over a period of 3, 5, and 10 years. A 10% decline over 10 years was not evaluated.

Annual Decline	3 years	5 years	10 years
1%	60.6	71	80.8
3%	78.8	88.4	97.6
5%	84.4	97.8	99
10%	97.4	98.2	NA

Table 40. Difference between the estimated slopes for predicted annual trend for true abundance and estimated abundances for a protocol where 80 sites are visited 4 times and abundances are estimated using N-mixture model. Trends were examined for 1, 3, 5, and 10% annual declines over a period of 3, 5 and 10 years. A 10% decline over 10 years was not evaluated.

Annual Decline	3 years	5 years	10 years
1%	-0.0005 (-0.0618, 0.0656)	-0.0012 (-0.0406, 0.0358)	-0.0003 (-0.0138, 0.0137)
3%	-0.0030 (-0.0723, 0.0632)	-0.0001 (-0.0399, 0.0350)	0.0007 (-0.0152, 0.0167)
5%	0.0018 (-0.0637, 0.0695)	0.0009 (-0.0343, 0.0.371)	0.0011 (-0.0161, 0.0201)
10%	-0.0007 (-0.0801, 0.0720)	0.0014 (-0.0400, -0.0468)	NA

Table 41. Results of simulations evaluating the effects of a covariate on estimates of abundance for the recommended protocols for the N-mixture models under 6 different scenarios. Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of survey sites, λ = mean abundance per site, p = mean probability of detection; CV = coefficient of variation for total population size (Total N), N.site = estimated number of dusky grouse per survey site, alpha.lam = intercept from linear covariate model, alpha1.lam = slope coefficient (i.e. effect size) estimating linear relationship between local abundance and site covariate X.

Simulation Parameters				Bias in alpha.lam	Bias in alpha1.lam	Bias in *p*	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	Protocol meets Management Requirements
R	J	λ	*p*								
170	4	0.31 - 1X	0.37	-0.02 (-0.33, 0.27)	0.00 (-0.47, 0.46)	0.00 (-0.08, 0.08)	2.13 (-8.23, 13.10)	0.01 (-0.05, 0.08)	0.11 (0.08, 0.16)	0.08	yes
240	4	0.18 - 1X	0.37	-0.04 (-0.41, 0.26)	-0.02 (-0.55, 0.48)	0.00 (-0.08, 0.09)	0.89 (-7.29, 10.95)	0.00 (-0.03, 0.05)	0.11 (0.07, 0.16)	0.07	yes
490	4	0.08 - 1X	0.37	-0.04 (-0.40, 0.29)	-0.03 (-0.56, 0.47)	0.00 (-0.08, 0.08)	1.26 (-5.84, 8.93)	0.00 (-0.01, 0.02)	0.11 (0.07, 0.15)	0.05	yes
60	4	0.31 - 1X	0.57	-0.10 (-0.61, 0.34)	-0.07 (-0.82, 0.64)	-0.02 (-0.13, 0.10)	0.81 (-1.96, 4.17)	0.01 (-0.03, 0.07)	0.09 (0.05, 0.15)	0.06	yes
80	4	0.18 - 1X	0.57	-0.13 (-0.73, 0.36)	-0.13 (-1.17, 0.68)	-0.01 (-0.13, 0.10)	0.58 (-1.45, 2.70)	0.01 (-0.02, 0.03)	0.09 (0.05, 0.15)	0.06	yes
140	4	0.08 - 1X	0.57	-0.20 (-1.01, 0.39)	-0.12 (-1.25, 0.88)	-0.02 (-0.16, 0.11)	0.41 (-1.36, 2.05)	0.00 (-0.01, 0.01)	0.10 (0.04, 0.19)	0.11	yes-ish
170	4	0.31 - 0.5X	0.37	-0.03 (-0.35, 0.27)	-0.03 (-0.49, 0.43)	-0.01 (-0.09, 0.08)	1.82 (-7.37, 13.90)	0.01 (-0.04, 0.08)	0.12 (0.08, 0.16)	0.10	yes
240	4	0.18 - 0.5X	0.37	-0.05 (-0.41, 0.29)	0.00 (-0.51, 0.48)	0.00 (-0.09, 0.08)	1.19 (-5.98, 9.97)	0.00 (-0.02, 0.04)	0.11 (0.08, 0.16)	0.10	yes
490	4	0.08 - 0.5X	0.37	-0.04 (-0.38, 0.28)	-0.01 (-0.59, 0.47)	0.00 (-0.08, 0.08)	1.13 (-5.64, 8.03)	0.00 (-0.01, 0.02)	0.11 (0.07, 0.16)	0.07	yes
60	4	0.31 - 0.5X	0.57	-0.08 (-0.59, 0.31)	-0.04 (-0.77, 0.70)	-0.01 (-0.12, 0.10)	0.56 (-1.77, 3.07)	0.01 (-0.03, 0.05)	0.08 (0.05, 0.14)	0.03	yes
80	4	0.18 - 0.5X	0.57	-0.14 (-0.77, 0.33)	-0.10 (-1.01, 0.81)	-0.01 (-0.13, 0.11)	0.53 (-1.39, 2.42)	0.01 (-0.02, 0.03)	0.09 (0.05, 0.18)	0.07	yes
140	4	0.08 - 0.5X	0.57	-0.19 (-0.96, 0.34)	-0.08 (-1.19, 0.95)	-0.01 (-0.16, 0.12)	0.39 (-1.39, 1.87)	0.00 (-0.01, 0.01)	0.11 (0.04, 0.21)	0.10	yes

*Table printed as image here to fit the page; a spreadsheet of this table is available in provided supplemental materials

Table 42. Results of simulations evaluating the effects of a covariate on estimates of abundance for the recommended protocols for the hierarchical distance sampling with line transects under 6 different scenarios. Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of transect sites, λ = mean abundance per site, sigma = mean sigma; CV = coefficient of variation for total population size (Total N), N.site = estimated number of dusky grouse per survey site, alpha.lam = intercept from linear covariate model, alpha1.lam = slope coefficient (i.e. effect size) estimating linear relationship between local abundance and site covariate X.

Simulation Parameters			Bias in alpha λ	Bias in alpha1 λ	Bias in *sigma*	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	Protocol meets Management Requirements
R	λ	*sigma*								
25	0.31 - 1X	42	-0.05 (-0.33, 0.19)	-0.02 (-0.39, 0.33)	2.00 (-5.83, 10.76)	-1.44 (-32.52, 31.34)	-0.06 (-1.30, 1.25)	0.12 (0.10, 0.14)	0.00	yes
40	0.18 - 1X	42	-0.06 (-0.33, 0.20)	-0.03 (-0.42, 0.30)	2.18 (-5.07, 10.98)	-1.46 (-29.90, 30.30)	-0.04 (-0.75, 0.76)	0.12 (0.11, 0.14)	0.01	yes
90	0.08 - 1X	42	-0.05 (-0.34, 0.21)	-0.02 (-0.38, 0.36)	2.20 (-5.62, 11.67)	-3.24 (-33.06, 26.71)	-0.04 (-0.37, 0.30)	0.12 (0.11, 0.14)	0.00	yes
20	0.31 - 1X	51	-0.07 (-0.32, 0.19)	-0.01 (-0.38, 0.31)	5.72 (-7.13, 21.23)	-3.87 (-28.62, 21.93)	-0.19 (-1.43, 1.10)	0.12 (0.10, 0.14)	0.02	yes
35	0.18 - 1X	51	-0.07 (-0.37, 0.20)	-0.02 (-0.38, 0.34)	5.01 (-7.51, 21.35)	-3.35 (-28.62, 28.19)	-0.10 (-0.82, 0.81)	0.12 (0.10, 0.14)	0.01	yes
70	0.08 - 1X	51	-0.07 (-0.37, 0.21)	-0.01 (-0.39, 0.35)	4.91 (-7.14, 20.40)	-2.61 (-25.38, 22.62)	-0.04 (-0.36, 0.32)	0.13 (0.11, 0.15)	0.04	yes
25	0.31 - 0.5X	42	-0.05 (-0.32, 0.21)	-0.03 (-0.42, 0.32)	2.09 (-5.65, 12.64)	-1.96 (-30.25, 26.81)	-0.08 (-1.21, 1.07)	0.13 (0.11, 0.14)	0.01	yes
40	0.18 - 0.5X	42	-0.06 (-0.36, 0.21)	-0.01 (-0.40, 0.32)	3.08 (-5.95, 15.07)	-3.13 (-30.61, 27.95)	-0.08 (-0.77, 0.70)	0.13 (0.12, 0.15)	0.02	yes
90	0.08 - 0.5X	42	-0.05 (-0.34, 0.22)	-0.01 (-0.40, 0.36)	2.65 (-6.20, 14.01)	-1.68 (-30.45, 30.50)	-0.02 (-0.34, 0.34)	0.13 (0.12, 0.15)	0.02	yes
20	0.31 - 0.5X	51	-0.07 (-0.36, 0.22)	-0.01 (-0.41, 0.36)	5.50 (-7.29, 22.14)	-2.59 (-26.33, 24.25)	-0.13 (-1.32, 1.21)	0.13(0.11, 0.15)	0.04	yes
35	0.18 - 0.5X	51	-0.06 (-0.35, 0.18)	-0.01 (-0.37, 0.38)	6.17 (-7.22, 21.61)	-3.55 (-25.22, 20.53)	-0.10 (-0.72, 0.59)	0.13 (0.11, 0.14)	0.02	yes
70	0.08 - 0.5X	51	-0.07 (-0.39, 0.22)	-0.01 (-0.38, 0.36)	5.91 (-9.03, 22.60)	-2.09 (21.41, 23.72)	-0.03 (-0.31, 0.34)	0.13 (0.11, 0.15)	0.08	yes

*Table printed as image here to fit the page; a spreadsheet of this table is available in provided supplemental materials

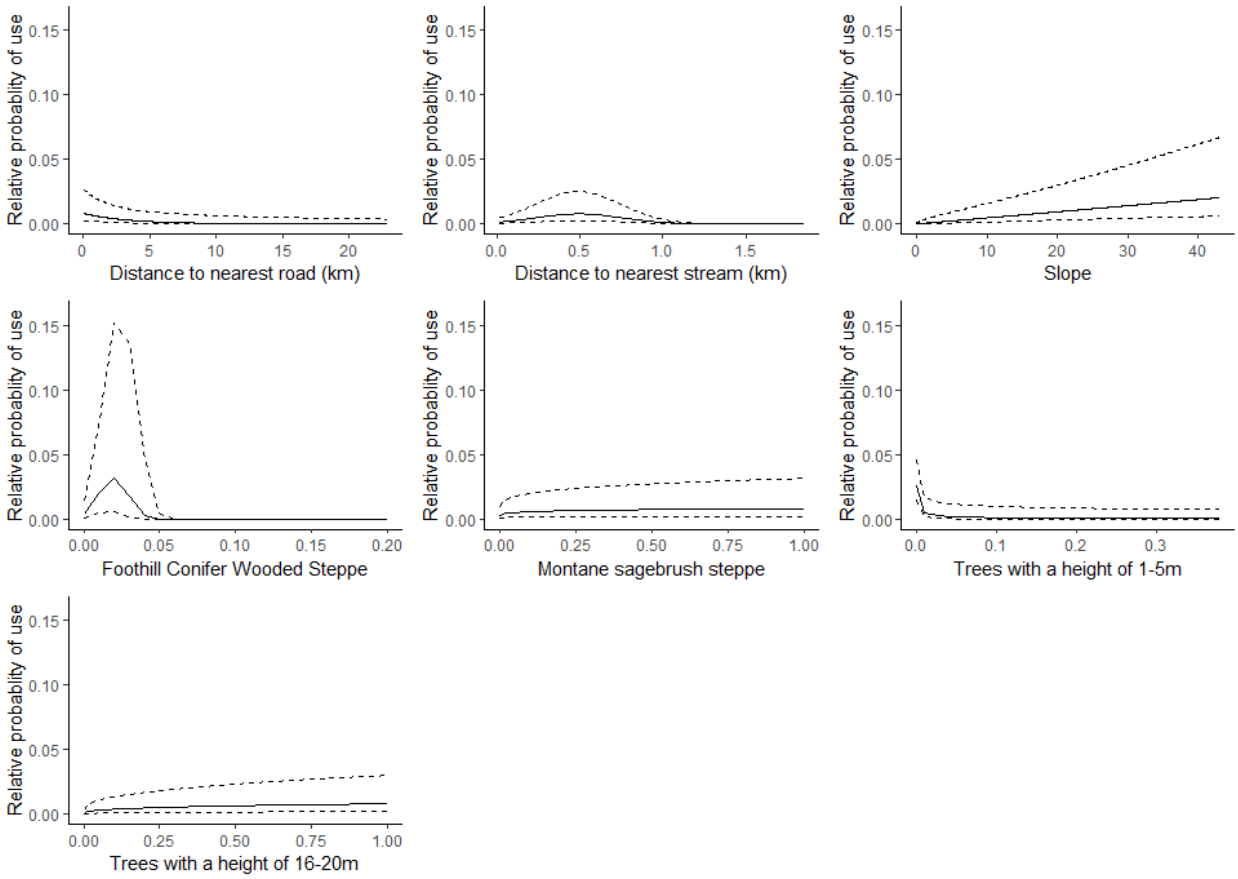


Figure 1. Predicted relative probability of use for the covariates in the RSF model with 95% confidence intervals (dashed lines) while all other covariates held at their average value.

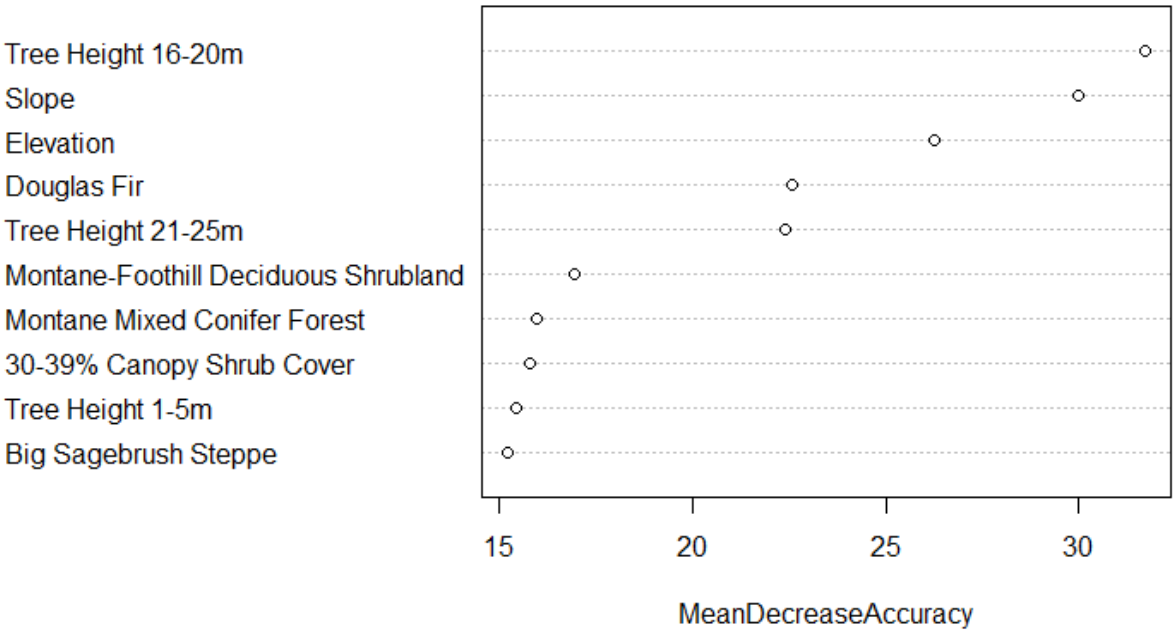


Figure 2. Variable importance plot for the top 10 important variables from the random forest model. Variable importance was calculated as the impact of removing a variable on the model or mean decrease in accuracy.

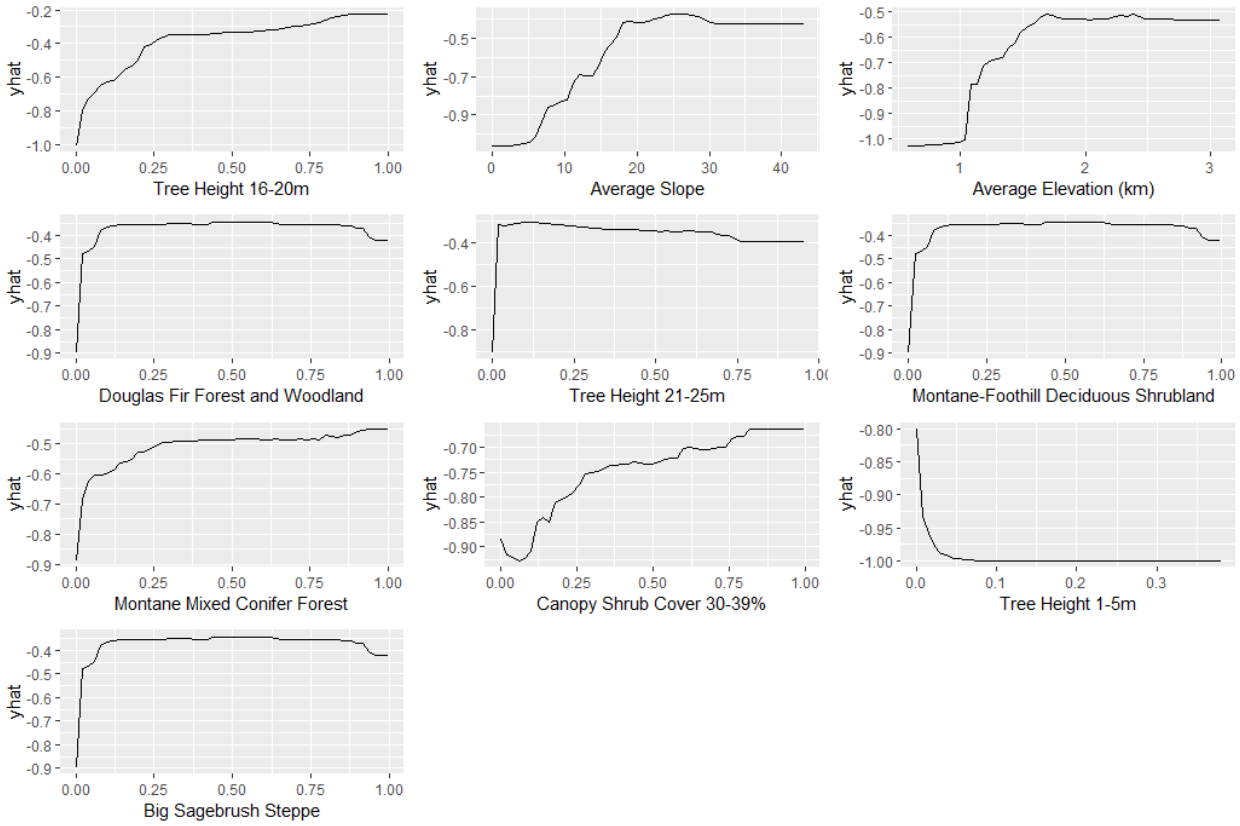


Figure 3. Partial dependency plots for the variables of greatest importance for fitting the random forest model to evaluate the marginal effect of a variable on the random forest's predictions.

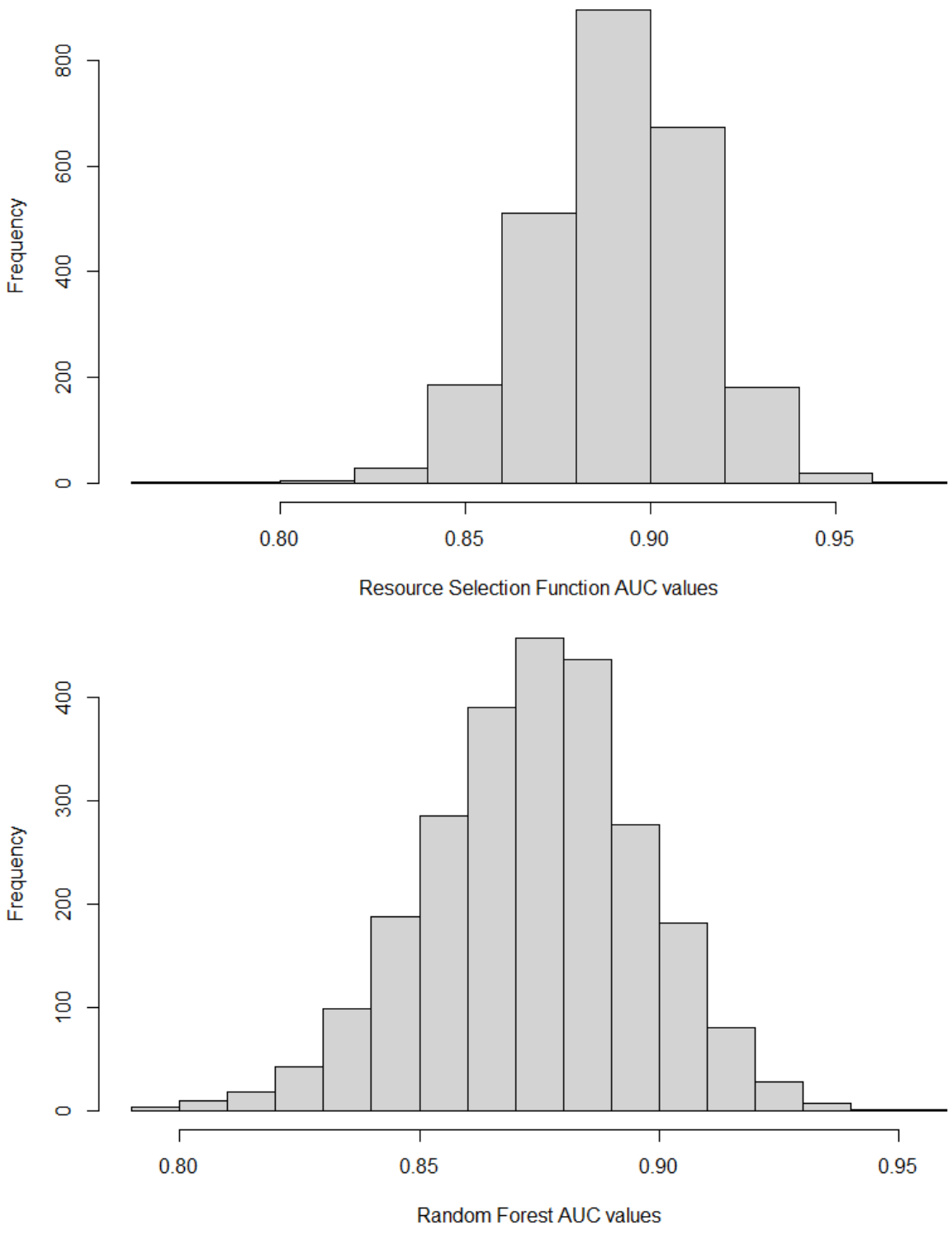


Figure 4. Histogram of the AUC values from the repeated k-fold cross validation for the resource selection model (top) and random forest model (bottom). Average AUC for the RSF model was 0.89 (95% CI: 0.85-0.93) and for the RF model was 0.87 (95% CI: 0.82, 0.92).

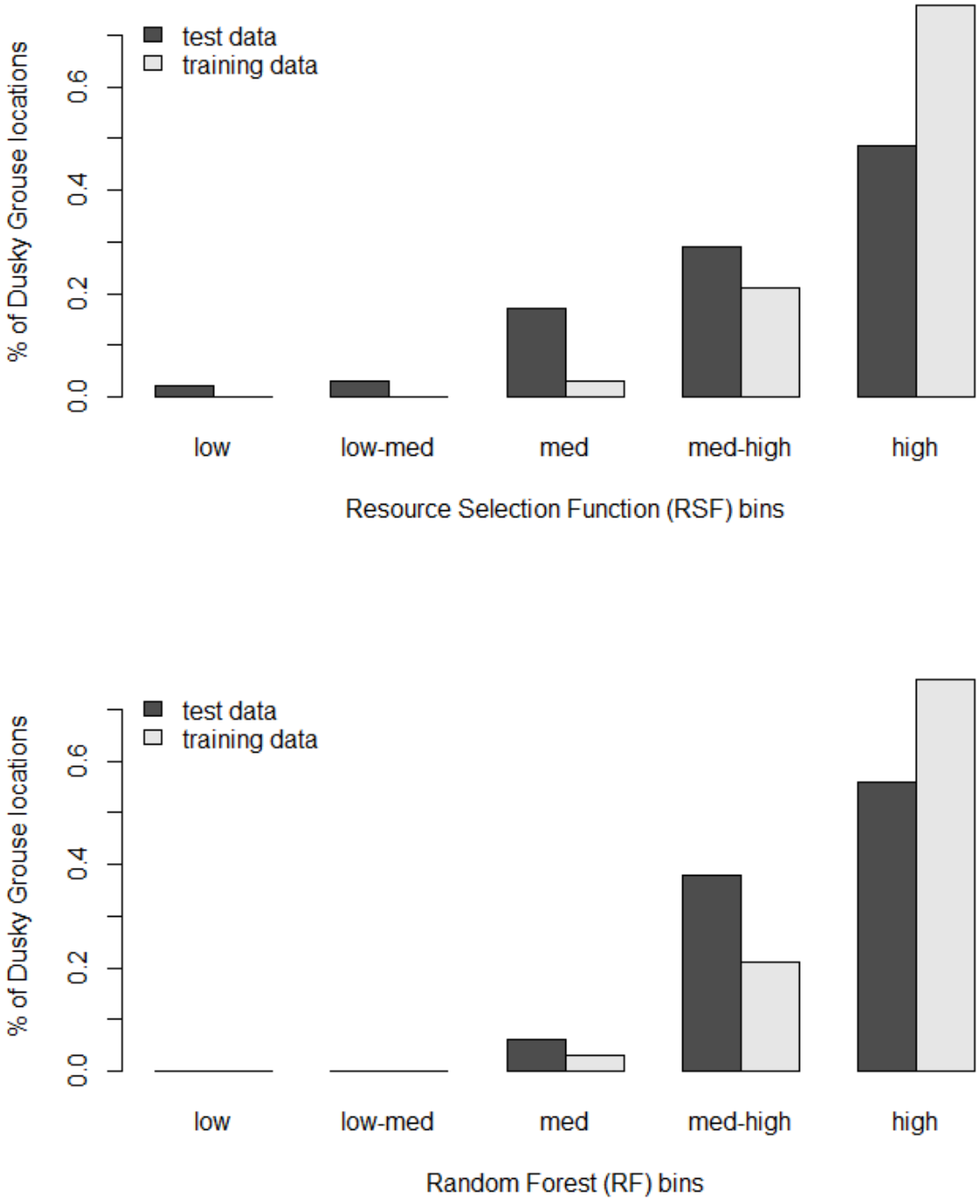


Figure 5. Proportion of Dusky Grouse locations in five bins of increasing relative probability of use values for resource selection function values (top), random forest model values (bottom) that we used to train (n = 132) and test (n = 193; 1 location was outside MT) the different models of predicted Dusky Grouse habitat. A good predictive model will assign most of the training and test Dusky Grouse locations to medium-high or high categories of predicted use.

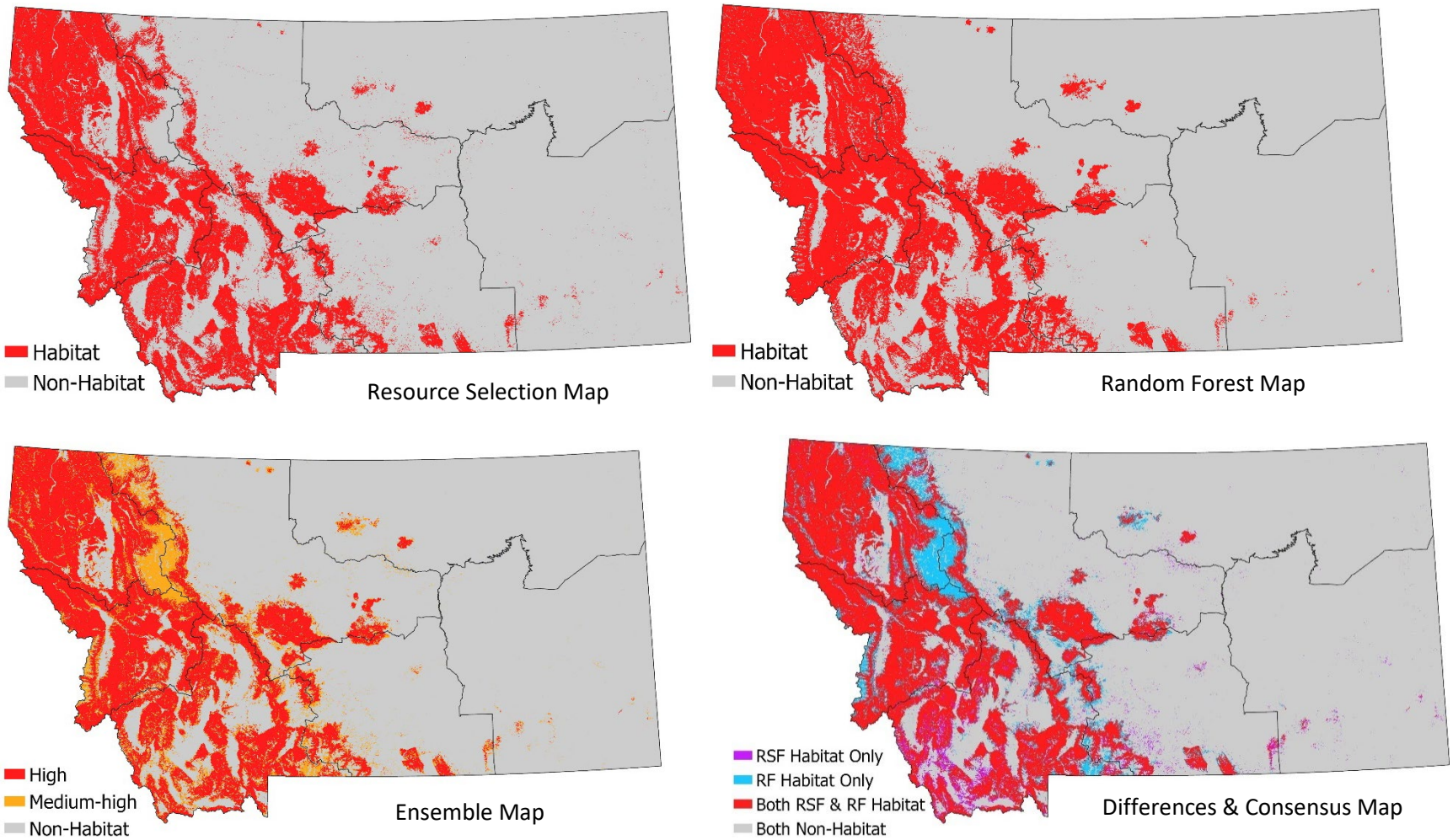


Figure 6. Predicted Dusky Grouse habitat (red) for the resource selection function map (top left) and random forest map (top right). Predicted Dusky Grouse habitat for the ensemble model (bottom left) where red represents habitat with high probability of use, orange represents habitat with medium-high probability of use, and gray represents non-habitat. Areas of consensus and differences (bottom right) in predicted Dusky Grouse habitat between the RSF and RF models, where areas both models predict habitat are red, where only RSF predicted habitat are purple, areas where only RF predicted habitat are blue, and areas where both models predict non-habitat are gray. MFWP administrative regions are delineated in gray (left top to bottom: Regions 1, 2, 3; center top to bottom: Regions 4, 5; and right top to bottom: 6, 7).

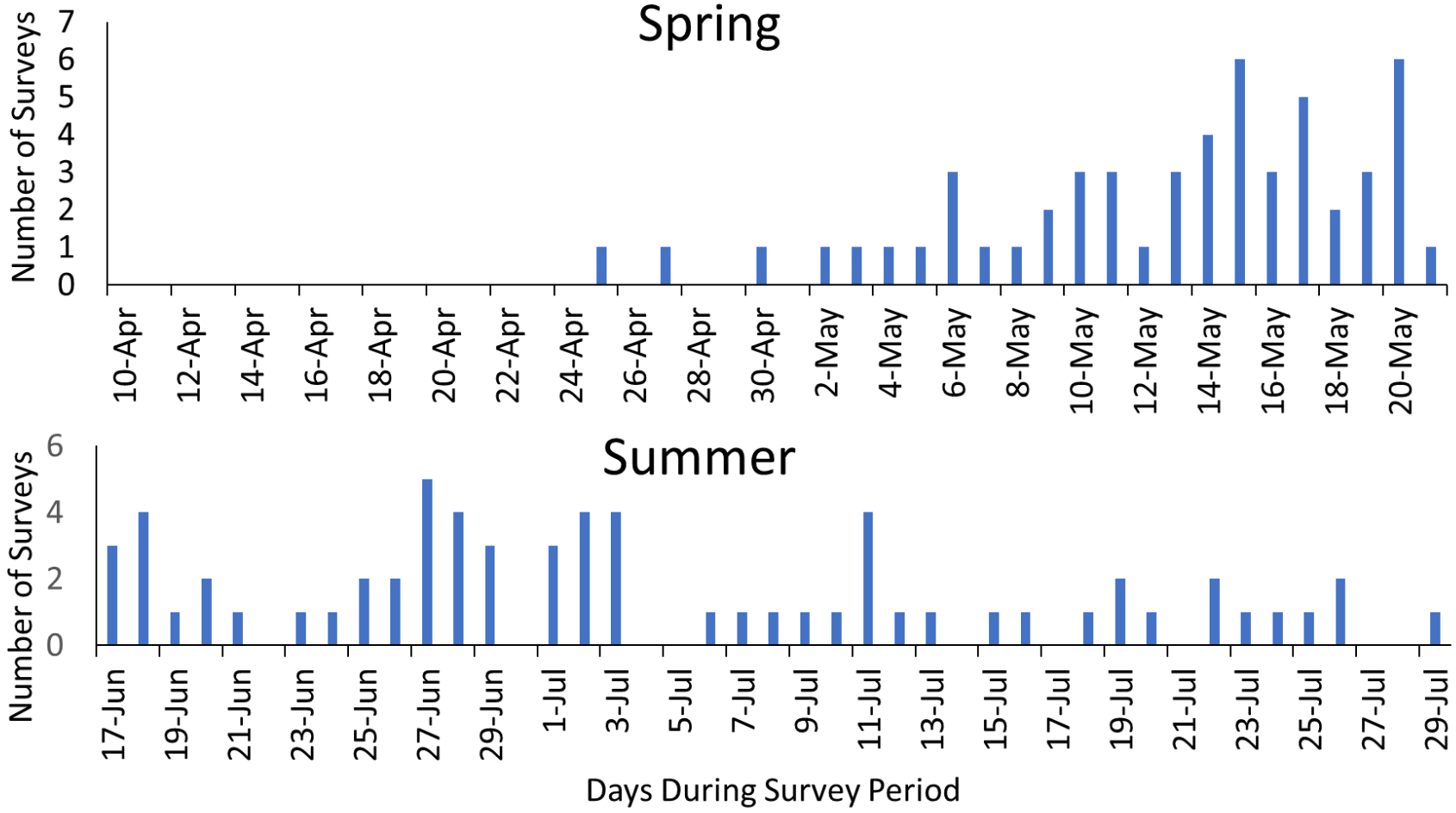


Figure 7. Daily survey effort represented by the number of surveys completed each day for dusky grouse surveys conducted in spring and summer 2019.

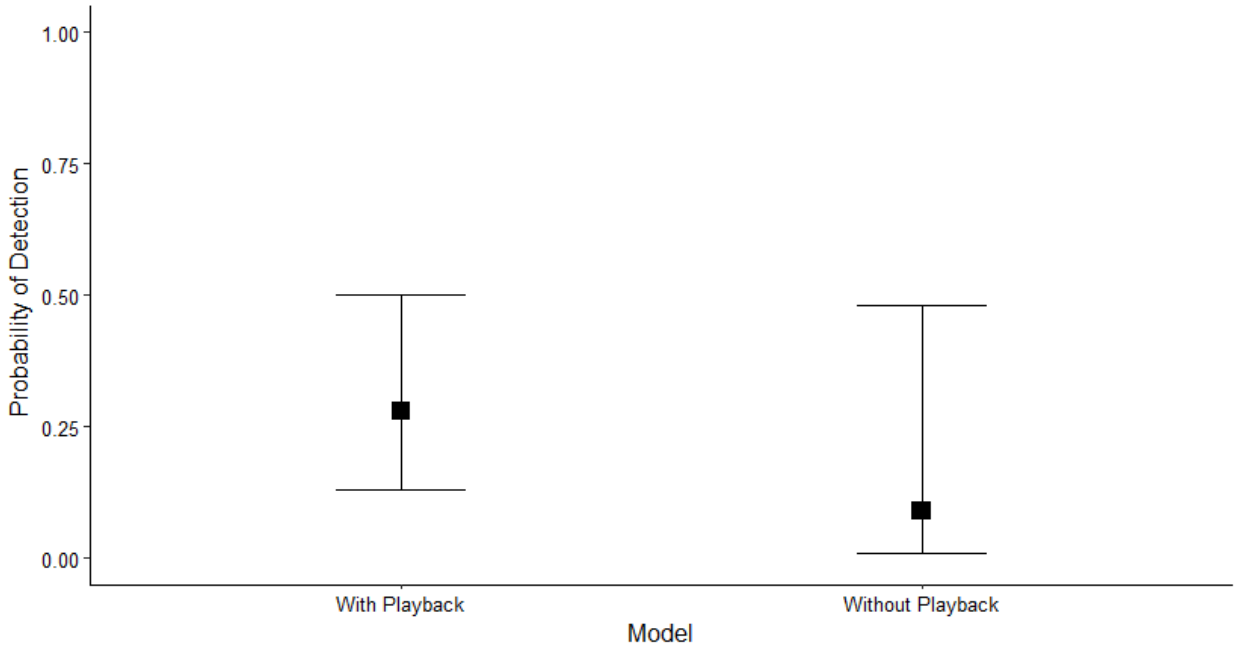


Figure 8. The impacts of electronic playback on probability of detecting a dusky grouse with 95% confidence intervals. Data from spring 2019 dusky grouse surveys, where female calls were used to elicit male dusky grouse responses.

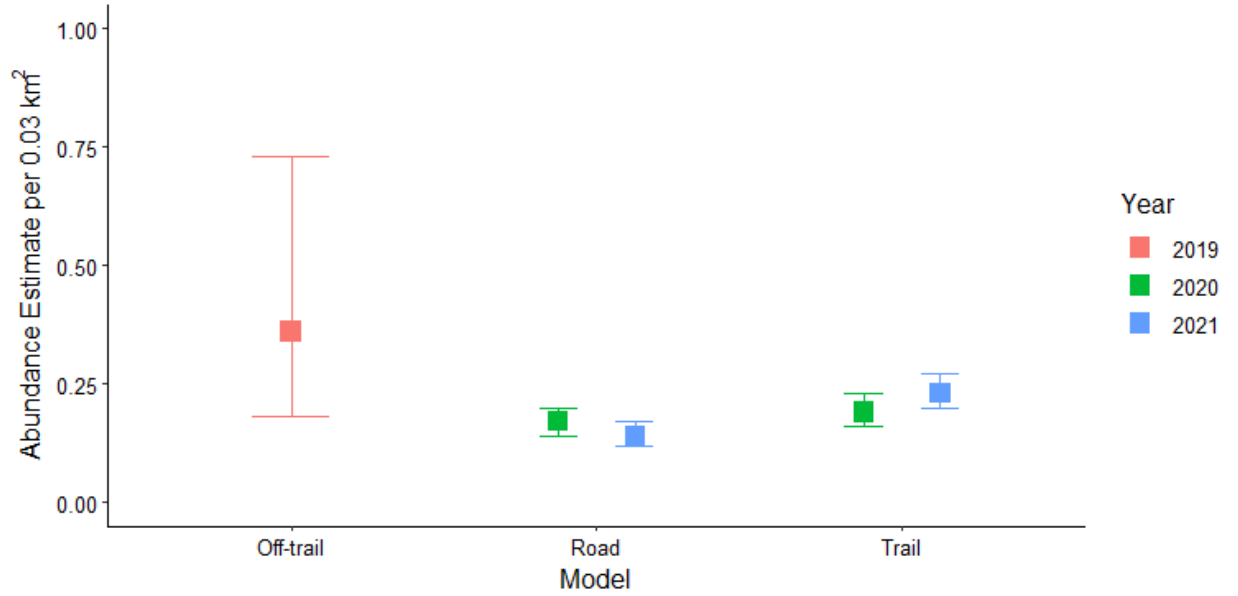


Figure 9. Local abundance estimates evaluated using single season N-mixture models of dusky grouse with 95% confidence intervals for point counts conducted along different route types: off-trail, road, and trail. Data for the off-trail transects come from the 2019 pilot year surveys conducted in MFWP region 3. Data for the road and trail transects comes from the 2020 and 2021 surveys conducted across western Montana.

