**A preliminary Bayesian species distribution model framework for status reporting for the Boreal Monitoring Strategy**

Steven L. Van Wilgenburg, David T. Iles, and Samuel Haché

*Introduction*

Over the past decade, the Boreal Avian Modeling (BAM) project has made a number of major strides in estimating and reporting on the distribution and abundance of boreal forest birds (Cumming et al. 2014; Stralberg et al. 2015a,b). While BAMs has provided major methodological advances (Sólymos et al. 2013, 2020) and insights into factors driving the abundance and distribution of boreal birds at a national scale (Cumming et al. 2014; Stralberg et al. 2015a,b), spatio-temporal biases in the data and the complexity of the modeling present several challenges to status reporting. A key example is that BAM population size estimates represent population size over an ill-defined time-frame (circa 1990 – 2018) and the model currently does not generate population size estimates for specified temporal intervals. Ideally, status reporting could generate population size estimates within defined time-frames meaningful for species listing mechanisms such as COSEWIC. Specifically, reporting estimated population sizes for the most recent 10-year period in advance of status assessments would be one key objective for a national boreal bird monitoring strategy (*hereafter* BMS; ECCC 2020a).

There are a number of possible approaches to modeling and reporting on population status over 10-year time-frames. The most logical approach would be to fit models to data collected exclusively within the 10-year interval of interest. ECCC has recently implemented more rigorous systematic sampling for boreal bird monitoring in a number of regions (Van Wilgenburg et al. 2020, ECCC 2020a), which could contribute to more frequent status reporting. As data are now becoming available, it is worthwhile contemplating alternative modeling frameworks that could be employed for status reporting.

In addition to status reporting, the national boreal bird monitoring strategy (ECCC 2020a) aims to produce unbiased estimates of species trend, distribution, and habitat associations. A key impetus for many of the BMS objectives is to inform conservation and mitigation. For example, data, estimates, and models from BMS can be used directly in impact assessments as baselines against which data collected for EIAs can be compared (ECCC 2020b). As such, an ideal model would be capable of simultaneously addressing all of the above objectives and provide outputs that are relatively easy to interpret. While recent efforts by BAM do an excellent job of predicting species distribution, the machine learning approaches are often difficult to explain and many of the habitat relationships are difficult to interpret and thus apply in impact mitigation (for example). Indeed, BAM originally intended to build upon initial machine learning approaches by using variable importance and structure of regression trees to inform regression modeling (S.G. Cumming, *personal communication*; Cumming et al. 2014). Here, we build on work by BAM and provide a preliminary description of a Bayesian zero-inflated Poisson regression modelling framework potentially suited to status reporting given the hierarchical nature of BMS sampling.

*Methods*

We selected primary sampling units (PSUs) and secondary sampling units (SSUs, or point-count sampling stations) nested within PSUs using a spatially-balanced hierarchical sampling framework according to the “Boreal Optimal Sampling Strategy” design (*hereafter* BOSS; Van Wilgenburg et al. 2020). Surveys in Saskatchewan began in the summer of 2014 using a pre-cursor to the BOSS design, and sampling modified to the BOSS design in 2017. BOSS sampling was initiated in Northwest Territories in 2019. In total, we sampled 3251 secondary sampling units (point-count stations) distributed amongst 325 primary sampling units (Figure 1) across Bird Conservation Region 6 (n = 1049 SSUs), Bird Conservation Region 6 (n = 1243 SSUs), and Bird Conservation Region 8 (n = 959 SSUs).

We conducted point count surveys at selected SSUs using standard 10-minute point counts conducted by trained observers following protocols recommended by Matsuoka et al. 2014. We only conducted surveys during suitable weather conditions from 30 minutes prior to sunrise until 4-5 hours after sunrise, from the last week of May to the first week of July. We conducted a portion (X) of the surveys using autonomous recording units (*hereafter* ARUs). We transcribed between three to six recordings per SSU from the dawn chorus. We initially transcribed three 10 minute recordings (2014-2018) per SSU in Saskatchewan, but based on analyses by Bayne et al. (2017), have since upgraded transcription from 2017-2019 to one 10 minute and five 3-minute recordings per SSU. Wherever possible, we attempted to record over ≥ 4 mornings of good survey conditions; however, ARUs were occasionally deployed for as little as a single night. We pre-programmed ARUs to record ≥ six 10-minute intervals over the course of a dawn chorus during the same time-period as point counts.

