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Statistical guidelines for assessing marine avian hotspots and coldspots: A case study on wind energy development in the U.S. Atlantic Ocean



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ABSTRACT

Estimating patterns of habitat use is challenging for marine avian species because seabirds tend to aggregate in large groups and it can be difficult to locate both individuals and groups in vast marine environments. We developed an approach to estimate the statistical power of discrete survey events to identify species-specific hotspots and coldspots of long-term seabird abundance in marine environments. We illustrate our approach using historical seabird data from survey transects in the U.S. Atlantic Ocean Outer Continental Shelf (OCS), an area that has been divided into "lease blocks" for proposed offshore wind energy development. For our power analysis, we examined whether discrete lease blocks within the region could be defined as hotspots (3× mean abundance in the OCS) or coldspots (1/3×) for individual species within a given season. For each of 74 species/season combinations, we determined which of eight candidate statistical distributions (ranging in their degree of skewedness) best fit the count data. We then used the selected distribution and estimates of regional prevalence to calculate and map statistical power to detect hotspots and coldspots, and estimate the *p*-value from Monte Carlo significance tests that specific lease blocks are in fact hotspots or coldspots relative to regional average abundance. The power to detect species-specific hotspots was higher than that of coldspots for most species because species-specific prevalence was relatively low (mean: 0.111; SD: 0.110). The number of surveys required for adequate power (>0.6) was large for most species (tens to hundreds) using this hotspot definition. Regulators may need to accept higher proportional effect sizes, combine species into groups, and/or broaden the spatial scale by combining lease blocks in order to determine optimal placement of wind farms. Our power analysis approach provides a general framework for both retrospective analyses and future avian survey design and is applicable to a broad range of research and conservation problems.

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1. Introduction

Understanding the distribution and abundance patterns of marine species is important not only to address fundamental ecological questions on species habitat use and movement but also to evaluate potential impacts of human activities, such as energy development, on marine populations and communities (Louzao et al., 2006; Nur et al., 2011). Offshore renewable energy development is increasingly common in both Europe and the United States with potential long-term consequences for marine species (Garthe and Hüppop, 2004). Wind farms can cause declines in seabird populations through direct impacts from collision (Hüppop et al., 2006) or indirect impacts such as displacement due to disturbance and habitat loss or disruption of migratory pathways (Drewitt and Langston, 2006). Evaluating the potential consequences of

alternative energy development necessitates a clear understanding of species spatial distributions, abundances, and habitat use to identify sensitive areas in need of protection (Huettman and Diamond, 2001; Ford et al., 2004). One important way to reduce risks associated with offshore energy facilities is through scientifically informed marine spatial planning processes that identify and avoid areas that are seabird "hotspots" (high use areas). It is equally useful to determine "coldspot" locations (areas of low use) where wind farms can be safely implemented with minimal risks to seabirds.

There are several difficulties in identifying species hotspots and coldspots in marine environments. The first is that sampling in the ocean, particularly in offshore areas, is expensive and logistically difficult due to remote survey locations and variable climatic conditions. Although seabird sampling methodology is relatively standardized, data can be collected using either aircraft or ships and continuous or discrete transects (Tasker et al., 1984). Additionally, the number and duration of studies is much smaller as compared to terrestrial locations, such that it

is difficult to use any one survey effort to determine hotspot/coldspot locations and combining data requires standardizing across sampling discrepancies (Smith et al., 2014). The second issue is that seabird populations tend to have patchy aggregations with extremely skewed distributions (Beauchamp, 2011). Thus, typical statistical distributions that are used to model counts (e.g., Poisson, negative binomial) may not be appropriate for seabird data (Zipkin et al., 2014). The disparate data on seabirds and the uncertainty on how to model available data creates a challenge for identification of consistent long-term patterns in occurrence and abundance of marine birds.

We present a framework for assessing species hotspots and coldspots - including the necessary amount of data - which accounts for the extreme skewedness observed in seabird count data. We apply our approach to data from the Outer Continental Shelf (OCS) of the Atlantic Ocean in the eastern United States, a proposed area for offshore wind energy development (Bowes and Allegro, 2012). Ongoing research efforts have focused on compiling all available seabird data in the OCS into the Atlantic Seabird Compendium (O'Connell et al., 2009), allowing an unprecedented opportunity to examine species' uses of the marine environment. Detailed spatio-temporal models of the occurrence and abundance of birds and other highly mobile species in the offshore marine environment are challenging (Smith et al., 2014). Our purpose here is not to create such a complicated model, but instead to develop a general framework that can be applied with a minimum of input data to provide a first-order estimate of retrospective and prospective statistical power to guide interpretation of past data collection efforts and planning of future surveys. Although we focus our approach on seabirds in the Atlantic Ocean for the specific topic of wind energy development, our framework should be useful in identifying hotspots/ coldspots for other animal species that aggregate (e.g., insects, fish).