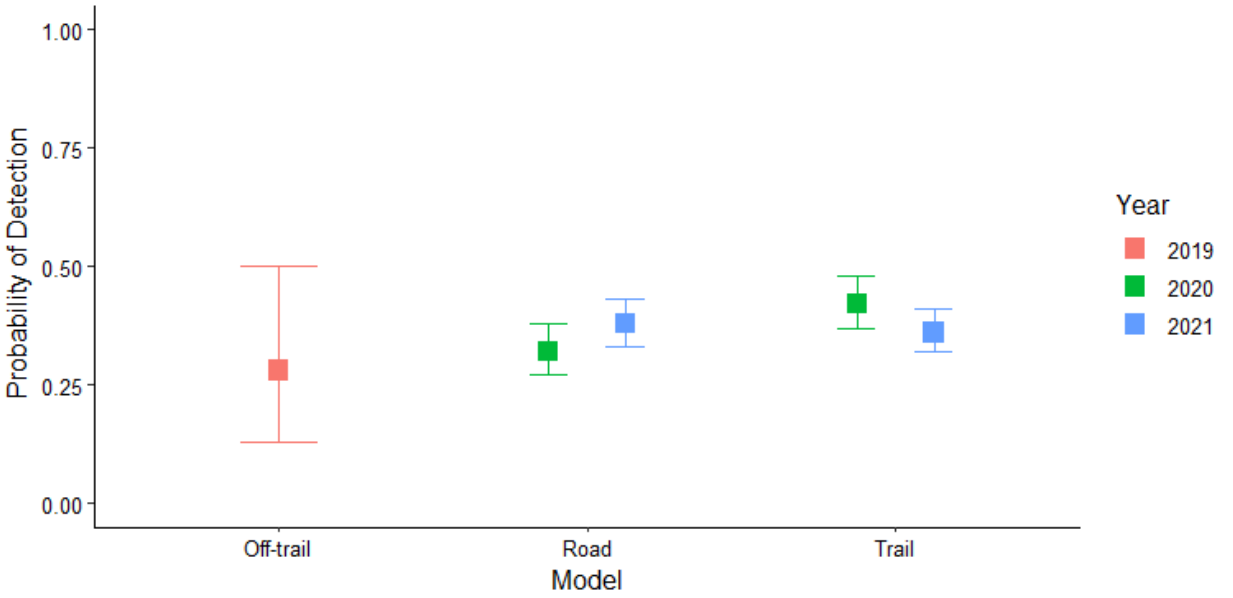


Figure 10. Probability of detection estimates evaluated using single season N-mixture models of dusky grouse with 95% confidence intervals for point counts conducted along different route types: off-trail, road, and trail. Data for the off-trail transects come from the 2019 pilot year surveys conducted in MFWP region 3. Data for the road and trail transects comes from the 2020 and 2021 surveys conducted across western Montana.

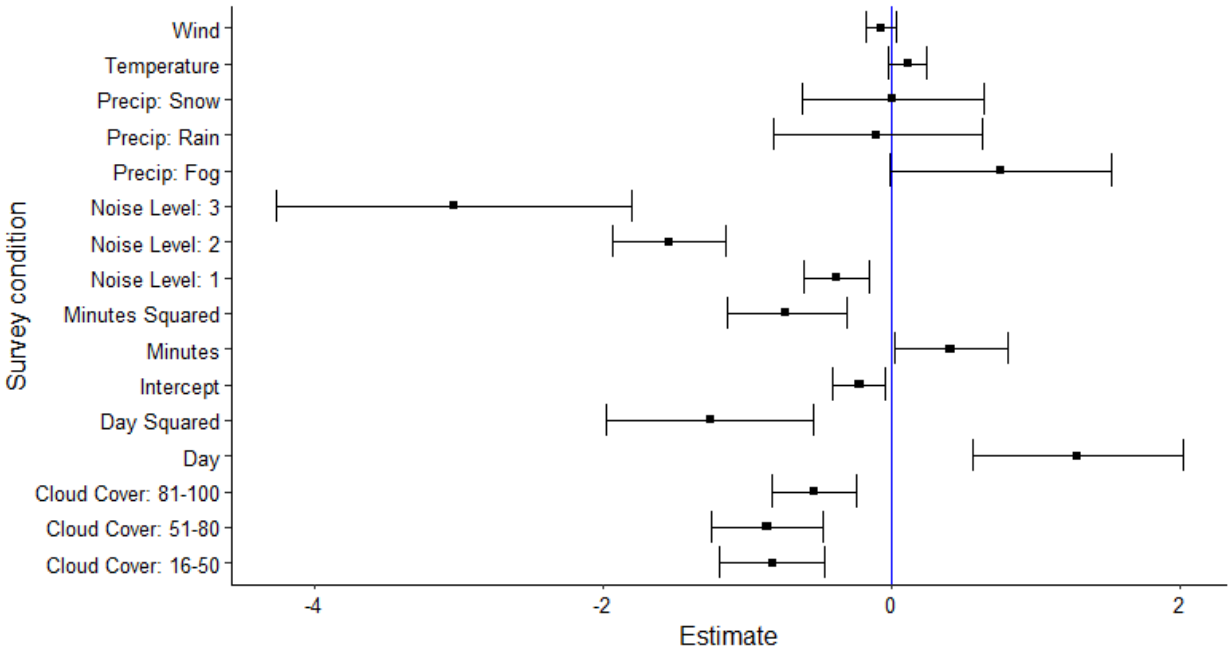


Figure 11. Standardized effects with 95% confidence intervals of survey conditions on the probability of detection from a single-season N-mixture model where abundance (per point count area) was held constant and detection was modeled based on precipitation, cloud cover, noise level, day during the sampling period, minutes since sunrise, temperature, and wind speed. Reference level for noise level is noise level: 0, for precipitation is none, and for cloud cover is 0-15%.

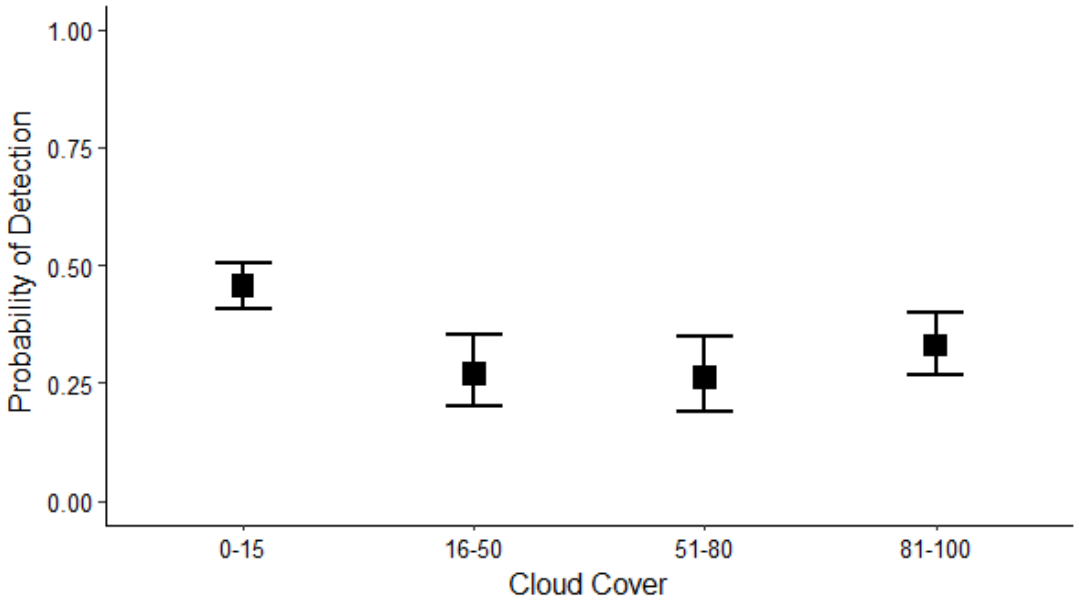


Figure 12. Estimated probability of detection for different cloud cover categories: 0-15% cloud cover, 16-50% cloud cover, 51-80% cloud cover, 81-100% cloud cover while minutes since sunrise, day during the sampling period, and temperature were held constant, wind was held at minimum wind speed, precipitation was held at none, and noise level was held at 0.

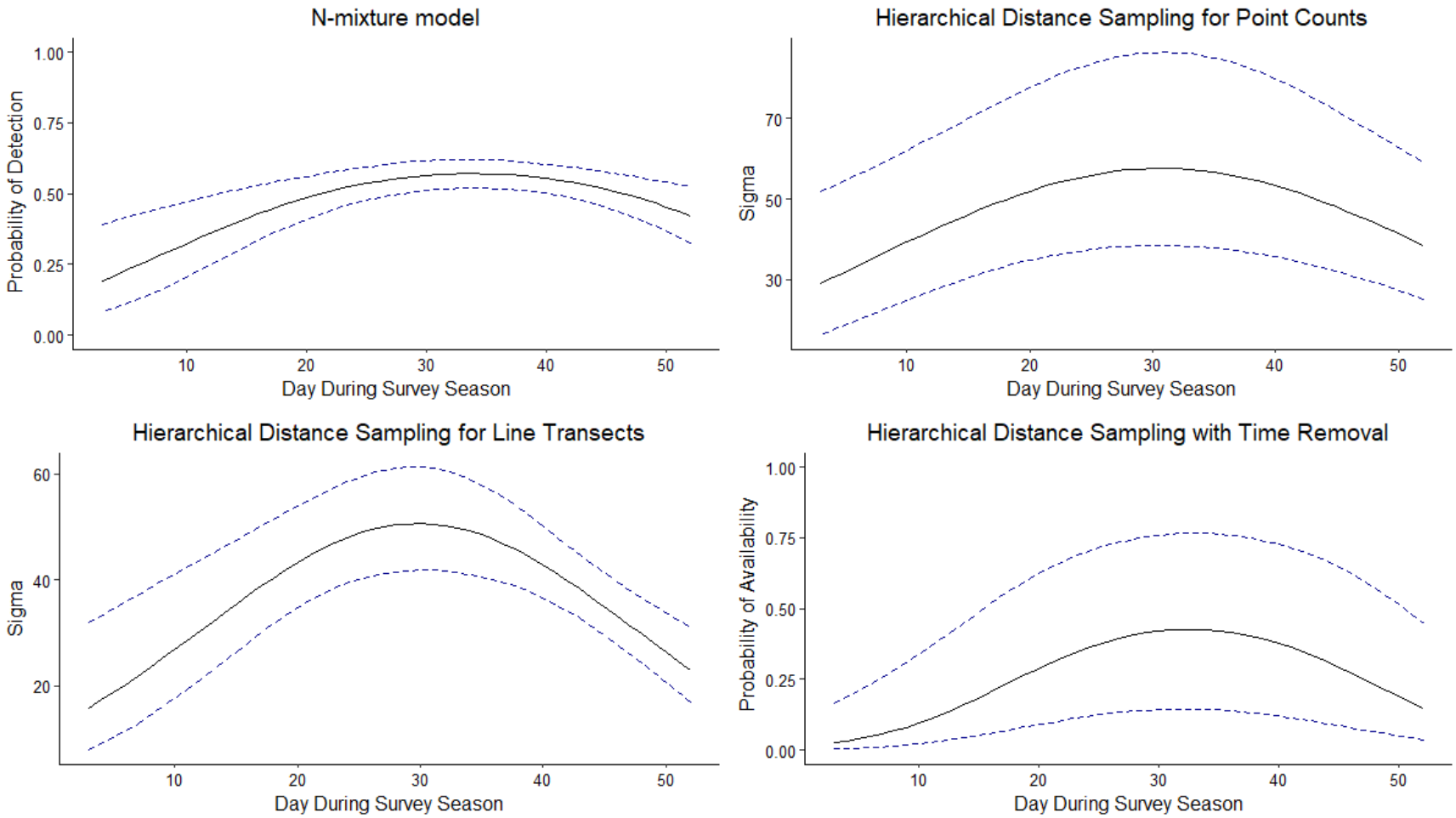


Figure 13. Effect of day during the survey season on probability of detection, sigma, or availability for 4 models. 3 models for point counts: N-mixture, hierarchical distance sampling, hierarchical distance sampling with time removal. 1 model for line transects: hierarchical distance sampling. Probability of detection was highest for the N-mixture model on day 34 (May 13th, sigma was highest for the hierarchical distance sampling for point counts on day 31 (May 10th), sigma was highest for hierarchical distance sampling for line transects on day 30 (May 9th), and availability was highest on day 33 (May 12th) for hierarchical distance sampling with time removal models.

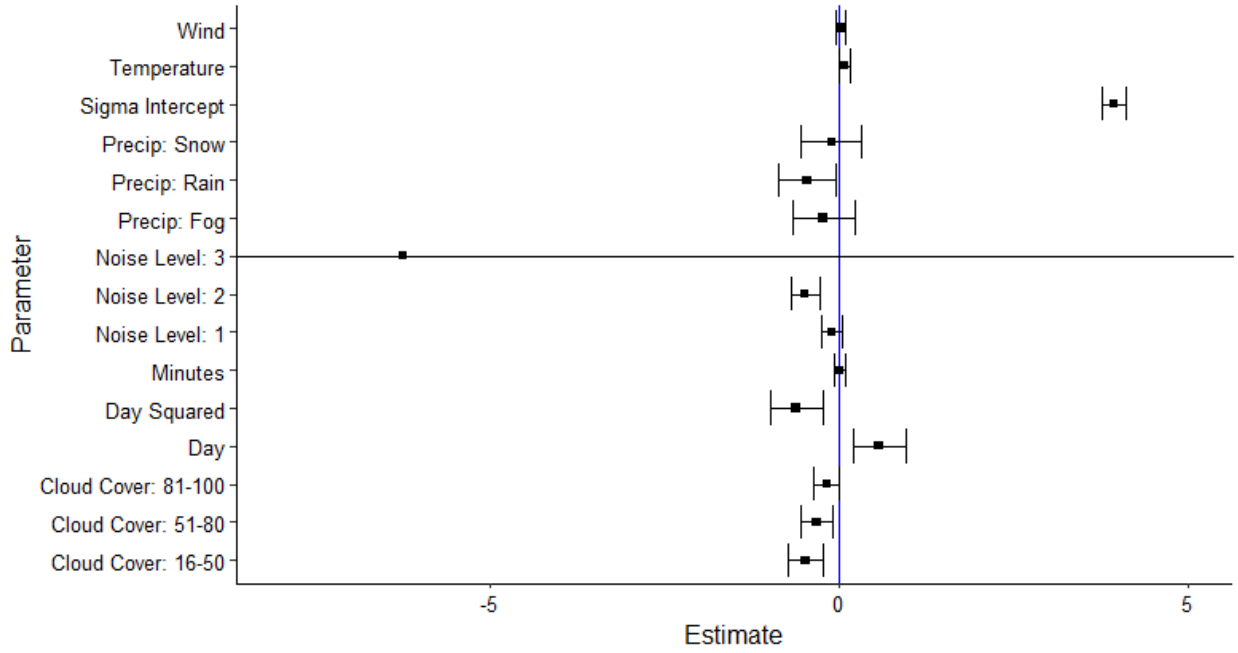


Figure 14. Standardized effects with 95% confidence intervals of survey conditions on sigma (used to estimate the detection function) from a hierarchical distance sampling model for point counts where abundance (per point count area) was held constant and sigma was modeled based on precipitation, cloud cover, noise level, day during the sampling period, minutes since sunrise, temperature, and wind speed. Reference level for noise level is noise level: 0, for precipitation is none, and for cloud cover is 0-15%.

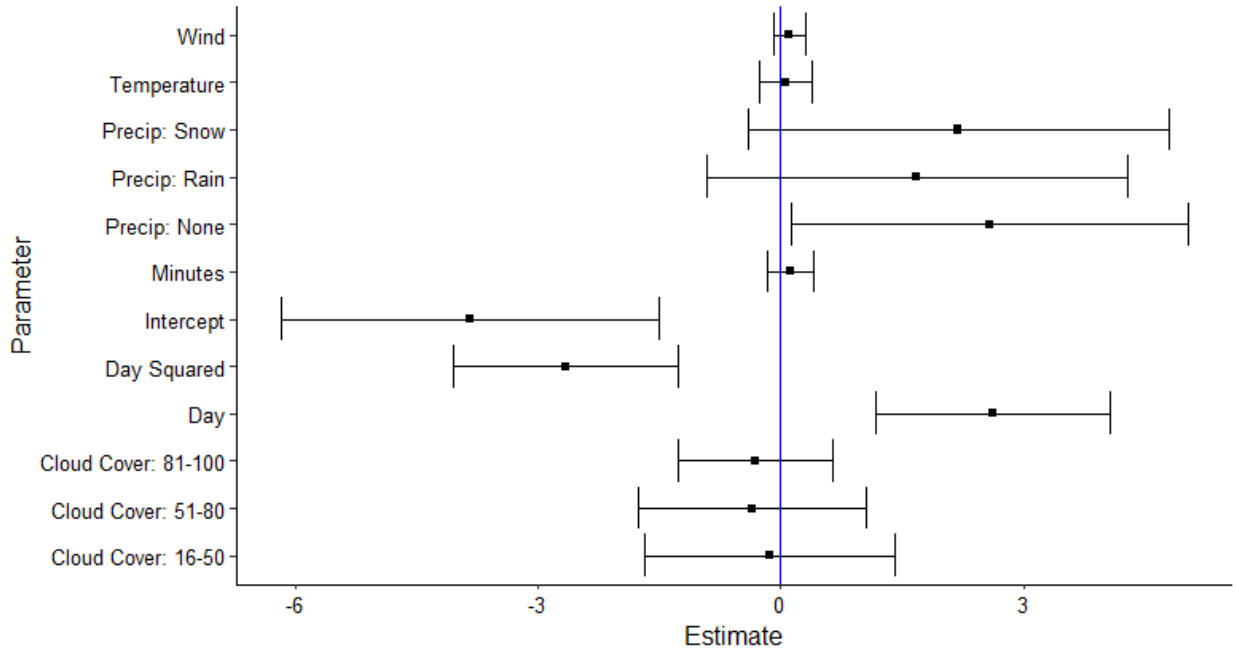


Figure 15. Standardized effects with 95% confidence intervals of survey conditions on probability of availability from a hierarchical distance sampling with time removal model for point counts where abundance (per point count area) was held constant, sigma (for the detection function) was modeled based on noise level, and availability was modeled based on precipitation, cloud cover, noise level, day during the sampling period, minutes since sunrise, temperature, and wind speed. Reference level for noise level is noise level: 0, for precipitation is fog, and for cloud cover is 0-15%.

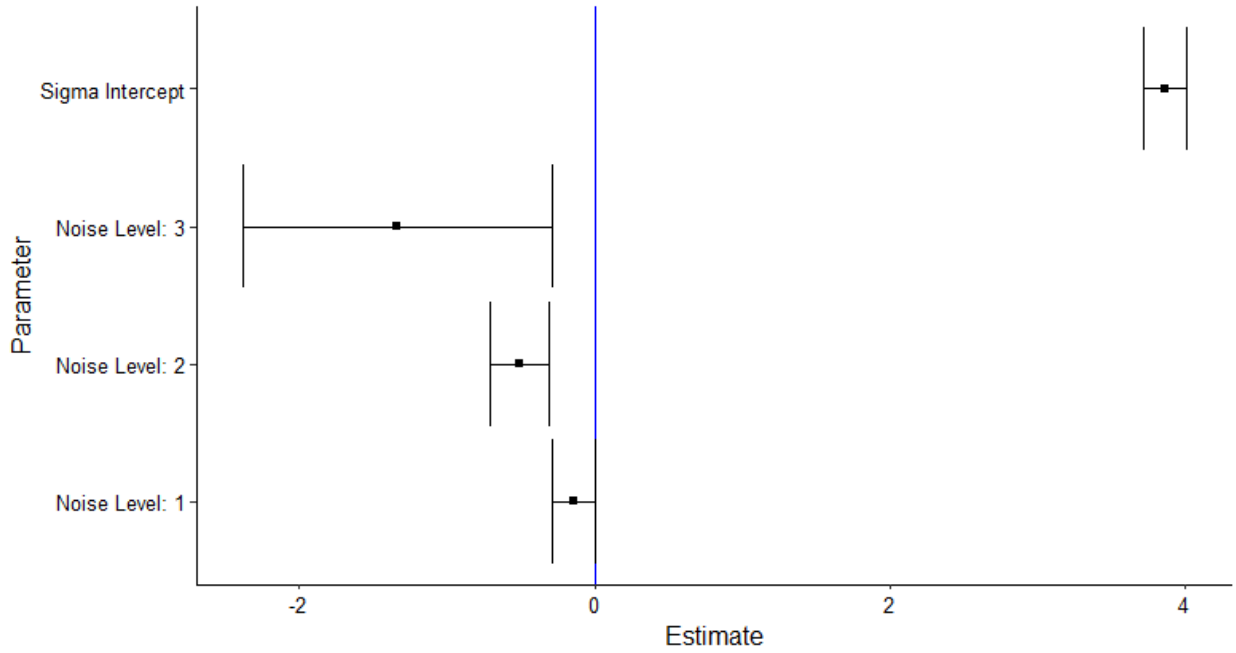


Figure 16. Standardized effects with 95% confidence intervals of noise level on sigma from a hierarchical distance sampling with time removal model for point counts where abundance (per point count area) was held constant, sigma (for the detection function) was modeled based on noise level, and availability was modeled based on precipitation, cloud cover, noise level, day during the sampling period, minutes since sunrise, temperature, and wind speed. Reference level for noise level is noise level: 0, for precipitation is fog, and for cloud cover is 0-15%.

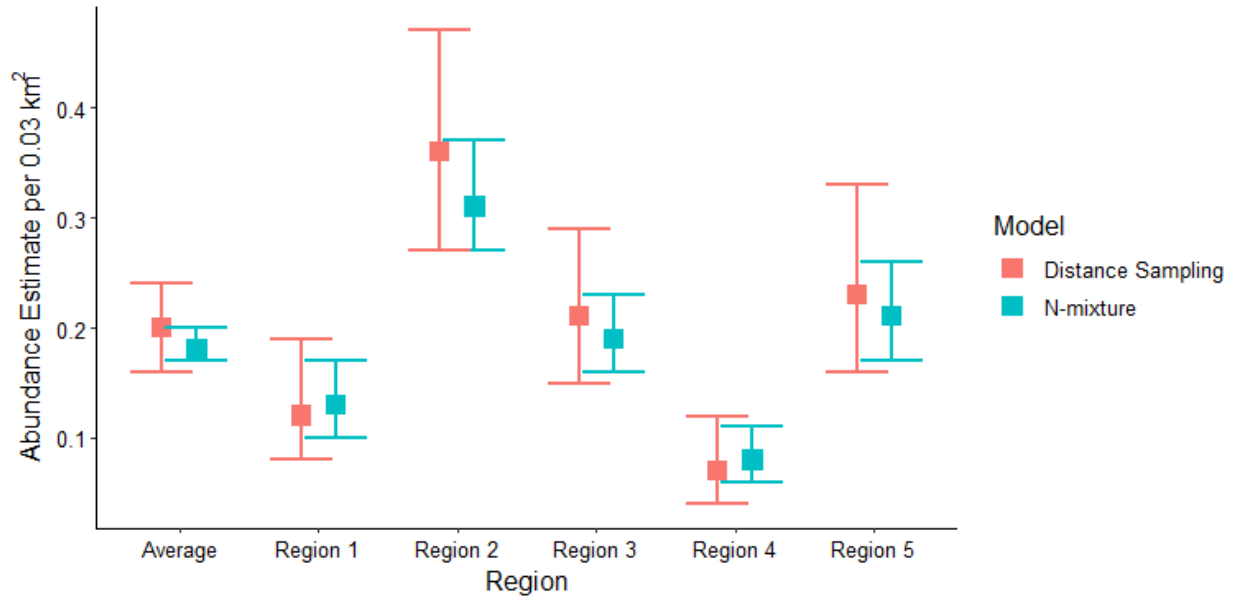


Figure 17. Abundance estimates per point count with 95% confidence intervals across FWP Regions 1-5 based on N-mixture and Distance Sampling model where detection (p or sigma) was held constant and abundance was allowed to vary by region. There is also average abundance from N-mixture and Distance Sampling models where both detection (p or sigma) and abundance was held constant.

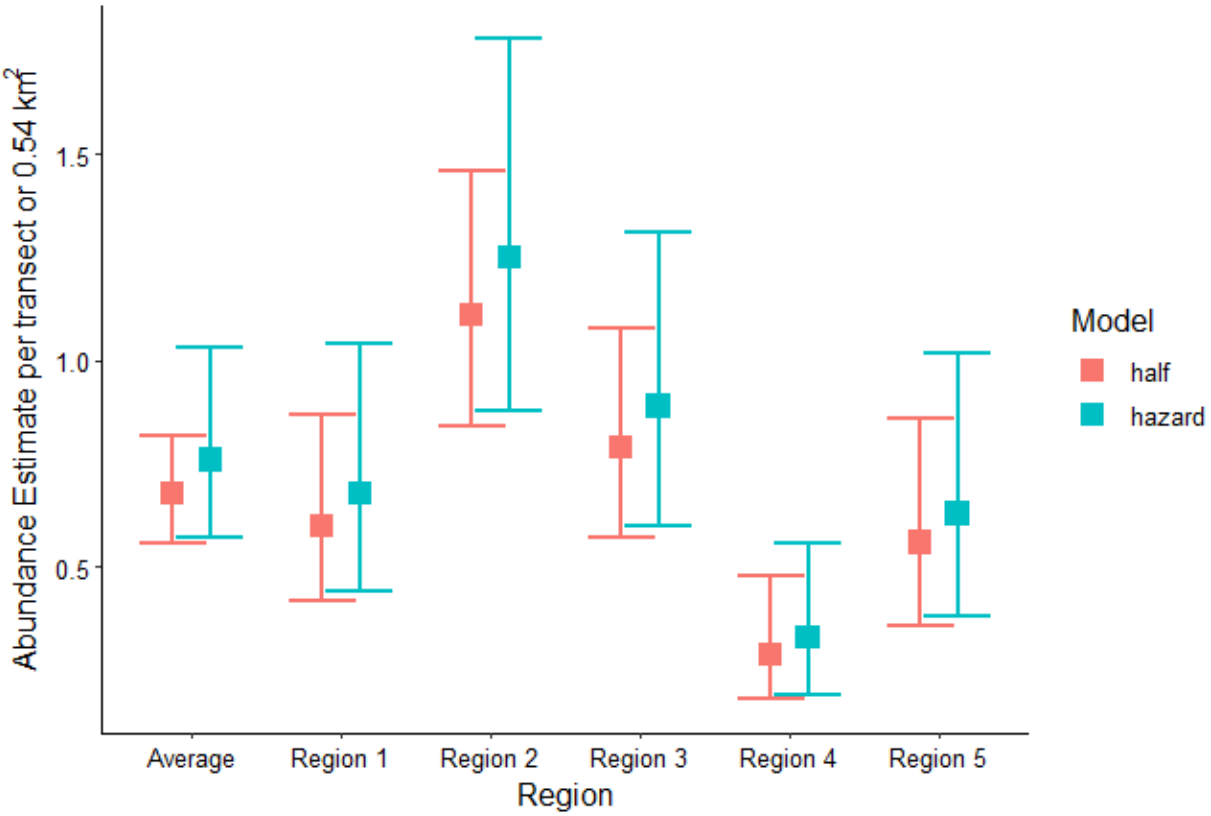


Figure 18. Abundance estimates per point count with 95% confidence intervals across FWP Regions 1-5 based on hierarchical distance sampling models with a half-normal detection function and a hazard-rate detection function where detection (sigma) was held constant and abundance was allowed to vary by region. There is also average abundance from the distance sampling models where both detection (sigma) and abundance were held constant.

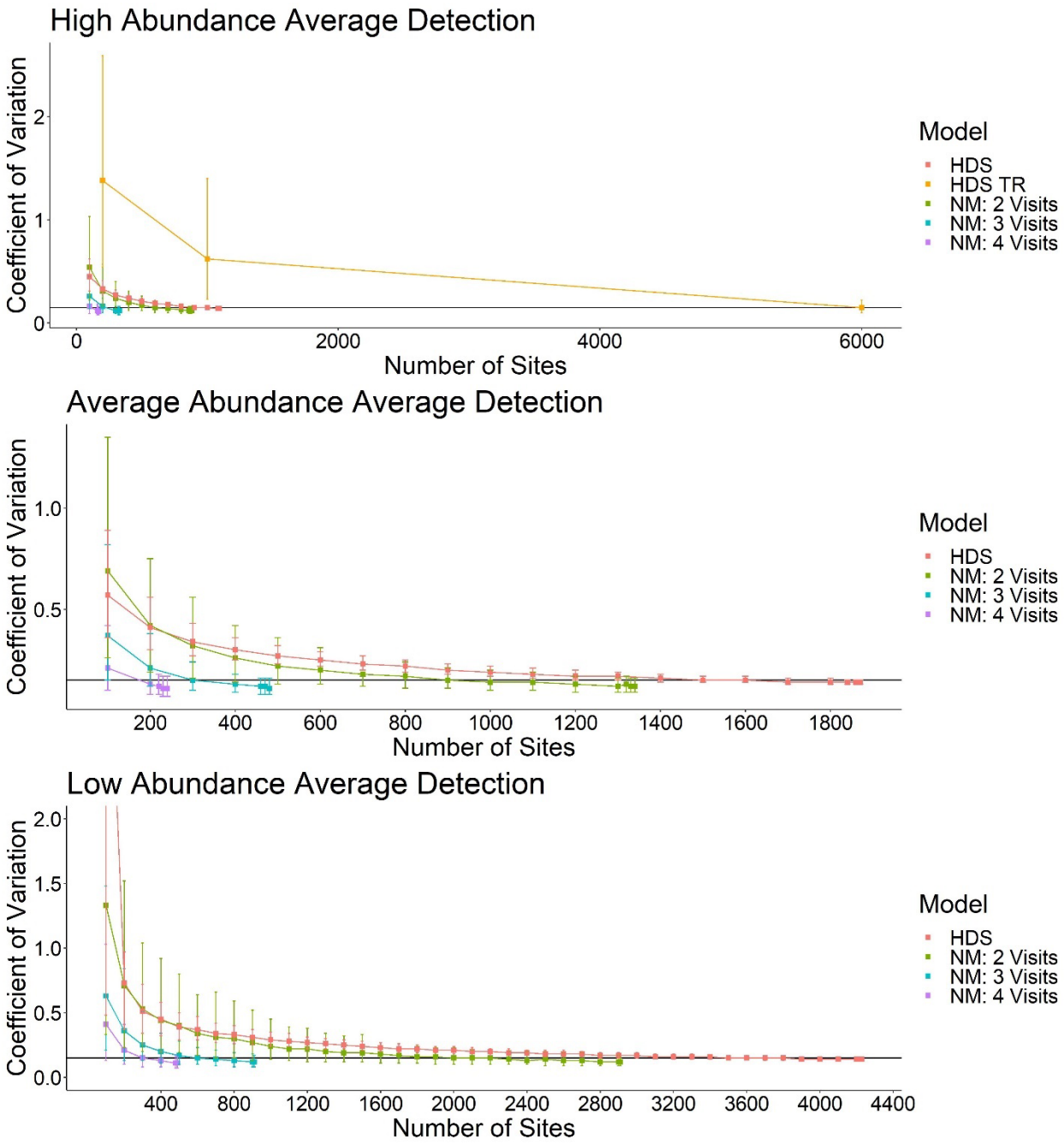


Figure 19. Coefficient of variation for estimates of population size for number of sites visited under different protocols for N-mixture and hierarchical distance sampling models under different scenarios with varying abundance and average detection. For the N-mixture model, protocols with 2, 3, or 4 visits are evaluated. NM = N-mixture model, HDS = hierarchical distance sampling model, HDS TR = hierarchical distance sampling with time removal model. Horizontal line represents the goal of a coefficient of variation of 0.15 or lower.

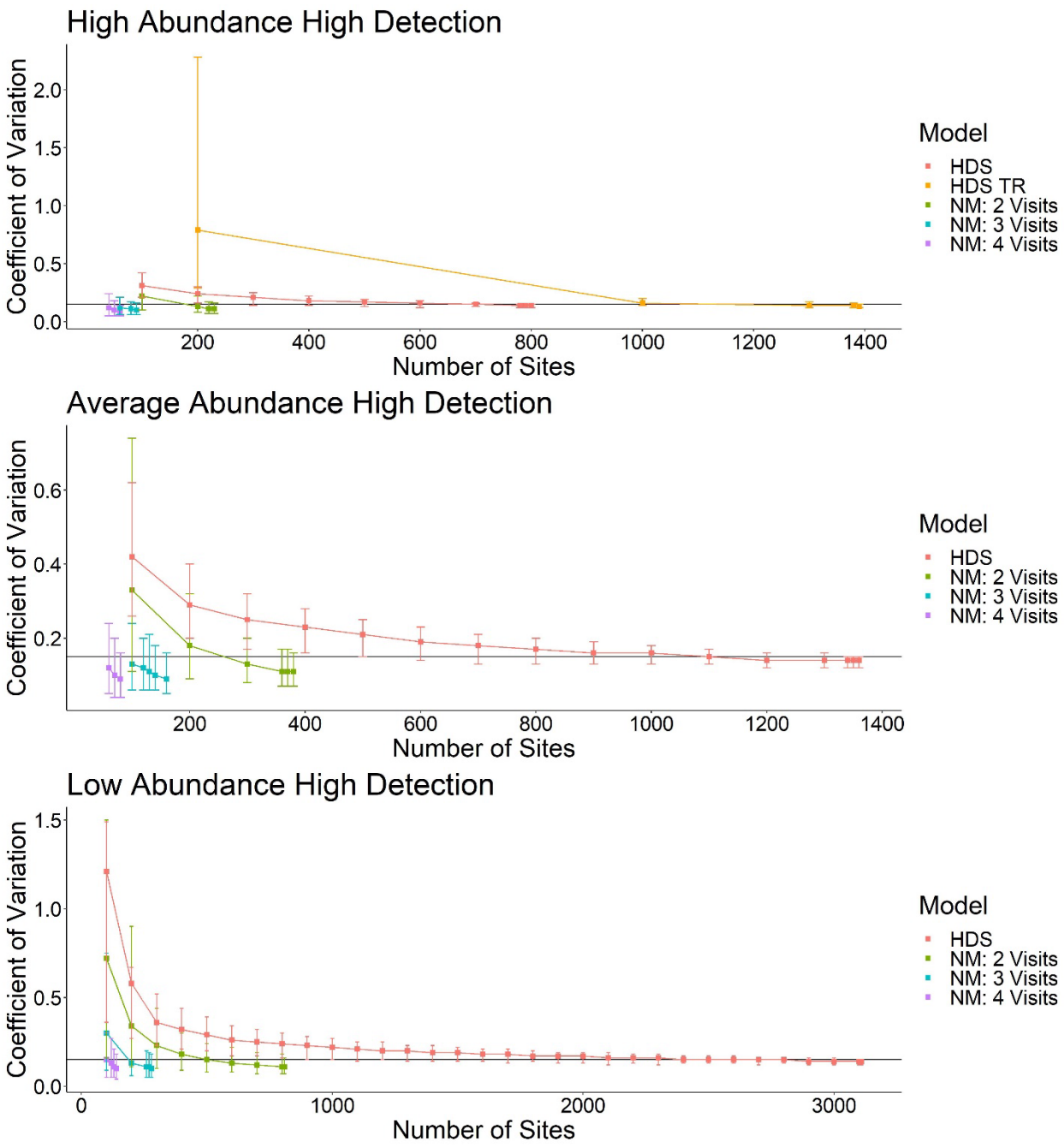


Figure 20. Coefficient of variation for estimates of population size for number of sites visited under different protocols for N-mixture and hierarchical distance sampling models under different scenarios with varying abundance and high detection. For the N-mixture model, protocols with 2, 3, or 4 visits are evaluated. NM = N-mixture model, HDS = hierarchical distance sampling model, HDS TR = hierarchical distance sampling with time removal model. Horizontal line represents the goal of a coefficient of variation of 0.15 or lower.

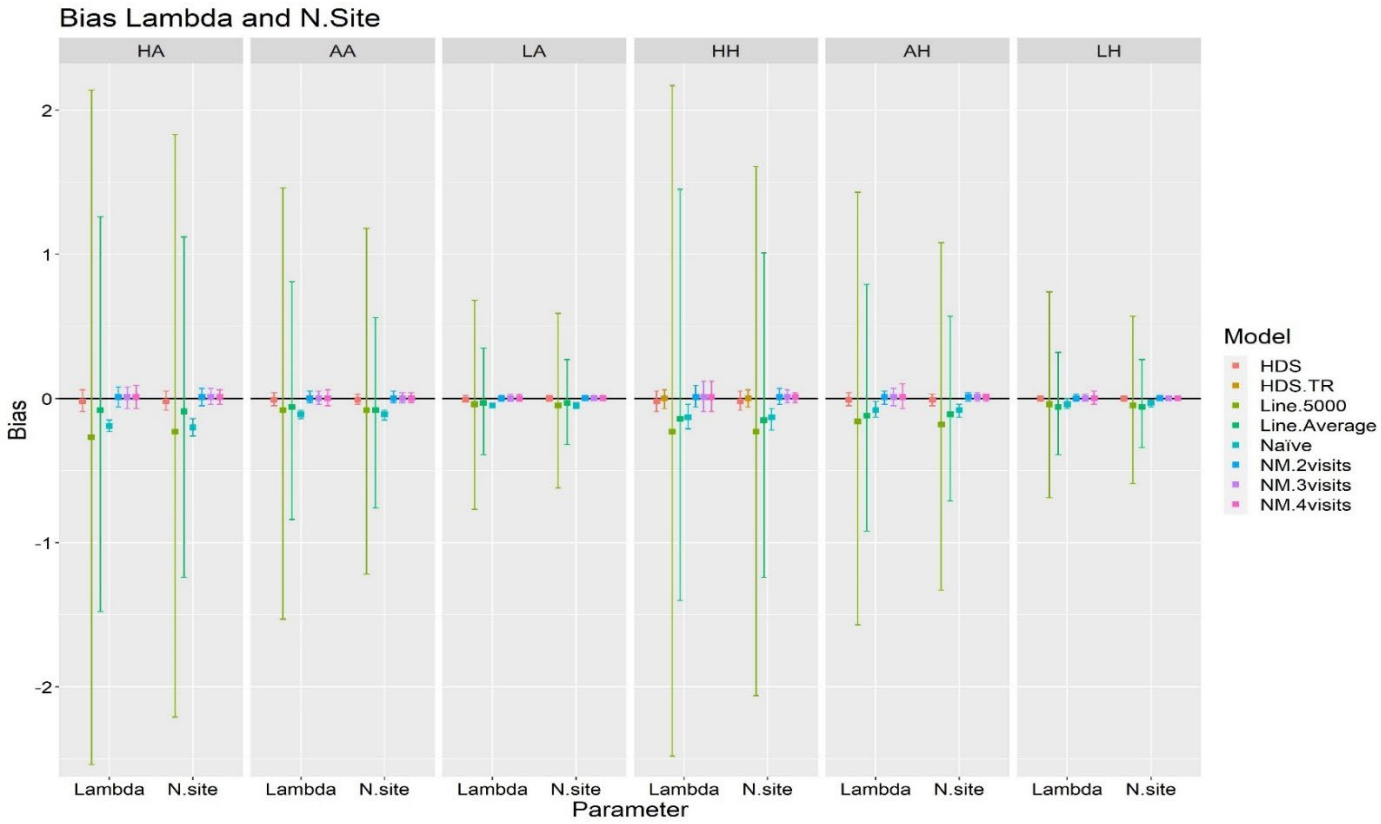


Figure 21. Parameter bias over 500 simulations under 6 scenarios with varying abundance and detection/sigma. Parameters are average local/point count abundance (lambda) and abundance at each site (N.site). Scenarios include, HA = high abundance, average detection, AA = average abundance, average detection, LA = low abundance, average detection, HH = high abundance, high detection, AH = average abundance, high detection, and LH = low abundance, high detection. There 8 models evaluated: HDS = hierarchical distance sampling for point counts, HDS.TR = hierarchical distance sampling with time removal, Line.5000 = hierarchical distance sampling for line transects 5000m in length, Line.Average = hierarchical distance sampling for line transects of average (2,681m) length, Naïve = naïve model, and NM with varying visits = N-mixture model with either 2, 3, or 4 visits.