Statistical analyses

Based on the success of BAM in modeling species distributions using climatic, topographic and landcover covariates (Cumming et al. 2014, Stralberg et al. 2015, Sólymos et al. 2020), we chose to model avian density as a function of the similar covariates (see below). However, unlike BAM, we chose to model avian density using a hierarchical modeling framework rather than using boosted regression trees. Given the high proportion of counts in our data consisting of repeated observations, the usual modeling approach for such data would entail using N-mixture models (Royle 2004). We chose not to use an N-mixture modeling approach because the method has been met with several recent criticisms that call into question the ability of the models to reliably model both counts (N) and detection probability (p) from count data of unmarked individuals alone (Barker et al. 2018). Instead, we develop count models in which we simply treat repeated observations as repeated measurements of a mean density at a given SSU and instead account for detection probability using inclusion of statistical offsets estimated separately based on time-removal and distance estimation using the QPAD approach of BAM (Sólymos et al. 2013).

To model species distribution, we assumed that geographically broad sampling would cross species range limits, and thus a large component of extra-binomial variation (or zero-inflation) in counts would caused by sampling beyond a species range extent. We therefore modeled counts as a zero-inflated Poisson process. Cumming et al. (2014) previously described the hierarchical nature of species responses to both climate and vegetation in the boreal region. Their models generally showed climatic variables tending to discriminate amongst species presence-absence whereas higher abundances tended to be driven by local vegetation (Cumming et al. 2014). In keeping with these findings, we generated initial models where the zero-inflation process was modeled as a function of climatic covariates, and the count component was modeled as a function of vegetation variables.

Specifically, the observed count at site *i* on survey occasion *t* was modeled as:

|  |  |
| --- | --- |
|  | (1) |

is a latent indicator variable (i.e., presence/absence) that is 1 if the site has non-zero density and 0 if the site contributes to the “zero-inflation” component of the model. Accordingly, was modeled as a Bernoulli-distributed logit-linear function of covariates:

|  |  |
| --- | --- |
|  | (2) |
|  | (3) |

The non-zero component of the model describes the expected counts at sites that are potentially occupied. This was modeled as a log-linear function of covariates, with random effects for PSU to account for local-scale autocorrelation in residual density among SSUs:

|  |  |
| --- | --- |
|  | (4) |
|  | (5) |

Offsets were calculated for each site, during each survey location, according to standard approaches described in Sólymos et al. (2013) and Sólymos (2016).

An estimate of density (males per hectare) at a site, given site-level covariates, is therefore given by:

|  |  |
| --- | --- |
|  | (6) |

Across an entire landscape (i.e., a raster comprised of *n* pixels), an estimate of total abundance is given by:

|  |  |
| --- | --- |
|  | (6) |

Based on previous analyses (Cumming et al. 2014; Stralberg et al. 2015a,b) we derived estimates of mean annual temperature (°C), climate moisture index (mean annual precipitation - potential evapotranspiration), degree days below 0°C, and degree days above 5°C. In addition to climatic covariates, we obtained digital elevation model derived indices including terrain roughness index which indexes changes in slope (Wilson et al. 2007) and topographic wetness index (Sörensen et al. 2006) which quantifies topographic control on hydrological processes and correlates with soil attributes such as horizon depth, silt percentage, and organic matter content. Climatic and terrain based covariates were obtained using the ‘envirem’ package (Title and Bemmels 2018) in the R statistical computing environment (R Core Team 2019).

We also derived a series of local vegetation variables representing forest structure, composition and biomass. Specifically, we obtained estimates percent tree cover (250m resolution), stand age, stand height (m), stand canopy closure, proportion of the stand biomass comprised of needle-leaf trees, and proportion of the stand biomass comprised of broadleaf-leaf trees. Percent tree cover was derived from the MODIS vegetation continuous fields version 6 product (DiMiceli et al. 2021). All other forest composition variables were derived from the products of Beaudoin et al (2014), which used a combination of 26 geospatial data layers and national forest inventory data to derive Canada wide estimates of forest attributes.

