**Modeling trends of Leach’s Storm-petrel and Atlantic puffin** – paper outline/first draft

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# INTRODUCTION

Despite their presence in huge numbers on coasts and islands across the world, seabird populations present particular obstacles to population monitoring. Seabird colonies are often large (e.g. range?), diffuse, geographically isolated, and in some cases include a very large presence of non-breeding individuals that confound estimates of breeding totals (refs). Many seabird species also nest in burrows under soil or rock, such that variable detectability of breeders further complicates population censusing (e.g. Buxton et al. 2015, Arneill et al. 2019, Lavers et al. 2019). Given these multiple challenges, seabird population monitoring has often been conducted sporadically and with inconsistent methods (refs?). Estimating the population status and trend of colonial seabirds at regional scales is therefore a considerable challenge.

Adding urgency to these estimation difficulties, numerous colonial seabird populations are declining and at risk from anthropogenic threats and ongoing environmental changes (e.g. Paleczny et al. 2015, Dias et al. 2019). In addition to long-term fisheries bycatch impacts (e.g. Anderson et al. 2011, Regular et al. 2013, Grémillet et al. 2018, Christensen-Dalsgaard et al. 2019), seabirds are now increasingly vulnerable to effects of offshore energy production, light attraction, pollution, and invasive species (e.g. Ronconi et al. 2015, Dias et al. 2019, Gilmour et al. 2023). Climate change represents a further pervasive challenge for seabirds in both their marine and terrestrial habitats (e.g. Sandvik et al. 2012, Dias et al. 2019), such that cumulative stressors can be particularly strong among widespread species (Lieske et al. 2020, Phillips et al. 2023).

In Atlantic Canada, Leach’s storm-petrel (*Hydrobates leucorhous*, hereafter ‘storm-petrel’) and Atlantic puffin (*Fratercula arctica*, hereafter ‘puffin’) are two burrow-nesting species of conservation concern that also exemplify many challenges to population monitoring. Storm-petrels are small-bodied ‘tube-nose’ that nest in small and often concealed burrows, and are active only at night at the colony. They have a broad distribution across the Northern hemisphere, including numerous breeding colonies across Atlantic Canada ranging in size from approximately xx-xx (ref). They are exposed to many threats to their persistence (Lieske et al. 2020, Pollet et al. 2023), showing a population decline of over 50% since the 1970s (COSEWIC 2020, d’Entremont et al. 2020, Wilhelm et al. 2020) that led to their designation in 2020 as Threatened by the Committee on the Status of Endangered Wildlife in Canada. Puffins have a similarly diffuse breeding distribution across the coasts and islands of eastern Canada and colonies ranging in size from approximately xx-xx (refs). But unlike storm-petrels, and in contrast to many other regions (e.g. int’l puffin refs?), the Canadian puffin population has grown in recent decades, possibly linked to the closure of gill-net fisheries in the region (Regular et al. 2013, other refs?). Breeding distributions for storm-petrels and puffins in Atlantic Canada are illustrated in Figure 1.

Sentence reiterating why these two spp are interesting/contrasting case studies: e.g. unique censusing requirements, and Atlantic Canada puffin story in particular isn’t well known (international context, i.e. Canadian pops doing better than elsewhere). A bit more detail on distribution /censusing/ trends of these two spp in Atlantic Canada (e.g. some varying survey methods over time, occupied area estimate is improving over time; could mention also the small QC LHSP colonies as having conservation importance at margins of distribution even though they don’t represent much in terms of numbers; also some changes to QC ATPU colonies too…

Pgph on GAMM approach (background, justification/suitability here etc)

In the context of ongoing environmental change and increasing pressures on seabirds in the North Atlantic, the objectives of this study were: (1) to provide robust regional trend estimates for Leach’s storm-petrel and Atlantic puffin in eastern Canada, (2) to illustrate the GAMM approach to modeling population trends for sporadically-censused burrow-nesting birds such as these, and (3) to explore sensitivity of trend estimates to input parameters (e.g. additive/multiplicative error, number of knots, diff approaches to determining overall regional trend from individual colonies? -Dave can refine wording here). [*maybe one final sentence for big picture context/implications*?]