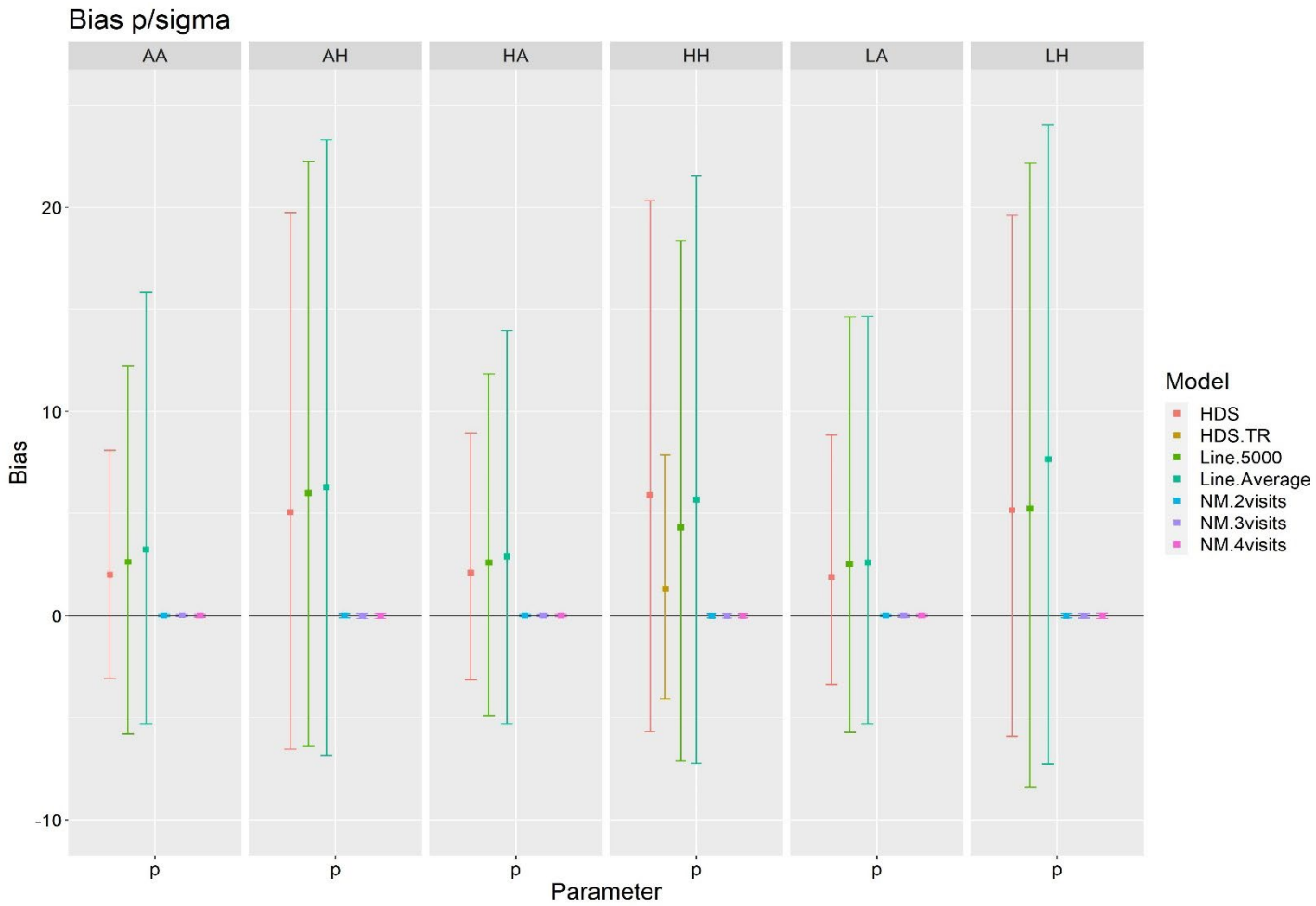


Figure 22. Bias over 500 simulations under 6 scenarios with varying abundance and detection/sigma for probability of detection (N-mixture model) and sigma (all hierarchical distance sampling models). Scenarios include, HA = high abundance, average detection, AA = average abundance, average detection, LA = low abundance, average detection, HH = high abundance, high detection, AH = average abundance, high detection, and LH = low abundance, high detection. There 7 models evaluated: HDS = hierarchical distance sampling for point counts, HDS.TR = hierarchical distance sampling with time removal, Line.5000 = hierarchical distance sampling for line transects 5000m in length, Line.Average = hierarchical distance sampling for line transects of average (2,681m) length, and NM with varying visits = N-mixture model with either 2, 3, or 4 visits.

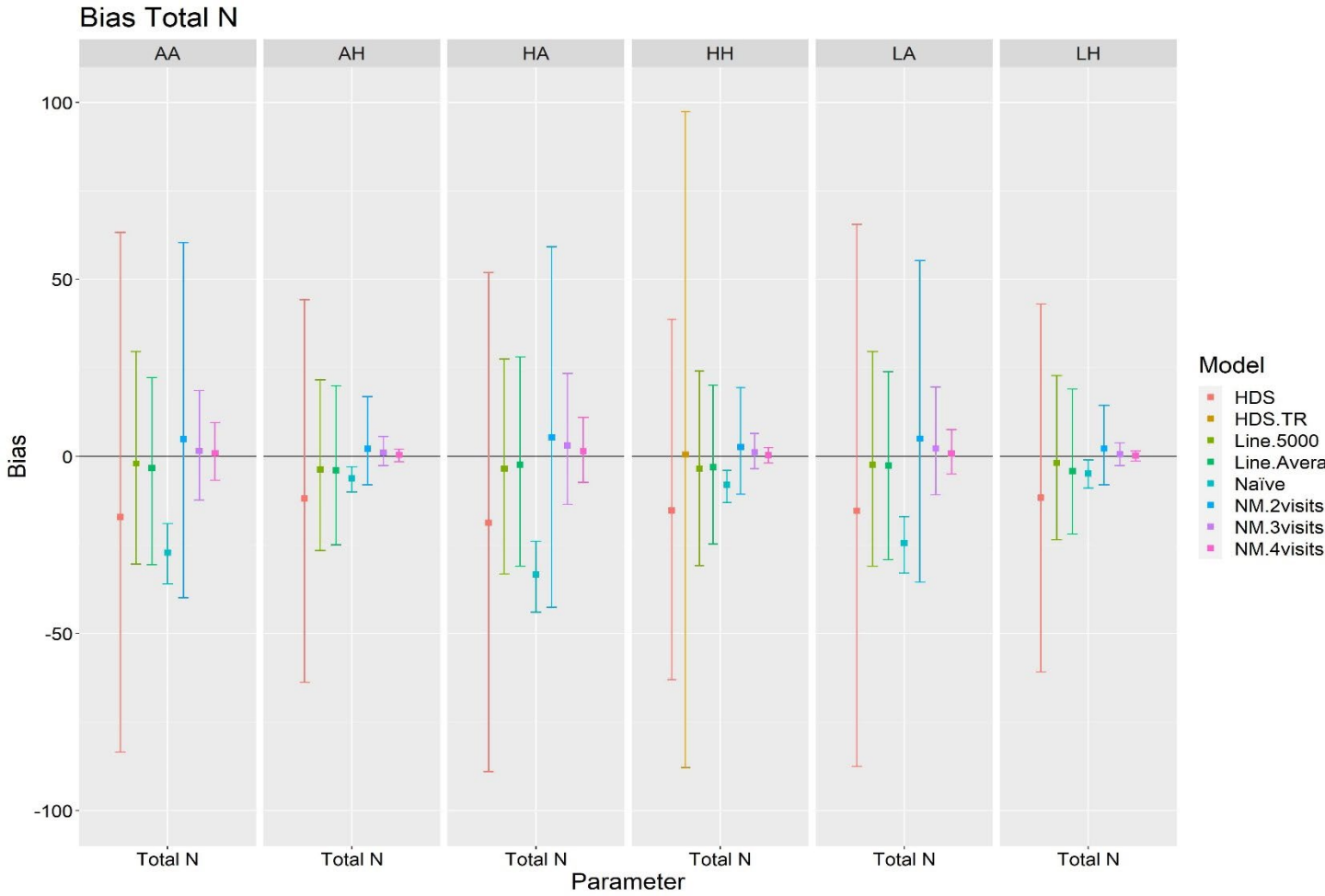


Figure 23. Bias over 500 simulations under 6 scenarios with varying abundance and detection/sigma for total population size (Total N). Scenarios include, HA = high abundance, average detection, AA = average abundance, average detection, LA = low abundance, average detection, HH = high abundance, high detection, AH = average abundance, high detection, and LH = low abundance, high detection. There 7 models evaluated: HDS = hierarchical distance sampling for point counts, HDS.TR = hierarchical distance sampling with time removal, Line.5000 = hierarchical distance sampling for line transects 5000m in length, Line.Average = hierarchical distance sampling for line transects of average (2,681m) length, and NM with varying visits = N-mixture model with either 2, 3, or 4 visits.

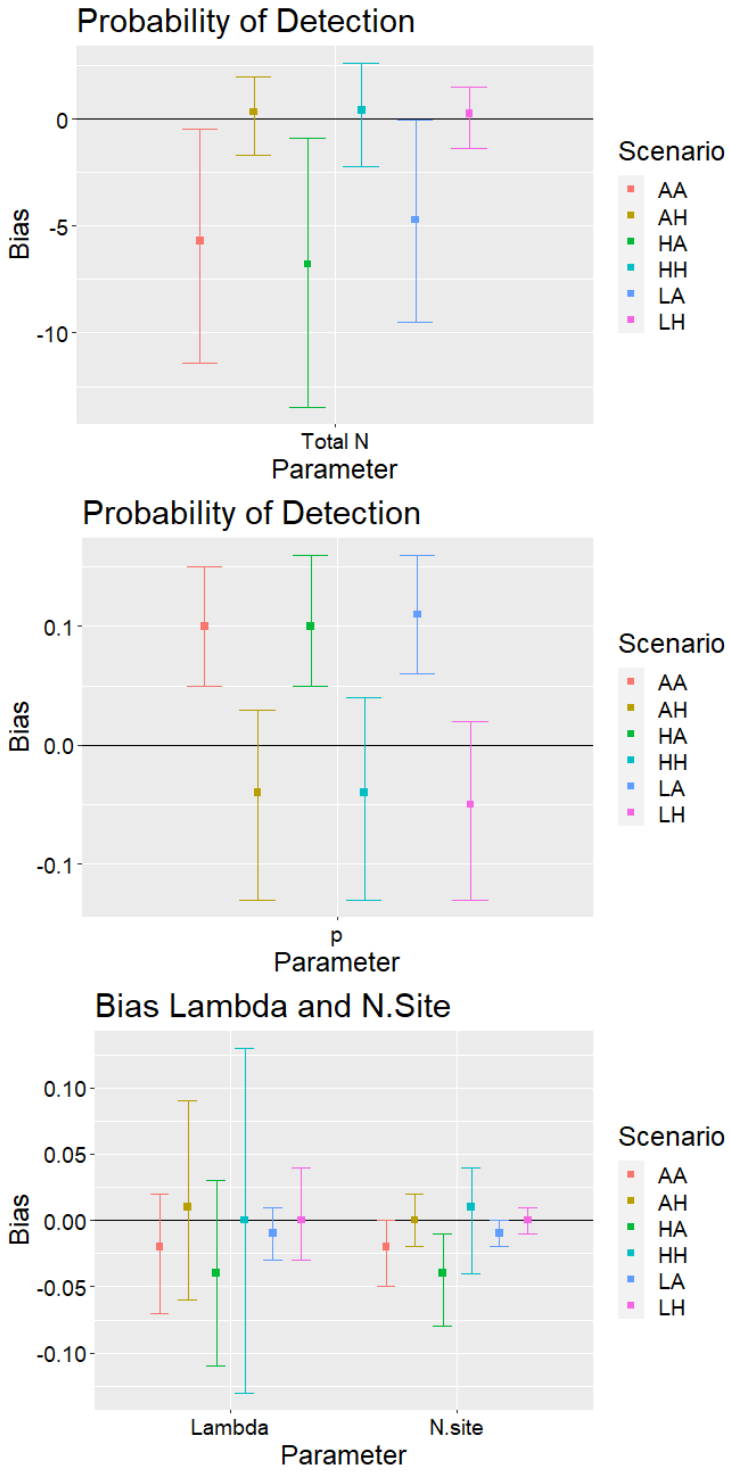
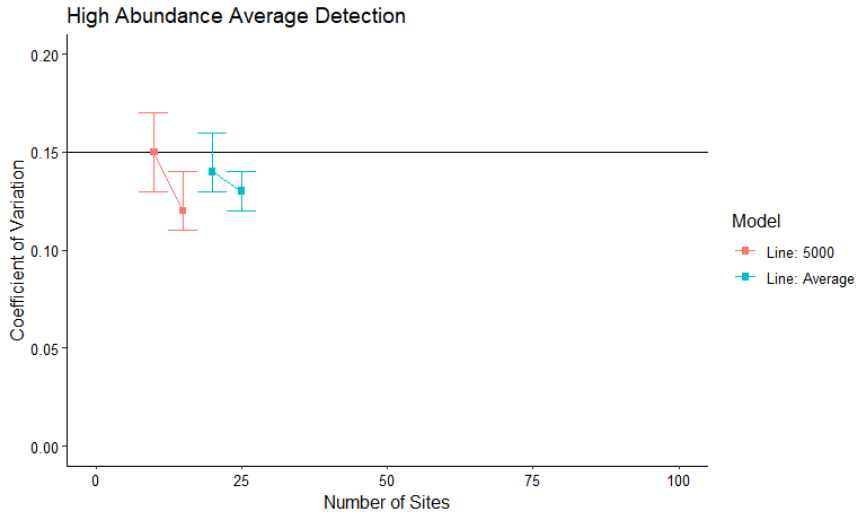
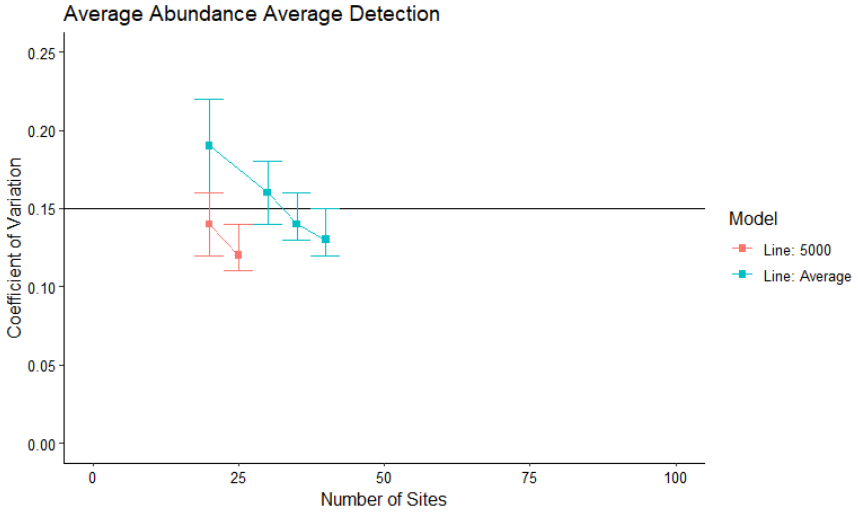
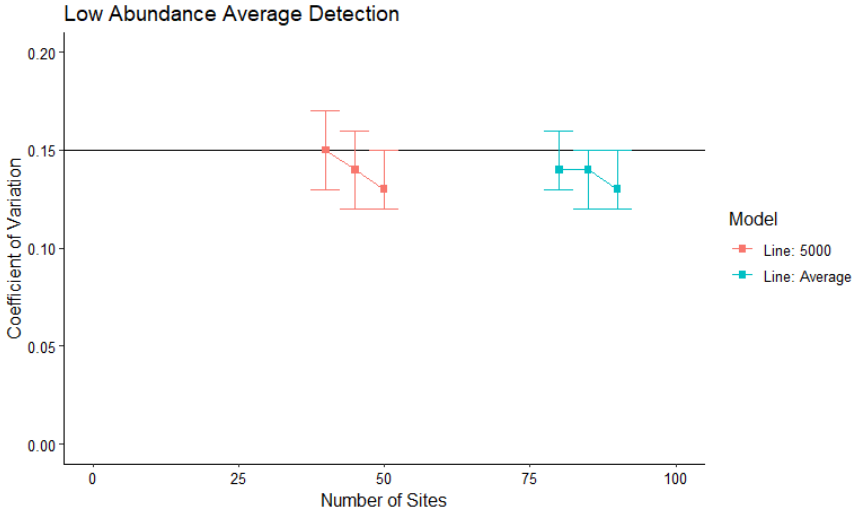


Figure 24. Bias over 500 simulations under 6 scenarios with varying abundance and detection/sigma for total population size (Total N). Scenarios are HA = high abundance, average detection, AA = average abundance, average detection, LA = low abundance, average detection, HH = high abundance, high detection, AH = average abundance, high detection, and LH = low abundance, high detection. Models evaluated are the 'best' protocols from the N-mixture models with 4 visits.


High Abundance Average Detection
Coefficient of Variation
0.20
0.15
0.10
0.05
0.00
0
25
50
75
100
Number of Sites
Model
Line: 5000
Line: Average


Average Abundance Average Detection
Coefficient of Variation
0.25
0.20
0.15
0.10
0.05
0.00
0
25
50
75
100
Number of Sites
Model
Line: 5000
Line: Average


Low Abundance Average Detection
Coefficient of Variation
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0.15
0.10
0.05
0.00
0
25
50
75
100
Number of Sites
Model
Line: 5000
Line: Average

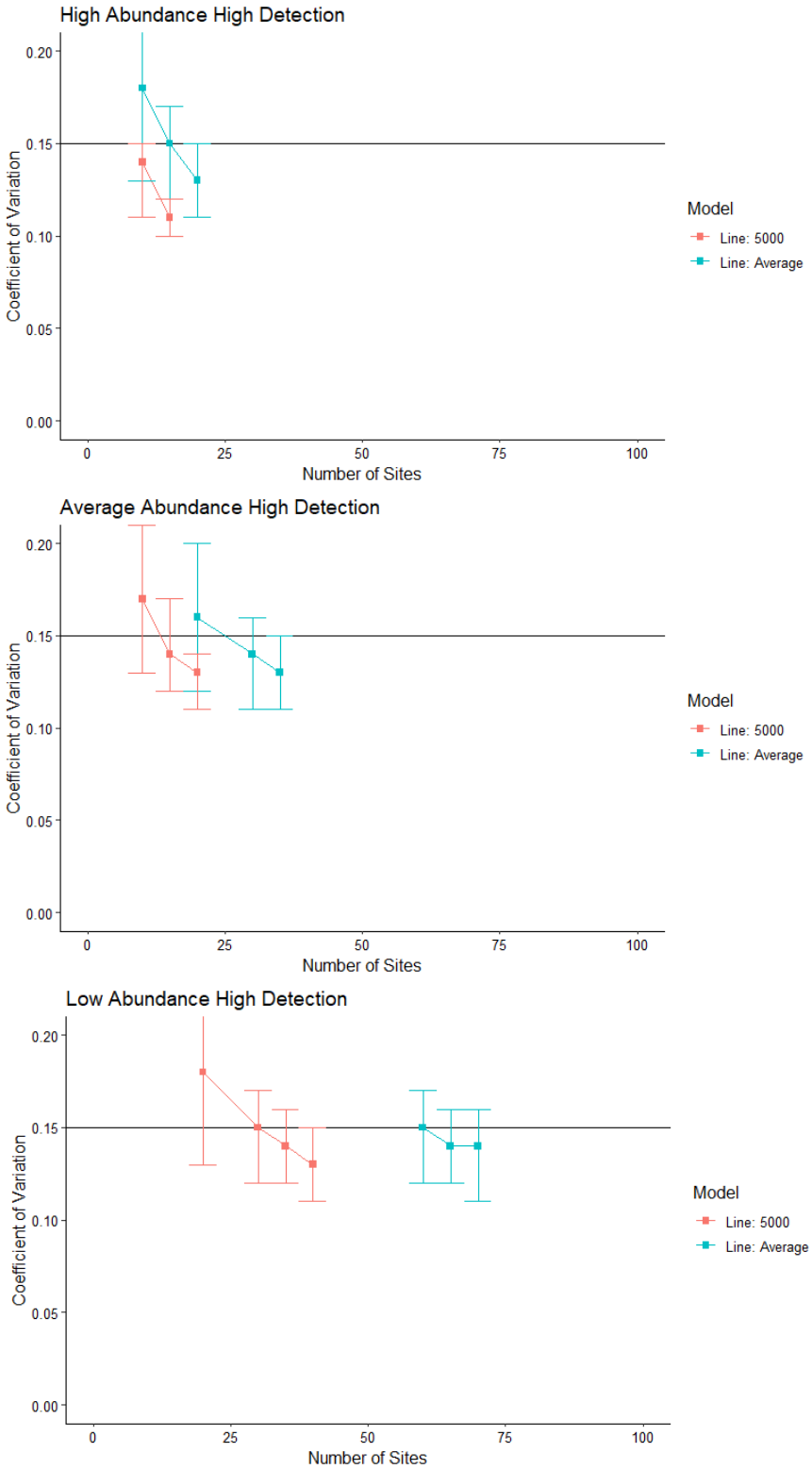

Figure 25. Coefficient of variation with 95% credible intervals for average transect length (2,681m) and 5,000m transect length across differing number of sites visited for six different scenarios where abundance varied (high, average, and low) and detection varied (average and high).

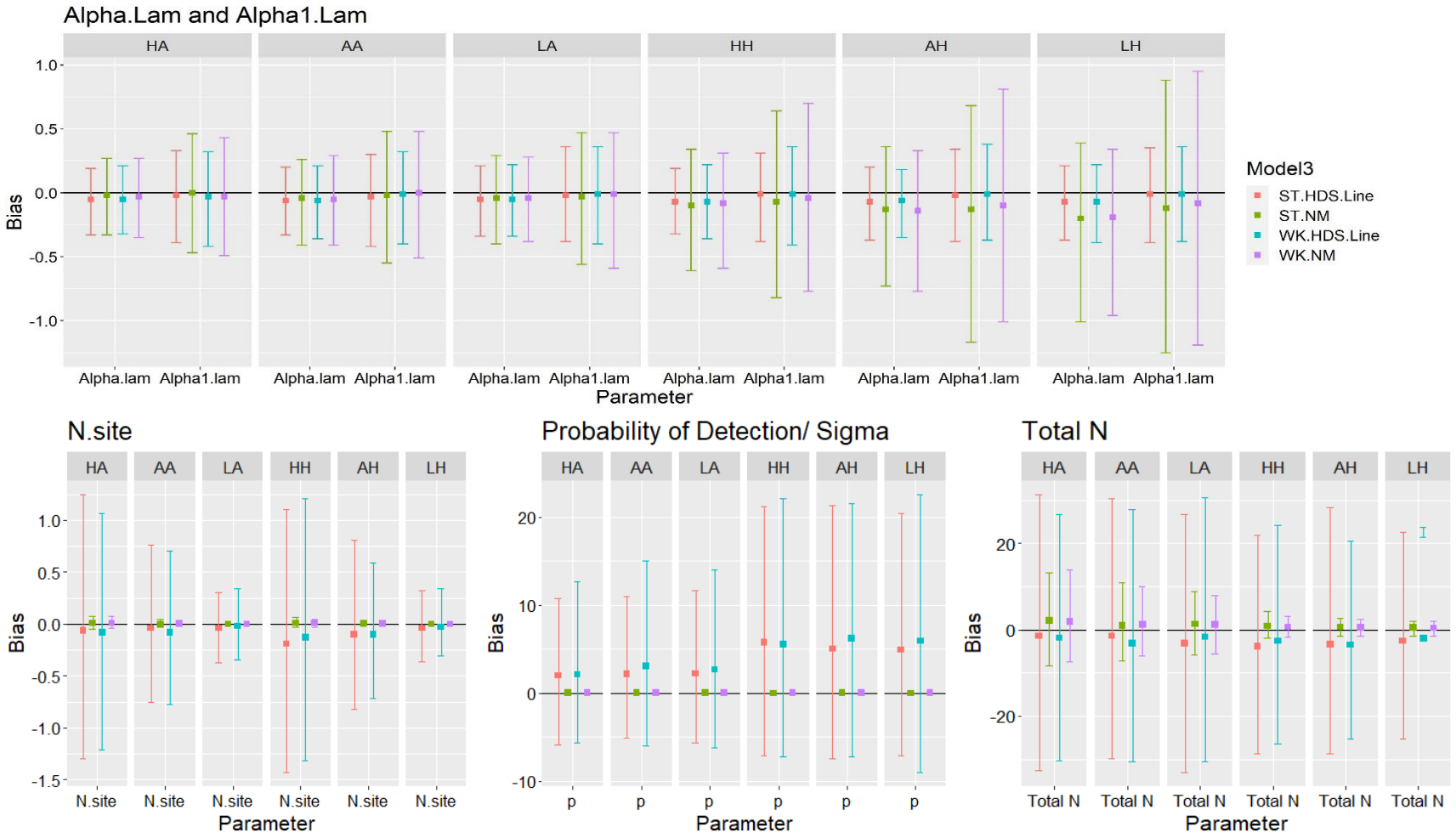

Figure 26. Bias over 500 simulations under 6 scenarios with varying abundance and detection/sigma for total population size (Total N). Scenarios are HA = high abundance, average detection, AA = average abundance, average detection, LA = low abundance, average detection, HH = high abundance, high detection, AH = average abundance, high detection, and LH = low abundance, high detection. Models evaluated are the 'best' protocols from the N-mixture models with 4 visits and hierarchical distance sampling for line transects (2,681m long) with either a strong or weak covariate effect on lambda. Alpha.lam = intercept from linear covariate model, alpha1.lam = slope coefficient estimating linear relationship between local dusky grouse abundance and site covariate X.

Literature Cited

Aldridge, C. L., D. J. Saher, T. M. Childers, K. E. Stahlnecker, and Z. H. Bowen. 2012. Crucial nesting habitat for gunnison sage-grouse: A spatially explicit hierarchical approach. The Journal of Wildlife Management 76:391-406.

Amundson, C. L., J. A. Royle, C. M. Handel. 2014. A hierarchical model combining distance sampling and time removal to estimate detection probability during avian point counts. The Auk 131(4):476-494.

Araùjo, M. B., and New, M. 2006. Ensemble forecasting of species distributions. Trends in Ecology and Evolution. 22:42-47

Arnold, T. W. 2010. Uninformative parameters and model selection using Akaike's information criterion. Journal of Wildlife Management 74:1175-1178.

Bates, D., M. Machler, B. Bolker, and S. Walker. 2015. Fitting linear mixed-effects models using lme4. Journal of Statistical Software 67:1-48.

Beyer, H. L. 2015. Version 0.7.4.0.

Bendell, J. F., P. W. Elliot. 1967. Behavior and the regulation of numbers in blue grouse. Canadian Wildlife Service Report Series: 4, Department of Indian Affairs and Northern Development. Ottawa.

Boyce, M. S., and L. L. McDonald. 1999. Relating populations to habitats using resource selection functions. TREE 14(7):268-272

Boyce, M. S., P. R. Vernier, S. E. Nielsen, and F. K. A. Schmiegelow. 2002. Evaluating resource selection functions. Ecological Modelling 157:281-300.

Breiman, L. 2001. Random forests. Machine learning 45:5-32.

Buckland, S.T., D. R. Anderson, K. P. Burnham, J. L. Laake, D. L. Borchers, and L. Thomas. 2001. Introduction to distance sampling. Oxford University Press, Oxford.

Burnham, K. P., and D. R. Anderson. 2002. Model Selection and Multimodel Inference A practical information-theoretic approach. Second edition. Springer, New York.

Dugger, K. M., F. Wager, R. G. Anthony, and G. S. Olson. 2005. The relationship between habitat characteristics and demographic performance of northern spotted owls in southern Oregon. The Condor 107:863-878.

Evans, J. S., and S. A. Cushman. 2009. Gradient modeling of conifer species using random forests. Landscape Ecology 24:673-683.

Evans, J. S., M. A. Murphy, Z. A. Holden, and S. A. Cushman. 2011. Modeling species distribution and change using random forest. Pages 139-159 in Predictive species and habitat modeling in landscape ecology. Springer.

Farnsworth, Skyler Y. 2020. Forest Grouse Ecology and Management in the Bear River Range Northern Utah. Thesis. Utah State University, USA.

Fisk I., and R. Chandler. 2011. Unmarked: an R package for fitting hierarchical models of wildlife occurrence and abundance. Journal of Statistical Software 43(i10).

Franklin, A.B., D.R. Anderson, R.J. Gutierrez, and K. P. Burnham. 2000. Climate, habitat quality, and fitness in northern spotted owl populations in northwestern California. Ecological Monographs 70: 539-590.

Gelman, A., and D. B. Rubin. 1992. Inference from iterative simulation using multiple sequences. Statistical Science 7:457-511.

Guisan, A., and N. E. Zimmerman. 2000. Predictive habitat distribution models in ecology. Ecological Modelling 135:147-186.

Guisan, A., T. C. J. Edwards, and T. Hastie. 2002. Generalized linear and generalized additive models in studies of species distributions: setting the scene. Ecological Modelling 157:89-100.

Hanni, D. J., C. M. White, N. J. V. Lanen, J. J. Birek, J. M. Berven, and M. F. McLaren. 2018. Integrated Monitoring in Bird Conservation Regions (IMBCR): Field protocol for spatially-balanced sampling of land bird populations.

Heinze, G., C. Wallisch, and D. Dunkler. 2018. Variable selection – A review and recommendations for the praticing statistician. Biometrical Journal 60:431-449.

Hosmer, D. W., S. Lemeshow, and R. X. Sturdivant. 2013. Applied logistic regression. Wiley, New York.

Johnson, C. J., S. E. Nielsen, E. H. Merril, T. L. McDonald, and M. S. Boyce. 2006. Resource selection functions based on use-availability data: theoretical motivation and evaluationg methods. Journal of Wildlife Management 70:347-357.

Kellner, K. 2019. jagsUI: A wrapper around 'rjags' to streamline 'Jags' analyses. R package version 1.5.1. https://CRAN.R-project.org/package=jagsUI

Kery, M., and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom.

Kery, M., and M. Schaub. 2012. Bayesian Population Analysis Using WinBugs A hiearchical perspective. Elsevier Inc.

Kuhn, M. 2008. Caret package. Journal of Statistical Software 28.

Kuhn, M., K. Johnson. 2013. Applied Predictive Modeling. Springer.

Kuhn, M. 2019. The caret Package. https://topepo.github.io/caret/index.html. Accessed 25 April 2022.

LANDFIREa. 2016. LANDFIRE Existing Vegetation Canopy Layer, LANDFIRE 2016 Remap (LF 2.0.0). U.S. Department of the Interior, Geological Survey. Accessed September 2020 at http://landfire.cr.usgs.gov/viewer/.

LANDFIREb. 2016. LANDFIRE Existing Vegetation Height Layer, LANDFIRE 2016 Remap (LF 2.0.0). U.S. Department of the Interior, Geological Survey. Accessed September 2020 at http://landfire.cr.usgs.gov/viewer/.

LANDFIRE. 2016c. LANDFIRE Existing Vegetation Type Layer, LANDFIRE 2016 Remap (LF 2.0.0). U.S. Department of the Interior, Geological Survey. Accessed September 2020 at http://landfire.cr.usgs.gov/viewer/.

LANDFIRE. 2019. LANDFIRE product descriptions with references. U.S. Department of the Interior, Geological Survey.

LANDFIRE. 2020. LANDFIRE 2016 Remap (LF 2.0.0). U.S. Department of the Interior, Geological Survey.

Le Lay, G., R. Engler, E. Franc, and A. Guisan. 2010. Prospective sampling based on model ensembles improves the detection of rare species. Ecography 33:1015-1027.

Lunn, D.J., Thomas, A., Best, N., and Spiegelhalter, D. 2000. WinBUGS — a Bayesian modelling framework: concepts, structure, and extensibility. Statistics and Computing, 10:325–337.

Manly, B. F. J., L. L. McDonald, D. L. Thomas, T. L. McDonald, and W. P. Erickson. 2002. Resource Selection by Animals Statistical Design and Analysis for Field Studies. Second edition. Kluwer Academic Publishers, New York.

McNew, L. B., A. J. Gregory, and B. K. Sandercock. 2013. Spatial heterogeneity in habitat selection: Nest site selection by greater prairie-chickens. The Journal of Wildlife Management 77:791-801.

McNew, L. B., V. L. Winder, J. C. Pitman, and B. K. Sandercock. 2015. Alternative rangeland management strategies and the nesting ecology of greater prairie-chickens. Rangeland Ecology & Management 68:298-304.

McNew, L., Leipold, E., Gower, C., Berkeley, L. 2018. Estimating the occupancy, abundance, and density of dusky grouse: developing methods of unbiased population monitoring in Montana, Annual Report. Montana Fish, Wildlife, and Parks, Bozeman, Montana.

McNew, L., Leipold, E., Gower, C., Berkeley, L. 2021. Estimating the occupancy, abundance, and density of dusky grouse: developing methods of unbiased population monitoring in Montana, Annual Report. Montana Fish, Wildlife, and Parks, Bozeman, Montana.

Molnar, C. 2022. Interpretable Machine Larning: A Guide for Making Black Box Models Explainable (2nd. Ed.). christophm.github.io/interpretable-ml-book/

Montana Spatial Data Infrastructure (MSDI). Transportation Framework. 2017. Montana State Library. http://geoinfo.msl.mt.gov/msdi/hydrography

Montana Spatial Data Infrastructure (MSDI). Hydrography. 2018. Montana State Library. http://geoinfo.msl.mt.gov/msdi/transportation/

Pavlacky, D. C. J., J. A. Lukacs, R. C. Blakesley, D. S. Skokowsky, D. S. Klute, B. A. Hahn, V. J. Dreitz, T. L. George, and D. J. Hanni. 2017. A statistically rigours sampling design to integrate avian monitoring and management within Bird Conservation Regions. PLoS One 12.

R Core Team. 2017. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Royle, J.A. 2004. N-mixture models for estimating population size from spatially replicated counts. Biometrics 60:108–115.

Stirling, I. and J. F. Bendell. 1966. Census of blue grouse with recorded calls of a female. The Journal of Wildlife Management. 30: 184-187.

Stohlgren, T. J., P. Ma, S. Kumar, M. Rocca, J. T. Morisette, C. S. Jarnevich, and N. Benson. 2010. Ensemble habitat mapping of invasive plant species. Risk Analysis 30:224-235.

U.S. Geological Survey, The National Map, 2017, 3DEP products and services: The National Map, 3D Elevation Program Web page, accessed at https://nationalmap.gov/3DEP/3dep_prodserv.html.

Zurr, A. F. 2009. Mixed effects models and extensions in ecology with R. Springer, New York.

Zwickel, FC, and Bendell, JF. 2004. Blue Grouse: Their biology and natural history. NRC Research Press, Ottawa, Ontario, Canada.

SUPPLEMENTARY INFORMATION

S1. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for point counts analyzed using N-mixture models where local abundance and probability of detection were kept constant.

```
# Function for simulating and analyzing data using a N-mixture model for point counts in which average local abundance and probability of detection are kept constant.

# Code adapted from:
#Kery, M. and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom.
# Kery, M. and M. Schaub. 2012. Bayesian population analysis using WinBUGS. A hierarchical perspective. Elsevier Inc.

# S = number of spatial reps/ number of sites
# V = number of visits at each site (temporal reps)
# lambda = average local abundance
# prob = probability of detection
# num.sim = number of simulations

#Simulate Data - Nmixture model. Parameters estimated: lambda and probability of detection
Sim.Nmix.fn <- function(S=S, V=V, lambda = lambda, prob = prob, num.sim = num.sim) {
  library(jagsUI) # use the JAGS for analyzing data within a Bayesian framework

  #***************
  # Define Bayesian Model
  #***************

  # Specify model in Bugs language
  sink("NMmodel.txt")
  cat("
    model {

    # Priors
      lambda ~ dgamma(0.005, 0.005)      # Standard vague prior for lambda
      p ~ dunif(0, 1) #vague prior for probability of detection

    # Likelihood
      # Biological model for true abundance
        for (i in 1:S) {
          N[i] ~ dpois(lambda) #describes spatial variation in abundance (N)
       # Observation model for replicated counts
          for (j in 1:V) {
            y[i,j] ~ dbin(p, N[i]) #count (observation) for each visit at each site
          } # j
       } # i

      #Derived parameters
      Ntotal <- sum(N[]) #total of abundance at each site (N)
    }
```

```
  ",fill = TRUE)
sink()

#************************************************
# Loop for replicating datasets and assessing bias
#************************************************

num.sim <- num.sim

# Create empty vectors to store results from replicated datasets
m.bias.Nsite <- vector("list",num.sim)  #examine bias in abundance (N) at each site
sd.bias.Nsite <- vector("list",num.sim)
baye.pvalue.Nsite <- vector("list",num.sim)

m.bias.p <- vector("list",num.sim) #bias in probability of detection
sd.bias.p <- vector("list",num.sim)
baye.pvalue.p <- vector("list",num.sim)

m.bias.Ntot <- vector("list",num.sim) #bias in total N
sd.bias.Ntot <- vector("list",num.sim)
baye.pvalue.Ntot <- vector("list",num.sim)

m.bias.lam <- vector("list",num.sim)  #bias in recovered lambda (mean abundance at site)
sd.bias.lam <- vector("list",num.sim)
baye.pvalue.lam <- vector("list",num.sim)


m.CV.lam <- vector("list",num.sim)  #coefficient of variation for lambda (mean abundance at site)
sd.CV.lam <- vector("list",num.sim)
prop.CV.lam <- vector("list", num.sim)

m.CV.Ntot <- vector("list",num.sim) #coefficient of variation for total N
sd.CV.Ntot <- vector("list",num.sim)
prop.CV.Ntot <- vector("list", num.sim)

#*******************
# Start Simulation
#*******************

# Stick simulation in loop and replicate num.sim times
system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

  #Simulate data
  S = S  # spatial reps
  V = V  # temporal reps
  lambda = lambda # mean abundance at site
  prob = prob # probablity of detection

  # Create structure to contain counts
  y <- array(dim = c(S,V))
```

```
# sample abundance from a Poisson (lambda = 0.3)
N <- rpois(n=S, lambda=lambda)

# sample counts from a Binomial distribution (N, prob = 0.3)
for (j in 1:V){
  y[,j] <- rbinom(n = S, size = N, prob = prob)
}

# Bundle data
win.data <- list(y = y, S = nrow(y), V = ncol(y))

# initial values
Nst <- apply(y, 1, max) + 1     # This line is vital
inits <- function() list(N = Nst)

# Define parameters to be monitored
params <- c("lambda", "p", "Ntotal", "N")

# MCMC settings
ni <- 5000
nt <- 1
nb <- 1000
nc <- 3

start.time = Sys.time()  #set timer
# run model
out <- jags(win.data, inits, params, "NMmodel.txt", n.chains = nc,
            n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)
print(out)

end.time = Sys.time()
elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

#************************************
#### Evaluate bias ####
#************************************
#Bias in N (site specific abundance)
bias.Nsite <- out$mean$N - N #calculates bias
m.bias.Nsite[k] <- mean(bias.Nsite) #averages bias and places within vector
sd.bias.Nsite[k] <- sd(bias.Nsite) #gets standard deviation of bias places within vector
baye.pvalue.Nsite[k] <-mean(N > out$mean$N)  #Bayesian P-value (proportion of simulations where
the true abundance was greater than the estimated abundance - values close to 0 or 1 indicate significant
bias)

#Bias in lambda (average local abundance) - descriptions same as above
bias.lam <- out$mean$lambda - lambda
m.bias.lam[k] <- mean(bias.lam)
sd.bias.lam[k] <- sd(bias.lam)
baye.pvalue.lam[k] <- mean(lambda > out$mean$lambda)
```

```
    #Bias in p - descriptions same as above
    bias.p <- out$mean$p - prob
    m.bias.p[k] <- mean(bias.p)
    sd.bias.p[k] <- sd(bias.p)
    baye.pvalue.p[k] <- mean(prob > out$mean$p)

    #Bias in Ntotal (total population size) - descriptions same as above
    bias.Ntot <- out$mean$Ntotal - sum(N)
    m.bias.Ntot[k] <- mean(bias.Ntot)
    sd.bias.Ntot[k] <- sd(bias.Ntot)
    baye.pvalue.Ntot[k] <- mean(sum(N) > out$mean$Ntotal)

    #Coefficient of Variation in Ntotal (total population size) - want to be under 15%
    CV.Ntot <- out$sd$Ntotal/out$mean$Ntotal #standard deviation divided by mean
    m.CV.Ntot[k] <- mean(CV.Ntot)
    sd.CV.Ntot[k] <- sd(CV.Ntot)
    prop.CV.Ntot[k] <- mean(CV.Ntot < 0.15)

    #Coefficient of Variation in local abundance (lambda / average local abundance)
    CV.lam <- out$sd$lambda/out$mean$lambda
    m.CV.lam[k] <- mean(CV.lam)
    sd.CV.lam[k] <- sd(CV.lam)
    prop.CV.lam[k] <- mean(CV.lam < 0.15)

  }  ) #This will be the end of the simulations

  #********************
  # Summary of Results
  #********************
  results <- c("lambda", "prob", "N.total", "N.site", "N.total.CV", "lambda.CV", "Prob.CV.Ntot",
"Prob.CV.lambda")
  mean.bias <- round(c((mean(unlist(m.bias.lam))), (mean(unlist(m.bias.p))), (mean(unlist(m.bias.Ntot))),
(mean(unlist(m.bias.Nsite))), (mean(unlist(m.CV.Ntot))), (mean(unlist(m.CV.lam))), NA, NA),2)

  lower.CI <- round(c((quantile(unlist(m.bias.lam), 0.05)), (quantile(unlist(m.bias.p), 0.05)),
(quantile(unlist(m.bias.Ntot), 0.05)), (quantile(unlist(m.bias.Nsite), 0.05)), (quantile(unlist(m.CV.Ntot),
0.05)), (quantile(unlist(m.CV.lam), 0.05)), NA, NA),2) #lower 95% credible interval

  upper.CI <- round(c((quantile(unlist(m.bias.lam), 0.95)), (quantile(unlist(m.bias.p), 0.95)),
(quantile(unlist(m.bias.Ntot), 0.95)), (quantile(unlist(m.bias.Nsite), 0.95)), (quantile(unlist(m.CV.Ntot),
0.95)), (quantile(unlist(m.CV.lam), 0.95)), NA, NA),2) #upper 95% credible interval

  greater.15.CV <- c(NA, NA, NA, NA, NA, NA, (mean(unlist(m.CV.Ntot) > 0.15)),
(mean(unlist(m.CV.lam) > 0.15))) #percent of CV's greater than 15%

  Baye.pvalue <- round(c((mean(unlist(baye.pvalue.lam))), (mean(unlist(baye.pvalue.p))),
(mean(unlist(baye.pvalue.Ntot))), (mean(unlist(baye.pvalue.Nsite))), NA, NA, NA, NA),2)

  sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a
table of results
  print(sim.results)
```

```
  #****************
  #Post processing
  #****************
  # Set plots so that six plots can be created in one image
  par(mfrow = c(6,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

  # Plots
  (hist(unlist(m.bias.Nsite), xlim=c(-1,1), breaks=120, main="", ylab="N.site"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.lam), xlim=c(-1,1), main="", ylab="lambda"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.p), xlim=c(-0.5,0.5), main="", ylab="Detection prob."))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.Ntot), xlim=c(-100,100), main="", ylab="Total N"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.CV.Ntot), xlim=c(0,0.5), main="", ylab="CV Ntotal"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.lam), xlim=c(0,0.5), main="", ylab="CV lambda"))
  (abline(v=0.15, col="red", lwd=3))

   return(list(sim.results=sim.results, m.bias.Nsite=unlist(m.bias.Nsite), m.bias.lam = unlist(m.bias.lam),
m.bias.p = unlist(m.bias.p), m.bias.Ntot = unlist(m.bias.Ntot), m.CV.Ntot = unlist(m.CV.Ntot), m.CV.lam
= unlist(m.CV.lam), lambda = lambda, prob = prob, S = S, V = V, num.sim = num.sim))
  }
```