In order to avoid multicollinearity, we removed all highly correlated variables (r>0.60) prior to analyses; retaining the variables in correlated pairs that we felt would provide the best ecological explanatory power and biological interpretability. As a result, we removed degree days below 0°C and degree days above 5°C as they were highly correlated with mean annual temperature (°C, r >0.7). In addition, stand age, stand height and stand canopy closure were also correlated and we dropped stand height from consideration. In order to derive an orthogonal measure of stand closure, we modeled canopy closure as a function of stand height (using a quadratic fit in OLS regression) and save the residuals of this relationship as our measure of canopy closure. Proportion of the stand biomass composed of needle-leaf trees was inversely related to the proportion of broadleaf trees in the stand, and we retained needleleaf as the sole covariate of forest composition.

*Empirical example*

We modeled the distribution and density Olive-sided Flycatcher (*Contopus cooperi*) as a motivating example. We first began with a saturated model in which included stand age, stand age2, proportion needleleaf, proportion needleleaf2, residual canopy closure, and percent tree cover as fixed effect covariates and a random intercept for primary sampling unit in the count model. The zero-inflation component of the model included mean annual temperature, climate moisture index and topographic wetness index as covariates. A quadratic fit for mean annual temperature was also considered, but models would not converge using frequentist approaches. Using this saturated model, we then varied the inclusion of the variables in the zero-inflation component of the model and used Akaike’s Information Criterion to select the most parsimonious model formulation for zero-inflation. We then used the most parsimonious model formulation in a second stage of model selection where we varied the inclusion of variables in the count component of the model. Prior to analyses, all covariates were centered and standardized to improve model convergence. We only considered main effects and no interactions in the analyses. Models also included offsets to account for detection probability. Offsets were calculated using version 3 of the QPAD models (Sólymos 2016).

Based on the above analyses, the most parsimonious model was then used to build two competing Bayesian models, and we used posterior predictive checks to select which model formulation was more appropriate. The two competing models varied only in whether or not the zero-inflation component of the model included a quadratic effect for mean annual temperature. Bayesian models were run in the JAGS environment interfaced with the R programming language using the jagsUI library. We ran 35000 iterations with a burnin of 5000 iterations and stored every 50th iteration to estimate the posterior probability densities.

We generated pixel based population size estimates (following Sólymos et al. 2020) by generating spatially explicit predictions of bird densities onto the spatially explicit raster covariate layers and summing the densities across all non-water pixels. When estimates were back-transformed to produced the density estimates, we applied a lognormal bias correction as sum of the log-scale prediction plus 0.5 times the between site (PSU) variance following Sprugel (1983). One raster prediction was made per saved Markov Chain Monte Carlo iteration, and we used percentiles of the posterior distributions to quantify uncertainty in density and population size estimates respectively.

*Simulation*

To confirm the statistical model can accurately estimate provincial abundance, we conducted spatially explicit simulations for seven species of boreal passerines: Olive-sided Flycatcher, Dark-eyed Junco (*Junco hyemalis*), Orange-crowned Warbler (*Oreothlypis celata*), Ovenbird (*Seiurus aurocapilla*), Blackpoll Warbler (*Setophaga striata*), Yellow-rumped Warbler (*Setophaga coronata*), and Canada Warbler (*Cardellina canadensis*) (BAM 2020a-g).

For each species at each survey location, we extracted local density values from BAM national density model output raster maps. On each survey occasion, we generated Poisson-distributed count data while also incorporating empirical QPAD detectability offsets. We then fit the statistical model (equations 1-5) to the simulated count data. Specifically, each species simulated density at the survey locations was modeled using mean annual temperature and mean annual temperature2 along with climate moisture index as covariates for the zero-inflation submodel (equation 3), and stand age, proportion needleleaf, residual canopy closure, and percent tree cover in the count submodel (equation 4).

We then used the resulting parameter estimates (, , and ) for each species to generate estimates of population density in every pixel on the landscape (equation 6). These estimates and 95% equal-tailed credible intervals were compared to the “True” population size obtained by summing pixel values within the BAM mean species density maps.