# METHODS

## Study species and census methods

* brief intro to LHSP and ATPU
* Census approach: explain what the censuses look like for these two spp in Atlantic Canada (noting that minimal LHSP data for Quebec), could we use maximums and use a censored likelihood approach?

## Description of Hierarchical Population Model

We estimated colony- and regional-level population trajectories using hierarchical state-space models. These models decompose spatio-temporal variation in seabird counts into contributions from biological processes of interest (i.e., temporal changes in colony-level population indices) and observation processes (i.e., variation due to imprecision in survey counts).

The model assumes survey counts () arise from an over-dispersed Poisson process with mean for colony in year :

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

is a normally distributed random variable with mean equal to an expected count () and a variance term () that characterizes the magnitude of sampling error:

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

This explicitly recognizes that there are inevitable discrepancies between the numbers of birds estimated from surveys and the total number of birds that would be counted with a true colony census.

The model further decomposes expected counts into contributions from two terms:

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

where represents the general shape of each colony’s trajectory over time, and represents annual departures of population indices from the colony-level smooths (sometimes called “process variance”).

The primary goal of our analysis is to describe temporal patterns in and its variation among colonies. We accomplished this using hierarchical generalized additive mixed models (GAMMs) that fit smoothed temporal trajectories to each colony, using an approach described in Smith and Edwards (2021) where:

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

The term therefore includes effects of colony-level intercepts () and a semi-parametric “smoothed” temporal process defined by a generalized additive function (), involving the product of a series of colony-level smoothing parameters () and a design matrix () that is constructed from a series of basis functions multiplied by a smoothness penalty. Further details related to constructing are described in appendix XX.

In our analysis, we estimated the smoothing parameters as random effects arising from a shared distribution across colonies where . This allows the shape of colony-level trajectories to be partially conserved among colonies, if supported by the data, which can improve model predictions for colonies with sparse data. This is also a valuable feature if large-scale environmental processes (e.g., climate oscillations) affect an entire regional population in a similar way, leading to trajectories with similar shapes.

The term in equation 3 describes random annual departures from the colony-level smooths, which we modeled as:

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

These deviations can be driven by a wide variety of population processes, including random annual variation in breeding propensity or environmental effects affecting recruitment. While describes genuine year-to-year fluctuations in colony abundance around its temporal smooth, we focus inference for status and trend assessment on changes in , which represents longer-term and more persistent changes in the expected annual abundance at colonies.

Finally, our analysis included an additional sub-model to estimate the magnitude of sampling variation for in cases where estimates of were missing (i.e., where raw plot-level data to calculate this quantity was unavailable). In general, for plot-based surveys of burrow-nesting seabirds, can be calculated via design-based estimators of spatial population totals (Horvitz and Thompson 1952). Specifically, there is an extremely robust positive empirical relationship between and , based on surveys that had both quantities available (Figure SXX). We therefore estimated missing values of by nesting an additional linear regression within our Bayesian model:

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

## Estimation of Regional Population Totals and Trends

For each colony, we calculated estimates of annual population index as . This definition of population index removes the effects of observation error and random annual process variation, yielding an index that is represented by the colony’s long-term temporal smooth. We then calculated the regional population total as the sum of annual population indices across all the colonies within each year of study, using . This naturally constructs a regional population trajectory that weights colonies according to their relative abundance; larger colonies have a stronger impact on the calculation of regional population dynamics.

We estimated the regional population trend from year to as the geometric mean annual rate of population change over that interval, which can be expressed as a percent rate of change, using:

|  |  |
| --- | --- |
|  | (7) |

Mention how we chose “which colonies to include for the regional sum” if we decide not to use all colonies, and “which years to choose for t\_start and t\_end” (i.e., if we only use 1984 onwards, since Baccalieu does not have surveys prior to that date).

## Bayesian model specification

We fit the statistical model in a Bayesian framework using JAGS version 4.3.0 (Plummer 2003) through the jagsUI library version 1.5.2 (Kellner 2021) within the R programming language version 4.0.2 (R Core Team 2024). We used the ‘jagam’ function from the mgcv package (Wood & Wood 2015) to prepare a template for constructing hierarchical GAMs within the JAGS language, which we manually modified to incorporate colony-level random effects and observation error.