S2. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for point counts analyzed using N-mixture models where local abundance and probability of detection were kept constant, and point counts visits were correlated.

```
# Functions for simulating data for four visits per site that are correlated where visits 1 & 2 have a correlation of 0.67, 1 & 3 have a correlation of 0.41, 1 & 4 have a correlation of 0.44, 2 & 3 have a correlation of 0.48, 2 & 4 have a correlation of 0.47, and 3 & 4 have a correlation of 0.67. Correlations are based off point counts from 2020 and 2021 data where all counts occurred on the same day and visits 1 & 2, and visits 3 & 4 were back-to-back. There are two functions: rcorrbinom which simulates the correlated counts and Sim.Nmix.fn which uses rcorrbinom to simulate correlated data and then analyzes the data using an N-mixture model. Average local abundance (lambda) across and probability of detection are kept constant.

# rcorrbinom code adapted from:
#https://stats.stackexchange.com/questions/284996/generating-correlated-binomial-random-variables

# Sim.Nmix.fn code adapted from:
#Kery, M. and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom.
# Kery, M. and M. Schaub. 2012. Bayesian population analysis using WinBUGS. A hierarchical perspective. Elsevier Inc.

# S = number of spatial reps/ number of sites
# V = number of visits at each site (temporal reps)
# lambda = average local abundance
# prob = probability of detection
# num.sim = number of simulations

# n = number of observations
# size = number of trials
# prob = probability of detection
# corr1 = correlation between visit 1 & visit 2: 0.67
# corr2 = correlation between visit 2 & visit 3: 0.47
# corr3 = correlation between visit 3 & visit 4: 0.67

# Creates data where visit 1 is correlated with visit 2, visit 2 is correlated with visit 3, and visit 3 is correlated with visit 4
# Creates correlated Bernoulli random variables, which frequently resulted in correlation between the binomial values
rcorrbinom <- function(n, size = size, prob, corr1 = corr1, corr2 = corr2, corr3 = corr3) {
  #Check inputs
  if (!is.numeric(n))            { stop('Error: n must be numeric') }
  if (length(n) != 1)            { stop('Error: n must be a single number') }
  if (as.integer(n) != n)        { stop('Error: n must be a positive integer') }
  if (n < 1)                     { stop('Error: n must be a positive integer') }
  if (!is.numeric(size))         { stop('Error: n must be numeric') }
  if (length(size) != 1)         { stop('Error: n must be a single number') }
  if (as.integer(size) != size)  { stop('Error: n must be a positive integer') }
  if (size < 1)                  { stop('Error: n must be a positive integer') }
  if (!is.numeric(prob))         { stop('Error: prob1 must be numeric') }
```

```
 if (length(prob) != 1)        { stop('Error: prob1 must be a single number') }
 if (prob < 0)                 { stop('Error: prob1 must be between 0 and 1') }
 if (prob > 1)                 { stop('Error: prob1 must be between 0 and 1') }
 if (!is.numeric(corr1))         { stop('Error: corr must be numeric') }
 if (length(corr1) != 1)         { stop('Error: corr must be a single number') }
 if (corr1 < -1)               { stop('Error: corr must be between -1 and 1') }
 if (corr1 > 1)                { stop('Error: corr must be between -1 and 1') }
 if (!is.numeric(corr2))         { stop('Error: corr must be numeric') }
 if (length(corr2) != 1)         { stop('Error: corr must be a single number') }
 if (corr2 < -1)               { stop('Error: corr must be between -1 and 1') }
 if (corr2 > 1)                { stop('Error: corr must be between -1 and 1') }
 if (!is.numeric(corr3))         { stop('Error: corr must be numeric') }
 if (length(corr3) != 1)         { stop('Error: corr must be a single number') }
 if (corr3 < -1)               { stop('Error: corr must be between -1 and 1') }
 if (corr3 > 1)                { stop('Error: corr must be between -1 and 1') }

  #Compute probabilities
 #Between visit 1 & visit 2
 P00.1   <- (1-prob)*(1-prob) + corr1*sqrt(prob*prob*(1-prob)*(1-prob))
 P01.1   <- 1 - prob - P00.1
 P10.1   <- 1 - prob - P00.1
 P11.1   <- P00.1 + prob + prob - 1
 PROBS.1 <- c(P00.1, P01.1, P10.1, P11.1)
 if (min(PROBS.1) < 0)       { stop('Error: corr is not in the allowable range') }

 #Between visit 2 & visit 3
 P00.2   <- (1-prob)*(1-prob) + corr2*sqrt(prob*prob*(1-prob)*(1-prob))
 P01.2   <- 1 - prob - P00.2
 P10.2   <- 1 - prob - P00.2
 P11.2   <- P00.2 + prob + prob - 1
 PROBS.2a <- c(P00.2, P01.2) # First one is zero
 PROBS.2b <- c(P10.2, P11.2) # First one is not zero
 if (min(PROBS.2a) < 0)       { stop('Error: corr is not in the allowable range')}
 if (min(PROBS.2b) < 0)       { stop('Error: corr is not in the allowable range')}

 #Between visit 3 & visit 4
 P00.3   <- (1-prob)*(1-prob) + corr3*sqrt(prob*prob*(1-prob)*(1-prob))
 P01.3   <- 1 - prob - P00.3
 P10.3   <- 1 - prob - P00.3
 P11.3   <- P00.3 + prob + prob - 1
 PROBS.3a <- c(P00.3, P01.3) # First one is zero
 PROBS.3b <- c(P10.3, P11.3) # First one is not zero
 if (min(PROBS.3a) < 0)       { stop('Error: corr is not in the allowable range')}
 if (min(PROBS.3b) < 0)       { stop('Error: corr is not in the allowable range')}

 #Generate the output
 # Generates counts for visits 1 & 2
 # sample.int = n (number of items to choose from), size (number of items to choose), replace (sample
with replacement), prob (vector of probability weights for obtaining the elements of the vector beign
sampled)
 RAND.1 <- array(sample.int(4, size = n*size, replace = TRUE, prob = PROBS.1),
```

```
            dim = c(n, size)) #produces count group, 1 = 00, 2 = 01, 3 = 10 4 = 11
  VALS.1 <- array(0, dim = c(2, n, size)) # will hold results of each trial so could have multiple arrays if
size > 1
  OUT.1  <- array(0, dim = c(2, n)) # will hold counts

  for (i in 1:n)    {
    for (j in 1:size) {
      VALS.1[1,i,j] <- (RAND.1[i,j] %in% c(3, 4)) #is Rand.1 in count groups 3 or 4 (counts 10 or 11)
      VALS.1[2,i,j] <- (RAND.1[i,j] %in% c(2, 4)) }  # is Rand.1 in count groups 2 or 4 (counts 01 or 11)
    OUT.1[1, i]   <- sum(VALS.1[1,i,]) #sums number of detections in first visit -> count for visit 1
    OUT.1[2, i]   <- sum(VALS.1[2,i,]) #sums number of detections in second visit -> count for visit 2
    }

  # Section generates counts for visits 2 & 3, where visit 2 counts are identical to the previous visit 2
counts
  RAND.2 <- array(0, dim = c(n, n*size)) #creates array filled with zeros
  for (i in 1:n) {
    for (j in 1:size) {
      if (VALS.1[2,i,j] > 0) { #if for visit 2, count is greater than 0
        RAND.2[i,j] <- sample.int(2, size = 1, replace = TRUE, prob = PROBS.2b) #place in count group
        if (RAND.2[i,j] == 1) {
          RAND.2[i,j] <- 3 #if in group 1, gets placed in overall group 3 (1,0)
        }
        else {
          RAND.2[i,j] <- 4 #otherwise placed in overall group 4 (1,1)
        }
      }
      else {
        RAND.2[i,j] <- sample.int(2, size = 1, replace = TRUE, prob = PROBS.2a) #place in count group
1(0,0) or 2(0,1)

      }
    }
  }

  VALS.2 <- array(0, dim = c(2, n, size)) #will hold results of each trial
  OUT.2  <- array(0, dim = c(2, n)) #will hold counts

  for (i in 1:n)    {
    for (j in 1:size) {
      VALS.2[1,i,j] <- (RAND.2[i,j] %in% c(3, 4)) #is Rand.2 in probability groups 3 or 4 (counts 10 or
11)
      VALS.2[2,i,j] <- (RAND.2[i,j] %in% c(2, 4)) } # is Rand.2 in probability groups 2 or 4 (counts 01 or
11)
    OUT.2[1, i]   <- sum(VALS.2[1,i,]) #sums number of detections in second visit
    OUT.2[2, i]   <- sum(VALS.2[2,i,]) #sums number of detections in third visit
  }

  # Section generates counts for visits 3 & 4, where visit 3 counts are identical to the previous visit 3
counts
  RAND.3 <- array(0, dim = c(n, n*size)) #creates array filled with zeros
```

```
  for (i in 1:n) {
    for (j in 1:size) {
      if (VALS.2[2,i,j] > 0) { #if for visit 3, count is greater than 0
        RAND.3[i,j] <- sample.int(2, size = 1, replace = TRUE, prob = PROBS.3b) #place in count group
        if (RAND.3[i,j] == 1) {
          RAND.3[i,j] <- 3 #if in group 1, gets placed in overall group 3 (1,0)
        }
        else {
          RAND.3[i,j] <- 4 #otherwise placed in overall group 4 (1,1)
        }
      }
      else {
        RAND.3[i,j] <- sample.int(2, size = 1, replace = TRUE, prob = PROBS.3a) #place in count group
1(0,0) or 2(0,1)

      }
    }
  }

  VALS.3 <- array(0, dim = c(2, n, size)) #will hold results of each trial
  OUT.3  <- array(0, dim = c(2, n)) #will hold counts

  for (i in 1:n)    {
    for (j in 1:size) {
      VALS.3[1,i,j] <- (RAND.3[i,j] %in% c(3, 4)) #is Rand.3 in probability groups 3 or 4 (counts 10 or
11)
      VALS.3[2,i,j] <- (RAND.3[i,j] %in% c(2, 4)) } # is Rand.3 in probability groups 2 or 4 (counts 01 or
11)
    OUT.3[1, i]   <- sum(VALS.3[1,i,]) #sums number of detections in third visit
    OUT.3[2, i]   <- sum(VALS.3[2,i,]) #sums number of detections in fourth visit
  }

  # Give output- counts per visit per site
  y <- array(dim = c(n,4))
  y[,1] <- OUT.1[1,]
  y[,2] <- OUT.1[2,]
  y[,3] <- OUT.2[2,]
  y[,4] <- OUT.3[2,]
  y
}

# S = number of sites
# V = number of visits
# lambda = mean local abundance
# prob = probability of detection
# num.sim = number of simulations
# The code doesn't work perfectly for outputting correlated counts, so the corr values are the input to get
the correlation we want which is the rho values

#Simulate Data - Nmixture model. Parameters estimated: lambda and probability of detection
# corr1 & corr3 = 0.30, corr2 = -0.20
```

```
Sim.Nmix.fn <- function(S=S, V=V, lambda = lambda, prob = prob, num.sim = num.sim, corr1 = corr1,
corr2 = corr2, corr3 = corr3, rho1 = rho1, rho2 = rho2, rho3 = rho3) {
  library(jagsUI) # use the JAGS for analyzing data within a Bayesian framework

  #***************
  # Define Bayesian Model
  #***************

  # Specify model in Bugs language
  sink("modelCC.txt")
  cat("
    model {

    # Priors
      lambda ~ dgamma(0.005, 0.005)      # Standard vague prior for lambda
      p ~ dunif(0, 1) #vague prior for probability of detection

    # Likelihood
      # Biological model for true abundance
        for (i in 1:S) {
          N[i] ~ dpois(lambda) #describes spatial variation in abundance (N)
       # Observation model for replicated counts
          for (j in 1:V) {
            y[i,j] ~ dbin(p, N[i]) #count (observation) for each visit at each site
          } # j
        } # i

       #Derived parameters
       Ntotal <- sum(N[]) #total of abundance at each site (N)
    }
    ",fill = TRUE)
  sink()

  #************************************************
  # Loop for replicating datasets and assessing bias
  #************************************************

  num.sim <- num.sim

  # Create empty vectors to store results from replicated datasets
  m.bias.Nsite <- vector("list",num.sim)  #examine bias in abundance (N) at each site
  sd.bias.Nsite <- vector("list",num.sim)
  baye.pvalue.Nsite <- vector("list",num.sim)

  m.bias.p <- vector("list",num.sim) #bias in probability of detection
  sd.bias.p <- vector("list",num.sim)
  baye.pvalue.p <- vector("list",num.sim)

  m.bias.Ntot <- vector("list",num.sim) #bias in total N
  sd.bias.Ntot <- vector("list",num.sim)
  baye.pvalue.Ntot <- vector("list",num.sim)
```

```
m.bias.lam <- vector("list",num.sim)  #bias in recovered lambda (mean abundance at site)
sd.bias.lam <- vector("list",num.sim)
baye.pvalue.lam <- vector("list",num.sim)

  m.CV.lam <- vector("list",num.sim)  #coefficient of variation for lambda (mean abundance at site)
sd.CV.lam <- vector("list",num.sim)
prop.CV.lam <- vector("list", num.sim)

m.CV.Ntot <- vector("list",num.sim) #coefficient of variation for total N
sd.CV.Ntot <- vector("list",num.sim)
prop.CV.Ntot <- vector("list", num.sim)

#*********************
# Start Simulation
#*********************

# Stick simulation in loop and replicate num.sim times

  system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

  #Simulate data
  S = S  # spatial reps
  V = V  # temporal reps
  lambda = lambda # mean abundance at site
  prob = prob # probablity of detection
  rho1 = rho1 # desired correlation
  rho2 = rho2
  rho3 = rho3
  corr1 = corr1 # modified correlation
  corr2 = corr2
  corr3 = corr3

  # Create structure to contain counts
  y <- array(dim = c(S,V))

  for(f in 1:1000){ #if correlated counts fail to be created, then it tries again (prevents simulation from
crashing)
    N <- rpois(n=S, lambda=lambda) # sample abundance from a Poisson distribution
  # sample counts from a Binomial distribution
  for(m in 1:200000) { #tries for creating count from simulated abundance (N)

    my <- array(NA,dim = c(S,4)) #creates empty array for counts
    for (i in 1:S){
      NN <- N[i]
      if (NN > 0){ #if actual abundance is > 0, sample using the rcorrbinom function to create counts
        ymy <- rcorrbinom(n = 1, size = NN, prob = prob, corr1 = 0.30, corr2 = -0.20, corr3 = 0.30)
        my[i,] <- ymy
      }
      else { # if actual abundance is 0, then the counts are automatically 0
        my[i,] <- 0
```

```
    }
  }

  data.y.cor <- cor(my) # get correlation of count data and make sure that it is within 0.05 of the desired correlation
  cor1 <- (data.y.cor[1,2] >= (rho1 - 0.05) & data.y.cor[1,2] <= (rho1 + 0.05))
  cor2 <- (data.y.cor[2,3] >= (rho2 - 0.05) & data.y.cor[2,3] <= (rho2 + 0.05))
  cor3 <- (data.y.cor[3,4] >= (rho3 - 0.05) & data.y.cor[3,4] <= (rho3 + 0.05))
  cor13 <- (data.y.cor[1,3] >= (0.41 - 0.05) & data.y.cor[1,3] <= (0.41 + 0.05))
  cor14 <- (data.y.cor[1,4] >= (0.44 - 0.05) & data.y.cor[1,4] <= (0.44 + 0.05))
  cor24 <- (data.y.cor[2,4] >= (0.47 - 0.05) & data.y.cor[2,4] <= (0.47 + 0.05))

  if (cor1 %in% NA){
    cor1 <- FALSE
  }
  if (cor2 %in% NA){
    cor2 <- FALSE
  }
  if (cor3 %in% NA){
    cor3 <- FALSE
  }
  if (cor13 %in% NA){
    cor13 <- FALSE
  }
  if (cor14 %in% NA){
    cor14 <- FALSE
  }
  if (cor24 %in% NA){
    cor24 <- FALSE
  }

  # if count data has the correct correlation then export the count data and break the for loop
  if (cor1 == TRUE & cor2 == TRUE & cor3==TRUE & cor13==TRUE & cor14==TRUE & cor24==TRUE){
    y <- my
    cat("iteration ", m) #print how many iterations it took get count data
    break
  }
 }
  cat(" attempt", f ) #print how many times N had to be generated to get count data with correct correlation (created to keep simulation from stopping/crashing)
  if (is.na(mean(y)) == FALSE){
    break #exit for loop with count data
  }
 }

 # Bundle data
 win.data <- list(y = y, S = nrow(y), V = ncol(y))

 # initial values
 Nst <- apply(y, 1, max) + 1     # This line is vital
```

```
inits <- function() list(N = Nst)

# Define parameters to be monitored
params <- c("lambda", "p", "Ntotal", "N")

# MCMC settings
ni <- 30000
nt <- 1
nb <- 100
nc <- 3

start.time = Sys.time()  #set timer
# run model
out <- jags(win.data, inits, params, "modelCC.txt", n.chains = nc,
            n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)
print(out)

end.time = Sys.time()
elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

#************************************
#### Evaluate bias ####
#************************************
##Bias in N (site specific abundance)
bias.Nsite <- out$mean$N - N #calculates bias
m.bias.Nsite[k] <- mean(bias.Nsite) #averages bias and places within vector
sd.bias.Nsite[k] <- sd(bias.Nsite) #gets standard deviation of bias places within vector
baye.pvalue.Nsite[k] <-mean(N > out$mean$N)  #Bayesian P-value (proportion of simulations where the true abundance was greater than the estimated abundance - values close to 0 or 1 indicate significant bias)

##Bias in lambda (average local abundance) - descriptions same as above
bias.lam <- out$mean$lambda - lambda
m.bias.lam[k] <- mean(bias.lam)
sd.bias.lam[k] <- sd(bias.lam)
baye.pvalue.lam[k] <- mean(lambda > out$mean$lambda)

##Bias in p - descriptions same as above
bias.p <- out$mean$p - prob
m.bias.p[k] <- mean(bias.p)
sd.bias.p[k] <- sd(bias.p)
baye.pvalue.p[k] <- mean(prob > out$mean$p)

##Bias in Ntotal (total population size) - descriptions same as above
bias.Ntot <- out$mean$Ntotal - sum(N)
m.bias.Ntot[k] <- mean(bias.Ntot)
sd.bias.Ntot[k] <- sd(bias.Ntot)
baye.pvalue.Ntot[k] <- mean(sum(N) > out$mean$Ntotal)

##Coefficient of Variation in Ntotal (total population size) - want to be under 15%
```

```
   CV.Ntot <- out$sd$Ntotal/out$mean$Ntotal #standard deviation divided by mean
   m.CV.Ntot[k] <- mean(CV.Ntot)
   sd.CV.Ntot[k] <- sd(CV.Ntot)
   prop.CV.Ntot[k] <- mean(CV.Ntot < 0.15)

   #Coefficient of Variation in local abundance (lambda / average local abundance)
   CV.lam <- out$sd$lambda/out$mean$lambda
   m.CV.lam[k] <- mean(CV.lam)
   sd.CV.lam[k] <- sd(CV.lam)
   prop.CV.lam[k] <- mean(CV.lam < 0.15)

   }  ) #This will be the end of the simulations

  #*********************
  # Summary of Results
  #*********************
  results <- c("lambda", "prob", "N.total", "N.site", "N.total.CV", "lambda.CV", "Prob.CV.Ntot",
"Prob.CV.lambda")
  mean.bias <- round(c((mean(unlist(m.bias.lam))), (mean(unlist(m.bias.p))), (mean(unlist(m.bias.Ntot))),
(mean(unlist(m.bias.Nsite))), (mean(unlist(m.CV.Ntot))), (mean(unlist(m.CV.lam))), NA, NA),2)

  lower.CI <- round(c((quantile(unlist(m.bias.lam), 0.05)), (quantile(unlist(m.bias.p), 0.05)),
(quantile(unlist(m.bias.Ntot), 0.05)), (quantile(unlist(m.bias.Nsite), 0.05)), (quantile(unlist(m.CV.Ntot),
0.05)), (quantile(unlist(m.CV.lam), 0.05)), NA, NA),2) #lower 95% credible interval

  upper.CI <- round(c((quantile(unlist(m.bias.lam), 0.95)), (quantile(unlist(m.bias.p), 0.95)),
(quantile(unlist(m.bias.Ntot), 0.95)), (quantile(unlist(m.bias.Nsite), 0.95)), (quantile(unlist(m.CV.Ntot),
0.95)), (quantile(unlist(m.CV.lam), 0.95)), NA, NA),2) #upper 95% credible interval

  greater.15.CV <- c(NA, NA, NA, NA, NA, NA, (mean(unlist(m.CV.Ntot) > 0.15)),
(mean(unlist(m.CV.lam) > 0.15))) #percent of CV's greater than 15%

  Baye.pvalue <- round(c((mean(unlist(baye.pvalue.lam))), (mean(unlist(baye.pvalue.p))),
(mean(unlist(baye.pvalue.Ntot))), (mean(unlist(baye.pvalue.Nsite))), NA, NA, NA, NA),2)

  sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a
table of results
  print(sim.results)

  #****************
  #Post processing
  #****************
  # Set plots so that six plots can be created in one image
  par(mfrow = c(6,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

  # Plots
  (hist(unlist(m.bias.Nsite), xlim=c(-5,5), breaks=120, main="", ylab="N.site"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.lam), xlim=c(-1,1), main="", ylab="lambda"))
  (abline(v=0, col="red", lwd=3))
```

```
  (hist(unlist(m.bias.p), xlim=c(-0.5,0.5), main="", ylab="Detection prob."))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.Ntot), xlim=c(-100,100), main="", ylab="Total N"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.CV.Ntot), xlim=c(0,0.5), main="", ylab="CV Ntotal"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.lam), xlim=c(0,0.5), main="", ylab="CV lambda"))
  (abline(v=0.15, col="red", lwd=3))

  return(list(sim.results=sim.results, m.bias.Nsite=unlist(m.bias.Nsite), m.bias.lam = unlist(m.bias.lam),
m.bias.p = unlist(m.bias.p), m.bias.Ntot = unlist(m.bias.Ntot), m.CV.Ntot = unlist(m.CV.Ntot), m.CV.lam
= unlist(m.CV.lam), lambda = lambda, prob = prob, S = S, V = V, num.sim = num.sim))
}
```

S3. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for point counts analyzed using hierarchical distance sampling where local abundance and probability of detection (sigma) were kept constant.

```
# Function for simulating and analyzing data using a hierarchical distance sampling model for point counts where both abundance and detection is kept constant.
# Data is simulated over a square using average local abundance for the square (lambda) and then truncated into a circle with radius B with an average local abundance equal to the estimated average local abundance of a point count site from the 2020 & 2021 data

# Code adapted from: Kery, M. and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom

# nsites = number of sites
# lambda = average local abundance per site over a square with area 2B x 2B where B = radius of circle
# lambda1 = average local abundance per point count site (so average local abundance within a circle with a radius of B)
# sigma = sigma for the half-normal detection function
# num.sim = number of simulations

# SET WORKING DIRECTORY
Sim.HDS.point.fn <- function(nsites = nsites, lambda = lambda, sigma = sigma, num.sim = num.sim, lambda1 = lambda1) {
 library(jagsUI) # use the JAGS for analyzing data within a Bayesian framework

 #***************
 # Define Bayesian Model
 #***************

 # Specify model in Bugs language, but going to use JagsUI/jags
 sink("simHDSpointfunction.txt")
 cat("
model{
 # Priors
 sigma ~ dunif(0,100) #vague prior for sigma
 lambda ~ dgamma(0.001, 0.001) #standard vague prior for lambda
 for(i in 1:nind){
  dclass[i] ~ dcat(fc[site[i],]) # Part 1 of HM - model for distance class of the observed individuals
 }
 for(s in 1:nsites){
  # Construct cell probabilities for nD distance bands
  for(g in 1:nD){              # midpt = mid-point of each band
   log(p[s,g]) <- -midpt[g] * midpt[g] / (2 * sigma * sigma) # half-normal detection function
   pi[s,g] <- ((2 * midpt[g] ) / (B * B)) * delta # prob. per interval
   f[s,g] <- p[s,g] * pi[s,g]
   fc[s,g] <- f[s,g] / pcap[s]
  }
  pcap[s] <- sum(f[s,])          # Pr(capture): sum of rectangular areas
  ncap[s] ~ dbin(pcap[s], N[s])   # Part 2 of HM - describes imperfect detection leading to count n[s]
  N[s] ~ dpois(lambda)         # Part 3 of HM - describes spatial variation in local abundance N[s]
```

```
  }
  # Derived parameters
  Ntotal <- sum(N[]) #total of abundance at each site (N)
  area <- nsites*3.141*B*B/1000000 #area in meters of the point count area
  D <- Ntotal/area #calculates density
}
   ",fill = TRUE)
  sink()

  #************************************************
  # Loop for replicating datasets and assessing bias
  #************************************************

  num.sim <- num.sim

  # Create empty vectors to store results from replicated datasets
  m.bias.Nsite <- vector("list",num.sim)  #examine bias in abundance (N) at each site
  sd.bias.Nsite <- vector("list",num.sim)
  baye.pvalue.Nsite <- vector("list",num.sim)
  m.Ntrue <- vector("list",num.sim)
  m.N <- vector("list",num.sim)

  m.bias.sigma <- vector("list",num.sim) #bias in sigma
  sd.bias.sigma <- vector("list",num.sim)
  baye.pvalue.sigma <- vector("list",num.sim)
  m.sig <- vector("list", num.sim)

  m.bias.Ntot <- vector("list",num.sim) #bias in total N
  sd.bias.Ntot <- vector("list",num.sim)
  baye.pvalue.Ntot <- vector("list",num.sim)
  m.bias.Ntot <- vector("list", num.sim)
  m.Ntot.true <- vector("list", num.sim)
  m.Ntot <- vector("list", num.sim)

  m.bias.lam <- vector("list",num.sim)  #bias in recovered lambda (mean abundance at point count site)
  sd.bias.lam <- vector("list",num.sim)
  baye.pvalue.lam <- vector("list",num.sim)
  m.lambda <- vector("list", num.sim)

  m.bias.den <- vector("list", num.sim) # bias in density
  sd.bias.den <- vector("list", num.sim)
  baye.pvalue.den <- vector("list", num.sim)
  m.density <- vector("list", num.sim)
  m.density.true <- vector("list", num.sim)

  m.CV.lam <- vector("list",num.sim)  #coefficient of variation for lambda (mean abundance at site)
  sd.CV.lam <- vector("list",num.sim)
  prop.CV.lam <- vector("list", num.sim)

  m.CV.Ntot <- vector("list",num.sim) #coefficient of variation for total N
  sd.CV.Ntot <- vector("list",num.sim)
```

```
prop.CV.Ntot <- vector("list", num.sim)

#********************
# Start Simulation
#********************

# Stick simulation in loop and replicate num.sim times
system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

 # **************
 # Simulate Data
 # **************
 # Simulate abundance model (Poisson GLM for N)
 N <- rpois(nsites, lambda)     # site specific abundance for square
 N.true <- N                    # for point, those individuals located inside circle (radius = B)
 B <- 100 #radius for circle (meters)
 area <- nsites*3.141*B*B/1000000 #area for circle (meters squared)
 den.true <- sum(N.true)/area #density for point count circle

 # Simulate observation model - set up empty dataframe
 data <- NULL

 for(i in 1:nsites){
  if(N[i]==0){ #if abundance at a site is 0
   data <- rbind(data, c(i,NA,NA,NA,NA)) # save site, y=1, u, v, d
   next
  }

  # Simulation data on a square
  u <- runif(N[i], 0, 2*B)   #x coordinate for distance from middle of square/circle
  v <- runif(N[i], 0, 2*B)   #y coordinate for distance from middle of square/circle
  d <- sqrt((u-B)^2 + (v-B)^2)  #distance
  N.true[i] <- sum(d<= B)    # Population size inside of count circle

  # Can only count individuals in the circle, so set to zero probability of individuals in the corners
  p <- exp(-d *d / (2 * (sigma^2)))  # Detection probability - half normal detection function
  pp <- ifelse(d <= B, 1, 0) * p    # Inside or outside circle (times "inside" or "outside")
  y <- rbinom(N[i], 1, pp)  # Detection/non-detection of each individual

  # Subset to "captured" individuals only
  u <- u[y==1]
  v <- v[y==1]
  d <- d[y==1]
  y <- y[y==1]

  # Compile things into a matrix and insert NA if no individuals were captured at site i. Coordinates
(u,v) are not used here.
  if(sum(y) > 0)
   data <- rbind(data, cbind(rep(i, sum(y)), y, u, v, d))
  else
   data <- rbind(data, c(i,NA,NA,NA,NA)) # make a row of missing data
```

```
    }
    colnames(data) <- c("site", "y", "u", "v", "d") # name 1st column "site"

    # ************************
    # Prep Data for analysis
    # ************************
    ncap <- table(data[,1])           # ncap = 1 if no individuals captured
    sites0 <- data[is.na(data[,2]),][,1] # sites where nothing was seen
    ncap[as.character(sites0)] <- 0    # Fill in 0 for sites with no detections
    ncap <- as.vector(ncap)            # Number of individuals detected per site
    site <- data[!is.na(data[,2]),1]   # Site ID of each observation
    delta <- 25                       # Distance bin width for rectangular approximation
    midpt <- seq(delta/2, B, delta)    # Make mid-points and chop up data
    dclass <- data[,5] %/% delta + 1   # Convert distance to distance category
    nD <- length(midpt)               # Number of distance intervals
    dclass <- dclass[!is.na(data[,2])] # Observed categorical observations
    nind <- length(dclass)            # Total number of individuals detected

    # Bundle data
    win.data <- list(nsites=nsites, nind=nind, B=B, nD=nD, midpt=midpt, delta=delta, ncap=ncap,
dclass=dclass, site=site)

    # initial values
    Nst <- ncap + 1          # This line is vital
    inits <- function() list(N = Nst, sigma = runif(1,30,60))

    # Define parameters to be monitored
    params <- c("lambda", "sigma", "Ntotal", "D", "N")

    # MCMC settings
    ni <- 5000
    nt <- 1
    nb <- 1000
    nc <- 3

    start.time = Sys.time()  #set timer
    # run model
    out <- jags(win.data, inits, params, "simHDSpointfunction.txt", n.chains = nc,
            n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)
    print(out)

    end.time = Sys.time()
    elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
    cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

    #************************************
    #### Evaluate bias ####
    #************************************
    #Bias in N (site specific abundance)
    bias.Nsite <- out$mean$N - N.true #calculates bias
    m.bias.Nsite[k] <- mean(bias.Nsite) #averages bias and places within vector
```

```
   sd.bias.Nsite[k] <- sd(bias.Nsite) #gets standard deviation of bias places within vector
   baye.pvalue.Nsite[k] <-mean(N.true > out$mean$N)  #Bayesian P-value (proportion of simulations where the true abundance was greater than the estimated abundance - values close to 0 or 1 indicate significant bias)

   #Bias in lambda (average local abundance) - descriptions same as above
   bias.lam <- out$mean$lambda - lambda1 #calculates bias (estimated lambda for circle - true lambda per circle(lambda1))
   m.bias.lam[k] <- mean(bias.lam)
   sd.bias.lam[k] <- sd(bias.lam)
   baye.pvalue.lam[k] <- mean(lambda1 > out$mean$lambda)
   m.lambda[k] <- out$mean$lambda

   #Bias in sigma - descriptions same as above
   bias.sigma <- out$mean$sigma - sigma
   m.bias.sigma[k] <- mean(bias.sigma)
   sd.bias.sigma[k] <- sd(bias.sigma)
   baye.pvalue.sigma[k] <- mean(sigma > out$mean$sigma)
   m.sig[k] <- out$mean$sigma

   #Bias in Ntotal (total population size)  - descriptions same as above
   bias.Ntot <- out$mean$Ntotal - sum(N.true)
   m.bias.Ntot[k] <- mean(bias.Ntot)
   sd.bias.Ntot[k] <- sd(bias.Ntot)
   baye.pvalue.Ntot[k] <- mean(sum(N.true) > out$mean$Ntotal)
   m.Ntot.true[k] <- sum(N.true)
   m.Ntot[k] <- out$mean$Ntotal

   # Bias in density - descriptions same as above
   bias.den <- out$mean$D - den.true
   m.bias.den[k] <- mean(bias.den)
   sd.bias.den[k] <- sd(bias.den)
   baye.pvalue.den[k] <- mean(den.true > out$mean$D)
   m.density.true[k] <- mean(den.true)
   m.density[k] <- out$mean$D

   #Coefficient of Variation in Ntotal (total population size) - want to be under 15%
   CV.Ntot <- out$sd$Ntotal/out$mean$Ntotal #standard deviation divided by mean
   m.CV.Ntot[k] <- mean(CV.Ntot)
   sd.CV.Ntot[k] <- sd(CV.Ntot)
   prop.CV.Ntot[k] <- mean(CV.Ntot < 0.15) #percent with CV < 0.15

   #Coefficient of Variation in local abundance (lambda / average local abundance)
   CV.lam <- out$sd$lambda/out$mean$lambda
   m.CV.lam[k] <- mean(CV.lam)
   sd.CV.lam[k] <- sd(CV.lam)
   prop.CV.lam[k] <- mean(CV.lam < 0.15)

 }  ) #This will be the end of the simulations

 #********************
```

```
  # Summary of Results
  #********************
  results <- c("lambda", "sigma", "N.total", "N.site", "N.total.CV", "lambda.CV", "Prob.CV.Ntot",
"Prob.CV.lambda")
  mean.bias <- round(c((mean(unlist(m.bias.lam))), (mean(unlist(m.bias.sigma))),
(mean(unlist(m.bias.Ntot))), (mean(unlist(m.bias.Nsite))), (mean(unlist(m.CV.Ntot))),
(mean(unlist(m.CV.lam))), NA, NA),2)

  lower.CI <- round(c((quantile(unlist(m.bias.lam), 0.05)), (quantile(unlist(m.bias.sigma), 0.05)),
(quantile(unlist(m.bias.Ntot), 0.05)), (quantile(unlist(m.bias.Nsite), 0.05)), (quantile(unlist(m.CV.Ntot),
0.05)), (quantile(unlist(m.CV.lam), 0.05)), NA, NA),2) #lower 95% credible interval

  upper.CI <- round(c((quantile(unlist(m.bias.lam), 0.95)), (quantile(unlist(m.bias.sigma), 0.95)),
(quantile(unlist(m.bias.Ntot), 0.95)), (quantile(unlist(m.bias.Nsite), 0.95)), (quantile(unlist(m.CV.Ntot),
0.95)), (quantile(unlist(m.CV.lam), 0.95)), NA, NA),2) #upper 95% credible interval

  greater.15.CV <- c(NA, NA, NA, NA, NA, NA, (mean(unlist(m.CV.Ntot) > 0.15)),
(mean(unlist(m.CV.lam) > 0.15))) #percent of CV's greater than 15%

  Baye.pvalue <- round(c((mean(unlist(baye.pvalue.lam))), (mean(unlist(baye.pvalue.sigma))),
(mean(unlist(baye.pvalue.Ntot))), (mean(unlist(baye.pvalue.Nsite))), NA, NA, NA, NA),2)

  sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a
table of results
  print(sim.results)

  #****************
  #Post processing
  #****************
  # Set plots so that six plots can be created in one image
  par(mfrow = c(6,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

  # Plots
  (hist(unlist(m.bias.Nsite), xlim=c(-1,1), main="", ylab="N.site"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.lam), xlim=c(-1,1), main="", ylab="lambda"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.sigma), xlim=c(-10,10), main="", ylab="Sigma"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.Ntot), xlim=c(-200,200), main="", ylab="Total N"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.CV.Ntot), xlim=c(0,1), main="", ylab="CV Ntotal"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.lam), xlim=c(0,1), main="", ylab="CV lambda"))
  (abline(v=0.15, col="red", lwd=3))
```

```
  return(list(sim.results=sim.results, m.bias.Nsite=unlist(m.bias.Nsite), m.bias.lam = unlist(m.bias.lam),
m.bias.sigma = unlist(m.bias.sigma), m.bias.Ntot = unlist(m.bias.Ntot), m.CV.Ntot = unlist(m.CV.Ntot),
m.CV.lam = unlist(m.CV.lam), lambda = lambda, sigma = sigma, nsites = nsites, num.sim = num.sim,
density.true = unlist(m.density.true), m.density = unlist(m.density), Ntot.true = unlist(m.Ntot.true),
m.Ntot = unlist(m.Ntot), m.sigma = unlist(m.sig), m.lambda = unlist(m.lambda), out = out))
}
```