*Results*

*Empirical example*

Initial AIC based based selection followed by posterior predictive checks suggested that the model including mean annual temperature and mean annual temperature2 along with climate moisture index in the zero-inflation sub-model, and main effects for each of stand age, proportion of stand in needleleaf trees, residual canopy closure, and percent tree cover in the count submodel provided the best fit to the Olive-sided Flycatcher data. Our analyses suggests the probability of an Olive-sided flycatcher is detected follows a quadratic relationship with mean annual temperature (Table 1), with probability of occurrence being greatest in regions where mean annual temperature as ~ -0.4°C annually and decreased in warmer and colder areas respectively. Probability of occurrence also increased with climate moisture index (Table 1). Of the factors included in the count component of the model, only stand age showed evidence of a meaningful effect (credible interval not overlapping zero) on Olive-sided Flycatcher density, with Flycatcher density decreasing with increasing stand age (Table 1). Using our model, we generated spatially explicit predictions of Olive-sided Flycatcher density across Saskatchewan, which shows densities generally being greatest in the Boreal Shield shield ecozone (BCR8) in the central boreal south of Lake Athabasca (Figure 2). After remove waterbodies from consideration, the posterior median population size estimate for Saskatchewan was 887,588 (95% CI: 594,500 –1,446,650) after applying the lognormal bias correction (Figure 3). Prediction uncertainty is greatest in the boreal fringe near Prince Albert, Saskatchewan (Figure 4), where BOSS sampling does not occur (note that volunteer surveys from the Saskatchewan Breeding Bird Atlas have not been included here). The coefficient of variation was generally higher in the southern boreal forest, but was also higher on the southwestern and northwestern shores of Lake Athabasca (Figure 4).

*Simulation*

With the exception of Yellow-rumped Warbler and Ovenbird, 95% credible intervals for population size estimates encompassed the “true” population size for all the species we simulated (Figure 5). Population size estimates for both Yellow-rumped Warbler and Ovenbird were biased high, though this may is likely due to poor goodness-of-fit (Figure 5). Thus, even this relatively simple model structure generally produced unbiased estimates of species population sizes.

**Discussion**

Our preliminary results suggest that our Bayesian framework building upon previous work by BAM could provide a relatively simple approach to ongoing status reporting. Importantly, even applying a single model parameterization across multiple species appears capable of recovering unbiased estimates of population status with our design based sampling. Further refinements to the model should further improve both model accuracy and precision as well as ease of application to other species. Not only does our approach provide mapped estimates of species densities and population size estimation, but the derivation of relatively interpretable and graphable parameter estimates allow for relatively easy ecological interpretation. In addition, the natural approach to error propagation under a Bayesian approach makes it comparatively easy to publish and map degree of uncertainty in our estimates. These additional products not only improve our scientific credibility, but could also be used to inform further sampling.

*Future refinements*

One current limitation of BAM modeling approaches is that it does not currently leverage data sources aside from point count data. Data sources such as e-Bird and Breeding Bird Atlases have vast archives of data not fitting standardized point count methods that could be leveraged using Bayesian methods because the methods allow for multiple data sources to be combined within the joint likelihoods of models similar to those used here. Specifically, we envision

checklist data (with known survey effort) could be used to improve the estimation of the zero-inflation component of count models which would likely greatly improve precision and prediction accuracy. Developing a modeling framework including these data would have an immediate benefit for our partners as this would allow Birds Canada to incorporate a unified model into mapping for their Atlas products (instead of separate abundance and ‘PObs” models). Furthermore, testing this framework could also point to potential refinements to ECCC field programs and more easily leverage data outside of ECCC and not currently being used by BAM in modeling. For example, having ECCC staff regularly collect checklist data may improve our status and trend reporting if we had a unified model incorporating both checklist and point count data (both human and ARU). This would potentially be a major advantage over BAM machine learning approaches which can only incorporate point count data. However, the ongoing refinement of QPAD offset estimates, and further use of species-specific variable importance values (e.g. see Table C2 and C3 of Stralberg et al. 2015b) from BAMs previous modeling efforts could help drive model parameterization.

Here, we used relatively simple formulations for our preliminary models and limited ourselves to including climate and topographic variables to the zero-inflation sub-model, and habitat covariates to the count sub-model. Model fit was poor for two species, suggesting a need for alternative model formulations. Our models could be further refined in a number of ways, including creating a series of species-specific ‘indicator’ variables to indicate habitats that are likely structural-zeros. These indicator variables could be included in the zero-inflation sub-model to improve localized prediction of species presence/absence. In addition, it is likely that topographically derived variables such as the topographic wetness index or perhaps estimates of distance to water would be useful for predicting high abundance areas for species such as Yellow Warbler (*Setophaga petechia*).

One chief advantage of the BAM machine learning approach is that there is no need to go through a complicated model selection process for dozens of species. As previously mentioned, using previous BAM variable importance scores could greatly speed model parameterization and likelihood of success. One additional approach to partially automate estimation would be to use GAM smoothers on all linear covariates (while slow) to reduce the reliance on model selection issues and make our approach easier to apply across many species.