We specified vague priors on all model parameters. All variance parameters were priors of , except for process variance which we assigned a prior of ; this remained highly vague, but improved model convergence greatly. After a burn-in of 500,000 iterations, we stored every 2500th sample until we accumulated 2000 posterior samples from each of three MCMC chains. We assessed chain convergence by visual examination of MCMC traceplots and by evaluating that the Gelman–Rubin convergence statistic was close to 1 for all model parameters. Code and data to repeat these analyses is available at **\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**.

[Include description of how “regional population totals” are calculated]

* Intro to GAMMs and why these are a suitable approach for these two spp
* David’s GAMM structure/details (including variety of approaches to estimating trend?)
* Issues to consider:
  + Has the bias in surveys changed over time? Sabina mentioned something about this.
  + Small colonies, possibly modeled with truncated distribution / likelihood
  + Those colonies are more likely to go extinct
  + Conservation value of small colonies

## Simulations to evaluate model performance

## Application of GAMMs to seabird census data

* Application of GAMMs to real data
  + Dave to explore sensitivity of model results to “wiggliness” (number of knots, priors on variance in GAMM coefficients)
* Any other applications we might want to have at the end…? (I think we determined that using this approach to recommend best future census practices would be a different paper…?)

Prior specification: The hyper-parameters and were assigned diffuse priors.

Statistical models were fit using JAGS version 4.3.0 (Plummer 2003), interfaced with the R programming language version 4.0.2 (R Core Team 2024) using the jagsUI library version 1.5.2 (Kellner 2021). We used the ‘jagam’ function from the mgcv package (Wood & Wood 2015) to prepare basis functions and code template, which we modified to incorporate colony-level random effects and observation error.

We specified vague priors on all model parameters. After a burn-in of **\_\_\_\_**  iterations, we stored every **\_\_\_**th iteration until we accumulated **\_\_\_\_** posterior samples from each of three MCMC chains. We assessed chain convergence by visual examination of MCMC traceplots and by evaluating that the Gelman–Rubin convergence statistic was close to 1 for all model parameters. Code to repeat these analyses is available at **\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**.

# RESULTS

* Summarize census data for LHSP and ATPU
* Colony-specific and regional plots of estimated abundance
* Estimates of population trend over time
* Any other applications we want to include…

*Potential figures*: Map of colonies/relative colony size (DONE already by Dave!), lots of Dave’s pretty GAMM output J

*Potential tables:* census counts at major colonies? (or redundant w GAMM model figures?)

# DISCUSSION

## Trend estimation

* Importance of accuracy and precision in population estimates generally/why this is maybe especially challenging for colonial seabirds…
* Drivers of population trends… we can see how much detail we want to go into in this paper? (e.g. ATPU new stressor: food source alteration via climate change, no longer bycatch threat to adult survival with halting of gillnetting… We probably want to provide general context/discussion based on existing literature but not go much into detail in this paper)
* Ultimately knowing the error etc will help make surveys more efficient/prioritize future monitoring (with caution, i.e. can’t necesasrily assume that parallel trends among colonies in the past will continue indefinitely into the future...?)

## Methodological considerations

* History/range of applications of GAMMs/related approaches to this kind of question
* Methodological considerations/caveats/uncertainties
* Differences in colony size/structure/pressure e.g. between QC and Atlantic: implications for model structure and/or application
* Discussion about how much faith to put in the model’s projections of pre-survey-data trends?

## Inferences about petrel and puffin dynamics

* ATPU vs LHSP: synchrony vs differences in dynamics across colonies, e.g. three regions (NL, Labrador, elsewhere…?) -LHSP broad trends, ATPU more colony specific
* Maybe also some exploration of how much trend interpretation changes with inclusion/exclusion of some colonies (e.g. based on largest colonies only, vs. including small ones which give more context, or sub-region information-sharing where dynamics are linked within a section of Atlantic Canada but not necessarily across the whole region)
* Also modeling/discussion of cross-spp linkages btw ATPU-LHSP: we’ll find their dynamics differ, but could be interesting to show it anyway…

## Conclusions

* Implications for monitoring/conservation of these spp in particular, including remaining information gaps (e.g. specific colonies needing updates?)
* potential to apply this same approach to looking at ATPU and LHSP Atlantic wide (i.e. including European data, where colony trends may be very different than in Canada)
* Broader implications for best practices for monitoring of similar spp/etc

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