S4. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for line transects analyzed using hierarchical distance sampling where local abundance and probability of detection (sigma) were kept constant.

```
# Function for simulating and analyzing data using a hierarchical distance sampling model for line transects where both abundance and sigma (detection) are kept constant.

# Code adapted from: Kery, M. and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom

# nsites = number of sites
# lambda = average local abundance per transect
# sigma = sigma for the half-normal detection function
# num.sim = number of simulations
# L = transect length

Sim.HDS.line.fn <- function(nsites = nsites, lambda = lambda, sigma = sigma, num.sim = num.sim, L = L) {
  library(jagsUI) # use the JAGS for analyzing data within a Bayesian framework

  #***************
  # Define Bayesian Model
  #***************

  # Specify model in Bugs language, but going to use JagsUI/jags
  sink("simHDSlinefunction.txt")
  cat("
 model{
  # Priors
  sigma ~ dunif(0,100) #vague prior for sigma
  lambda ~ dgamma(0.001, 0.001) # vague prior for lambda
  for(i in 1:nind){
   dclass[i] ~ dcat(fc[site[i],]) # Part 1 of HM - model for distance class of the observed individuals
}
  for(s in 1:nsites){
    # Construct cell probabilities for nD distance bands
    for(g in 1:nD){               # midpt = mid-point of each band
      log(p[s,g]) <- -midpt[g] * midpt[g] / (2 * sigma * sigma) # half-normal detection function
      pi[s,g] <- delta/B # prob. per interval
      f[s,g] <- p[s,g] * pi[s,g]
      fc[s,g] <- f[s,g] / pcap[s]
    }
    pcap[s] <- sum(f[s,])          # Pr(capture): sum of rectangular areas
    ncap[s] ~ dbin(pcap[s], N[s])   # Part 2 of HM - describes imperfect detection leading to count n[s]
    N[s] ~ dpois(lambda)         # Part 3 of HM - describes spatial variation in local abundance N[s]
  }
  # Derived parameters
  Ntotal <- sum(N[]) #total of abundance at each site (N)
  area <- nsites*L*2*B/1000000 #area of transects
  D <- Ntotal/area #density
```

```
}
  ",fill = TRUE)
sink()


#************************************************
# Loop for replicating datasets and assessing bias
#************************************************

num.sim <- num.sim

# Create empty vectors to store results from replicated datasets
m.bias.Nsite <- vector("list",num.sim)  #examine bias in abundance (N) at each site
sd.bias.Nsite <- vector("list",num.sim)
baye.pvalue.Nsite <- vector("list",num.sim)
m.Ntrue <- vector("list",num.sim)
m.N <- vector("list",num.sim)

m.bias.sigma <- vector("list",num.sim) #bias in sigma
sd.bias.sigma <- vector("list",num.sim)
baye.pvalue.sigma <- vector("list",num.sim)
m.sig <- vector("list", num.sim)

m.bias.Ntot <- vector("list",num.sim) #bias in total N
sd.bias.Ntot <- vector("list",num.sim)
baye.pvalue.Ntot <- vector("list",num.sim)
m.bias.Ntot <- vector("list", num.sim)
m.Ntot.true <- vector("list", num.sim)
m.Ntot <- vector("list", num.sim)

m.bias.lam <- vector("list",num.sim)  #bias in recovered lambda (mean abundance at site)
sd.bias.lam <- vector("list",num.sim)
baye.pvalue.lam <- vector("list",num.sim)
m.lambda <- vector("list", num.sim)

m.bias.den <- vector("list", num.sim) #bias in density
sd.bias.den <- vector("list", num.sim)
baye.pvalue.den <- vector("list", num.sim)
m.density <- vector("list", num.sim)
m.density.true <- vector("list", num.sim)

m.CV.lam <- vector("list",num.sim)  #coefficient of variation for lambda (mean abundance at site)
sd.CV.lam <- vector("list",num.sim)
prop.CV.lam <- vector("list", num.sim)

m.CV.Ntot <- vector("list",num.sim) #coefficient of variation for total N
sd.CV.Ntot <- vector("list",num.sim)
prop.CV.Ntot <- vector("list", num.sim)

#*******************
# Start Simulation
```

```
#********************

# Stick simulation in loop and replicate num.sim times
system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

 # **************
 # Simulate Data
 # **************
 # Simulate abundance model (Poisson GLM for N)
 N <- rpois(nsites, lambda)                # site-specific abundances
 N.true <- N #true abundance at each site, for a transect this is the same as N (differs for point counts)
 B <- 100 #strip half-width
 L <- L #length of transect
 area <- nsites*L*2*B/1000000 #area meters squared
 den.true <- sum(N)/area # true density

 # Simulate observation model - set up empty dataframe
 data <- NULL

 for(i in 1:nsites){
  if(N[i]==0){ #if abundance at a site is 0
   data <- rbind(data, c(i,NA,NA,NA,NA)) # save site, y=1, u, v, d
   next
  }
  # Simulation of distances, uniformly, for each individual in population
  # note it piles up all N[i] guys on one side of the transect
  d <- runif(N[i], 0, B)
  p <- exp(-d *d / (2 * (sigma^2))) # half-normal detection function
  # Determine if individuals are captured or not
  y <- rbinom(N[i], 1, p)
  u <- v <- rep(NA, N[i])   # coordinates (u,v)
  # Subset to "captured" individuals only
  d <- d[y==1]
  u <- u[y==1]
  v <- v[y==1]
  y <- y[y==1]


  # Compile things into a matrix and insert NA if no individuals were
  # captured at site i. Coordinates (u,v) are not used here.
  if(sum(y) > 0)
   data <- rbind(data, cbind(rep(i, sum(y)), y, u, v, d))
  else
   data <- rbind(data, c(i,NA,NA,NA,NA)) # make a row of missing data
 }
 colnames(data) <- c("site", "y", "u", "v", "d") # name 1st col "site"

 # ************************
 # Prep Data for analysis
 # ************************
 ncap <- table(data[,1])           # ncap = 1 if no individuals captured
```

```
   sites0 <- data[is.na(data[,2]),1] # sites where nothing was seen
   ncap[as.character(sites0)] <- 0    # Fill in 0 for sites with no detections
   ncap <- as.vector(ncap)            # Number of individuals detected per site
   site <- data[!is.na(data[,2]),1]   # Site ID of each observation
   delta <- 10                        # Distance bin width for rect. approx.
   midpt <- seq(delta/2, B, delta)    # Make mid-points and chop up data
   dclass <- data[,5] %/% delta + 1   # Convert distance to distance category
   nD <- length(midpt)                # Number of distance intervals
   dclass <- dclass[!is.na(data[,2])] # Observed categorical observations
   nind <- length(dclass)             # Total number of individuals detected

   # Bundle data
   win.data <- list(nsites=nsites, nind=nind, B=B, nD=nD, midpt=midpt, delta=delta, ncap=ncap,
dclass=dclass, site=site, L=L)

   # initial values
   Nst <- ncap + 1          # This line is vital
   inits <- function() list(N = Nst, sigma = runif(1,30,60))

   # Define parameters to be monitored
   params <- c("lambda", "sigma", "Ntotal", "D", "N")

   # MCMC settings
   ni <- 5000
   nt <- 1
   nb <- 1000
   nc <- 3

   start.time = Sys.time()  #set timer
   # run model
   out <- jags(win.data, inits, params, "simHDSlinefunction.txt", n.chains = nc,
               n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)
   print(out)

   end.time = Sys.time()
   elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
   cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

   #************************************
   #### EValuate bias ####
   #************************************
   #Bias in N (site specific abundance)
   bias.Nsite <- out$mean$N - N.true #calculates bias
   m.bias.Nsite[k] <- mean(bias.Nsite) #averages bias and places within vector
   sd.bias.Nsite[k] <- sd(bias.Nsite) #gets standard deviation of bias places within vector
   baye.pvalue.Nsite[k] <-mean(N.true > out$mean$N)  #Bayesian P-value (proportion of simulations
where the true abundance was greater than the estimated abundance - values close to 0 or 1 indicate
significant bias)

   #Bias in lambda (average local abundance) - descriptions same as above
   bias.lam <- out$mean$lambda - lambda
```

```
   m.bias.lam[k] <- mean(bias.lam)
   sd.bias.lam[k] <- sd(bias.lam)
   baye.pvalue.lam[k] <- mean(lambda > out$mean$lambda)
   m.lambda[k] <- out$mean$lambda

   #Bias in sigma - descriptions same as above
   bias.sigma <- out$mean$sigma - sigma
   m.bias.sigma[k] <- mean(bias.sigma)
   sd.bias.sigma[k] <- sd(bias.sigma)
   baye.pvalue.sigma[k] <- mean(sigma > out$mean$sigma)
   m.sig[k] <- out$mean$sigma

   #Bias in Ntotal (total population size)  - descriptions same as above
   bias.Ntot <- out$mean$Ntotal - sum(N.true)
   m.bias.Ntot[k] <- mean(bias.Ntot)
   sd.bias.Ntot[k] <- sd(bias.Ntot)
   baye.pvalue.Ntot[k] <- mean(sum(N.true) > out$mean$Ntotal)
   m.Ntot.true[k] <- sum(N.true)
   m.Ntot[k] <- out$mean$Ntotal

   #Bias in density - descriptions same as above
   bias.den <- out$mean$D - den.true
   m.bias.den[k] <- mean(bias.den)
   sd.bias.den[k] <- sd(bias.den)
   baye.pvalue.den[k] <- mean(den.true > out$mean$D)
   m.density.true[k] <- mean(den.true)
   m.density[k] <- out$mean$D

   #Coefficient of Variation in Ntotal (total population size) - want to be under 15%
   CV.Ntot <- out$sd$Ntotal/out$mean$Ntotal #standard deviation divided by mean
   m.CV.Ntot[k] <- mean(CV.Ntot)
   sd.CV.Ntot[k] <- sd(CV.Ntot)
   prop.CV.Ntot[k] <- mean(CV.Ntot < 0.15)

   #Coefficient of Variation in local abundance (lambda / average local abundance)
   CV.lam <- out$sd$lambda/out$mean$lambda
   m.CV.lam[k] <- mean(CV.lam)
   sd.CV.lam[k] <- sd(CV.lam)
   prop.CV.lam[k] <- mean(CV.lam < 0.15)

  }  ) #This will be the end of the simulations

  #*********************
  # Summary of Results
  #*********************
  results <- c("lambda", "sigma", "N.total", "N.site", "N.total.CV", "lambda.CV", "Prob.CV.Ntot",
"Prob.CV.lambda")
  mean.bias <- round(c((mean(unlist(m.bias.lam))), (mean(unlist(m.bias.sigma))),
(mean(unlist(m.bias.Ntot))), (mean(unlist(m.bias.Nsite))), (mean(unlist(m.CV.Ntot))),
(mean(unlist(m.CV.lam))), NA, NA),2)
```

```
  lower.CI <- round(c((quantile(unlist(m.bias.lam), 0.05)), (quantile(unlist(m.bias.sigma), 0.05)),
(quantile(unlist(m.bias.Ntot), 0.05)), (quantile(unlist(m.bias.Nsite), 0.05)), (quantile(unlist(m.CV.Ntot),
0.05)), (quantile(unlist(m.CV.lam), 0.05)), NA, NA),2) #lower 95% credible interval

  upper.CI <- round(c((quantile(unlist(m.bias.lam), 0.95)), (quantile(unlist(m.bias.sigma), 0.95)),
(quantile(unlist(m.bias.Ntot), 0.95)), (quantile(unlist(m.bias.Nsite), 0.95)), (quantile(unlist(m.CV.Ntot),
0.95)), (quantile(unlist(m.CV.lam), 0.95)), NA, NA),2) #upper 95% credible interval

  greater.15.CV <- c(NA, NA, NA, NA, NA, NA, (mean(unlist(m.CV.Ntot) > 0.15)),
(mean(unlist(m.CV.lam) > 0.15))) #percent of CV's greater than 15%

  Baye.pvalue <- round(c((mean(unlist(baye.pvalue.lam))), (mean(unlist(baye.pvalue.sigma))),
(mean(unlist(baye.pvalue.Ntot))), (mean(unlist(baye.pvalue.Nsite))), NA, NA, NA, NA),2)

  sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a
table of results
  print(sim.results)

  #****************
  #Post processing
  #****************
  # Set plots so that six plots can be created in one image
  par(mfrow = c(6,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

  # Plots
  (hist(unlist(m.bias.Nsite), xlim=c(-10,10), main="", ylab="N.site"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.lam), xlim=c(-1,1), main="", ylab="lambda"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.sigma), xlim=c(-10,10), main="", ylab="Sigma"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.Ntot), xlim=c(-200,200), main="", ylab="Total N"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.CV.Ntot), xlim=c(0,1), main="", ylab="CV Ntotal"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.lam), xlim=c(0,1), main="", ylab="CV lambda"))
  (abline(v=0.15, col="red", lwd=3))

  return(list(sim.results=sim.results, m.bias.Nsite=unlist(m.bias.Nsite), m.bias.lam = unlist(m.bias.lam),
m.bias.sigma = unlist(m.bias.sigma), m.bias.Ntot = unlist(m.bias.Ntot), m.CV.Ntot = unlist(m.CV.Ntot),
m.CV.lam = unlist(m.CV.lam), lambda = lambda, sigma = sigma, nsites = nsites, num.sim = num.sim,
density.true = unlist(m.density.true), m.density = unlist(m.density), Ntot.true = unlist(m.Ntot.true),
m.Ntot = unlist(m.Ntot), m.sigma = unlist(m.sig), m.lambda = unlist(m.lambda), out = out))
}
```

S5. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for point counts analyzed using hierarchical distance sampling with time removal where local abundance and probability of detection (sigma) were kept constant.

```
# Function for simulating and analyzing data using a hierarchical distance sampling model and time removal for point counts where both abundance, detection, and availability is kept constant.
# Data is simulated over a square using average local abundance for the square (lambda) and then truncated into a circle with radius B with an average local abundance equal to the estimated average local abundance of a point count site from the 2020 & 2021 data

# Code adapted from:
#Kery, M. and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom.
#Amundson, C. L., J. A. Royle, C. M. Handel. 2014. A hierarchical model combining distance sampling and time removal to estimate detection probability during avian point counts. The Auk 131(4): 476-494.
#Hostetter, N. J., B. Gardner, T. S. Sillett, K. H. Pollock, T. R. Simmons. 2019. An integrated model decomposing the components of detection probability and abundance in unmarked populations. Ecosphere 10(3)

# nsites = number of sites
# lambda = average local abundance per site over a square with area 2B x 2B where B = radius of circle
# lambda1 = average local abundance per point count site (so average local abundance within a circle with a radius of B)
# sigma = sigma for the half-normal detection function
# num.sim = number of simulations
# p.avail = overall availability probability
# int.avail = time interval-specific availability probability

Sim.HDS.TR.function <- function(nsites = nsites, lambda = lambda, sigma = sigma, num.sim = num.sim, lambda1 = lambda1, p.avail = p.avail) {
  library(jagsUI) # use the JAGS for analyzing data within a Bayesian framework

  #***************
  # Define Model
  #***************

  # Specify model in Bugs language, but going to use JagsUI/jags
  sink("simHDS_TR.txt")
  cat("
model {
  # Prior distributions for basic parameters

  p.a ~ dunif(0,1) # vague prior for availability (during a)
  sigma ~ dunif(0,100) # vague prior for sigma
  lambda ~ dgamma(0.001, 0.001) # vague prior for abundance

for(s in 1:nsites){

    # Distance sampling detection probability model
    for(b in 1:nD){
```

```
    log(g[b,s]) <- -mdpts[b] * mdpts[b] / (2*sigma*sigma)  # Half-normal
    f[b,s] <- (2 * mdpts[b] * delta ) / (B*B) # Radial density function
    pi.pd[b,s] <- g[b,s]*f[b,s]  #  Product Pr(detect)*Pr(distribution)
    pi.pd.c[b,s] <- pi.pd[b,s]/pdet[s]  # Conditional probabilities
   }

   pdet[s] <- sum(pi.pd[,s])  # Probability of detection at all

   # Time-removal probabilities
   for (k in 1:K){
    pi.pa[k,s] <- p.a * pow(1-p.a, (k-1))
    pi.pa.c[k,s] <- pi.pa[k,s]/phi[s] # Conditional probabilities of availability
   }

   phi[s] <- sum(pi.pa[,s]) # Probability of ever available

  }
  # Conditional observation model for categorical covariates
  for(i in 1:nobs){
   dclass[i] ~ dcat(pi.pd.c[,site[i]])
   tint[i] ~ dcat(pi.pa.c[,site[i]])
  }
  # Abundance model
  for(s in 1:nsites){

   n[s] ~ dbin(pdet[s], N[s])    # counts related to probability of detection given availability
   N[s] ~ dbin(phi[s],M[s])      # Number of available individuals
   M[s] ~ dpois(lambda)       # Abundance per survey/site/point

  }

  # Derived quantities
  Mtot <- sum(M[])  # Total population size
  Ntot <- sum(N[])  # Total available population size
  PDETmean <- mean(pdet[]) # Mean perceptibility across sites
  PHImean <- mean(phi[]) # Mean availability across sites
}
   ",fill = TRUE)
  sink()

  #************************************************
  # Loop for replicating datasets and assessing bias
  #************************************************

  num.sim <- num.sim

  # Create empty vectors to store results from replicated datasets
  m.bias.Msite <- vector("list",num.sim)  #examine bias in abundance (M) at each site
  sd.bias.Msite <- vector("list",num.sim)
  baye.pvalue.Msite <- vector("list",num.sim)
  m.Mtrue <- vector("list",num.sim)
```

```
m.M <- vector("list",num.sim)

m.bias.sigma <- vector("list",num.sim) #bias in probablity of detection
sd.bias.sigma <- vector("list",num.sim)
baye.pvalue.sigma <- vector("list",num.sim)
m.sig <- vector("list", num.sim)

m.bias.PHImean <- vector("list",num.sim) #bias in probablity of availability
sd.bias.PHImean <- vector("list",num.sim)
baye.pvalue.PHImean <- vector("list",num.sim)
m.PHImean <- vector("list", num.sim)

m.bias.Mtot <- vector("list",num.sim) #bias in total M
sd.bias.Mtot <- vector("list",num.sim)
baye.pvalue.Mtot <- vector("list",num.sim)
m.bias.Mtot <- vector("list", num.sim)
m.Mtot.true <- vector("list", num.sim)
m.Mtot <- vector("list", num.sim)

m.bias.lam <- vector("list",num.sim)  #bias in recovered lambda (mean abundance at site)
sd.bias.lam <- vector("list",num.sim)
baye.pvalue.lam <- vector("list",num.sim)
m.lambda <- vector("list", num.sim)

m.CV.lam <- vector("list",num.sim)  #coefficient of variation for lambda (mean abundance at site)
sd.CV.lam <- vector("list",num.sim)
prop.CV.lam <- vector("list", num.sim)

m.CV.Mtot <- vector("list",num.sim) #coefficient of variation for total N
sd.CV.Mtot <- vector("list",num.sim)
prop.CV.Mtot <- vector("list", num.sim)

#********************
# Start Simulation
#********************

# Stick simulation in loop and replicate num.sim times
system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

  # **************
  # Simulate Data
  # **************
  # Simulate superpopulation abundance model for groups (Poisson GLM for M)
  M <- rpois(nsites, lambda)          # site-specific abundance for square
  M.true <- M                       # for point: inside of circle (radius = B)
  B <- 100 #radius for circle (meters)
  K <- 4 #number of time intervals


  # Simulate observation model - set up empty dataframe
  data <- NULL
```

```
   for(i in 1:nsites){
     if(M[i]==0){ #if abundance at a site is 0
       data <- rbind(data,c(i,NA,NA,NA,NA,NA)) # save site, y=1, u, v, d, tint
       next
     }

     # Simulation data on a square
     u <- runif(M[i], 0, 2*B)   #x
     v <- runif(M[i], 0, 2*B)   #y
     d <- sqrt((u-B)^2 + (v-B)^2)  #distance
     M.true[i] <- sum(d<= B)    # Population size inside of count circle

     # Can only count individuals in the circle, so set to zero probability of individuals in the corners
     p <- ifelse(d <= B, 1, 0) * exp(-d *d / (2 * (sigma^2))) #half-normal detection function

     # Time-removal
     int.avail <- 1 - (1-p.avail)^(1/K) #calculate time-interval specific availability probability
     rem.probs <- c(int.avail, ((1-int.avail)^(1:(K-1)))*int.avail) #calculate probability for each time
interval
     mn.probs <- c(rem.probs, 1-sum(rem.probs)) #probability for each time interval + probability not ever
available
     aux <- sample(1:(K+1), M[i], replace=TRUE, prob=mn.probs)
     aux[aux==(K+1)] <- 0 #if not capture during intervals 1-K, set to 0

     newp <-  p * as.numeric(aux!=0) #combine probability of detection with availability
     navail <- sum(aux!=0)

     if(navail==0){
       data <- rbind(data,c(i,NA,NA,NA,NA,NA)) # save site, y=1, u, v, d
       next
     }

     # generate count of birds based on combined probability of detection
     y <- rbinom(M[i], 1, newp)
     # Subset to "captured" individuals only
     u <- u[y==1]
     v <- v[y==1]
     d <- d[y==1]
     aux <- aux[y==1]
     y <- y[ y==1]

     # Now compile things into a matrix and insert NA if no individuals were
     # captured at site i. Coordinates (u,v) are not used here.
     if(sum(y)>0){
       data <- rbind(data, cbind(rep(i, sum(y)), y, u, v, d, aux))
     } else {
       data <- rbind(data, c(i,NA,NA,NA,NA,NA)) # make a row of missing data
     }
   } # end of for loop
   colnames(data)[1] <- "site"
```

```
# ************************
# Prep Data for analysis
# ************************
# Create the observed encounter frequencies per site (include the zeros! )
data <- data[!is.na(data[,2]),]   # Sites where detections did occur
n <- rep(0,nsites)               # The full site vector
names(n) <- 1:nsites
n[names(table(data[,1]))] <- table(data[,1])  # Put in the counts
site <- data[,1]
nobs <- nrow(data)

# Create the distance class data
nD <- 10            # Number of distance classes
delta <- B/nD       # bin size or width
mdpts <- seq(delta/2,B,delta) # midpoint distance of bins up to max distance
dclass <- data[,"d"] # distance class for each observation
dclass <- dclass%/%delta  +1
tint <- data[,"aux"]

# Bundle data and summarize
win.data<-list(n=n, site=site, dclass=as.numeric(dclass),nsites=nsites,
                nobs=nobs, delta=delta, nD=nD,mdpts=mdpts,B=B, K=K, tint=tint)

Mst <- Nst <- n + 1
inits <- function(){list(M=Mst, N=Nst)}
params <- c("PDETmean", "PHImean", "Mtot", "Ntot", "p.a", "sigma", "lambda", "N", "M")

# MCMC settings
ni <- 20000
nt <- 1
nb <- 1000
nc <- 3

start.time = Sys.time()  #set timer
# run model
out <- jags(win.data, inits, params, "simHDS_TR.txt", n.chains = nc, n.thin = nt, n.iter = ni, n.burnin =
nb, parallel = TRUE)
print(out)

end.time = Sys.time()
elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

#************************************
#### Evaluate bias ####
#************************************
##Bias in N (site specific abundance)
bias.Msite <- out$mean$M - M.true #calculates bias
m.bias.Msite[k] <- mean(bias.Msite) #averages bias and places within vector
sd.bias.Msite[k] <- sd(bias.Msite) #gets standard deviation of bias places within vector
```

```
   baye.pvalue.Msite[k] <-mean(M.true > out$mean$M)  #Bayesian P-value (proportion of simulations where the true abundance was greater than the estimated abundance - values close to 0 or 1 indicate significant bias)

   ##Bias in lambda (average local abundance) - descriptions same as above
   bias.lam <- out$mean$lambda - lambda1 #calculates bias (estimated lambda for circle - true lambda per circle(lambda1))
   m.bias.lam[k] <- mean(bias.lam)
   sd.bias.lam[k] <- sd(bias.lam)
   baye.pvalue.lam[k] <- mean(lambda1 > out$mean$lambda)
   m.lambda[k] <- out$mean$lambda

   ##Bias in sigma - descriptions same as above
   bias.sigma <- out$mean$sigma - sigma
   m.bias.sigma[k] <- mean(bias.sigma)
   sd.bias.sigma[k] <- sd(bias.sigma)
   baye.pvalue.sigma[k] <- mean(sigma > out$mean$sigma)
   m.sig[k] <- out$mean$sigma

   ##Bias in availability - descriptions same as above
   bias.PHImean <- out$mean$PHImean - p.avail
   m.bias.PHImean[k] <- mean(bias.PHImean)
   sd.bias.PHImean[k] <- sd(bias.PHImean)
   baye.pvalue.PHImean[k] <- mean(p.avail > out$mean$PHImean)
   m.PHImean[k] <- out$mean$PHImean

   ##Bias in Mtotal (total population size)  - descriptions same as above
   bias.Mtot <- out$mean$Mtot - sum(M.true)
   m.bias.Mtot[k] <- mean(bias.Mtot)
   sd.bias.Mtot[k] <- sd(bias.Mtot)
   baye.pvalue.Mtot[k] <- mean(sum(M.true) > out$mean$Mtot)
   m.Mtot.true[k] <- sum(M.true)
   m.Mtot[k] <- out$mean$Mtot

   ##Coefficient of Variation in Mtotal (total population size) - want to be under 15%
   CV.Mtot <- out$sd$Mtot/out$mean$Mtot #standard deviation divided by mean
   m.CV.Mtot[k] <- mean(CV.Mtot)
   sd.CV.Mtot[k] <- sd(CV.Mtot)
   prop.CV.Mtot[k] <- mean(CV.Mtot < 0.15)

   #Coefficient of Variation in local abundance (lambda / average local abundance)
   CV.lam <- out$sd$lambda/out$mean$lambda
   m.CV.lam[k] <- mean(CV.lam)
   sd.CV.lam[k] <- sd(CV.lam)
   prop.CV.lam[k] <- mean(CV.lam < 0.15)

 }  ) #This will be the end of the simulations

 #********************
 # Summary of Results
 #********************
```

```
  results <- c("lambda", "sigma", "PHImean", "M.total", "M.site", "N.total.CV", "lambda.CV",
"Prob.CV.Ntot", "Prob.CV.lambda")
  mean.bias <- round(c((mean(unlist(m.bias.lam))), (mean(unlist(m.bias.sigma))),
(mean(unlist(m.bias.PHImean))), (mean(unlist(m.bias.Mtot))), (mean(unlist(m.bias.Msite))),
(mean(unlist(m.CV.Mtot))), (mean(unlist(m.CV.lam))), NA, NA),2)

  lower.CI <- round(c((quantile(unlist(m.bias.lam), 0.05)), (quantile(unlist(m.bias.sigma), 0.05)),
(quantile(unlist(m.bias.PHImean), 0.05)), (quantile(unlist(m.bias.Mtot), 0.05)),
(quantile(unlist(m.bias.Msite), 0.05)), (quantile(unlist(m.CV.Mtot), 0.05)), (quantile(unlist(m.CV.lam),
0.05)), NA, NA),2) #lower 95% credible interval

  upper.CI <- round(c((quantile(unlist(m.bias.lam), 0.95)), (quantile(unlist(m.bias.sigma), 0.95)),
(quantile(unlist(m.bias.PHImean), 0.95)), (quantile(unlist(m.bias.Mtot), 0.95)),
(quantile(unlist(m.bias.Msite), 0.95)), (quantile(unlist(m.CV.Mtot), 0.95)), (quantile(unlist(m.CV.lam),
0.95)), NA, NA),2) #upper 95% credible interval

  greater.15.CV <- c(NA, NA, NA, NA, NA, NA, NA, (mean(unlist(m.CV.Mtot) > 0.15)),
(mean(unlist(m.CV.lam) > 0.15))) #percent of CV's greater than 15%

  Baye.pvalue <- round(c((mean(unlist(baye.pvalue.lam))), (mean(unlist(baye.pvalue.sigma))),
(mean(unlist(baye.pvalue.PHImean))), (mean(unlist(baye.pvalue.Mtot))),
(mean(unlist(baye.pvalue.Msite))), NA, NA, NA, NA),2)

  sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a
table of results
  print(sim.results)

  #****************
  #Post processing
  #****************
  # Set plots so that seven plots can be created in one image
  par(mfrow = c(7,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

  # Plots
  (hist(unlist(m.bias.Msite), xlim=c(-10,10), main="", ylab="M.site"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.lam), xlim=c(-1,1), main="", ylab="lambda"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.sigma), xlim=c(-10,10), main="", ylab="Sigma"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.PHImean), xlim=c(-10,10), main="", ylab="PHI mean"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.Mtot), xlim=c(-200,200), main="", ylab="Total M"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.CV.Mtot), xlim=c(0,1), main="", ylab="CV Mtotal"))
  (abline(v=0.15, col="red", lwd=3))
```

```
  (hist(unlist(m.CV.lam), xlim=c(0,1), main="", ylab="CV lambda"))
  (abline(v=0.15, col="red", lwd=3))

  return(list(sim.results=sim.results, m.bias.Msite=unlist(m.bias.Msite), m.bias.lam = unlist(m.bias.lam),
m.bias.sigma = unlist(m.bias.sigma), m.bias.PHImean = unlist(m.bias.PHImean), m.bias.Mtot =
unlist(m.bias.Mtot), m.CV.Mtot = unlist(m.CV.Mtot), m.CV.lam = unlist(m.CV.lam), lambda = lambda,
sigma = sigma, p.avail= p.avail, nsites = nsites, num.sim = num.sim, Mtot.true = unlist(m.Mtot.true),
m.Mtot = unlist(m.Mtot), m.sigma = unlist(m.sig), m.PHImean = unlist(m.PHImean), m.lambda =
unlist(m.lambda), out = out))
}
```

S6. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for point counts analyzed using naïve models where local abundance and probability of detection were kept constant.

```
# Function for simulating and analyzing data using a naive model where average local abundance is estimated without take probability of detection into account for point counts. Local abundance is kept similar across all sites and probability of detection is kept constant.

# S = number of spatial reps/ number of sites
# V = number of visits at each site (temporal reps) - which was 1 for these simulations
# lambda = average local abundance
# prob = probability of detection
# num.sim = number of simulations

#Simulate Data - Nmixture model. Parameters estimated: lambda and probability of detection
Sim.Naive.fn <- function(S=S, V=V, lambda = lambda, prob = prob, num.sim = num.sim) {
 library(jagsUI)

 #***************
 # Define Model
 #***************

 # Specify model in Bugs language, but going to use JagsUI/jags
 sink("Naive.txt")
 cat("
  model {

  # Priors
    lambda ~ dgamma(0.005, 0.005)      # Standard vague prior for lambda

  # Likelihood
    # Biological model for true abundance
      for (i in 1:S) {
        N[i] ~ dpois(lambda)

      } # i
  #Derived parameters
     Ntotal <- sum(N[])

  }
  ",fill = TRUE)
sink()

#************************************************
# Loop for replicating datasets and assessing bias
#************************************************

num.sim <- num.sim

m.bias.Nsite <- vector("list",num.sim)  #examine bias in abundance (N) at each site
sd.bias.Nsite <- vector("list",num.sim)
```

```
baye.pvalue.Nsite <- vector("list",num.sim)

m.bias.Ntot <- vector("list",num.sim) #bias in total N
sd.bias.Ntot <- vector("list",num.sim)
baye.pvalue.Ntot <- vector("list",num.sim)

m.bias.lam <- vector("list",num.sim)  #bias in recovered lambda (mean abundance at site)
sd.bias.lam <- vector("list",num.sim)
baye.pvalue.lam <- vector("list",num.sim)


m.CV.lam <- vector("list",num.sim)  #coefficient of variation for lambda (mean abundance at site)
sd.CV.lam <- vector("list",num.sim)
prop.CV.lam <- vector("list", num.sim)

#********************
# Start Simulation
#********************

# Stick simulation in loop and replicate num.sim times
system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

  #Simulate data
  S = S  # spatial reps
  V = V  # temporal reps
  lambda = lambda # mean abundance at site
  prob = prob # probability of detection

  # Create structure to contain counts
  y <- array(dim = c(S,V))

  # sample abundance from a Poisson distribution
  N <- rpois(n=S, lambda=lambda)

  # sample counts from a Binomial distribution (N, prob)
  for (j in 1:V){
    y[,j] <- rbinom(n = S, size = N, prob = prob)
  }

  Count.data <- apply(y,1,max) #max count if more than 1 visit, if 1 visit then counts for that visit

  win.data <- list(N = Count.data, S = nrow(y))

  # initial values
  inits <- function() list(lambda = 1)

  # Define parameters to be monitored
  params <- c("lambda", "Ntotal", "N")

  # MCMC settings
  ni <- 3000
```

```
   nt <- 1
   nb <- 100
   nc <- 3

   start.time = Sys.time()  #set timer
   # run model
   out <- jags(win.data, inits, params, "Naive.txt", n.chains = nc,
               n.thin = nt, n.iter = ni, n.burnin = nb)
   print(out)

   end.time = Sys.time()
   elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
   cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

   #************************************
   #### Evaluate bias ####
   #************************************
   #Bias in N (site specific abundance)
   bias.Nsite <- out$mean$N - N #calculates bias
   m.bias.Nsite[k] <- mean(bias.Nsite) #averages bias and places within vector
   sd.bias.Nsite[k] <- sd(bias.Nsite) #gets standard deviation of bias places within vector
   baye.pvalue.Nsite[k] <-mean(N > out$mean$N)  #Bayesian P-value (proportion of simulations where
the true abundance was greater than the estimated abundance - values close to 0 or 1 indicate significant
bias)

   #Bias in lambda (average local abundance) - descriptions same as above
   bias.lam <- out$mean$lambda - lambda
   m.bias.lam[k] <- mean(bias.lam)
   sd.bias.lam[k] <- sd(bias.lam)
   baye.pvalue.lam[k] <- mean(lambda > out$mean$lambda)

   #Bias in Ntotal (total population size)  - descriptions same as above
   bias.Ntot <- out$mean$Ntotal - sum(N)
   m.bias.Ntot[k] <- mean(bias.Ntot)
   sd.bias.Ntot[k] <- sd(bias.Ntot)
   baye.pvalue.Ntot[k] <- mean(sum(N) > out$mean$Ntotal)

   #Coefficient of Variation in local abundance (lambda / average local abundance)
   CV.lam <- out$sd$lambda/out$mean$lambda #standard deviation divided by mean
   m.CV.lam[k] <- mean(CV.lam)
   sd.CV.lam[k] <- sd(CV.lam)
   prop.CV.lam[k] <- mean(CV.lam < 0.15)

  }  ) #This will be the end of the simulations

  #********************
  # Summary of Results
  #********************
  results <- c("lambda", "N.total", "N.site", "lambda.CV", "Prob.CV.lambda")
  mean.bias <- round(c((mean(unlist(m.bias.lam))), (mean(unlist(m.bias.Ntot))),
(mean(unlist(m.bias.Nsite))), (mean(unlist(m.CV.lam))), NA),2)
```

```
  lower.CI <- round(c((quantile(unlist(m.bias.lam), 0.05)), (quantile(unlist(m.bias.Ntot), 0.05)),
(quantile(unlist(m.bias.Nsite), 0.05)), (quantile(unlist(m.CV.lam), 0.05)), NA),2) #upper 95% credible
interval

  upper.CI <- round(c((quantile(unlist(m.bias.lam), 0.95)), (quantile(unlist(m.bias.Ntot), 0.95)),
(quantile(unlist(m.bias.Nsite), 0.95)), (quantile(unlist(m.CV.lam), 0.95)), NA),2) #lower 95% credible
interval

  greater.15.CV <- c(NA, NA, NA, NA, (mean(unlist(m.CV.lam) > 0.15)))

  Baye.pvalue <- round(c((mean(unlist(baye.pvalue.lam))), (mean(unlist(baye.pvalue.Ntot))),
(mean(unlist(baye.pvalue.Nsite))), NA, NA),2)

  sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a
table of results
  print(sim.results)

  #****************
  #Post processing
  #****************
  # Set plots so that six plots can be created in one image, which is then saved in a
  # word document Liz_Sim_Results_Figures
  par(mfrow = c(4,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

  # Plots
  (hist(unlist(m.bias.Nsite), xlim=c(-5,5), breaks=120, main="", ylab="N.site"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.lam), xlim=c(-1,1), main="", ylab="lambda"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.Ntot), xlim=c(-100,100), main="", ylab="Total N"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.CV.lam), xlim=c(0,0.5), main="", ylab="CV lambda"))
  (abline(v=0.15, col="red", lwd=3))

  return(list(sim.results=sim.results, m.bias.Nsite=unlist(m.bias.Nsite), m.bias.lam = unlist(m.bias.lam),
m.bias.Ntot = unlist(m.bias.Ntot), m.CV.lam = unlist(m.CV.lam), lambda = lambda, prob = prob, S = S,
V = V, num.sim = num.sim))
}
```

Table S7. Results of simulations evaluating the efficacy of survey protocols using parameters from the 2020 and 2021 spring survey data analyzed using hierarchical distance sampling with time removal models. Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of survey sites, λ = mean abundance per site, sigma = mean sigma, p.avail = mean probability of availability; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site.

Simulation Parameters				Bias in λ	Bias in *sigma*	p.avail	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	Protocol meets Management Requirements
R	**λ**	***sigma***	***p.avail***								
High abundance, average detection											
200	0.31	43	0.65	0.32 (-0.15, 1.27)	11.04 (-7.40, 30.23)	-0.03 (-0.27, 0.24)	64.52 (-29.02, 256.44)	0.32 (-0.15, 1.28)	1.38 (0.54, 2.59)	1.00	no
1000	0.31	43	0.65	0.17 (-0.10, 0.65)	2.26 (-4.49, 11.99)	-0.04 (-0.29, 0.18)	175.90 (-99.60, 658.26)	0.18 (-0.10, 0.66)	0.62 (0.23, 1.40)	1.00	no
6000	0.31	43	0.65	0.01 (-0.06, 0.09)	0.44, (-2.33 3.35)	-0.01 (-0.12, 0.09)	63.86 (-313.64, 563.16)	0.01 (-0.05, 0.09)	0.15 (0.10, 0.22)	0.33	no
High abundance, high detection											
200	0.31	48	0.89	0.15 (-0.13, 0.55)	10.90 (-6.77, 26.49)	-0.08 (-0.32, 0.07)	30.64 (-22.93, 115.62)	0.15 (-0.11, 0.58)	0.79 (0.29, 2.28)	1.00	no
1000	0.31	48	0.89	0.00 (-0.08, 0.09)	2.49 (-4.59, 12.39)	-0.02 (-0.10, 0.05)	1.32 (-70.19, 86.43)	0.00 (-0.07, 0.09)	0.16 (0.14, 0.20)	0.78	no
1300	0.31	48	0.89	0.00 (-0.09, 0.07)	1.83 (-4.18, 10.15)	-0.01 (-0.09, 0.04)	0.20 (-88.30, 82.51)	0.00 (-0.07, 0.06)	0.14 (0.12, 0.17)	0.18	no
1380	0.31	48	0.89	0.00 (-0.07, 0.07)	1.49 (-4.37, 9.16)	-0.02 (-0.09, 0.04)	4.77 (-80.91, 95.09)	0.00 (-0.06, 0.07)	0.14 (0.12, 0.16)	0.11	yes-ish
1390	0.31	48	0.89	-0.01 (-0.07, 0.06)	1.88 (-4.21, 8.61)	-0.01 (-0.08, 0.04)	-5.11 (-92.07, 91.14)	0.00 (-0.07, 0.07)	0.13 (0.12, 0.15)	0.09	yes
1400	0.31	48	0.89	0.00 (-0.07, 0.08)	1.47 (-4.37, 8.64)	-0.01 (-0.07, 0.04)	2.80 (-87.32, 106.15)	0.00 (-0.06, 0.08)	0.13 (0.12, 0.15)	0.06	yes
1500	0.31	48	0.89	0.00 (-0.07, 0.06)	1.31 (-4.08, 7.88)	-0.01 (-0.09, 0.04)	0.52 (-87.88, 97.36)	0.00 (-0.06, 0.06)	0.13 (0.12, 0.15)	0.04	yes

* Table is printed here as an image in order to fit the page; a spreadsheet of this table is available in the provided supplemental materials

Table S8. Results of simulations evaluating the efficacy of survey protocols using parameters from the 2020 and 2021 spring survey data analyzed using single season N-mixture models. Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of survey sites, J = number of replicate visits, λ = mean abundance per site, p = mean detection probability; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site.