Finally, broader application of an approach such as that used here (e.g. the NA Pops project, A. Smith, personal communication) could be applied post-hoc to the BAM data set. Having a suite of Bayesian models at national and regional scales could improve status reporting in several ways. First, deriving national or regional models fit to historic data sets would allow us to use parameter estimates from those models as informative priors when creating or updating status reports using data collected over a narrower time-frame. Since the use of informative priors can greatly improve model precision, parameter estimates from national models fit using an approach similar to ours could greatly improve our ability to detect changes in population status. In addition, both map products and changes in parameter estimates could also point to changes in species distribution and/or habitat selection using a single modeling framework and thus allow greater insight into factors influencing avian populations.

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Table 1. Parameter estimates from a preliminary zero-inflated Poisson count model fit to Olive-sided Flycatcher (*Contopus cooperi*) counts from Saskatchewan and Manitoba.

|  |  |  |  |
| --- | --- | --- | --- |
|  |  | 95% Credible Interval | |
| Parameter | *β* | LCL | UCL |
| *Zero-inflation sub-model* |  |  |  |
| Intercept | 2.25 | 1.26 | 3.86 |
| Mean Annual Temperature | -1.22 | -1.79 | -0.71 |
| Mean Annual Temperature2 | -1.84 | -2.91 | -1.04 |
| Climate moisture index | 0.46 | -0.39 | 0.11 |
|  |  |  |  |
| *Count sub-model* |  |  |  |
| Intercept | -4.78 | -5.27 | -4.35 |
| Percent Needleleaf | -7.5x10-3 | -0.24 | 0.22 |
| Stand Age | -0.28 | -0.58 | 2.0x10-3 |
| Percent tree cover | 0.01 | -0.17 | 0.19 |
| Residual stand closure | -0.02 | -0.15 | 0.11 |

Figure 1. Geographic distribution of sampling using the “Boreal Optimal Sampling Strategy” design in Manitoba, Saskatchewan and Northwest Territories (2014-2019). Red dots indicate the location of 3251 secondary sampling units (point-count stations), distributed amongst 325 primary sampling units.

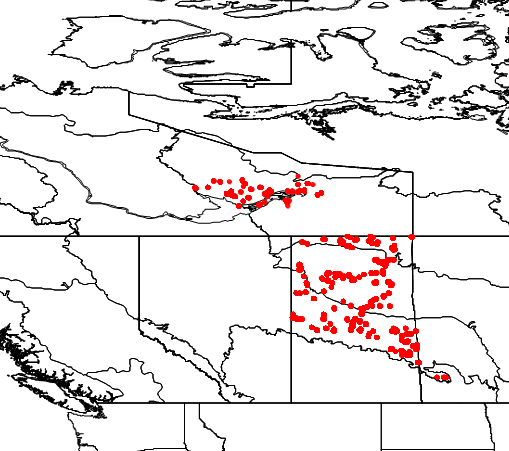


Figure 2. Mean posterior predicted density of Olive-sided Flycatcher (*Contopus cooperi*) in Saskatchewan, Canada (2014-2019).