2. Material and methods

Our objective is to determine the number of surveys required for sufficient statistical power to detect whether the long-term mean of a species count of individuals (0,1,2,...,100,...) in standardized surveys at a given location is larger (i.e., a hotspot) or smaller (i.e., a coldspot) than some a priori reference mean by a meaningful amount. The terms hotspot and coldspot have held a variety of interpretations in the scientific community and popular literature. In this case, we define a location as a species-specific hotspot if the mean count of individuals (i.e., abundance) of that species, conditional on presence, is more than three times the mean of the non-zero counts in some predefined reference region. We similarly define a species-specific coldspot as a location where the mean count of individuals of that species, conditional on presence, is less than one-third the mean of the non-zero counts in some predefined reference region. Other proportional effect sizes could easily be substituted, as appropriate. Our analyses are focused on defining hotspots and coldspots for individual species based on their prevalence in a region and their abundance at specific locations within seasons. Other metrics, such as species richness or community composition, could be used for defining hotspots/coldspots but are not considered here.

We assume that the abundance of a given species at a particular location in time is the outcome of a two-component random process known as a hurdle model (Mullahy, 1986). In a hurdle model, abundance is 0 with probability $1-\emptyset$, and non-zero with probability \emptyset (also referred to as the occurrence probability) according to a Bernoulli distribution. If abundance is non-zero, then the count of individuals (i.e., the group sizes 1,2,3,...) is distributed according to a discrete probability mass function with positive integer support.

Using this modeling framework, we can calculate the probability of detecting a hotspot/coldspot given that a location is a hotspot/coldspot for a specific number of sampling events. Conversely, we can determine the number of sampling events that are necessary to detect a hotspot/coldspot with a certain level of power. With spatially referenced count

data, we can also use the mean of a location's counts and the number of surveys that have been conducted to calculate a *p*-value for evaluation of the null hypothesis that the location is not a hotspot/coldspot. To do this, we must determine for each species: 1) its prevalence (occurrence probability) in the reference region (for the Bernoulli portion of the hurdle model) and 2) the discrete probability distribution that best describes the distribution of non-zero counts (i.e., the species' group sizes) within the reference region (for the abundance component of the hurdle model). We then implement a one-sample Monte Carlo significance test (Hope, 1968; Section 2.3) to test for either hotspots/ coldspots at given sampling locations using the estimate of prevalence (as a surrogate for the \varnothing parameter), the mean of the fitted distribution (as a surrogate of the mean for the reference region), and the parameter estimates from the fitted discrete statistical distribution that describes the non-zero counts.

2.1. Atlantic Seabird Compendium

The data for each seabird species come from the Atlantic Seabird Compendium, which contains the largest collection of scientific seabird surveys conducted within the Atlantic Ocean (O'Connell et al., 2009). We defined our reference region as the Outer Continental Shelf (OCS), the area currently being considered for renewable energy leasing by the Bureau of Ocean Energy Management (BOEM). This area has been divided into 48,446 lease blocks that are roughly 4.8 km \times 4.8 km in area (Appendix A, Figure A1).

The raw data consist of ship-based and aerial visual observations along fixed-width survey-transects recording the species and number of birds seen in each discrete time strip, or at each location along continuous time strips. Observers were generally trained to avoid double counting individuals but survey-specific observation errors are unknown. We used a total of 32 datasets that were collected between 1978 and 2010, 28 of which were ship-based while the remaining 4 were conducted from fixed-wing aircraft (Appendix A, Table A1, Figures A2-A6). Most of the surveys (28 total; 24 ship-based and 4 aerial) were conducted using the continuous time strip method. The four discrete time strip surveys were all ship-based and generally conducted for fixed 15-minute intervals on ships traveling at approximately 10 knots. We segmented all continuous time strip survey data (both ship-based and aerial) into transects of 4.63 km, equivalent to the distance covered by a ship moving at 10 knots for 15 min, to standardize the data across the two survey platforms and to match the discrete time surveys. We eliminated all transect segments shorter than 60% (2.78 km) of this distance, and any discrete time strip surveys shorter than 10 min (n = 209 removed transects). This allowed the remaining discrete and continuous time strip transect segments to be compared on an approximately common basis, "15-minute-ship-survey-equivalents." The resulting data consisted of 44,176 transects that covered our reference region (the OCS) with approximately 84% having lengths of 4.63 km (and the remainder having lengths no less than 2.78 km). Each standardized transect segment was then assigned to a BOEM lease block based on its centroid, such that all count data from a specific transect was assumed to have been observed in the corresponding lease block. All count data for a single species were then summed for each transect, date, dataset combination. We tabulated the number of samples for each lease block within each season and assumed that if a transect was flown/cruised and a given species was not recorded then it was not present (because none of the surveys recorded species absences). Although it is likely that this standardization did not fully resolve all differences among survey platforms and protocols, we believe that it accounted for the major differences among surveys.

Because species habitat uses and aggregations can vary throughout the year, we analyzed the count data for each species separately by season (spring = March 1 to May 31; summer = June 1 to August 31; fall = September 1 to November 30; winter = December 1 to February 28/29) and only considered counts where individuals were identified to Download English Version:

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