Simulation Parameters				Bias in λ	Bias in *p*	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	Protocol meets Management Requirements
R	J	λ	*p*							
High abundance, Average detection										
100	4	0.31	0.37	0.02, (-0.10, 0.15)	0.00, (-0.12, 0.10)	1.88, (-5.03, 11.22)	0.02, (-0.05, 0.11)	0.16, (0.09, 0.27)	0.51	no
160	4	0.31	0.37	0.02, (-0.07, 0.13)	-0.01, (-0.09, 0.08)	2.16, (-6.31, 13.34)	0.01, (-0.04, 0.08)	0.12, (0.08, 0.18)	0.15	no
170	4	0.31	0.37	0.01, (-0.07, 0.09)	0.00, (-0.08, 0.08)	1.42, (-7.40, 11.02)	0.01, (-0.04, 0.06)	0.11, (0.08, 0.16)	0.08	yes
180	4	0.31	0.37	0.00, (-0.07, 0.10)	0.00, (-0.08, 0.07)	1.06, (-8.16, 11.67)	0.01, (-0.05, 0.06)	0.11, (0.08, 0.15)	0.07	yes
200	4	0.31	0.37	0.01, (-0.07, 0.10)	0.00, (-0.07, 0.07)	1.26, (-8.35, 12.68)	0.01, (-0.04, 0.06)	0.10, (0.07, 0.14)	0.02	yes
100	3	0.31	0.37	0.04, (-0.10, 0.20)	0.00, (-0.12, 0.12)	3.53, (-6.05, 17.46)	0.04, (-0.06, 0.17)	0.26, (0.14, 0.45)	0.90	no
200	3	0.31	0.37	0.02, (-0.07, 0.14)	0.00, (-0.10, 0.10)	3.35, (-9.88, 20.19)	0.02, (-0.05, 0.10)	0.16, (0.10, 0.24)	0.50	no
300	3	0.31	0.37	0.01, (-0.06, 0.10)	0.00, (-0.07, 0.08)	2.29, (-12.37, 21.36)	0.01, (-0.04, 0.07)	0.12, (0.09, 0.16)	0.11	yes-ish
320	3	0.31	0.37	0.01, (-0.07, 0.09)	0.00, (-0.08, 0.08)	2.75, (-16.97, 25.09)	0.01, (-0.05, 0.08)	0.12, (0.08, 0.16)	0.11	yes-ish
330	3	0.31	0.37	0.01, (-0.07, 0.08)	0.00, (-0.07, 0.07)	3.13, (-13.59, 23.44)	0.01, (-0.04, 0.07)	0.12, (0.08, 0.16)	0.07	yes
340	3	0.31	0.37	0.00, (-0.06, 0.08)	0.00, (-0.08, 0.08)	2.75, (-14.55, 22.55)	0.01, (-0.04, 0.07)	0.11, (0.08, 0.15)	0.07	yes
360	3	0.31	0.37	0.00, (-0.06, 0.09)	0.00, (-0.07, 0.07)	1.33, (-16.21, 22.25)	0.00, (-0.05, 0.06)	0.11, (0.08, 0.14)	0.03	yes
380	3	0.31	0.37	0.01, (-0.06, 0.08)	0.00, (-0.07, 0.08)	2.01, (-17.62, 22.76)	0.01, (-0.05, 0.06)	0.10, (0.08, 0.14)	0.02	yes
400	3	0.31	0.37	0.01, (-0.06, 0.09)	0.00, (-0.07, 0.07)	2.95, (-15.44, 27.48)	0.01, (-0.04, 0.07)	0.10, (0.08, 0.14)	0.02	yes
100	2	0.31	0.37	0.12, (-0.11, 0.54)	0.00, (-0.18, 0.18)	11.37, (-9.03, 52.50)	0.11, (-0.09, 0.53)	0.54, (0.22, 1.03)	1.00	no
200	2	0.31	0.37	0.04, (-0.11, 0.25)	0.01, (-0.14, 0.16)	8.57, (-17.49, 47.24)	0.04, (-0.09, 0.24)	0.31, (0.16, 0.57)	0.96	no
300	2	0.31	0.37	0.03, (-0.09, 0.20)	0.00, (-0.13, 0.13)	9.45, (-20.66, 58.09)	0.03, (-0.07, 0.19)	0.24, (0.14, 0.40)	0.91	no
400	2	0.31	0.37	0.02, (-0.07, 0.16)	0.00, (-0.11, 0.12)	7.60, (-25.18, 54.73)	0.02, (-0.06, 0.14)	0.20, (0.12, 0.31)	0.82	no
500	2	0.31	0.37	0.01, (-0.07, 0.11)	0.00, (-0.10, 0.10)	5.90, (-29.56, 47.75)	0.01, (-0.06, 0.10)	0.17, (0.12, 0.26)	0.67	no
600	2	0.31	0.37	0.00, (-0.07, 0.09)	0.01, (-0.08, 0.10)	2.89, (-36.00, 50.37)	0.00, (-0.06, 0.08)	0.15, (0.10, 0.21)	0.42	no
700	2	0.31	0.37	0.01, (-0.07, 0.10)	0.01, (-0.08, 0.09)	4.77, (-38.69, 61.93)	0.01, (-0.06, 0.09)	0.14, (0.10, 0.19)	0.28	no
800	2	0.31	0.37	0.01, (-0.06, 0.09)	0.01, (-0.08, 0.09)	5.10, (-41.06, 66.28)	0.01, (-0.05, 0.08)	0.13, (0.09, 0.17)	0.15	no
860	2	0.31	0.37	0.01, (-0.05, 0.09)	0.00, (-0.07, 0.08)	5.46, (-41.03, 64.88)	0.01, (-0.05, 0.08)	0.12, (0.09, 0.16)	0.11	yes-ish
870	2	0.31	0.37	0.01, (-0.05, 0.09)	0.00, (-0.08, 0.08)	7.37, (-44.62, 75.69)	0.01, (-0.05, 0.09)	0.12, (0.09, 0.16)	0.13	no
880	2	0.31	0.37	0.01, (-0.06, 0.08)	0.00, (-0.07, 0.08)	5.38, (-42.59, 59.15)	0.01, (-0.05, 0.07)	0.12, (0.09, 0.16)	0.10	yes
890	2	0.31	0.37	0.00, (-0.06, 0.08)	0.01, (-0.08, 0.08)	4.27, (-45.13, 69.79)	0.00, (-0.05, 0.08)	0.12, (0.09, 0.16)	0.10	yes
900	2	0.31	0.37	0.01, (-0.06, 0.08)	0.01, (-0.07, 0.09)	2.69, (-49.32, 65.74)	0.00, (-0.05, 0.07)	0.12, (0.09, 0.16)	0.08	yes
Low abundance, Average detection										

100	4	0.08	0.37	0.02, (-0.03, 0.10)	0.00, (-0.17, 0.19)	1.58, (-2.01, 7.60)	0.02, (-0.02, 0.08)	0.41, (0.13, 1.03)	0.90	no
200	4	0.08	0.37	0.01, (-0.03, 0.06)	0.00, (-0.13, 0.13)	1.31, (-3.15, 7.74)	0.01, (-0.02, 0.04)	0.21, (0.10, 0.41)	0.68	no
300	4	0.08	0.37	0.00, (-0.03, 0.04)	0.00, (-0.10, 0.11)	0.88, (-4.64, 6.58)	0.00, (-0.02, 0.02)	0.15, (0.08, 0.26)	0.42	no
400	4	0.08	0.37	0.00, (-0.02, 0.04)	0.00, (-0.10, 0.09)	1.34, (-4.70, 8.78)	0.00, (-0.01, 0.02)	0.13, (0.08, 0.20)	0.22	no
480	4	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.09, 0.08)	1.01, (-4.93, 7.82)	0.00, (-0.01, 0.02)	0.11, (0.07, 0.17)	0.11	yes-ish
490	4	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.08, 0.08)	0.81, (-5.01, 7.52)	0.00, (-0.01, 0.02)	0.11, (0.07, 0.16)	0.08	yes
500	4	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.09, 0.08)	1.15, (-5.55, 9.20)	0.00, (-0.01, 0.02)	0.11, (0.07, 0.17)	0.10	yes
100	3	0.08	0.37	0.03, (-0.04, 0.16)	0.01, (-0.19, 0.22)	3.15, (-2.93, 15.56)	0.03, (-0.03, 0.16)	0.63, (0.21, 1.48)	0.99	no
200	3	0.08	0.37	0.01, (-0.04, 0.08)	0.01, (-0.16, 0.19)	2.72, (-3.90, 14.95)	0.01, (-0.02, 0.07)	0.36, (0.13, 0.84)	0.92	no
300	3	0.08	0.37	0.01, (-0.03, 0.06)	0.00, (-0.15, 0.14)	2.45, (-6.08, 15.59)	0.01, (-0.02, 0.05)	0.25, (0.13, 0.51)	0.85	no
400	3	0.08	0.37	0.01, (-0.02, 0.05)	0.00, (-0.12, 0.13)	2.45, (-6.62, 15.33)	0.01, (-0.02, 0.04)	0.20, (0.11, 0.34)	0.73	no
500	3	0.08	0.37	0.00, (-0.03, 0.04)	0.00, (-0.11, 0.12)	2.38, (-7.97, 16.00)	0.00, (-0.02, 0.03)	0.17, (0.10, 0.28)	0.62	no
600	3	0.08	0.37	0.00, (-0.02, 0.04)	0.00, (-0.10, 0.11)	2.07, (-8.32, 16.37)	0.00, (-0.01, 0.03)	0.15, (0.10, 0.23)	0.44	no
700	3	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.08, 0.09)	1.97, (-8.20, 13.22)	0.00, (-0.01, 0.02)	0.14, (0.09, 0.21)	0.29	no
800	3	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.09, 0.11)	1.71, (-10.78, 18.78)	0.00, (-0.01, 0.02)	0.13, (0.08, 0.19)	0.22	no
900	3	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.09, 0.08)	2.03, (-10.17, 16.32)	0.00, (-0.01, 0.02)	0.12, (0.08, 0.18)	0.13	no
910	3	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.09, 0.09)	2.24, (-10.80, 19.64)	0.00, (-0.01, 0.02)	0.12, (0.08, 0.17)	0.12	no
920	3	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.08, 0.08)	1.46, (-10.82, 17.11)	0.00, (-0.01, 0.02)	0.12, (0.08, 0.17)	0.10	yes
940	3	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.07, 0.09)	1.94, (-11.25, 16.90)	0.00, (-0.01, 0.02)	0.11, (0.08, 0.16)	0.08	yes
960	3	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.08, 0.08)	2.13, (-10.50, 16.33)	0.00, (-0.01, 0.02)	0.12, (0.08, 0.16)	0.09	yes
980	3	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.08, 0.08)	1.97, (-11.36, 17.12)	0.00, (-0.01, 0.02)	0.11, (0.08, 0.16)	0.08	yes
1000	3	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.08, 0.08)	2.27, (-10.53, 17.82)	0.00, (-0.01, 0.02)	0.11, (0.08, 0.16)	0.07	yes
100	2	0.08	0.37	0.06, (-0.05, 0.24)	0.04, (-0.16, 0.31)	5.56, (-3.76, 21.43)	0.06, (-0.04, 0.21)	1.33, (0.33, 2.23)	1.00	no
200	2	0.08	0.37	0.04, (-0.04, 0.17)	0.02, (-0.18, 0.26)	7.00, (-5.71, 32.15)	0.04, (-0.03, 0.16)	0.71, (0.23, 1.52)	0.99	no
300	2	0.08	0.37	0.03, (-0.03, 0.12)	0.02, (-0.17, 0.21)	7.42, (-7.29, 39.62)	0.02, (-0.02, 0.13)	0.53, (0.20, 1.04)	0.99	no
400	2	0.08	0.37	0.02, (-0.03, 0.11)	0.01, (-0.18, 0.19)	8.36, (-9.54, 43.31)	0.02, (-0.02, 0.11)	0.44, (0.19, 0.92)	0.99	no
500	2	0.08	0.37	0.02, (-0.03, 0.08)	0.00, (-0.17, 0.16)	9.59, (-10.82, 44.49)	0.02, (-0.02, 0.09)	0.40, (0.19, 0.80)	0.99	no
600	2	0.08	0.37	0.02, (-0.03, 0.08)	0.00, (-0.16, 0.15)	9.36, (-12.34, 46.55)	0.02, (-0.02, 0.08)	0.34, (0.17, 0.64)	0.98	no
700	2	0.08	0.37	0.01, (-0.02, 0.07)	0.01, (-0.14, 0.16)	7.69, (-12.79, 46.84)	0.01, (-0.02, 0.07)	0.31, (0.15, 0.66)	0.95	no
800	2	0.08	0.37	0.01, (-0.02, 0.06)	0.00, (-0.15, 0.14)	9.14, (-16.62, 48.21)	0.01, (-0.02, 0.06)	0.30, (0.15, 0.59)	0.95	no
900	2	0.08	0.37	0.01, (-0.02, 0.05)	0.01, (-0.12, 0.15)	7.25, (-17.19, 40.63)	0.01, (-0.02, 0.05)	0.27, (0.13, 0.52)	0.91	no
1000	2	0.08	0.37	0.01, (-0.02, 0.04)	0.00, (-0.12, 0.12)	7.82, (-18.24, 41.21)	0.01, (-0.02, 0.04)	0.24, (0.14, 0.45)	0.89	no
1100	2	0.08	0.37	0.01, (-0.02, 0.04)	0.01, (-0.11, 0.13)	5.25, (-19.37, 41.46)	0.00, (-0.02, 0.04)	0.22, (0.13, 0.39)	0.85	no
1200	2	0.08	0.37	0.00, (-0.02, 0.04)	0.00, (-0.11, 0.12)	6.14, (-20.92, 48.08)	0.01, (-0.02, 0.04)	0.22, (0.12, 0.38)	0.83	no
1300	2	0.08	0.37	0.01, (-0.02, 0.04)	0.01, (-0.11, 0.12)	6.49, (-22.34, 48.53)	0.00, (-0.02, 0.04)	0.20, (0.12, 0.34)	0.74	no
1400	2	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.11, 0.11)	6.12, (-21.42, 45.54)	0.00, (-0.02, 0.03)	0.19, (0.12, 0.32)	0.74	no
1500	2	0.08	0.37	0.01, (-0.02, 0.03)	0.00, (-0.10, 0.10)	8.10, (-22.94, 50.46)	0.01, (-0.02, 0.03)	0.19, (0.12, 0.33)	0.71	no
1600	2	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.10, 0.10)	7.07, (-24.16, 51.10)	0.00, (-0.02, 0.03)	0.18, (0.11, 0.27)	0.66	no
1700	2	0.08	0.37	0.00, (-0.02, 0.03)	0.01, (-0.09, 0.10)	4.55, (-26.91, 47.20)	0.00, (-0.02, 0.03)	0.17, (0.11, 0.26)	0.55	no
1800	2	0.08	0.37	0.00, (-0.02, 0.03)	0.01, (-0.10, 0.11)	5.79, (-28.18, 50.65)	0.00, (-0.02, 0.03)	0.16, (0.11, 0.24)	0.52	no
1900	2	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.09, 0.10)	6.06, (-29.78, 51.22)	0.00, (-0.02, 0.03)	0.16, (0.10, 0.23)	0.49	no
2000	2	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.09, 0.10)	6.81, (-26.32, 52.48)	0.00, (-0.01, 0.03)	0.15, (0.10, 0.23)	0.43	no
2100	2	0.08	0.37	0.00, (-0.02, 0.03)	0.00, (-0.08, 0.10)	4.50, (-32.48, 48.72)	0.00, (-0.02, 0.02)	0.15, (0.10, 0.21)	0.39	no
2200	2	0.08	0.37	0.00, (-0.01, 0.03)	0.00, (-0.09, 0.09)	6.71, (-29.46, 55.89)	0.00, (-0.01, 0.03)	0.15, (0.10, 0.22)	0.33	no
2300	2	0.08	0.37	0.00, (-0.02, 0.02)	0.01, (-0.09, 0.09)	4.95, (-29.89, 51.25)	0.00, (-0.01, 0.02)	0.14, (0.10, 0.20)	0.27	no

2400	2	0.08	0.37	0.00, (-0.02, 0.02)	0.01, (-0.08, 0.09)	4.08, (-35.24, 50.71)	0.00, (-0.01, 0.02)	0.13, (0.10, 0.20)	0.23	no
2500	2	0.08	0.37	0.00, (-0.02, 0.02)	0.01, (-0.08, 0.09)	5.56, (-35.94, 53.71)	0.00, (-0.01, 0.02)	0.14, (0.09, 0.20)	0.24	no
2600	2	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.08, 0.09)	4.58, (-34.24, 53.14)	0.00, (-0.01, 0.02)	0.13, (0.09, 0.19)	0.18	no
2700	2	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.08, 0.09)	6.38, (-34.09, 54.91)	0.00, (-0.01, 0.02)	0.13, (0.09, 0.19)	0.18	no
2800	2	0.08	0.37	0.00, (-0.01, 0.02)	0.01, (-0.07, 0.08)	3.69, (-36.63, 57.70)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.17)	0.11	yes-ish
2900	2	0.08	0.37	0.00, (-0.01, 0.02)	0.01, (-0.07, 0.08)	3.57, (-37.58, 51.97)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.17)	0.12	no
2910	2	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.07, 0.08)	5.02, (-35.49, 55.29)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.15)	0.08	yes
2920	2	0.08	0.37	0.00, (-0.02, 0.02)	0.01, (-0.06, 0.08)	2.61, (-34.79, 51.97)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.15)	0.06	yes
2940	2	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.08, 0.08)	4.05, (-35.93, 60.19)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.16)	0.08	yes
2960	2	0.08	0.37	0.00, (-0.01, 0.02)	0.00, (-0.07, 0.08)	4.75, (-36.66, 57.51)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.15)	0.07	yes
2980	2	0.08	0.37	0.00, (-0.02, 0.02)	0.01, (-0.07, 0.08)	3.26, (-36.81, 58.49)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.15)	0.05	yes
3000	2	0.08	0.37	0.00, (-0.02, 0.02)	0.00, (-0.07, 0.08)	5.78, (-37.41, 53.92)	0.00, (-0.01, 0.02)	0.12, (0.09, 0.15)	0.07	yes
Average abundance, Average detection										
100	4	0.18	0.37	0.01, (-0.07, 0.11)	0.01, (-0.12, 0.14)	1.11, (-3.95, 7.48)	0.01, (-0.04, 0.07)	0.21, (0.10, 0.42)	0.69	no
200	4	0.18	0.37	0.01, (-0.04, 0.07)	0.00, (-0.08, 0.09)	1.36, (-4.86, 8.47)	0.01, (-0.02, 0.04)	0.13, (0.08, 0.19)	0.20	no
220	4	0.18	0.37	0.01, (-0.05, 0.07)	0.00, (-0.09, 0.09)	1.25, (-6.32, 9.73)	0.01, (-0.03, 0.04)	0.12, (0.08, 0.18)	0.18	no
230	4	0.18	0.37	0.01, (-0.05, 0.07)	0.00, (-0.08, 0.09)	1.28, (-5.73, 9.49)	0.01, (-0.02, 0.04)	0.11, (0.07, 0.17)	0.11	yes-ish
240	4	0.18	0.37	0.00, (-0.05, 0.06)	0.00, (-0.09, 0.09)	0.89, (-6.76, 9.53)	0.00, (-0.03, 0.04)	0.11, (0.07, 0.17)	0.09	yes
260	4	0.18	0.37	0.01, (-0.04, 0.06)	0.00, (-0.09, 0.08)	1.37, (-6.84, 10.57)	0.01, (-0.03, 0.04)	0.11, (0.07, 0.16)	0.08	yes
280	4	0.18	0.37	0.00, (-0.04, 0.06)	0.00, (-0.08, 0.07)	1.33, (-5.95, 9.43)	0.00, (-0.02, 0.03)	0.10, (0.07, 0.15)	0.04	yes
300	4	0.18	0.37	0.00, (-0.05, 0.06)	0.00, (-0.07, 0.07)	1.00, (-7.05, 9.48)	0.00, (-0.02, 0.03)	0.10, (0.07, 0.14)	0.03	yes
100	3	0.18	0.37	0.03, (-0.08, 0.21)	0.00, (-0.17, 0.16)	3.44, (-4.89, 16.05)	0.03, (-0.05, 0.16)	0.37, (0.15, 0.82)	0.95	no
200	3	0.18	0.37	0.02, (-0.06, 0.11)	0.00, (-0.13, 0.11)	3.41, (-7.04, 19.31)	0.02, (-0.04, 0.10)	0.21, (0.12, 0.38)	0.76	no
300	3	0.18	0.37	0.01, (-0.04, 0.07)	0.00, (-0.11, 0.11)	2.63, (-8.97, 17.91)	0.01, (-0.03, 0.06)	0.15, (0.10, 0.24)	0.44	no
400	3	0.18	0.37	0.01, (-0.04, 0.07)	0.00, (-0.09, 0.09)	2.39, (-10.22, 18.97)	0.01, (-0.03, 0.05)	0.13, (0.09, 0.18)	0.20	no
460	3	0.18	0.37	0.01, (-0.04, 0.06)	0.00, (-0.09, 0.08)	2.49, (-11.72, 21.05)	0.01, (-0.03, 0.05)	0.12, (0.08, 0.16)	0.11	yes-ish
470	3	0.18	0.37	0.00, (-0.04, 0.05)	0.00, (-0.09, 0.08)	2.17, (-13.10, 20.65)	0.00, (-0.03, 0.04)	0.12, (0.08, 0.16)	0.12	no
480	3	0.18	0.37	0.00, (-0.04, 0.05)	0.01, (-0.07, 0.08)	1.54, (-12.38, 18.62)	0.00, (-0.03, 0.04)	0.11, (0.08, 0.16)	0.07	yes
500	3	0.18	0.37	0.01, (-0.04, 0.06)	0.00, (-0.09, 0.08)	1.90, (-14.07, 21.18)	0.00, (-0.03, 0.04)	0.11, (0.08, 0.15)	0.07	yes
100	2	0.18	0.37	0.09, (-0.08, 0.39)	0.02, (-0.18, 0.25)	8.78, (-6.90, 35.60)	0.09, (-0.07, 0.36)	0.69, (0.26, 1.35)	0.99	no
200	2	0.18	0.37	0.05, (-0.07, 0.25)	0.01, (-0.18, 0.19)	9.48, (-10.33, 46.88)	0.05, (-0.05, 0.23)	0.42, (0.19, 0.75)	0.99	no
300	2	0.18	0.37	0.03, (-0.06, 0.16)	0.00, (-0.15, 0.15)	8.66, (-13.87, 46.58)	0.03, (-0.05, 0.16)	0.32, (0.16, 0.56)	0.98	no
400	2	0.18	0.37	0.02, (-0.05, 0.12)	0.00, (-0.14, 0.14)	7.97, (-13.87, 46.58)	0.02, (-0.04, 0.12)	0.26, (0.14, 0.42)	0.93	no
500	2	0.18	0.37	0.01, (-0.05, 0.10)	0.00, (-0.12, 0.13)	6.41, (-21.90, 44.79)	0.01, (-0.04, 0.09)	0.22, (0.13, 0.36)	0.89	no
600	2	0.18	0.37	0.01, (-0.04, 0.09)	0.00, (-0.11, 0.11)	7.27, (-21.72, 53.29)	0.01, (-0.04, 0.09)	0.20, (0.13, 0.31)	0.82	no
700	2	0.18	0.37	0.01, (-0.04, 0.08)	0.01, (-0.10, 0.10)	6.19, (-24.29, 51.59)	0.01, (-0.03, 0.07)	0.18, (0.12, 0.17)	0.72	no
800	2	0.18	0.37	0.01, (-0.04, 0.08)	0.01, (-0.10, 0.10)	8.45, (-25.50, 56.03)	0.01, (-0.03, 0.07)	0.17, (0.11, 0.24)	0.64	no
900	2	0.18	0.37	0.01, (-0.04, 0.07)	0.01, (-0.09, 0.09)	5.08, (-31.26, 52.11)	0.01, (-0.03, 0.06)	0.15, (0.11, 0.21)	0.49	no
1000	2	0.18	0.37	0.01, (-0.04, 0.05)	0.01, (-0.08, 0.10)	3.42, (-32.63, 49.22)	0.00, (-0.03, 0.05)	0.14, (0.10, 0.20)	0.38	no
1100	2	0.18	0.37	0.01, (-0.03, 0.06)	0.00, (-0.08, 0.08)	6.42, (-31.86, 58.32)	0.01, (-0.03, 0.05)	0.14, (0.10, 0.19)	0.28	no
1200	2	0.18	0.37	0.01, (-0.04, 0.05)	0.01, (-0.07, 0.09)	3.69, (-36.53, 52.85)	0.00, (-0.03, 0.04)	0.13, (0.09, 0.17)	0.16	no
1300	2	0.18	0.37	0.01, (-0.04, 0.05)	0.01, (-0.07, 0.09)	2.23, (-38.73, 53.64)	0.00, (-0.03, 0.04)	0.12, (0.09, 0.16)	0.11	yes-ish
1320	2	0.18	0.37	0.00, (-0.03, 0.05)	0.00, (-0.08, 0.07)	6.10, (-35.34, 59.26)	0.00, (-0.03, 0.04)	0.13, (0.09, 0.17)	0.14	no
1330	2	0.18	0.37	0.00, (-0.04, 0.05)	0.00, (-0.09, 0.08)	4.99, (-41.55, 65.46)	0.00, (-0.03, 0.05)	0.12, (0.09, 0.16)	0.11	yes-ish

1340	2	0.18	0.37	0.00, (-0.03, 0.05)	0.00, (-0.08, 0.08)	4.90, (-39.91, 60.40)	0.00, (-0.03, 0.05)	0.12, (0.09, 0.16)	0.10	yes
1360	2	0.18	0.37	0.00, (-0.03, 0.04)	0.01, (-0.06, 0.08)	1.61, (-39.08, 49.20)	0.00, (-0.03, 0.04)	0.12, (0.09, 0.15)	0.06	yes
1380	2	0.18	0.37	0.00, (-0.04, 0.05)	0.00, (-0.08, 0.08)	3.96, (-40.50, 61.42)	0.00, (-0.03, 0.04)	0.12, (0.09, 0.16)	0.09	yes
1400	2	0.18	0.37	0.00, (-0.03, 0.04)	0.01, (-0.07, 0.08)	2.88, (-41.57, 55.45)	0.00, (-0.03, 0.04)	0.12, (0.09, 0.16)	0.07	yes
High abundance, High Detection										
40	4	0.31	0.57	0.02, (-0.13, 0.20)	-0.01, (-0.15, 0.12)	0.52, (-1.46, 2.65)	0.01, (-0.04, 0.07)	0.12, (0.05, 0.24)	0.21	no
50	4	0.31	0.57	0.01, (-0.12, 0.15)	-0.01, (-0.14, 0.11)	0.46, (-1.75, 2.79)	0.01, (-0.03, 0.06)	0.10, (0.05, 0.18)	0.11	yes-ish
60	4	0.31	0.57	0.01, (-0.11, 0.14)	-0.01, (-0.12, 0.10)	0.34, (-1.86, 2.51)	0.01, (-0.03, 0.04)	0.08, (0.05, 0.14)	0.04	yes
80	4	0.31	0.57	0.01, (-0.10, 0.12)	-0.01, (-0.12, 0.09)	0.54, (-2.26, 3.09)	0.01, (-0.03, 0.04)	0.07, (0.04, 0.11)	0.01	yes
100	4	0.31	0.57	0.00, (-0.09, 0.10)	-0.01, (-0.09, 0.08)	0.46, (-2.30, 3.21)	0.00, (-0.02, 0.03)	0.06, (0.04, 0.09)	0.00	yes
80	3	0.31	0.57	0.01, (-0.09, 0.15)	-0.02, (-0.15, 0.10)	1.04, (-3.19, 5.81)	0.01, (-0.04, 0.07)	0.12, (0.06, 0.21)	0.20	no
90	3	0.31	0.57	0.01, (-0.09, 0.14)	-0.01, (-0.14, 0.09)	1.17, (-2.98, 6.04)	0.01, (-0.03, 0.07)	0.11, (0.06, 0.17)	0.11	yes-ish
100	3	0.31	0.57	0.01, (-0.09, 0.12)	-0.02, (-0.13, 0.10)	1.17, (-3.50, 6.48)	0.01, (-0.03, 0.06)	0.10, (0.06, 0.16)	0.07	yes
100	2	0.31	0.57	0.03, (-0.10, 0.20)	-0.01, (-0.18, 0.14)	3.10, (-5.43, 15.37)	0.03, (-0.05, 0.15)	0.22, (0.10, 0.42)	0.71	no
200	2	0.31	0.57	0.01, (-0.07, 0.12)	-0.01, (-0.15, 0.11)	3.09, (-8.55, 18.66)	0.02, (-0.04, 0.09)	0.13, (0.08, 0.22)	0.27	no
260	2	0.31	0.57	0.01, (-0.06, 0.10)	-0.02, (-0.13, 0.09)	3.93, (-8.86, 19.64)	0.02, (-0.03, 0.08)	0.11, (0.07, 0.17)	0.11	yes-ish
270	2	0.31	0.57	0.01, (-0.06, 0.09)	-0.01, (-0.12, 0.10)	2.65, (-10.68, 19.44)	0.01, (-0.04, 0.07)	0.11, (0.07, 0.16)	0.10	yes
280	2	0.31	0.57	0.01, (-0.06, 0.09)	-0.01, (-0.12, 0.10)	2.89, (-11.67, 18.31)	0.01, (-0.04, 0.07)	0.10, (0.07, 0.16)	0.06	yes
300	2	0.31	0.57	0.01, (-0.06, 0.08)	0.00, (-0.12, 0.11)	2.38, (-11.06, 17.92)	0.01, (-0.04, 0.06)	0.10, (0.06, 0.14)	0.05	yes
Average abundance, High detection										
60	4	0.18	0.57	0.01, (-0.08, 0.12)	-0.01, (-0.16, 0.11)	0.40, (-1.35, 1.93)	0.01, (-0.02, 0.03)	0.12, (0.05, 0.24)	0.19	no
70	4	0.18	0.57	0.00, (-0.08, 0.09)	-0.01, (-0.16, 0.13)	0.40, (-1.40, 2.08)	0.01, (-0.02, 0.03)	0.10, (0.04, 0.20)	0.13	no
80	4	0.18	0.57	0.01, (-0.07, 0.10)	-0.01, (-0.15, 0.11)	0.44, (-1.53, 2.09)	0.01, (-0.02, 0.03)	0.09, (0.04, 0.16)	0.08	yes
100	4	0.18	0.57	0.00, (-0.06, 0.07)	-0.01, (-0.11, 0.10)	0.38, (-1.78, 2.14)	0.00, (-0.02, 0.02)	0.08, (0.04, 0.12)	0.02	yes
100	3	0.18	0.57	0.01, (-0.06, 0.09)	-0.02, (-0.16, 0.11)	0.92, (-2.17, 4.61)	0.01, (-0.02, 0.05)	0.13, (0.06, 0.24)	0.29	no
120	3	0.18	0.57	0.01, (-0.06, 0.08)	-0.01, (-0.15, 0.11)	0.90, (-2.83, 5.00)	0.01, (-0.02, 0.04)	0.12, (0.06, 0.20)	0.20	no
130	3	0.18	0.57	0.01, (-0.05, 0.08)	-0.02, (-0.16, 0.10)	0.94, (-2.47, 5.02)	0.01, (-0.02, 0.04)	0.11, (0.06, 0.21)	0.14	no
140	3	0.18	0.57	0.01, (-0.05, 0.07)	-0.01, (-0.15, 0.11)	1.04, (-2.65, 5.62)	0.01, (-0.02, 0.04)	0.10, (0.06, 0.18)	0.10	yes
160	3	0.18	0.57	0.01, (-0.06, 0.07)	-0.01, (-0.13, 0.10)	0.81, (-3.10, 5.26)	0.01, (-0.02, 0.03)	0.09, (0.05, 0.16)	0.06	yes
180	3	0.18	0.57	0.00, (-0.05, 0.07)	-0.01, (-0.12, 0.09)	0.75, (-3.39, 5.10)	0.00, (-0.02, 0.03)	0.09, (0.05, 0.14)	0.03	yes
200	3	0.18	0.57	0.00, (-0.05, 0.05)	0.00, (-0.10, 0.09)	0.37, (-4.24, 4.27)	0.00, (-0.02, 0.02)	0.08, (0.05, 0.12)	0.01	yes
100	2	0.18	0.57	0.04, (-0.06, 0.17)	-0.03, (-0.25, 0.17)	3.64, (-4.01, 14.15)	0.04, (-0.04, 0.14)	0.33, (0.11, 0.74)	0.87	no
200	2	0.18	0.57	0.02, (-0.04, 0.09)	-0.02, (-0.18, 0.12)	2.95, (-5.82, 15.54)	0.01, (-0.03, 0.08)	0.18, (0.09, 0.32)	0.60	no
300	2	0.18	0.57	0.01, (-0.04, 0.06)	-0.01, (-0.14, 0.11)	2.68, (-7.26, 14.43)	0.01, (-0.02, 0.05)	0.13, (0.08, 0.20)	0.26	no
360	2	0.18	0.57	0.01, (-0.04, 0.06)	0.00, (-0.11, 0.11)	2.08, (-8.82, 14.99)	0.01, (-0.02, 0.04)	0.11, (0.07, 0.17)	0.12	no
370	2	0.18	0.57	0.01, (-0.04, 0.06)	0.00, (-0.13, 0.10)	2.10, (-8.79, 17.11)	0.01, (-0.02, 0.05)	0.11, (0.07, 0.17)	0.12	no
380	2	0.18	0.57	0.01, (-0.04, 0.05)	0.00, (-0.12, 0.10)	2.16, (-8.01, 16.90)	0.01, (-0.02, 0.04)	0.11, (0.07, 0.16)	0.09	yes
400	2	0.18	0.57	0.00, (-0.04, 0.05)	-0.01, (-0.12, 0.09)	2.35, (-8.74, 15.74)	0.01, (-0.02, 0.04)	0.11, (0.07, 0.16)	0.08	yes
Low abundance, High detection										
100	4	0.08	0.57	0.00, (-0.04, 0.06)	-0.01, (-0.17, 0.14)	0.32, (-0.94, 1.51)	0.00, (-0.01, 0.02)	0.15, (0.05, 0.30)	0.27	no
120	4	0.08	0.57	0.00, (-0.04, 0.05)	-0.02, (-0.18, 0.13)	0.34, (-0.93, 1.65)	0.00, (-0.01, 0.01)	0.13, (0.05, 0.27)	0.20	no
130	4	0.08	0.57	0.00, (-0.04, 0.04)	-0.01, (-0.16, 0.12)	0.33, (-1.29, 1.86)	0.00, (-0.01, 0.01)	0.11, (0.05, 0.21)	0.15	no

140	4	0.08	0.57	0.00, (-0.04, 0.05)	-0.01, (-0.15, 0.13)	0.25, (-1.34, 1.57)	0.00, (-0.01, 0.01)	0.10, (0.04, 0.18)	0.10	yes
160	4	0.08	0.57	0.00, (-0.03, 0.04)	-0.01, (-0.16, 0.11)	0.36, (-1.20, 1.78)	0.00, (-0.01, 0.01)	0.09, (0.04, 0.18)	0.10	yes
180	4	0.08	0.57	0.00, (-0.03, 0.04)	-0.02, (-0.14, 0.10)	0.40, (-1.27, 1.87)	0.00, (-0.01, 0.01)	0.08, (0.04, 0.15)	0.05	yes
200	4	0.08	0.57	0.00, (-0.03, 0.03)	-0.01, (-0.14, 0.11)	0.32, (-1.51, 1.95)	0.00, (-0.01, 0.01)	0.07, (0.04, 0.14)	0.04	yes
100	3	0.08	0.57	0.01, (-0.04, 0.06)	-0.03, (-0.25, 0.16)	1.07, (-1.30, 4.70)	0.01, (-0.01, 0.05)	0.30, (0.09, 0.75)	0.71	no
200	3	0.08	0.57	0.01, (-0.03, 0.05)	-0.01, (-0.17, 0.13)	0.83, (-2.19, 3.84)	0.00, (-0.01, 0.02)	0.13, (0.06, 0.27)	0.28	no
260	3	0.08	0.57	0.00, (-0.03, 0.04)	-0.01, (-0.15, 0.11)	0.64, (-2.90, 4.18)	0.00, (-0.01, 0.02)	0.11, (0.05, 0.20)	0.14	no
270	3	0.08	0.57	0.00, (-0.03, 0.03)	-0.01, (-0.15, 0.12)	0.80, (-2.34, 4.55)	0.00, (-0.01, 0.02)	0.11, (0.05, 0.19)	0.14	no
280	3	0.08	0.57	0.00, (-0.02, 0.03)	-0.01, (-0.14, 0.12)	0.65, (-2.59, 3.81)	0.00, (-0.01, 0.01)	0.10, (0.05, 0.18)	0.10	yes
300	3	0.08	0.57	0.00, (-0.02, 0.04)	-0.01, (-0.12, 0.11)	0.60, (-2.60, 4.04)	0.00, (-0.01, 0.01)	0.09, (0.05, 0.16)	0.06	yes
100	2	0.08	0.57	0.03, (-0.04, 0.17)	-0.04, (-0.31, 0.20)	3.48, (-1.87, 17.18)	0.03, (-0.02, 0.17)	0.72, (0.16, 1.50)	0.96	no
200	2	0.08	0.57	0.02, (-0.03, 0.08)	-0.03, (-0.27, 0.18)	3.35, (-3.14, 16.23)	0.02, (-0.02, 0.08)	0.34, (0.11, 0.90)	0.85	no
300	2	0.08	0.57	0.01, (-0.03, 0.05)	-0.02, (-0.21, 0.14)	2.51, (-4.26, 12.63)	0.01, (-0.01, 0.04)	0.23, (0.10, 0.44)	0.74	no
400	2	0.08	0.57	0.01, (-0.02, 0.04)	-0.01, (-0.16, 0.14)	2.33, (-5.14, 13.15)	0.01, (-0.01, 0.03)	0.18, (0.09, 0.30)	0.56	no
500	2	0.08	0.57	0.00, (-0.02, 0.03)	0.00, (-0.15, 0.12)	1.73, (-6.34, 13.81)	0.00, (-0.01, 0.03)	0.15, (0.08, 0.24)	0.38	no
600	2	0.08	0.57	0.00, (-0.02, 0.03)	-0.01, (-0.15, 0.11)	2.12, (-6.84, 14.17)	0.00, (-0.01, 0.02)	0.13, (0.08, 0.22)	0.26	no
700	2	0.08	0.57	0.00, (-0.02, 0.03)	-0.01, (-0.13, 0.10)	2.05, (-7.04, 12.92)	0.00, (-0.01, 0.02)	0.12, (0.07, 0.19)	0.18	no
800	2	0.08	0.57	0.00, (-0.02, 0.02)	-0.01, (-0.14, 0.10)	2.55, (-8.43, 14.68)	0.00, (-0.01, 0.02)	0.11, (0.07, 0.18)	0.12	no
810	2	0.08	0.57	0.00, (-0.02, 0.03)	-0.01, (-0.12, 0.11)	2.21, (-8.07, 14.45)	0.00, (-0.01, 0.02)	0.11, (0.07, 0.16)	0.09	yes
820	2	0.08	0.57	0.00, (-0.02, 0.03)	-0.01, (-0.12, 0.11)	2.34, (-8.14, 15.44)	0.00, (-0.01, 0.02)	0.11, (0.06, 0.16)	0.09	yes
840	2	0.08	0.57	0.00, (-0.02, 0.03)	-0.01, (-0.12, 0.10)	2.03, (-7.51, 13.65)	0.00, (-0.01, 0.02)	0.11, (0.07, 0.16)	0.07	yes
860	2	0.08	0.57	0.00, (-0.02, 0.03)	-0.01, (-0.13, 0.09)	2.71, (-8.18, 16.54)	0.00, (-0.01, 0.02)	0.11, (0.07, 0.16)	0.09	yes
880	2	0.08	0.57	0.00, (-0.02, 0.02)	-0.01, (-0.13, 0.09)	2.42, (-8.03, 16.64)	0.00, (-0.01, 0.02)	0.10, (0.07, 0.16)	0.07	yes
900	2	0.08	0.57	0.00, (-0.02, 0.02)	-0.01, (-0.11, 0.09)	1.90, (-8.58, 13.68)	0.00, (-0.01, 0.02)	0.10, (0.07, 0.15)	0.05	yes

Table S9. Results of simulations evaluating the efficacy of survey protocols using parameters from the 2020 and 2021 spring survey data analyzed hierarchical distance sampling models. Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of survey sites, λ = mean abundance per site, sigma = sigma for calculating the half-normal detection function; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site.