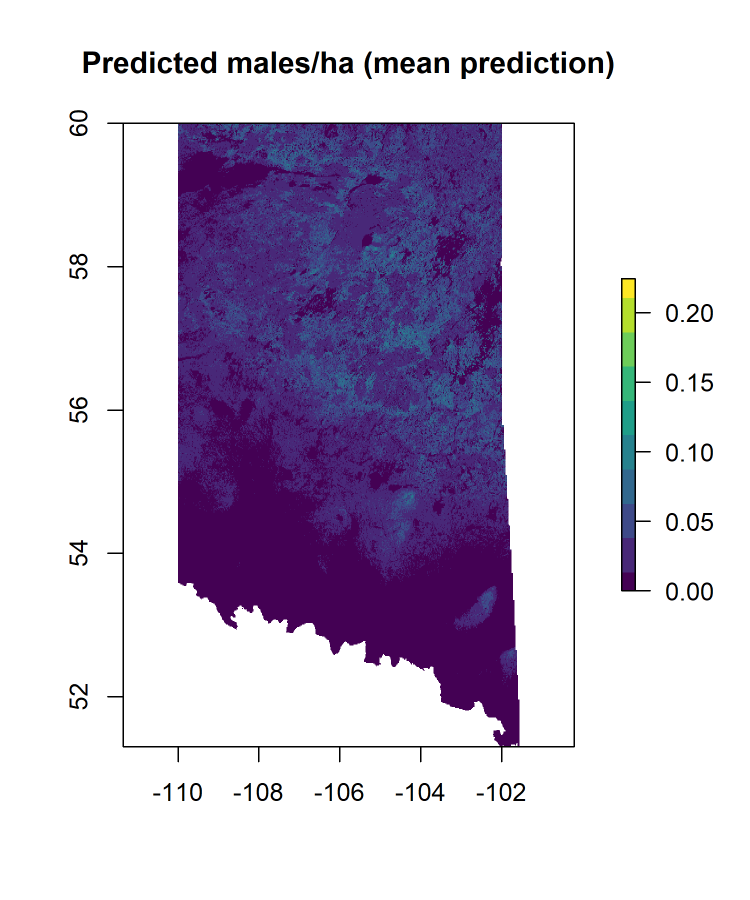


Figure 3. Distribution of posterior population size estimates for Olive-sided Flycatcher (*Contopus cooperi*) in Saskatchewan from a Bayesian species distribution model.

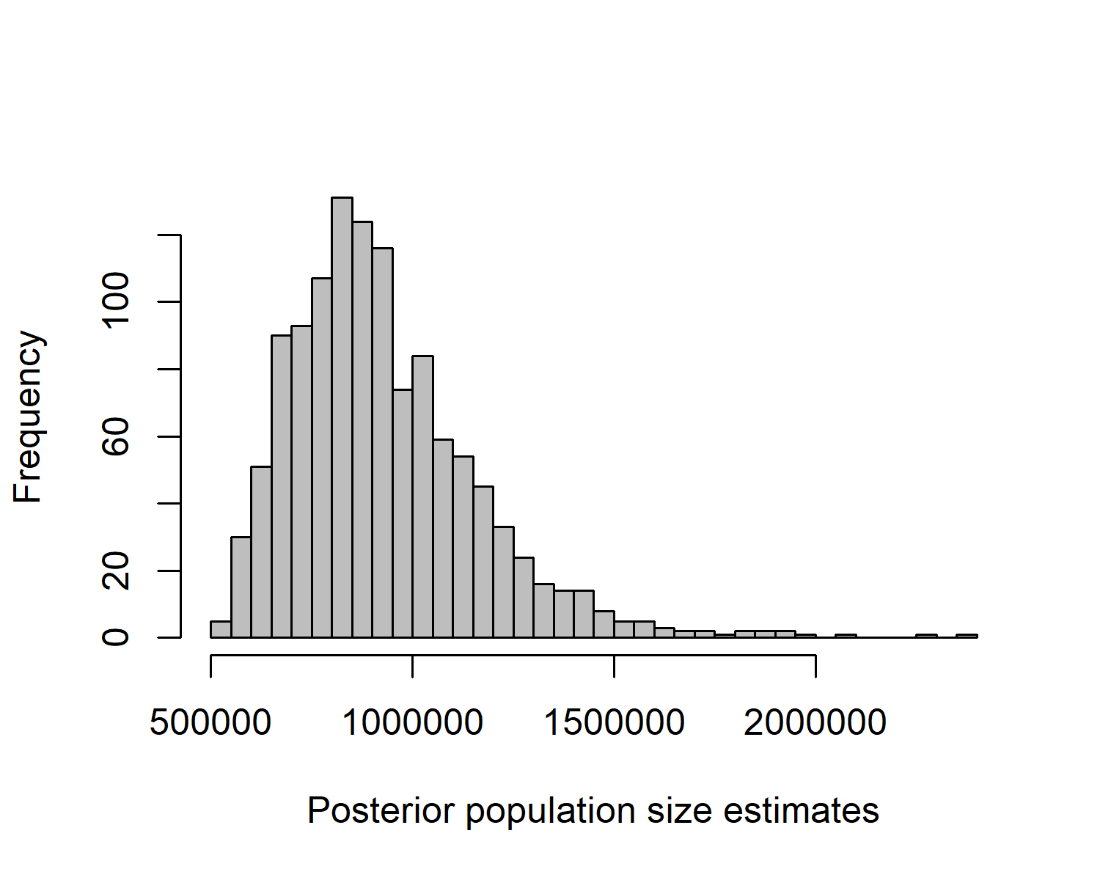


Figure 4. Coefficient of variation in predicted densities of Olive-sided Flycatcher (*Contopus cooperi*) in Saskatchewan, Canada (2014-2019).

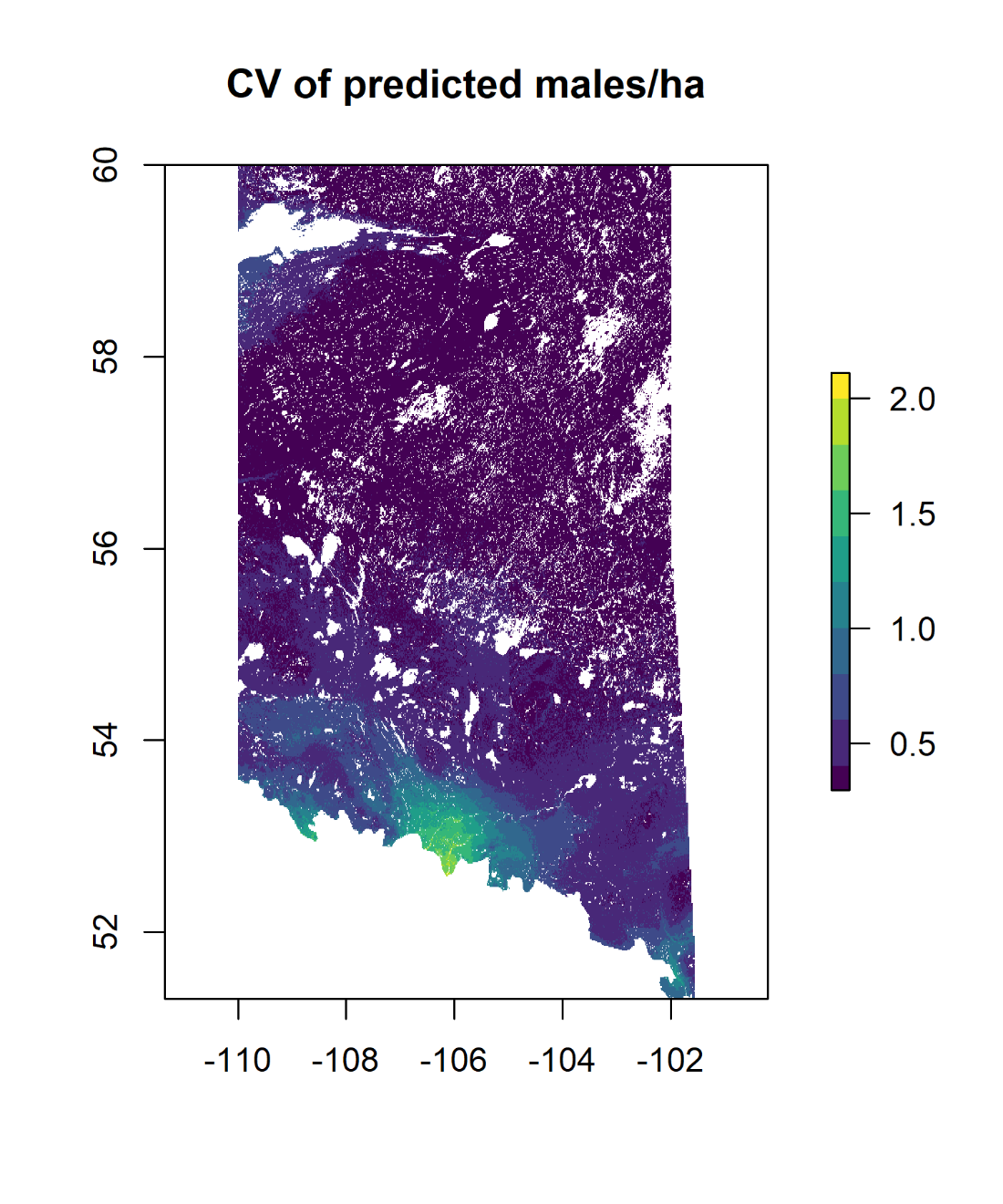


Figure 5. Performance of a pixel based population size estimation for seven species of passerine using a Bayesian zero-inflated Poisson regression model incorporating climatic, topographic and local habitat covariates (see Methods). Black line indicates 1:1 correspondence, dots and error bars represent mean and 95% Credible Intervals for population size estimates respectively.