Simulation Parameters			**Bias in λ**	**Bias in *sigma***	**Bias in Total N**	**Bias in N.site**	**CV Total N**	**Probability CV N.total > 0.15**	**Protocol meets Management Requirements**
R	**λ**	***sigma***							
High abundance, Average detection									
100	0.31	43	-0.03, (-0.18, 0.25)	12.49, (-8.02, 31.07)	-2.69 (-18.05, 23.53)	-0.03, (-0.18, 0.24)	0.45 (0.31, 0.62)	1.00	no
200	0.31	43	-0.04, (-0.16, 0.15)	9.33, (-6.36, 27.07)	-5.86 (-29.45, 26.54)	-0.03, (-0.15, 0.13)	0.33 (0.27, 0.41)	1.00	no
300	0.31	43	-0.03, (-0.15, 0.12)	6.76, (-6.15, 24.38)	-6.83 (-37.74, 34.02)	-0.02, (-0.13, 0.11)	0.27 (0.23, 0.32)	1.00	no
400	0.31	43	-0.03, (-0.13, 0.10)	5.06, (-4.71, 20.20)	-8.67 (-51.63, 37.50)	-0.02, (-0.13, 0.09)	0.24 (0.20, 0.27)	1.00	no
500	0.31	43	-0.02, (-0.13, 0.09)	4.09, (-5.55, 18.37)	-10.39 (-58.87, 46.26)	-0.02, (-0.12, 0.09)	0.21 (0.18, 0.24)	1.00	no
600	0.31	43	-0.02, (-0.11, 0.09)	3.20, (-4.32, 13.62)	-9.94 (-62.57, 46.39)	-0.02, (-0.10, 0.08)	0.19 (0.17, 0.22)	1.00	no
700	0.31	43	-0.02, (-0.11, 0.07)	2.80, (-4.63, 12.15)	-13.90 (-69.13, 40.18)	-0.02, (-0.10, 0.06)	0.18 (0.16, 0.20)	0.99	no
800	0.31	43	-0.02, (-0.10, 0.07)	2.41, (-4.33, 10.63)	-12.23 (-76.15, 54.38)	-0.02, (-0.10, 0.07)	0.16 (0.14, 0.18)	0.85	no
900	0.31	43	-0.02, (-0.10, 0.06)	2.38, (-3.72, 11.16)	-14.95 (-79.90, 56.56)	-0.02, (-0.09, 0.06)	0.15 (0.14, 0.17)	0.62	no
1000	0.31	43	-0.02, (-0.09, 0.05)	1.86, (-3.68, 9.58)	-15.56 (-86.52, 58.16)	-0.02, (-0.09, 0.06)	0.15 (0.13, 0.16)	0.30	no
1080	0.31	43	-0.02, (-0.09, 0.06)	1.93, (-3.45, 9.13)	-17.44 (-89.20, 60.15)	-0.02, (-0.08, 0.06)	0.14 (0.13, 0.15)	0.11	yes-ish
1090	0.31	43	-0.02, (-0.09, 0.06)	2.10, (-3.15, 8.94)	-18.79 (-88.97, 51.88)	-0.02, (-0.08, 0.05)	0.14 (0.13, 0.15)	0.09	yes
1100	0.31	43	-0.02, (-0.09, 0.06)	1.96, (-3.74, 8.62)	-18.82 (-88.62, 61.83)	-0.02, (-0.08, 0.06)	0.14 (0.13, 0.15)	0.09	yes
Low abundance, Average detection									
100	0.08	43	-0.01, (-0.08, 0.14)	14.28, (-8.12, 29.67)	1.51 (-6.81, 13.36)	-0.02, (-0.07, 0.13)	4.13 (0.48, 32.36)	1.00	no
200	0.08	43	0.00, (-0.06, 0.10)	14.16, (-8.22, 31.40)	0.24 (-10.30, 17.32)	-0.00, (-0.05, 0.09)	0.73 (0.37, 0.97)	1.00	no
300	0.08	43	-0.01, (-0.05, 0.06)	13.25, (-7.69, 30.94)	-1.77 (-14.30, 16.92)	-0.01, (-0.05, 0.06)	0.51 (0.34, 0.72)	1.00	no
400	0.08	43	-0.01, (-0.05, 0.06)	11.85, (-8.94, 29.75)	-2.12 (-18.13, 22.77)	-0.01, (-0.05, 0.06)	0.45 (0.32, 0.58)	1.00	no
500	0.08	43	-0.01, (-0.05, 0.06)	11.98, (-8.15, 32.05)	-3.51 (-21.65, 25.54)	-0.01, (-0.04, 0.05)	0.39 (0.29, 0.50)	1.00	no
600	0.08	43	-0.01, (-0.05, 0.05)	10.85, (-7.17, 28.07)	-4.69 (-25.74, 23.21)	-0.01, (-0.04, 0.04)	0.37 (0.29, 0.47)	1.00	no
700	0.08	43	-0.01, (-0.04, 0.04)	9.18, (-7.45, 28.12)	-3.42 (-27.03, 28.64)	-0.00, (-0.04, 0.04)	0.34 (0.27, 0.42)	1.00	no
800	0.08	43	-0.01, (-0.04, 0.04)	9.77, (-5.85, 28.00)	-7.49 (-30.99, 25.53)	-0.01, (-0.04, 0.03)	0.33 (0.26, 0.40)	1.00	no
900	0.08	43	-0.01, (-0.04, 0.03)	9.45, (-5.57, 27.95)	-8.05 (-36.32, 26.72)	-0.01, (-0.04, 0.03)	0.31 (0.25, 0.37)	1.00	no
1000	0.08	43	-0.01, (-0.04, 0.03)	8.49, (-5.67, 27.47)	-7.70 (-36.40, 29.51)	-0.01, (-0.04, 0.03)	0.29 (0.24, 0.35)	1.00	no
1100	0.08	43	-0.01, (-0.04, 0.03)	7.01, (-5.92, 24.80)	-7.10 (-38.17, 31.39)	-0.01, (-0.03, 0.03)	0.28 (0.24, 0.34)	1.00	no
1200	0.08	43	-0.01, (-0.04, 0.03)	7.12, (-6.04, 25.24)	-8.17 (-42.23, 33.67)	-0.01, (-0.04, 0.03)	0.27 (0.22, 0.31)	1.00	no
1300	0.08	43	-0.01, (-0.04, 0.03)	6.33, (-5.33, 23.55)	-8.84 (-47.22, 37.38)	-0.01, (-0.04, 0.03)	0.26 (0.22, 0.30)	1.00	no
1400	0.08	43	-0.01, (-0.04, 0.02)	5.88, (-5.18, 21.26)	-9.01 (-47.30, 31.65)	-0.01, (-0.03, 0.02)	0.25 (0.22, 0.29)	1.00	no
1500	0.08	43	-0.01, (-0.04, 0.03)	5.93, (-5.74, 23.13)	-10.50 (-49.78, 38.86)	-0.01, (-0.03, 0.03)	0.24 (0.21, 0.28)	1.00	no
1600	0.08	43	-0.01, (-0.03, 0.03)	4.62, (-5.59, 20.75)	-7.98 (-51.29, 40.44)	-0.00, (-0.03, 0.03)	0.23 (0.20, 0.27)	1.00	no

1700	0.08	43	-0.01, (-0.03, 0.02)	4.70, (-4.88, 17.78)	-9.67 (-53.32, 36.98)	-0.01, (-0.03, 0.02)	0.22 (0.19, 0.26)	1.00	no
1800	0.08	43	-0.01, (-0.03, 0.02)	5.36, (-4.89, 20.75)	-12.04 (-55.40, 39.73)	-0.01, (-0.03, 0.02)	0.22 (0.19, 0.25)	1.00	no
1900	0.08	43	-0.01, (-0.03, 0.02)	4.19, (-4.65, 19.10)	-9.98 (-55.93, 40.14)	-0.01, (-0.03, 0.02)	0.21 (0.19, 0.24)	1.00	no
2000	0.08	43	-0.01, (-0.03, 0.02)	3.86, (-4.76, 16.80)	-10.47 (-58.77, 40.46)	-0.01, (-0.03, 0.02)	0.21 (0.18, 0.24)	1.00	no
2100	0.08	43	-0.01, (-0.03, 0.02)	4.34, (-4.39, 17.04)	-14.75 (-61.60, 37.68)	-0.01, (-0.03, 0.02)	0.20 (0.18, 0.23)	1.00	no
2200	0.08	43	-0.01, (-0.03, 0.02)	3.81, (-4.39, 15.32)	-10.29 (-60.64, 47.19)	-0.00, (-0.03, 0.02)	0.20 (0.17, 0.22)	1.00	no
2300	0.08	43	-0.01, (-0.03, 0.02)	3.97, (-3.96, 15.66)	-13.67 (-66.91, 39.67)	-0.01, (-0.03, 0.02)	0.19 (0.17, 0.22)	1.00	no
2400	0.08	43	-0.01, (-0.03, 0.02)	3.57, (-4.75, 14.64)	-11.85 (-64.28, 46.87)	-0.00, (-0.03, 0.02)	0.19 (0.17, 0.21)	1.00	no
2500	0.08	43	-0.01, (-0.03, 0.02)	2.97, (-4.48, 13.56)	-11.60 (-67.65, 46.84)	-0.00, (-0.03, 0.02)	0.18 (0.16, 0.21)	1.00	no
2600	0.08	43	-0.01, (-0.03, 0.02)	3.48, (-3.70, 12.30)	-15.97 (-66.83, 44.16)	-0.01, (-0.03, 0.02)	0.18 (0.16, 0.21)	1.00	no
2700	0.08	43	-0.00, (-0.03, 0.02)	2.58, (-5.09, 12.59)	-8.92 (-65.01, 55.51)	-0.00, (-0.02, 0.02)	0.18 (0.16, 0.20)	0.99	no
2800	0.08	43	-0.01, (-0.03, 0.02)	3.19, (-4.47, 14.46)	-14.18 (-70.89, 48.19)	-0.01, (-0.03, 0.02)	0.17 (0.15, 0.19)	0.98	no
2900	0.08	43	-0.01, (-0.03, 0.02)	2.82, (-4.05, 11.38)	-13.56 (-70.86, 46.23)	-0.00, (-0.02, 0.02)	0.17 (0.15, 0.19)	0.96	no
3000	0.08	43	-0.01, (-0.03, 0.02)	2.59, (-3.95, 11.75)	-12.63 (-77.32, 55.70)	-0.00, (-0.04, 0.02)	0.17 (0.15, 0.19)	0.91	no
3100	0.08	43	-0.01, (-0.03, 0.02)	2.67, (-4.22, 11.36)	-13.99 (-74.71, 50.46)	-0.00, (-0.02, 0.02)	0.16 (0.15, 0.18)	0.91	no
3200	0.08	43	-0.01, (-0.03, 0.02)	2.42, (-3.86, 11.09)	-12.78 (-72.98, 48.70)	-0.00, (-0.02, 0.02)	0.16 (0.14, 0.18)	0.84	no
3300	0.08	43	-0.01, (-0.03, 0.01)	2.75, (-3.53, 11.68)	-17.05 (-76.50, 47.78)	-0.01, (-0.02, 0.01)	0.16 (0.14, 0.18)	0.79	no
3400	0.08	43	-0.01, (-0.03, 0.01)	2.29, (-3.60, 10.31)	-14.90 (-75.36, 53.96)	-0.00, (-0.02, 0.01)	0.16 (0.14, 0.17)	0.71	no
3500	0.08	43	-0.01, (-0.03, 0.01)	2.55, (-4.12, 11.03)	-18.15 (-78.58, 51.00)	-0.01, (-0.02, 0.01)	0.15 (0.14, 0.17)	0.63	no
3600	0.08	43	-0.01, (-0.03, 0.02)	2.33, (-3.43, 10.19)	-16.56 (-80.80, 57.00)	-0.00, (-0.02, 0.02)	0.15 (0.14, 0.17)	0.54	no
3700	0.08	43	-0.00, (-0.02, 0.02)	2.14, (-3.73, 9.85)	-14.32 (-81.42, 55.24)	-0.00, (-0.02, 0.01)	0.15 (0.13, 0.16)	0.42	no
3800	0.08	43	-0.01, (-0.02, 0.01)	2.10, (-3.73, 9.33)	-15.58 (-79.81, 52.56)	-0.00, (-0.02, 0.01)	0.15 (0.13, 0.16)	0.33	no
3900	0.08	43	-0.01, (-0.02, 0.01)	1.94, (-4.04, 8.77)	-14.41 (-80.78, 54.87)	-0.00, (-0.02, 0.01)	0.14 (0.13, 0.16)	0.25	no
4000	0.08	43	-0.01, (-0.03, 0.01)	2.39, (-3.36, 9.73)	-19.42 (-87.05, 50.46)	-0.00, (-0.02, 0.01)	0.14 (0.13, 0.16)	0.22	no
4100	0.08	43	-0.01, (-0.02, 0.01)	1.91, (-3.33, 8.78)	-16.27 (-84.71, 56.91)	-0.00, (-0.02, 0.01)	0.14 (0.13, 0.16)	0.17	no
4200	0.08	43	-0.01, (-0.02, 0.01)	2.05, (-3.31, 9.73)	-18.75 (-93.80, 54.63)	-0.00, (-0.02, 0.01)	0.14 (0.13, 0.15)	0.13	no
4220	0.08	43	-0.01, (-0.02, 0.01)	1.83, (-3.33, 8.36)	-16.98 (-82.82, 57.28)	0.00, (-0.02, 0.01)	0.14 (0.13, 0.15)	0.11	yes-ish
4230	0.08	43	-0.01, (-0.02, 0.02)	1.88, (-3.38, 8.84)	-15.39 (-87.53, 65.58)	0.00, (-0.02, 0.02)	0.14 (0.13, 0.15)	0.08	yes
4240	0.08	43	-0.01, (-0.02, 0.01)	2.29, (-3.36, 8.51)	-21.31 (-92.40, 52.07)	-0.01, (-0.02, 0.01)	0.14 (0.13, 0.15)	0.08	yes
4260	0.08	43	0.00, (-0.02, 0.02)	1.67, (-3.96, 8.20)	-15.67 (-85.26, 62.21)	0.00, (-0.02, 0.01)	0.14 (0.13, 0.15)	0.10	yes
4280	0.08	43	-0.01, (-0.02, 0.01)	2.06, (-2.99, 9.06)	-20.57 (-89.29, 51.27)	0.00, (-0.02, 0.01)	0.14 (0.13, 0.15)	0.07	yes
4300	0.08	43	-0.01, (-0.02, 0.01)	1.72, (-3.70, 7.72)	-15.77 (-88.18, 56.97)	-0.00, (-0.02, 0.01)	0.14 (0.13, 0.15)	0.08	yes
Average abundance, Average detection									
100	0.18	43	-0.00, (-0.12, 0.17)	15.49, (-7.38, 31.57)	0.13 (-11.95, 16.33)	0.00, (-0.12, 0.16)	0.57 (0.36, 0.89)	1.00	no
200	0.18	43	-0.00, (-0.11, 0.13)	12.14, (-7.20, 29.91)	-3.59 (-21.45, 26.09)	-0.02, (-0.11, 0.13)	0.41 (0.30, 0.56)	1.00	no
300	0.18	43	-0.01, (-0.09, 0.10)	9.61, (-7.65, 28.24)	-3.79 (-26.80, 29.27)	-0.01, (-0.09, 0.10)	0.34 (0.27, 0.43)	1.00	no
400	0.18	43	-0.01, (-0.09, 0.09)	7.97, (-6.91, 26.01)	-5.38 (-33.14, 30.68)	-0.01, (-0.08, 0.08)	0.30 (0.25, 0.36)	1.00	no
500	0.18	43	-0.02, (-0.08, 0.07)	7.65, (-5.88, 25.75)	-9.19 (-43.12, 31.31)	-0.02, (-0.09, 0.06)	0.27 (0.23, 0.32)	1.00	no
600	0.18	43	-0.02, (-0.08, 0.07)	6.20, (-6.02, 23.24)	-9.85 (-46.30, 36.80)	-0.02, (-0.08, 0.06)	0.25 (0.22, 0.29)	1.00	no
700	0.18	43	-0.02, (-0.08, 0.05)	5.83, (-5.39, 22.42)	-11.67 (-55.37, 34.89)	-0.02, (-0.08, 0.05)	0.23 (0.20, 0.27)	1.00	no
800	0.18	43	-0.01, (-0.07, 0.05)	4.98, (-4.78, 18.80)	-11.43 (-57.57, 38.71)	-0.01, (-0.07, 0.05)	0.22 (0.19, 0.25)	1.00	no
900	0.18	43	-0.01, (-0.07, 0.05)	4.13, (-4.87, 17.00)	-11.08 (-66.05, 43.72)	-0.01, (-0.07, 0.05)	0.20 (0.18, 0.23)	1.00	no
1000	0.18	43	-0.01, (-0.06, 0.05)	3.60, (-4.64, 14.11)	-11.68 (-62.54, 44.27)	-0.01, (-0.06, 0.04)	0.19 (0.17, 0.22)	1.00	no
1100	0.18	43	-0.01, (-0.06, 0.04)	3.30, (-3.83, 13.09)	-13.53 (-67.11, 40.76)	-0.01, (-0.06, 0.04)	0.18 (0.16, 0.21)	1.00	no

1200	0.18	43	-0.01, (-0.06, 0.05)	3.03, (-4.29, 12.80)	-12.82 (-66.73, 51.98)	-0.01, (-0.06, 0.04)	0.17 (0.15, 0.20)	0.98	no
1300	0.18	43	-0.01, (-0.06, 0.04)	3.07, (-3.36, 11.84)	-17.82 (-76.43, 44.09)	-0.01, (-0.06, 0.03)	0.17 (0.15, 0.19)	0.95	no
1400	0.18	43	-0.01, (-0.06, 0.05)	2.50, (-3.88, 10.64)	-15.13 (-74.78, 57.71)	-0.01, (-0.05, 0.04)	0.16 (0.14, 0.18)	0.84	no
1500	0.18	43	-0.01, (-0.05, 0.04)	2.21, (-3.47, 8.91)	-14.60 (-75.93, 54.73)	-0.01, (-0.05, 0.04)	0.15 (0.14, 0.17)	0.67	no
1600	0.18	43	-0.01, (-0.05, 0.04)	2.18, (-3.71, 9.73)	-16.56 (-83.86, 54.38)	-0.01, (-0.05, 0.03)	0.15 (0.14, 0.17)	0.46	no
1700	0.18	43	-0.01, (-0.05, 0.04)	2.32, (-3.26, 9.01)	-18.61 (-84.83, 56.63)	-0.01, (-0.05, 0.03)	0.14 (0.13, 0.16)	0.28	no
1800	0.18	43	-0.01, (-0.05, 0.03)	2.03, (-3.37, 8.46)	-18.09 (-92.63, 56.68)	-0.01, (-0.05, 0.03)	0.14 (0.13, 0.16)	0.13	no
1860	0.18	43	-0.01, (-0.05, 0.04)	1.82, (-3.30, 8.48)	-17.80 (-90.37, 60.18)	-0.01, (-0.05, 0.03)	0.14 (0.13, 0.15)	0.11	yes-ish
1870	0.18	43	-0.01, (-0.05, 0.04)	1.99, (-3.09, 8.08)	-17.12 (-83.53, 63.25)	-0.01, (-0.04, 0.03)	0.14 (0.13, 0.15)	0.06	yes
1880	0.18	43	-0.01, (-0.05, 0.03)	1.85, (-3.38, 8.26)	-17.15 (-86.41, 52.00)	-0.01, (-0.05, 0.03)	0.14 (0.13, 0.15)	0.06	yes
1900	0.18	43	-0.01, (-0.05, 0.04)	1.86, (-3.59, 7.59)	-18.32 (-85.32, 60.60)	-0.01, (-0.04, 0.03)	0.14 (0.12, 0.15)	0.06	yes
High abundance, High detection									
100	0.31	58	-0.02, (-0.14, 0.14)	10.09, (-8.59, 22.55)	-1.09 (-11.26, 12.84)	-0.01, (-0.11, 0.13)	0.31 (0.21, 0.42)	1.00	no
200	0.31	58	-0.02, (-0.11, 0.12)	9.78, (-7.40, 24.12)	-3.68 (-19.30, 21.72)	-0.02, (-0.10, 0.11)	0.24 (0.16, 0.30)	0.97	no
300	0.31	58	-0.02, (-0.11, 0.11)	8.14, (-8.13, 23.82)	-4.21 (-27.23, 30.31)	-0.01, (-0.09, 0.10)	0.21 (0.14, 0.25)	0.93	no
400	0.31	58	-0.02, (-0.11, 0.09)	7.40, (-7.80, 23.03)	-5.78 (-34.83, 35.01)	-0.01, (-0.09, 0.09)	0.18 (0.14, 0.22)	0.90	no
500	0.31	58	-0.02, (-0.09, 0.08)	6.68, (-6.91, 21.36)	-7.48 (-39.28, 37.20)	-0.01, (-0.08, 0.07)	0.17 (0.13, 0.19)	0.87	no
600	0.31	58	-0.02, (-0.10, 0.06)	6.90, (-7.22, 22.48)	-11.47 (-51.76, 38.69)	-0.02, (-0.09, 0.06)	0.16 (0.12, 0.18)	0.75	no
700	0.31	58	-0.02, (-0.09, 0.06)	6.03, (-6.39, 19.76)	-12.12 (-54.45, 42.24)	-0.02, (-0.08, 0.06)	0.15 (0.13, 0.16)	0.41	no
780	0.31	58	-0.02, (-0.09, 0.06)	6.15, (-6.42, 21.11)	-14.02 (-61.94, 47.12)	-0.02, (-0.08, 0.06)	0.14 (0.12, 0.15)	0.13	no
790	0.31	58	-0.02, (-0.08, 0.06)	5.72, (-5.60, 18.78)	-13.11 (-58.29, 40.61)	-0.02, (-0.07, 0.05)	0.14 (0.12, 0.15)	0.11	yes-ish
800	0.31	58	-0.02, (-0.09, 0.05)	5.90, (-5.70, 20.32)	-15.31 (-63.06, 38.67)	-0.02, (-0.08, 0.05)	0.14 (0.12, 0.15)	0.07	yes
Average abundance, High detection									
100	0.18	58	0.00, (-0.10, 0.15)	7.71, (-13.26, 21.42)	0.83 (-7.59, 13.95)	0.01, (-0.08, 0.14)	0.42 (0.26, 0.62)	1.00	no
200	0.18	58	-0.01, (-0.08, 0.09)	10.25, (-8.05, 22.96)	-2.08 (-13.86, 14.53)	-0.01, (-0.07, 0.07)	0.29 (0.20, 0.40)	1.00	no
300	0.18	58	-0.01, (-0.07, 0.09)	9.23, (-10.02, 24.04)	-2.12 (-18.90, 23.19)	-0.01, (-0.06, 0.08)	0.25 (0.17, 0.32)	0.98	no
400	0.18	58	-0.01, (-0.06, 0.08)	8.15, (-9.92, 23.51)	-2.03 (-23.80, 28.60)	-0.01, (-0.06, 0.07)	0.23 (0.16, 0.28)	0.97	no
500	0.18	58	-0.01, (-0.06, 0.06)	7.94, (-7.61, 22.71)	-4.11 (-27.47, 27.83)	-0.01, (-0.05, 0.06)	0.21 (0.15, 0.25)	0.95	no
600	0.18	58	-0.01, (-0.06, 0.06)	7.92, (-9.48, 22.36)	-6.11 (-33.32, 34.50)	-0.01, (-0.06, 0.06)	0.19 (0.14, 0.23)	0.93	no
700	0.18	58	-0.01, (-0.06, 0.06)	7.28, (-7.67, 23.09)	-6.49 (-35.11, 34.33)	-0.01, (-0.05, 0.05)	0.18 (0.13, 0.21)	0.89	no
800	0.18	58	-0.01, (-0.06, 0.06)	7.65, (-9.07, 23.18)	-7.84 (-42.33, 39.52)	-0.01, (-0.05, 0.05)	0.17 (0.13, 0.20)	0.83	no
900	0.18	58	-0.01, (-0.05, 0.05)	6.39, (-8.22, 22.16)	-7.78 (-43.56, 44.66)	-0.01, (-0.05, 0.05)	0.16 (0.13, 0.19)	0.85	no
1000	0.18	58	-0.01, (-0.05, 0.04)	6.83, (-6.72, 21.75)	-10.79 (-49.12, 38.50)	-0.01, (-0.05, 0.04)	0.16 (0.13, 0.18)	0.75	no
1100	0.18	58	-0.01, (-0.05, 0.05)	6.13, (-7.44, 20.08)	-10.78 (-49.51, 43.62)	-0.01, (-0.05, 0.04)	0.15 (0.13, 0.17)	0.61	no
1200	0.18	58	-0.01, (-0.05, 0.04)	6.50, (-5.82, 20.76)	-12.26 (-53.03, 37.08)	-0.01, (-0.04, 0.03)	0.14 (0.12, 0.16)	0.36	no
1300	0.18	58	-0.01, (-0.05, 0.04)	5.12, (-6.20, 19.93)	-10.41 (-61.06, 45.39)	-0.01, (-0.05, 0.03)	0.14 (0.12, 0.16)	0.17	no
1340	0.18	58	-0.01, (-0.05, 0.03)	4.95, (-6.75, 18.81)	-10.71 (-57.01, 38.66)	-0.01, (-0.04, 0.03)	0.14 (0.12, 0.15)	0.11	yes-ish
1350	0.18	58	-0.01, (-0.05, 0.04)	5.38, (-6.36, 19.01)	-12.58 (-58.27, 40.85)	-0.01, (-0.04, 0.03)	0.14 (0.12, 0.15)	0.12	no
1360	0.18	58	-0.01, (-0.05, 0.04)	5.05, (-6.55, 19.75)	-11.90 (-63.80, 44.26)	-0.01, (-0.05, 0.03)	0.14 (0.12, 0.15)	0.08	yes
1380	0.18	58	-0.01, (-0.05, 0.03)	5.15, (-6.16, 19.62)	-13.08 (-61.06, 41.45)	-0.01, (-0.04, 0.03)	0.14 (0.12, 0.15)	0.07	yes
1400	0.18	58	-0.01, (-0.05, 0.04)	4.36, (-7.56, 18.45)	-9.17 (-58.23, 50.97)	-0.01, (-0.04, 0.04)	0.14 (0.12, 0.15)	0.06	yes
Low abundance, high detection									

100	0.08	58	0.02, (-0.05, 0.13)	5.48, (-20.85, 19.54)	2.59 (-4.04, 12.89)	0.03, (-0.04, 0.13)	1.21 (0.36, 1.49)	1.00	no
200	0.08	58	0.00, (-0.04, 0.07)	7.98, (-13.24, 21.30)	0.72 (-7.48, 13.90)	0.00, (-0.04, 0.07)	0.58 (0.27, 0.67)	1.00	no
300	0.08	58	0.00, (-0.04, 0.06)	8.30, (-11.25, 21.53)	0.71 (-9.00, 15.79)	0.00, (-0.03, 0.05)	0.36 (0.23, 0.52)	1.00	no
400	0.08	58	0.00, (-0.04, 0.05)	8.19, (-11.23, 22.25)	0.00 (-11.74, 17.47)	0.00, (-0.03, 0.04)	0.32 (0.21, 0.44)	1.00	no
500	0.08	58	0.00, (-0.03, 0.04)	8.66, (-10.65, 22.78)	-0.33 (-11.98, 19.26)	0.00, (-0.02, 0.04)	0.29 (0.20, 0.39)	1.00	no
600	0.08	58	0.00, (-0.03, 0.03)	9.75, (-8.83, 23.85)	-2.22 (-15.78, 19.92)	0.00, (-0.03, 0.03)	0.26 (0.17, 0.34)	0.99	no
700	0.08	58	-0.01, (-0.03, 0.03)	9.31, (-8.07, 23.65)	-2.32 (-16.86, 18.75)	0.00, (-0.02, 0.03)	0.25 (0.17, 0.32)	0.99	no
800	0.08	58	0.00, (-0.03, 0.03)	8.95, (-7.86, 23.35)	-2.93 (-20.13, 21.50)	0.00, (-0.03, 0.03)	0.24 (0.16, 0.30)	0.97	no
900	0.08	58	0.00, (-0.03, 0.03)	8.83, (-7.93, 24.28)	-3.17 (-23.30, 23.45)	0.00, (-0.03, 0.03)	0.23 (0.15, 0.28)	0.95	no
1000	0.08	58	-0.01, (-0.03, 0.02)	9.43, (-7.93, 23.04)	-5.59 (-25.15, 25.45)	-0.01, (-0.03, 0.03)	0.22 (0.15, 0.27)	0.95	no
1100	0.08	58	-0.01, (-0.03, 0.03)	8.64, (-8.63, 24.51)	-4.62 (-26.64, 23.74)	0.00, (-0.02, 0.02)	0.21 (0.14, 0.25)	0.93	no
1200	0.08	58	0.00, (-0.03, 0.03)	7.57, (-9.11, 22.10)	-4.06 (-27.77, 28.33)	0.00, (-0.02, 0.02)	0.20 (0.15, 0.25)	0.95	no
1300	0.08	58	0.00, (-0.03, 0.02)	7.59, (-8.74, 23.67)	-4.74 (-30.13, 28.41)	0.00, (-0.02, 0.02)	0.20 (0.14, 0.23)	0.92	no
1400	0.08	58	-0.01, (-0.03, 0.02)	7.48, (-8.38, 22.72)	-5.41 (-30.14, 29.74)	0.00, (-0.02, 0.02)	0.19 (0.14, 0.23)	0.93	no
1500	0.08	58	-0.01, (-0.03, 0.02)	7.60, (-7.38, 21.62)	-6.25 (-32.28, 27.84)	0.00, (-0.02, 0.02)	0.19 (0.14, 0.22)	0.92	no
1600	0.08	58	-0.01, (-0.03, 0.02)	7.30, (-8.74, 23.07)	-5.39 (-35.20, 37.24)	0.00, (-0.02, 0.02)	0.18 (0.14, 0.21)	0.91	no
1700	0.08	58	-0.01, (-0.03, 0.02)	8.12, (-6.56, 23.34)	-9.18 (-38.67, 30.63)	-0.01, (-0.02, 0.02)	0.18 (0.13, 0.21)	0.86	no
1800	0.08	58	-0.01, (-0.03, 0.02)	7.10, (-7.04, 21.88)	-7.74 (-37.97, 32.14)	0.00, (-0.02, 0.02)	0.17 (0.14, 0.20)	0.89	no
1900	0.08	58	-0.01, (-0.03, 0.02)	7.06, (-7.84, 22.71)	-7.80 (-42.93, 36.47)	0.00, (-0.02, 0.02)	0.17 (0.13, 0.19)	0.84	no
2000	0.08	58	-0.01, (-0.03, 0.02)	7.16, (-7.82, 21.61)	-8.67 (-42.97, 35.06)	0.00, (-0.02, 0.02)	0.17 (0.13, 0.19)	0.83	no
2100	0.08	58	-0.01, (-0.03, 0.02)	7.29, (-6.62, 23.00)	-10.84 (-45.52, 35.68)	-0.01, (-0.02, 0.02)	0.16 (0.12, 0.19)	0.81	no
2200	0.08	58	-0.01, (-0.02, 0.02)	6.36, (-8.34, 22.27)	-8.32 (-46.97, 38.45)	0.00, (-0.02, 0.02)	0.16 (0.13, 0.18)	0.80	no
2300	0.08	58	-0.01, (-0.03, 0.02)	7.07, (-6.73, 23.50)	-11.29 (-51.19, 40.76)	0.00, (-0.02, 0.02)	0.16 (0.12, 0.18)	0.75	no
2400	0.08	58	-0.01, (-0.02, 0.02)	5.93, (-7.91, 20.79)	-8.74 (-51.42, 42.91)	0.00, (-0.02, 0.02)	0.15 (0.13, 0.17)	0.72	no
2500	0.08	58	-0.01, (-0.03, 0.02)	6.02, (-6.98, 21.08)	-10.76 (-51.31, 42.65)	0.00, (-0.02, 0.02)	0.15 (0.13, 0.17)	0.65	no
2600	0.08	58	-0.01, (-0.02, 0.02)	6.11, (-6.88, 20.47)	-12.31 (-53.13, 36.12)	0.00, (-0.02, 0.01)	0.15 (0.13, 0.17)	0.56	no
2700	0.08	58	-0.01, (-0.02, 0.01)	6.55, (-6.84, 22.10)	-13.41 (-56.32, 40.97)	0.00, (-0.02, 0.02)	0.15 (0.12, 0.16)	0.45	no
2800	0.08	58	-0.01, (-0.02, 0.02)	5.48, (-6.41, 18.93)	-10.59 (-52.51, 43.38)	0.00, (-0.02, 0.02)	0.15 (0.13, 0.16)	0.32	no
2900	0.08	58	-0.01, (-0.02, 0.01)	5.76, (-6.24, 21.57)	-12.78 (-58.46, 41.17)	0.00, (-0.02, 0.01)	0.14 (0.12, 0.16)	0.23	no
3000	0.08	58	-0.01, (-0.02, 0.02)	5.47, (-6.33, 18.87)	-12.03 (-57.94, 42.01)	0.00, (-0.02, 0.01)	0.14 (0.12, 0.16)	0.20	no
3100	0.08	58	-0.01, (-0.02, 0.01)	5.73, (-4.96, 19.82)	-14.70 (-62.94, 39.28)	0.00, (-0.02, 0.01)	0.14 (0.12, 0.15)	0.11	yes-ish
3110	0.08	58	0.00, (-0.02, 0.01)	5.16, (-5.92, 19.60)	-11.62 (-60.84, 43.04)	0.00, (-0.02, 0.01)	0.14 (0.12, 0.15)	0.09	yes
3120	0.08	58	-0.01, (-0.02, 0.01)	5.25, (-6.20, 21.17)	-11.99 (-61.64, 39.36)	0.00, (-0.02, 0.01)	0.14 (0.12, 0.15)	0.10	yes
3140	0.08	58	-0.01, (-0.02, 0.01)	5.28, (-6.70, 19.55)	-13.07 (-59.33, 46.66)	0.00, (-0.02, 0.01)	0.14 (0.12, 0.15)	0.08	yes
3160	0.08	58	-0.01, (-0.02, 0.01)	5.08, (-6.43, 20.59)	-11.48 (-61.55, 50.74)	0.00, (-0.02, 0.02)	0.14 (0.12, 0.15)	0.08	yes
3180	0.08	58	-0.01, (-0.02, 0.01)	5.39, (-6.59, 20.17)	-12.14 (-58.57, 48.50)	0.00, (-0.02, 0.02)	0.14 (0.12, 0.15)	0.07	yes
3200	0.08	58	-0.01, (-0.02, 0.02)	5.33, (-6.77, 20.70)	-13.21 (-65.15, 49.01)	0.00, (-0.02, 0.02)	0.14 (0.12, 0.15)	0.07	yes

Table S10. Results of simulations evaluating the efficacy of survey protocols using parameters from the 2020 and 2021 spring survey data analyzed hierarchical distance sampling models for line transects with a length of 2,681 (average transect length from 2020 and 2021 surveys). Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of survey sites, λ = mean abundance per site, sigma = sigma for calculating the half-normal detection function; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site.

Simulation Parameters			**Bias in λ**	**Bias in *sigma***	**Bias in Total N**	**Bias in N.site**	**CV Total N**	**Probability CV N.total > 0.15**	**Protocol meets Management Requirements**
R	**λ**	***sigma***							
High abundance, Average detection									
20	5.54	42	-0.09 (-1.65, 1.58)	3.59 (-6.06, 17.96)	-2.54 (-29.47, 28.67)	-0.13 (-1.47, 1.43)	0.14 (0.13, 0.16)	0.27	no
25	5.54	42	-0.08 (-1.48, 1.26)	2.90 (-5.32, 13.94)	-2.34 (-31.01, 28.10)	-0.09 (-1.24, 1.12)	0.13 (0.12, 0.14)	0.01	yes
30	5.54	42	-0.05 (-1.27, 1.28)	1.43 (-5.66, 9.53)	-1.79 (-31.05, 28.58)	-0.06 (-1.03, 0.95)	0.12 (0.11, 0.13)	0.00	yes
40	5.54	42	-0.06 (-1.16, 1.14)	1.25 (-5.16, 8.51)	-2.89 (-36.80, 37.46)	-0.07 (-0.92, 0.94)	0.10 (0.09, 0.11)	0.00	yes
60	5.54	42	-0.08 (-0.85, 0.80)	1.16 (-3.70, 6.31)	-4.37 (-45.46, 42.31)	-0.07 (-0.76, 0.71)	0.08 (0.08, 0.09)	0.00	yes
80	5.54	42	-0.04 (-0.77, 0.73)	0.65 (-3.53, 5.19)	-2.71 (-57.15, 49.50)	-0.03 (-0.71, 0.62)	0.07 (0.07, 0.07)	0.00	yes
100	5.54	42	-0.01 (-0.66, 0.67)	0.55 (-2.85, 4.62)	-1.94 (-55.14, 59.02)	-0.02 (-0.55, 0.59)	0.06 (0.06, 0.07)	0.00	yes
Average abundance, Average detection									
20	3.22	42	-0.10 (-1.15, 1.24)	6.16 (-6.66, 23.52)	-2.16 (-19.42, 18.89)	-0.11 (-0.97, 0.94)	0.19 (0.16, 0.22)	0.99	no
30	3.22	42	-0.11 (-1.01, 0.98)	4.26 (-6.44, 19.45)	-2.64 (-25.97, 21.85)	-0.09 (-0.87, 0.73)	0.16 (0.14, 0.18)	0.71	no
35	3.22	42	-0.07 (-0.86, 0.85)	3.29 (-5.27, 15.88)	-2.67 (-26.82, 23.36)	-0.08 (-0.77, 0.67)	0.14 (0.13, 0.16)	0.29	no
40	3.22	42	-0.06 (-0.84, 0.81)	3.23 (-5.31, 15.81)	-3.31 (-30.55, 22.27)	-0.08 (-0.76, 0.56)	0.13 (0.12, 0.15)	0.04	yes
60	3.22	42	-0.04 (-0.72, 0.65)	1.63 (-4.63, 9.25)	-2.69 (-35.61, 33.99)	-0.04 (-0.59, 0.57)	0.11 (0.10, 0.12)	0.00	yes
80	3.22	42	-0.05 (-0.62, 0.53)	1.45 (-4.31, 8.60)	-3.22 (-40.71, 38.56)	-0.04 (-0.51, 0.48)	0.09 (0.09, 0.10)	0.00	yes
100	3.22	42	-0.03 (-0.51, 0.46)	1.01 (-3.88, 6.17)	-3.13 (-42.30, 40.99)	-0.03 (-0.42, 0.41)	0.08 (0.08, 0.09)	0.00	yes
Low abundance, Average detection									
100	1.43	42	-0.01 (-0.35, 0.34)	2.60 (-5.83, 12.97)	-1.81 (-32.22, 30.12)	-0.02 (-0.32, 0.30)	0.13 (0.12, 0.14)	0.01	yes
80	1.43	42	-0.03 (-0.41, 0.39)	3.41 (-6.44, 16.49)	-2.76 (-30.47, 24.64)	-0.03 (-0.38, 0.31)	0.14 (0.13, 0.16)	0.24	no
90	1.43	42	-0.03 (-0.39, 0.35)	2.58 (-5.32, 14.65)	-2.58 (-29.13, 23.93)	-0.03 (-0.32, 0.27)	0.13 (0.12, 0.15)	0.06	yes
85	1.43	42	-0.03 (-0.36, 0.38)	2.92 (-5.81, 13.87)	-2.62 (-26.72, 23.79)	-0.03 (-0.31, 0.28)	0.14 (0.12, 0.15)	0.11	yes-ish
High abundance, High detection									
10	5.54	51	-0.25 (-1.97, 1.78)	9.19 (-8.45, 26.34)	-2.64 (-15.51, 14.34)	-0.26 (-1.55, 1.43)	0.18 (0.13, 0.22)	0.84	no

15	5.54	51	-0.10 (-1.56, 1.83)	6.81 (-9.23, 23.51)	-1.79 (-19.00, 21.42)	-0.12 (-1.27, 1.43)	0.15 (0.12, 0.17)	0.45	no
20	5.54	51	-0.14 (-1.40, 1.45)	5.67 (-7.24, 21.52)	-3.04 (-24.75, 20.15)	-0.15 (-1.24, 1.01)	0.13 (0.11, 0.15)	0.04	yes
40	5.54	51	-0.13 (-1.23, 0.95)	3.45 (-5.73, 15.85)	-4.63 (-39.53, 29.92)	-0.12 (-0.99, 0.75)	0.09 (0.09, 0.10)	0.00	yes
60	5.54	51	-0.07 (-0.85, 0.81)	1.93 (-5.28, 10.23)	-4.25 (-48.17, 41.12)	-0.07 (-0.80, 0.69)	0.08 (0.07, 0.08)	0.00	yes
80	5.54	51	-0.05 (-0.71, 0.65)	1.03 (-4.26, 7.88)	-3.45 (-47.22, 37.54)	-0.04 (-0.59, 0.47)	0.07 (0.06, 0.07)	0.00	yes
100	5.54	51	-0.01 (-0.65, 0.71)	0.96 (-4.28, 6.81)	-2.32 (-52.68, 47.03)	-0.02 (-0.53, 0.47)	0.06 (0.06, 0.06)	0.00	yes
Average abundance, High detection									
20	3.22	51	-0.14 (-1.08, 1.04)	9.42 (-8.57, 26.65)	-3.06 (-18.03, 16.03)	-0.15 (-0.90, 0.80)	0.16 (0.12, 0.20)	0.73	no
30	3.22	51	-0.15 (-0.93, 0.72)	7.63 (-5.95, 24.20)	-4.65 (-22.60, 18.41)	-0.15 (-0.75, 0.61)	0.14 (0.11, 0.16)	0.20	no
35	3.22	51	-0.12 (-0.92, 0.79)	6.28 (-6.85, 23.29)	-3.94 (-24.98, 19.96)	-0.11 (-0.71, 0.57)	0.13 (0.11, 0.15)	0.02	yes
40	3.22	51	-0.10 (-0.85, 0.73)	5.18 (-7.40, 21.19)	-4.05 (-27.98, 23.58)	-0.10 (-0.70, 0.59)	0.12 (0.11, 0.14)	0.00	yes
60	3.22	51	-0.07 (-0.76, 0.61)	3.47 (-6.39, 16.87)	-3.40 (-35.24, 28.49)	-0.06 (-0.59, 0.47)	0.10 (0.0, 0.11)	0.00	yes
80	3.22	51	-0.06 (-0.62, 0.52)	2.52 (-5.84, 13.79)	-4.22 (-39.76, 32.49)	-0.05 (-0.50, 0.41)	0.09 (0.08, 0.09)	0.00	yes
100	3.22	51	-0.04 (-0.56, 0.46)	2.12 (-5.06, 11.52)	-4.91 (-45.84, 37.84)	-0.05 (-0.46, 0.38)	0.08 (0.07, 0.08)	0.00	yes
Low abundance, High detection									
60	1.43	51	-0.07 (-0.44, 0.42)	7.36 (-7.83, 24.88)	-3.36 (-21.23, 19.94)	-0.06 (-0.35, 0.33)	0.15 (0.12, 0.17)	0.45	no
65	1.43	51	-0.03 (-0.41, 0.42)	6.42 (-7.71, 22.17)	-1.66 (-20.76, 21.16)	-0.03 (-0.32, 0.33)	0.14 (0.12, 0.16)	0.25	no
70	1.43	51	-0.06 (-0.39, 0.32)	7.66 (-7.27, 24.01)	-4.18 (-21.92, 18.97)	-0.06 (-0.34, 0.27)	0.14 (0.11, 0.16)	0.10	yes
80	1.43	51	-0.04 (-0.37, 0.40)	6.17 (-7.75, 20.89)	-3.14 (-23.48, 23.70)	-0.04 (-0.29, 0.30)	0.13 (0.11, 0.14)	0.01	yes
100	1.43	51	-0.03 (-0.36, 0.32)	4.63 (-7.44, 20.77)	-3.65 (-30.02, 27.41)	-0.04 (-0.30, 0.27)	0.12 (0.10, 0.13)	0.00	yes

Table S11. Results of simulations evaluating the efficacy of survey protocols using parameters from the 2020 and 2021 spring survey data analyzed hierarchical distance sampling models for line transects with a length of 5,000m. Mean (95% credible interval) for bias and coefficient of variation from 500 simulation runs for each suite of parameters. Different scenarios include combinations of high, average, and low abundance paired with either average or high detection. R = number of survey sites, λ = mean abundance per site, sigma = sigma for calculating the half-normal detection function; CV = coefficient of variation for total population size (Total N) and N.site = estimated number of dusky grouse per survey site.

Simulation Parameters			Bias in λ	Bias in *sigma*	Bias in Total N	Bias in N.site	CV Total N	Probability CV N.total > 0.15	Protocol meets Management Requirements
R	**λ**	***sigma***							
High abundance, Average detection									
10	10.33	42	-0.36 (-3.42, 2.95)	4.59 (-5.73, 19.76)	-3.08 (-29.41, 24.03)	-0.31 (-2.94, 2.40)	0.15 (0.13, 0.17)	0.47	no
15	10.33	42	-0.27 (-2.54, 2.14)	2.58 (-4.90, 11.82)	-3.47 (-33.21, 27.46)	-0.23 (-2.21, 1.83)	0.12 (0.11, 0.14)	0.00	yes
20	10.33	42	-0.13 (-2.33, 2.03)	1.78 (-5.26, 9.68)	-2.99 (-40.46, 37.18)	-0.15 (-2.02, 1.86)	0.10 (0.10, 0.12)	0.00	yes
40	10.33	42	-0.05 (-1.51, 1.48)	0.74 (-3.61, 5.70)	-1.29 (-51.31, 44.90)	-0.03 (-1.28, 1.12)	0.07 (0.07, 0.08)	0.00	yes
60	10.33	42	-0.09 (-1.27, 1.20)	0.67 (-2.43, 4.70)	-5.92 (-69.32, 56.28)	-0.10 (-1.16, 0.94)	0.06 (0.06, 0.06)	0.00	yes
80	10.33	42	-0.04 (-1.05, 1.04)	0.47 (-2.39, 3.98)	-4.56 (-73.02, 62.47)	-0.06 (-0.91, 0.78)	0.05 (0.05, 0.05)	0.00	yes
100	10.33	42	-0.08 (-1.01, 0.99)	0.40 (-2.34, 3.01)	-8.19 (-84.39, 69.41)	-0.08 (-0.84, 0.69)	0.05 (0.04, 0.05)	0.00	yes
Average abundance, Average detection									
20	6	42	-0.10 (-1.72, 1.56)	3.06 (-5.41, 15.58)	-2.51 (-28.58, 25.43)	-0.13 (-1.43, 1.27)	0.14 (0.12, 0.16)	0.14	no
25	6	42	-0.08 (-1.53, 1.46)	2.62 (-5.81, 12.23)	-2.01 (-30.41, 29.61)	-0.08 (-1.22, 1.18)	0.12 (0.11, 0.14)	0.00	yes
30	6	42	-0.05 (-1.42, 1.33)	2.00 (-4.49, 11.27)	-2.08 (-36.65, 30.71)	-0.07 (-1.22, 1.02)	0.11 (0.10, 0.12)	0.00	yes
40	6	42	-0.04 (-1.04, 1.13)	1.19 (-4.56, 7.65)	-1.72 (-37.93, 34.09)	-0.04 (-0.95, 0.85)	0.10 (0.09, 0.10)	0.00	yes
60	6	42	-0.05 (-1.08, 0.78)	0.99 (-3.25, 6.33)	-3.26 (-51.41, 43.90)	-0.05 (-0.86, 0.73)	0.08 (0.07, 0.08)	0.00	yes
80	6	42	-0.02 (-0.79, 0.80)	0.51 (-3.34, 4.95)	-0.82 (-51.25, 48.55)	-0.01 (-0.64, 0.61)	0.07 (0.06, 0.07)	0.00	yes
100	6	42	-0.04 (-0.79, 0.70)	0.54 (-2.81, 4.36)	-4.23 (-62.13, 52.88)	-0.04 (-0.62, 0.53)	0.06 (0.06, 0.06)	0.00	yes
Low abundance, Average detection									
40	2.67	42	-0.08 (-0.84, 0.73)	3.86 (-5.99, 16.94)	-3.09 (-27.32, 23.42)	-0.08 (-0.68, 0.59)	0.15 (0.13, 0.17)	0.42	no
45	2.67	42	-0.08 (-0.76, 0.67)	3.68 (-4.89, 15.58)	-3.60 (-28.97, 25.27)	-0.08 (-0.64, 0.56)	0.14 (0.12, 0.16)	0.14	no
50	2.67	42	-0.04 (-0.77, 0.68)	2.52 (-5.73, 14.62)	-2.34 (-31.02, 29.58)	-0.05 (-0.62, 0.59)	0.13 (0.12, 0.15)	0.05	yes

60	2.67	42	-0.06 (-0.65, 0.60)	2.17 (-5.55, 12.34)	-3.22 (-35.98, 29.53)	-0.05 (-0.60, 0.49)	0.12 (0.11, 0.13)	0.00	yes
80	2.67	42	-0.05 (-0.59, 0.55)	1.95 (-4.65, 9.91)	-3.37 (-37.17, 35.92)	-0.04 (-0.46, 0.45)	0.10 (0.09, 0.11)	0.00	yes
100	2.67	42	-0.01 (-0.47, 0.46)	1.14 (-4.19, 6.95)	-1.38 (-36.59, 37.71)	-0.01 (-0.37, 0.38)	0.09 (0.09, 0.10)	0.00	yes
High abundance, High detection									
10	10.33	51	-0.37 (-2.89, 2.60)	6.23 (-7.93, 22.81)	-2.88 (-23.44, 22.58)	-0.29 (-2.34, 2.26)	0.14 (0.11, 0.15)	0.11	yes-ish
15	10.33	51	-0.23 (-2.48, 2.17)	4.32 (-7.13, 18.33)	-3.40 (-30.83, 24.10)	-0.23 (-2.06, 1.61)	0.11 (0.10, 0.12)	0.00	yes
20	10.33	51	-0.19 (-2.25, 1.91)	2.98 (-6.97, 16.01)	-2.94 (-37.56, 32.09)	-0.15 (-1.88, 1.60)	0.10 (0.09, 0.11)	0.00	yes
40	10.33	51	-0.18 (-1.49, 1.19)	1.66 (-4.07, 9.92)	-7.09 (-50.55, 39.84)	-0.18 (-1.26, 1.00)	0.07 (0.06, 0.07)	0.00	yes
60	10.33	51	-0.04 (-1.25, 1.07)	0.73 (-3.92, 6.40)	-2.17 (-61.66, 56.14)	-0.04 (-1.03, 0.94)	0.06 (0.05, 0.06)	0.00	yes
80	10.33	51	-0.07 (-1.10, 0.93)	1.02 (-3.48, 6.07)	-6.89 (-76.07, 53.61)	-0.09 (-0.95, 0.67)	0.05 (0.05, 0.05)	0.00	yes
100	10.33	51	-0.04 (-0.99, 0.85)	0.60 (-3.08, 5.30)	-2.65 (-77.98, 72.19)	-0.03 (-0.78, 0.72)	0.04 (0.04, 0.04)	0.00	yes
Average abundance, High detection									
10	6	51	-0.24 (-2.08, 1.90)	9.10 (-8.94, 26.79)	-2.25 (-16.35, 16.15)	-0.22 (-1.63, 1.61)	0.17 (0.13, 0.21)	0.81	no
15	6	51	-0.22 (-1.77, 1.44)	7.12 (-7.50, 24.09)	-3.36 (-21.34, 17.06)	-0.22 (-1.42, 1.14)	0.14 (0.12, 0.17)	0.34	no
20	6	51	-0.16 (-1.57, 1.43)	6.00 (-6.41, 22.23)	-3.68 (-26.62, 21.67)	-0.18 (-1.33, 1.08)	0.13 (0.11, 0.14)	0.01	yes
40	6	51	-0.06 (-1.15, 1.17)	2.34 (-6.25, 13.91)	-2.44 (-39.09, 34.63)	-0.06 (-0.98, 0.87)	0.09 (0.08, 0.10)	0.00	yes
60	6	51	-0.07 (-0.94, 0.79)	1.90 (-4.58, 10.08)	-5.19 (-49.50, 38.98)	-0.09 (-0.82, 0.65)	0.07 (0.07, 0.08)	0.00	yes
80	6	51	-0.04 (-0.78, 0.80)	1.09 (-4.84, 7.94)	-1.46 (-54.12, 49.80)	-0.02 (-0.68, 0.62)	0.06 (0.06, 0.07)	0.00	yes
100	6	51	-0.06 (-0.72, 0.57)	0.98 (-4.15, 6.88)	-3.24 (-56.26, 51.08)	-0.03 (-0.56, 0.51)	0.06 (0.05, 0.06)	0.00	yes
Low abundance, High detection									
20	2.67	51	-0.12 (-0.99, 0.93)	9.29 (-8.90, 26.61)	-2.43 (-14.89, 14.82)	-0.12 (-0.74, 0.74)	0.18 (0.13, 0.22)	0.84	no
30	2.67	51	-0.07 (-0.78, 0.86)	7.28 (-9.63, 24.44)	-2.46 (-20.13, 20.37)	-0.08 (-0.67, 0.68)	0.15 (0.12, 0.17)	0.54	no
35	2.67	51	-0.08 (-0.78, 0.75)	6.12 (-8.26, 22.59)	-2.56 (-22.43, 20.67)	-0.07 (-0.64, 0.59)	0.14 (0.12, 0.16)	0.23	no
40	2.67	51	-0.04 (-0.69, 0.74)	5.24 (-8.42, 22.15)	-1.84 (-23.56, 22.83)	-0.05 (-0.59, 0.57)	0.13 (0.11, 0.15)	0.07	yes
60	2.67	51	-0.05 (-0.58, 0.53)	4.27 (-6.23, 18.55)	-2.89 (-28.54, 25.77)	-0.05 (-0.48, 0.43)	0.11 (0.10, 0.12)	0.00	yes
80	2.67	51	-0.03 (-0.52, 0.50)	2.86 (-5.52, 15.18)	-3.57 (-35.98, 30.26)	-0.04 (-0.45, 0.38)	0.10 (0.09, 0.10)	0.00	yes
100	2.67	51	-0.04 (-0.48, 0.47)	2.78 (-5.09, 13.67)	-4.16 (-39.69, 33.94)	-0.04 (-0.40, 0.34)	0.09 (0.08, 0.09)	0.00	yes

S12. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for point counts using N-mixture models in a population in which average local abundance declined with a hypothetical covariate X and probability of detection was kept constant.

```
# Function for simulating and analyzing data using a N-mixture model for point counts in which local abundance declined strongly (or weakly), B = -1, (or B = -0.5) with standardized hypothetical site covariate. Probability of detection is kept constant.

# Code adapted from:
#Kery, M. and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom.
# Kery, M. and M. Schaub. 2012. Bayesian population analysis using WinBUGS. A hierarchical perspective. Elsevier Inc.

# S = number of spatial reps/ number of sites
# V = number of visits at each site (temporal reps)
# lambda.orig = average local abundance per transect estimated from the 2020 & 2021 data
# alpha (log(lambda.orig)) & alpha1 = intercept and slope of log-linear regression relating abundance to site covariate X
# xmin & xmas = lower and upper limits of distribution when generating covariate X
# prob = probability of detection
# num.sim = number of simulations

#Simulate Data - Nmixture model. Parameters estimated: lambda and probability of detection
Sim.Nmix.fn.Lam.Cov <- function(S=S, V=V, lambda.orig = lambda.orig, alpha1.lam = alpha1.lam, xmin = xmin, xmax = xmax, prob = prob, num.sim = num.sim) {
  library(jagsUI) # use the JAGS for analyzing data within a Bayesian framework

  #***************
  # Define Bayesian Model
  #***************

  # Specify model in Bugs language, but going to use JagsUI/jags
  sink("Nmix.Lam.Cov.txt")
  cat("
    model {

    # Priors
      alpha ~ dunif(-10,10) #vague prior for alpha (intercept for log-linear regression relating abundance to site covariate X)
      alpha1 ~ dunif(-10,10) #vague prior for alpha1 (slope for log-linear regression relating abundance to site covariate X)
      p ~ dunif(0, 1) #vague prior for probability of detection

    # Likelihood
      # Biological model for true abundance
        for (i in 1:S) {
          N[i] ~ dpois(lambda[i]) #describes spatial variation in abundance (N)
          log(lambda[i]) <- alpha + alpha1 * X[i] #relationship between local abundance per site and site covariate X
       # Observation model for replicated counts
          for (j in 1:V) {
            y[i,j] ~ dbin(p, N[i]) #count (observation) for each visit at each site
          } # j
        } # i
```

```
    #Derived parameters
    Ntotal <- sum(N[]) #total of abundance at each site (N)
  }
  ",fill = TRUE)
sink()

#************************************************
# Loop for replicating datasets and assessing bias
#************************************************

num.sim <- num.sim

# Create empty vectors to store results from replicated datasets
m.bias.Nsite <- vector("list",num.sim)  #examine bias in abundance (N) at each site
sd.bias.Nsite <- vector("list",num.sim)
baye.pvalue.Nsite <- vector("list",num.sim)

m.bias.p <- vector("list",num.sim) #bias in probability of detection
sd.bias.p <- vector("list",num.sim)
baye.pvalue.p <- vector("list",num.sim)

m.bias.Ntot <- vector("list",num.sim) #bias in total N
sd.bias.Ntot <- vector("list",num.sim)
baye.pvalue.Ntot <- vector("list",num.sim)

m.bias.alpha.lam <- vector("list",num.sim)  #bias in alpha (intercept for model for lambda)
sd.bias.alpha.lam <- vector("list",num.sim)
baye.pvalue.alpha.lam <- vector("list",num.sim)

m.bias.alpha1.lam <- vector("list",num.sim)  #bias in alpha1 (slope for model for lambda)
sd.bias.alpha1.lam <- vector("list",num.sim)
baye.pvalue.alpha1.lam <- vector("list",num.sim)

m.CV.alpha.lam <- vector("list",num.sim)  #coefficient of variation for alpha (intercept for model for lambda)
sd.CV.alpha.lam <- vector("list",num.sim)
prop.CV.alpha.lam <- vector("list", num.sim)

m.CV.alpha1.lam <- vector("list",num.sim)  #coefficient of variation for alpha1 (slope for model for lambda)
sd.CV.alpha1.lam <- vector("list",num.sim)
prop.CV.alpha1.lam <- vector("list", num.sim)

m.CV.Ntot <- vector("list",num.sim) #coefficient of variation for total N
sd.CV.Ntot <- vector("list",num.sim)
prop.CV.Ntot <- vector("list", num.sim)

#********************
# Start Simulation
#********************

# Stick simulation in loop and replicate num.sim times
system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

  #Simulate data
  S = S  # spatial reps
  V = V  # temporal reps
```

```
xmin = xmin
xmax = xmax
alpha.lam = log(lambda.orig)
alpha1.lam = alpha1.lam
prob = prob # probablity of detection

# Create structure to contain counts
y <- array(dim = c(S,V))

# sample abundance from a Poisson
X <- sort(runif(n=S, min=xmin, max=xmax)) #covariate values
lambda <- exp(alpha.lam + alpha1.lam * X) #relationship between expected lambda and covariate
N <- rpois(n=S, lambda=lambda) # site-specific abundances

# sample counts from a Binomial distribution (N, prob)
for (j in 1:V){
  y[,j] <- rbinom(n = S, size = N, prob = prob)
}

# Bundle data
win.data <- list(y = y, S = nrow(y), V = ncol(y), X = X)

# initial values
Nst <- apply(y, 1, max) + 1          # This line is vital
inits <- function() list(N = Nst, alpha = runif(1,-1,1), alpha1 = runif(1,-1,1))

# Define parameters to be monitored
params <- c("alpha", "alpha1", "p", "Ntotal", "N")

# MCMC settings
ni <- 5000
nt <- 1
nb <- 100
nc <- 3

start.time = Sys.time()  #set timer
# run model
out <- jags(win.data, inits, params, "Nmix.Lam.Cov.txt", n.chains = nc,
            n.thin = nt, n.iter = ni, n.burnin = nb)
print(out)

end.time = Sys.time()
elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

#************************************
#### EValuate bias ####
#************************************
#Bias in N (site specific abundance)
bias.Nsite <- out$mean$N - N #calculates bias
m.bias.Nsite[k] <- mean(bias.Nsite) #averages bias and places within vector
sd.bias.Nsite[k] <- sd(bias.Nsite) #gets standard deviation of bias places within vector
baye.pvalue.Nsite[k] <-mean(N > out$mean$N)  #Bayesian P-value (proportion of simulations where the true
abundance was greater than the estimated abundance - values close to 0 or 1 indicate significant bias)
```

```
   #Bias in intercept for log-linear regression of expected abundance per site on a habitat covariate - descriptions same as above
   bias.alpha.lam <- out$mean$alpha - alpha.lam
   m.bias.alpha.lam[k] <- mean(bias.alpha.lam)
   sd.bias.alpha.lam[k] <- sd(bias.alpha.lam)
   baye.pvalue.alpha.lam[k] <- mean(alpha.lam > out$mean$alpha)

   #Bias in slope for log-linear regression of expected abundance per site on a habitat covariate - descriptions same as above
   bias.alpha1.lam <- out$mean$alpha1 - alpha1.lam
   m.bias.alpha1.lam[k] <- mean(bias.alpha1.lam)
   sd.bias.alpha1.lam[k] <- sd(bias.alpha1.lam)
   baye.pvalue.alpha1.lam[k] <- mean(alpha1.lam > out$mean$alpha1)

   #Bias in p (probability of detection) - descriptions same as above
   bias.p <- out$mean$p - prob
   m.bias.p[k] <- mean(bias.p)
   sd.bias.p[k] <- sd(bias.p)
   baye.pvalue.p[k] <- mean(prob > out$mean$p)

   #Bias in Ntotal (total population size) - descriptions same as above
   bias.Ntot <- out$mean$Ntotal - sum(N)
   m.bias.Ntot[k] <- mean(bias.Ntot)
   sd.bias.Ntot[k] <- sd(bias.Ntot)
   baye.pvalue.Ntot[k] <- mean(sum(N) > out$mean$Ntotal)

   #Coefficient of Variation in Ntotal (total population size) - want to be under 15%
   CV.Ntot <- out$sd$Ntotal/out$mean$Ntotal #standard deviation divided by mean
   m.CV.Ntot[k] <- mean(CV.Ntot)
   sd.CV.Ntot[k] <- sd(CV.Ntot)
   prop.CV.Ntot[k] <- mean(CV.Ntot < 0.15)

   #Coefficient of Variation in local abundance (lambda / average local abundance) for alpha
   CV.alpha.lam <- abs(out$sd$alpha/out$mean$alpha)
   m.CV.alpha.lam[k] <- mean(CV.alpha.lam)
   sd.CV.alpha.lam[k] <- sd(CV.alpha.lam)
   prop.CV.alpha.lam[k] <- mean(CV.alpha.lam < 0.15)

   #Coefficient of Variation in local abundance (lambda / average local abundance) for alpha1
   CV.alpha1.lam <- abs(out$sd$alpha1/out$mean$alpha1)
   m.CV.alpha1.lam[k] <- mean(CV.alpha1.lam)
   sd.CV.alpha1.lam[k] <- sd(CV.alpha1.lam)
   prop.CV.alpha1.lam[k] <- mean(CV.alpha1.lam < 0.15)

  }  ) #This will be the end of the simulations

  #********************
  # Summary of Results
  #********************
  results <- c("alpha", "alpha1", "prob", "N.total", "N.site", "N.total.CV", "lambda.alpha.CV", "lambda.alpha1.CV",
"Prob.CV.Ntot", "Prob.CV.alpha.lambda", "Prob.CV.alpha1.lambda")
  mean.bias <- round(c((mean(unlist(m.bias.alpha.lam))), (mean(unlist(m.bias.alpha1.lam))),
(mean(unlist(m.bias.p))), (mean(unlist(m.bias.Ntot))), (mean(unlist(m.bias.Nsite))), (mean(unlist(m.CV.Ntot))),
(mean(unlist(m.CV.alpha.lam))), (mean(unlist(m.CV.alpha1.lam))), NA, NA, NA),2)
```

```
  lower.CI <- round(c((quantile(unlist(m.bias.alpha.lam), 0.05)), (quantile(unlist(m.bias.alpha1.lam), 0.05)),
(quantile(unlist(m.bias.p), 0.05)), (quantile(unlist(m.bias.Ntot), 0.05)), (quantile(unlist(m.bias.Nsite), 0.05)),
(quantile(unlist(m.CV.Ntot), 0.05)), (quantile(unlist(m.CV.alpha.lam), 0.05)), (quantile(unlist(m.CV.alpha1.lam),
0.05)), NA, NA, NA),2) #lower 95% credible interval

  upper.CI <- round(c((quantile(unlist(m.bias.alpha.lam), 0.95)), (quantile(unlist(m.bias.alpha1.lam), 0.95)),
(quantile(unlist(m.bias.p), 0.95)), (quantile(unlist(m.bias.Ntot), 0.95)), (quantile(unlist(m.bias.Nsite), 0.95)),
(quantile(unlist(m.CV.Ntot), 0.95)), (quantile(unlist(m.CV.alpha.lam), 0.95)), (quantile(unlist(m.CV.alpha1.lam),
0.95)), NA, NA, NA),2) #upper 95% credible interval

  greater.15.CV <- c(NA, NA, NA, NA, NA, NA, NA, NA, (mean(unlist(m.CV.Ntot) > 0.15)),
(mean(unlist(m.CV.alpha.lam) > 0.15)), (mean(unlist(m.CV.alpha1.lam) > 0.15))) #percent of CV's greater than
15%

  Baye.pvalue <- round(c((mean(unlist(baye.pvalue.alpha.lam))),(mean(unlist(baye.pvalue.alpha1.lam))),
(mean(unlist(baye.pvalue.p))), (mean(unlist(baye.pvalue.Ntot))), (mean(unlist(baye.pvalue.Nsite))), NA, NA, NA,
NA, NA, NA),2)

  sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a table of
results
  print(sim.results)

  #****************
  #Post processing
  #****************
  # Set plots so that eight plots can be created in one image
  par(mfrow = c(8,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

  # Plots
  (hist(unlist(m.bias.Nsite), xlim=c(-5,5), breaks=120, main="", ylab="N.site"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.alpha.lam), xlim=c(-1,1), main="", ylab="alpha lambda"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.alpha1.lam), xlim=c(-1,1), main="", ylab="alpha1 lambda"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.p), xlim=c(-0.5,0.5), main="", ylab="Detection prob."))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.bias.Ntot), xlim=c(-100,100), main="", ylab="Total N"))
  (abline(v=0, col="red", lwd=3))

  (hist(unlist(m.CV.Ntot), xlim=c(0,0.5), main="", ylab="CV Ntotal"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.alpha.lam), xlim=c(0,0.5), main="", ylab="CV alpha lambda"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.alpha1.lam), xlim=c(0,0.5), main="", ylab="CV alpha lambda"))
  (abline(v=0.15, col="red", lwd=3))

  return(list(sim.results=sim.results, m.bias.Nsite=unlist(m.bias.Nsite), m.bias.alpha.lam = unlist(m.bias.alpha.lam),
m.bias.alpha1.lam = unlist(m.bias.alpha1.lam), m.bias.p = unlist(m.bias.p), m.bias.Ntot = unlist(m.bias.Ntot),
m.CV.Ntot = unlist(m.CV.Ntot), m.CV.alpha.lam = unlist(m.CV.alpha.lam), m.CV.alpha1.lam =
```

```
unlist(m.CV.alpha1.lam), alpha.lam = alpha.lam, alpha1.lam = alpha1.lam, prob = prob, S = S, V = V, num.sim =
num.sim))
}
```

S13. Complete Bayesian model specification and simulation code in R language for evaluating dusky grouse survey protocols for line transects using hierarchical distance sampling in a population in which average local abundance declined with a hypothetical covariate X and probability of detection was kept constant.

```
# Function for simulating and analyzing data using a hierarchical distance sampling model for line transects in which local abundance declined strongly (or weakly), B = -1, (or B = -0.5) with standardized hypothetical site covariate. Sigma is kept constant.

# Code adapted from:
#Kery, M. and J. A. Royle. 2016. Applied hierarchical modeling in ecology: analysis of distribution, abundance, and species richness in R and BUGS. Academic Press, London, United Kingdom.
# Kery, M. and M. Schaub. 2012. Bayesian population analysis using WinBUGS. A hierarchical perspective. Elsevier Inc.

# nsites = number of sites
# lambda.orig = average local abundance per transect estimated from the 2020 & 2021 data
# alpha (log(lambda.orig)) & alpha1 = intercept and slope of log-linear regression relating abundance to site covariate X
# sigma = sigma for the half-normal detection function
# num.sim = number of simulations
# L = transect length
# xmin & xmas = lower and upper limits of distribution when generating covariate X

Sim.HDS.line.fn.Lam.Cov <- function(nsites = nsites, lambda.orig = lambda.orig, alpha1 = alpha1, sigma = sigma, num.sim = num.sim, L = L, xmin = xmin, xmax = xmax) {
  library(jagsUI) # use the JAGS for analyzing data within a Bayesian framework

  #***************
  # Define Bayesian Model
  #***************

  # Specify model in Bugs language, but going to use JagsUI/jags
  sink("line.Lam.Cov.txt")
  cat("
 model{
  # Priors
  sigma ~ dunif(0,100) #vague prior for sigma
  alpha ~ dunif(-10,10) #vague prior for alpha (intercept for log-linear regression relating abundance to site covariate X)
  alpha1 ~ dunif(-10,10) #vague prior for alpha1 (slope for log-linear regression relating abundance to site covariate X)
  for(i in 1:nind){
   dclass[i] ~ dcat(fc[site[i],]) # Part 1 of HM - model for distance class of the observed individuals
}
  for(s in 1:nsites){
    # Construct cell probabilities for nD distance bands
    for(g in 1:nD){              # midpt = mid-point of each band
      log(p[s,g]) <- -midpt[g] * midpt[g] / (2 * sigma * sigma) # half-normal detection function
      pi[s,g] <- delta/B # prob. per interval
      f[s,g] <- p[s,g] * pi[s,g]
      fc[s,g] <- f[s,g] / pcap[s]
    }
    pcap[s] <- sum(f[s,])          # Pr(capture): sum of rectangular areas
    ncap[s] ~ dbin(pcap[s], N[s])   # Part 2 of HM - describes imperfect detection leading to count n[s]
```

```
  N[s] ~ dpois(lambda[s])         # Part 3 of HM - describes spatial variation in local abundance N[s]
  log(lambda[s]) <- alpha + alpha1 * X[s] # linear model for abundance
 }
 # Derived parameters
 Ntotal <- sum(N[]) #total of abundance at each site (N)
 area <- nsites*L*2*B/1000000 #area of transects
 D <- Ntotal/area #density
}
  ",fill = TRUE)
 sink()

 #************************************************
 # Loop for replicating datasets and assessing bias
 #************************************************
  num.sim <- num.sim

 # Create empty vectors to store results from replicated datasets
 m.bias.Nsite <- vector("list",num.sim)  #examine bias in abundance (N) at each site
 sd.bias.Nsite <- vector("list",num.sim)
 baye.pvalue.Nsite <- vector("list",num.sim)
 m.Ntrue <- vector("list",num.sim)
 m.N <- vector("list",num.sim)

 m.bias.sigma <- vector("list",num.sim) #bias in sigma (for the half-normal detection function)
 sd.bias.sigma <- vector("list",num.sim)
 baye.pvalue.sigma <- vector("list",num.sim)
 m.sig <- vector("list", num.sim)

 m.bias.Ntot <- vector("list",num.sim) #bias in total N
 sd.bias.Ntot <- vector("list",num.sim)
 baye.pvalue.Ntot <- vector("list",num.sim)
 m.bias.Ntot <- vector("list", num.sim)
 m.Ntot.true <- vector("list", num.sim)
 m.Ntot <- vector("list", num.sim)

 m.bias.alpha <- vector("list",num.sim)  #bias in alpha (intercept for model for lambda)
 sd.bias.alpha <- vector("list",num.sim)
 baye.pvalue.alpha <- vector("list",num.sim)
 m.alpha <- vector("list", num.sim)

 m.bias.alpha1 <- vector("list",num.sim)  #bias in alpha1 (slope for model for lambda)
 sd.bias.alpha1 <- vector("list",num.sim)
 baye.pvalue.alpha1 <- vector("list",num.sim)
 m.alpha1 <- vector("list", num.sim)

 m.bias.den <- vector("list", num.sim) #bias in density
 sd.bias.den <- vector("list", num.sim)
 baye.pvalue.den <- vector("list", num.sim)
 m.density <- vector("list", num.sim)
 m.density.true <- vector("list", num.sim)

 m.CV.alpha <- vector("list",num.sim)  #coefficient of variation for alpha (intercept for model for lambda)
 sd.CV.alpha <- vector("list",num.sim)
 prop.CV.alpha <- vector("list", num.sim)

 m.CV.alpha1 <- vector("list",num.sim)  #coefficient of variation for alpha1 (slope for model for lambda)
```

```
  sd.CV.alpha1 <- vector("list",num.sim)
  prop.CV.alpha1 <- vector("list", num.sim)

  m.CV.Ntot <- vector("list",num.sim) #coefficient of variation for total N
  sd.CV.Ntot <- vector("list",num.sim)
  prop.CV.Ntot <- vector("list", num.sim)

  #********************
  # Start Simulation
  #********************

  # Stick simulation in loop and replicate num.sim times
  system.time(for (k in 1:num.sim) {  #keep track of how long simulation takes

    # **************
    # Simulate Data
    # **************
    # Simulate abundance model (Poisson GLM for N)
    alpha <- log(lambda.orig) #intercept of log-linear regression of expected lambda per site on covariate
    X <- sort(runif(n=nsites, min=xmin, max=xmax)) #covariate values
    lambda <- exp(alpha + alpha1 * X) # relationship between expected abundance (lambda) and covariate X /
density per "square"

    # Simulate abundance model (Poisson GLM for N)
    N <- rpois(nsites, lambda)                # site-specific abundances
    N.true <- N  #true abundance at each site, for a transect this is the same as N (differs for point counts)
    B <- 100 #half-width of transect
    L <- L #length of transect
    area <- nsites*L*2*B/1000000 #area (meters squared)
    den.true <- sum(N)/area #true density

    # Simulate observation model - set up empty dataframe
    data <- NULL

    for(i in 1:nsites){
      if(N[i]==0){ #if abundance at a site is 0
        data <- rbind(data, c(i,NA,NA,NA,NA)) # save site, y=1, u, v, d
        next
      }
      # Simulation of distances, uniformly, for each individual in population
      # note it piles up all N[i] guys on one side of the transect
      d <- runif(N[i], 0, B)
      p <- exp(-d *d / (2 * (sigma^2))) #half-normal detection function
      # Determine if individuals are captured or not
      y <- rbinom(N[i], 1, p)
      u <- v <- rep(NA, N[i])   # coordinates (u,v)
      # Subset to "captured" individuals only
      d <- d[y==1]
      u <- u[y==1]
      v <- v[y==1]
      y <- y[y==1]

      # Compile things into a matrix and insert NA if no individuals were
      # captured at site i. Coordinates (u,v) are not used here.
      if(sum(y) > 0)
        data <- rbind(data, cbind(rep(i, sum(y)), y, u, v, d))
```

```
  else
    data <- rbind(data, c(i,NA,NA,NA,NA)) # make a row of missing data
  }
  colnames(data) <- c("site", "y", "u", "v", "d") # name 1st col "site"

  # *************************
  # Prep Data for analysis
  # *************************
  ncap <- table(data[,1])           # ncap = 1 if no individuals captured
  sites0 <- data[is.na(data[,2]),1] # sites where nothing was seen
  ncap[as.character(sites0)] <- 0    # Fill in 0 for sites with no detections
  ncap <- as.vector(ncap)           # Number of individuals detected per site
  site <- data[!is.na(data[,2]),1]   # Site ID of each observation
  delta <- 10                       # Distance bin width for rectangular approximation
  midpt <- seq(delta/2, B, delta)    # Make mid-points and chop up data
  dclass <- data[,5] %/% delta + 1   # Convert distance to distance category
  nD <- length(midpt)               # Number of distance intervals
  dclass <- dclass[!is.na(data[,2])] # Observed categorical observations
  nind <- length(dclass)            # Total number of individuals detected

  # Bundle data
  win.data <- list(nsites=nsites, nind=nind, B=B, nD=nD, midpt=midpt, delta=delta, ncap=ncap, dclass=dclass,
site=site, L=L, X=X)

  # initial values
  Nst <- ncap + 1             # This line is vital
  inits <- function() list(N = Nst, sigma = runif(1,30,60))

  # Define parameters to be monitored
  params <- c("alpha", "alpha1", "sigma", "Ntotal", "D", "N")

  # MCMC settings
  ni <- 5000
  nt <- 1
  nb <- 1000
  nc <- 3

  start.time = Sys.time()  #set timer
  # run model
  out <- jags(win.data, inits, params, "line.Lam.Cov.txt", n.chains = nc,
          n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)
  print(out)

  end.time = Sys.time()
  elapsed.time = round(difftime(end.time, start.time, units = 'mins'), dig = 2)
  cat('sim', k,', Posterior computed in ', elapsed.time, ' minutes\n\n', sep='')

  #************************************
  #### EValuate bias ####
  #************************************
  #Bias in N (site specific abundance)
  bias.Nsite <- out$mean$N - N.true #calculates bias
  m.bias.Nsite[k] <- mean(bias.Nsite) #averages bias and places within vector
  sd.bias.Nsite[k] <- sd(bias.Nsite) #gets standard deviation of bias places within vector
  baye.pvalue.Nsite[k] <-mean(N.true > out$mean$N)  #Bayesian P-value (proportion of simulations where the true
abundance was greater than the estimated abundance - values close to 0 or 1 indicate significant bias)
```

```
   #Bias in intercept for log-linear regression of expected abundance per site on a habitat covariate - descriptions
same as above
   bias.alpha <- out$mean$alpha - alpha
   m.bias.alpha[k] <- mean(bias.alpha)
   sd.bias.alpha[k] <- sd(bias.alpha)
   baye.pvalue.alpha[k] <- mean(alpha > out$mean$alpha)
   m.alpha[k] <- out$mean$alpha

   #Bias in slope for log-linear regression of expected abundance per site on a habitat covariate - descriptions same
as above
   bias.alpha1 <- out$mean$alpha1 - alpha1
   m.bias.alpha1[k] <- mean(bias.alpha1)
   sd.bias.alpha1[k] <- sd(bias.alpha1)
   baye.pvalue.alpha1[k] <- mean(alpha1 > out$mean$alpha1)
   m.alpha1[k] <- out$mean$alpha1

   #Bias in sigma - descriptions same as above
   bias.sigma <- out$mean$sigma - sigma
   m.bias.sigma[k] <- mean(bias.sigma)
   sd.bias.sigma[k] <- sd(bias.sigma)
   baye.pvalue.sigma[k] <- mean(sigma > out$mean$sigma)
   m.sig[k] <- out$mean$sigma

   #Bias in Ntotal (total population size)  - descriptions same as above
   bias.Ntot <- out$mean$Ntotal - sum(N.true)
   m.bias.Ntot[k] <- mean(bias.Ntot)
   sd.bias.Ntot[k] <- sd(bias.Ntot)
   baye.pvalue.Ntot[k] <- mean(sum(N.true) > out$mean$Ntotal)
   m.Ntot.true[k] <- sum(N.true)
   m.Ntot[k] <- out$mean$Ntotal

   #Bias in density - descriptions same as above
   bias.den <- out$mean$D - den.true
   m.bias.den[k] <- mean(bias.den)
   sd.bias.den[k] <- sd(bias.den)
   baye.pvalue.den[k] <- mean(den.true > out$mean$D)
   m.density.true[k] <- mean(den.true)
   m.density[k] <- out$mean$D

   #Coefficient of Variation in Ntotal (total population size) - want to be under 15%
   CV.Ntot <- out$sd$Ntotal/out$mean$Ntotal #standard deviation divided by mean
   m.CV.Ntot[k] <- mean(CV.Ntot)
   sd.CV.Ntot[k] <- sd(CV.Ntot)
   prop.CV.Ntot[k] <- mean(CV.Ntot < 0.15)

   #Coefficient of Variation in intercept for log-linear regression of expected abundance per site on a habitat
covariate
   CV.alpha <- abs(out$sd$alpha/out$mean$alpha)
   m.CV.alpha[k] <- mean(CV.alpha)
   sd.CV.alpha[k] <- sd(CV.alpha)
   prop.CV.alpha[k] <- mean(CV.alpha < 0.15)

   #Coefficient of Variation in slope for log-linear regression of expected abundance per site on a habitat covariate
   CV.alpha1 <- abs(out$sd$alpha1/out$mean$alpha1)
   m.CV.alpha1[k] <- mean(CV.alpha1)
```

```
  sd.CV.alpha1[k] <- sd(CV.alpha1)
  prop.CV.alpha1[k] <- mean(CV.alpha1 < 0.15)

 }  ) #This will be the end of the simulations

 #********************
 # Summary of Results
 #********************
 results <- c("alpha", "alpha1", "sigma", "N.total", "N.site", "N.total.CV", "CV.alpha", "CV.alpha1",
"Prob.CV.Ntot", "Prob.CV.alpha", "Prob.CV.alpha1")
 mean.bias <- round(c((mean(unlist(m.bias.alpha))), (mean(unlist(m.bias.alpha1))), (mean(unlist(m.bias.sigma))),
(mean(unlist(m.bias.Ntot))), (mean(unlist(m.bias.Nsite))), (mean(unlist(m.CV.Ntot))), (mean(unlist(m.CV.alpha))),
(mean(unlist(m.CV.alpha1))),NA, NA, NA),2)

 lower.CI <- round(c((quantile(unlist(m.bias.alpha), 0.05)), (quantile(unlist(m.bias.alpha1), 0.05)),
(quantile(unlist(m.bias.sigma), 0.05)), (quantile(unlist(m.bias.Ntot), 0.05)), (quantile(unlist(m.bias.Nsite), 0.05)),
(quantile(unlist(m.CV.Ntot), 0.05)), (quantile(unlist(m.CV.alpha), 0.05)), (quantile(unlist(m.CV.alpha1), 0.05)),NA,
NA, NA),2) #lower 95% credible interval

 upper.CI <- round(c((quantile(unlist(m.bias.alpha), 0.95)),(quantile(unlist(m.bias.alpha1), 0.95)),
(quantile(unlist(m.bias.sigma), 0.95)), (quantile(unlist(m.bias.Ntot), 0.95)), (quantile(unlist(m.bias.Nsite), 0.95)),
(quantile(unlist(m.CV.Ntot), 0.95)), (quantile(unlist(m.CV.alpha), 0.95)), (quantile(unlist(m.CV.alpha1), 0.95)),NA,
NA, NA),2) #upper 95% credible interval

 greater.15.CV <- c(NA, NA, NA, NA, NA, NA, NA, NA, (mean(unlist(m.CV.Ntot) >
0.15)),(mean(unlist(m.CV.alpha) > 0.15)), (mean(unlist(m.CV.alpha1) > 0.15))) #percent of CV's greater than 15%

 Baye.pvalue <- round(c((mean(unlist(baye.pvalue.alpha))), (mean(unlist(baye.pvalue.alpha1))),
(mean(unlist(baye.pvalue.sigma))), (mean(unlist(baye.pvalue.Ntot))), (mean(unlist(baye.pvalue.Nsite))), NA, NA,
NA, NA, NA, NA),2)

 sim.results <- data.frame(results,mean.bias,lower.CI, upper.CI, Baye.pvalue, greater.15.CV) #creates a table of
results
 print(sim.results)

 #****************
 #Post processing
 #****************
 # Set plots so that eight plots can be created in one image
 par(mfrow = c(8,1), mai=c(0.5,0.2,0.2,0.2), mar=c(1,5,1,2), oma=c(1,1,1,1), las=1)

 # Plots
 (hist(unlist(m.bias.Nsite), xlim=c(-10,10), main="", ylab="N.site"))
 (abline(v=0, col="red", lwd=3))

 (hist(unlist(m.bias.alpha), xlim=c(-1,1), main="", ylab="alpha"))
 (abline(v=0, col="red", lwd=3))

 (hist(unlist(m.bias.alpha1), xlim=c(-1,1), main="", ylab="alpha1"))
 (abline(v=0, col="red", lwd=3))

 (hist(unlist(m.bias.sigma), xlim=c(-10,10), main="", ylab="Sigma"))
 (abline(v=0, col="red", lwd=3))

 (hist(unlist(m.bias.Ntot), xlim=c(-200,200), main="", ylab="Total N"))
 (abline(v=0, col="red", lwd=3))
```

```
  (hist(unlist(m.CV.Ntot), xlim=c(0,1), main="", ylab="CV Ntotal"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.alpha), xlim=c(0,1), main="", ylab="CV alpha"))
  (abline(v=0.15, col="red", lwd=3))

  (hist(unlist(m.CV.alpha1), xlim=c(0,1), main="", ylab="CV alpha1"))
  (abline(v=0.15, col="red", lwd=3))

  return(list(sim.results=sim.results, m.bias.Nsite=unlist(m.bias.Nsite), m.bias.alpha = unlist(m.bias.alpha),
m.bias.alpha1 = unlist(m.bias.alpha1), m.bias.sigma = unlist(m.bias.sigma), m.bias.Ntot = unlist(m.bias.Ntot),
m.CV.Ntot = unlist(m.CV.Ntot), m.CV.alpha = unlist(m.CV.alpha), m.CV.alpha1 = unlist(m.CV.alpha1), alpha =
alpha, alpha1 = alpha1, sigma = sigma, nsites = nsites, num.sim = num.sim, density.true = unlist(m.density.true),
m.density = unlist(m.density), Ntot.true = unlist(m.Ntot.true), m.Ntot = unlist(m.Ntot), m.sigma = unlist(m.sig),
m.alpha = unlist(m.alpha), m.alpha1 = unlist(m.alpha1), out = out))
}
```