Marine Important Bird Areas in Alaska
Identifying Globally Significant Sites
Using Colony and At-Sea Survey Data

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ABSTRACT

An ongoing challenge for marine spatial ecologists is how to delineate important areas at sea. Effective marine bird conservation requires knowledge of places necessary for nesting, foraging, and migration. Using an extensive colony database, and over 30 years of at-sea survey data, we developed a spatial analysis method for identifying persistent seabird hotspots in Alaska waters by filtering survey data, creating abundance gradient maps, drawing core area boundaries, and validating marine Important Bird Areas (IBAs).

Here we present methods for identifying global IBAs in two categories: nesting colonies and pelagic foraging areas that hold more than 1% of the population of a species. We used a moving window analysis to group nearby colonies (e.g., on adjoining cliffs or islets) into meta-colonies for globally significant populations of seabirds, resulting in 59 colony groups identified for 22 species. This included 25.8 million birds in globally significant populations or 32.2 million seabirds of all species present. Our meta-colony IBAs captured 89% of the colonial birds in Alaska using 15% of the mapped colonies. The most important colonial nesting areas occur along the Aleutian Islands chain, remote islands within the Bering Sea (e.g. Pribilofs, Diomedes, St. Lawrence), and islands in the Gulf of Alaska (e.g. Semidis, Barren, Kodiak Archipelago).

For pelagic IBAs, we computed average densities of each species within spatial bins overlaying the study area, and filtered the data to select for areas of persistent use. We then used a moving window analysis to create gradient maps summarizing total species abundance and drew core area polygons around major concentrations exceeding an established abundance threshold. We advanced to IBA status those core areas which (a) encompassed more than 1% of the global seabird or North American waterbird population (adequate abundance) (b) resulted from five or more independent surveys (sufficient survey effort), and (c) had the species recorded on those surveys in two or more different years (good persistence). Pelagic core areas tended to be associated with the continental shelf break, and boundaries between major water masses or marine ecosystems (e.g., Aleutian passes, Bering Strait). We identified 64 pelagic IBAs for 45 species; this included 18.4 million birds in globally significant populations or 23 million birds of all species present. The IBAs captured about 38% of all pelagic seabirds in Alaska waters, within only 6% of the area.

Spanning 20 degrees of latitude and 56 degrees of longitude, we identified IBAs in two different oceans, with climates ranging from temperate to polar, for 49 out of 58 assessed species. These methods should be broadly applicable across ecosystem types and species guilds, including both short- and long-range foragers, and locally common to widely abundant species. We built the final steps into geoprocessing tools to standardize and automate marine IBA identification, further contributing to the use of IBAs as a "global currency" for conservation.

1. INTRODUCTION

Effective seabird conservation requires management of key locations for nesting, foraging, and migration. The identification of critical marine bird colonies and pelagic concentration areas has a varied history with many definitions applied. Important Bird Areas (IBAs) are based on an established program that uses standardized criteria to identify essential habitats (BirdLife International 2012b; National Audubon Society 2012b), which are areas that hold a significant proportion of the population of one or more bird species. BirdLife International, in partnership with the National Audubon Society, developed standardized criteria defining Important Bird Areas, establishing a global "currency" for bird conservation (National Audubon Society 2012a). Since the 1980s when the IBAs program began, over 11,000 sites have been identified in 200 countries (BirdLife International 2012b). To qualify as a globally significant IBA, a proposed site must hold a significant number of a globally threatened species, or a significant percentage of a global population (National Audubon Society 2012a), as evidenced by documented, repeated observation of substantial congregations in an area.

Historically, IBAs have focused on identification of important sites for terrestrial bird species. Extending that concept to identification of marine IBAs and/or Marine Protected Areas (MPAs) has been the focus of recent seabird conservation work (Carr et al. 2003; Amorim et al. 2009; BirdLife International 2009; Louzao et al. 2009; BirdLife International 2010; Arcos et al. 2012; Lascelles et al. In press; Oppel et al. In press; Ronconi et al. In press). Although standard IBA criteria require a certain abundance of a species to be present at a site, currently there are not rules on how IBAs should be spatially defined. The criteria do not prescribe what concentration of a species is considered important, how to draw core area boundaries, or how to merge overlapping important areas for multiple species for multiple seasons.

1.1 Past Efforts to Identify Seabird Hotspots

Past efforts to identify important areas for seabirds have included expert consultation or a variety of methods using spatial data analysis or modeling. Before the proliferation and accessibility of spatial analysis tools, expert consultation to draw boundaries around core areas was widely used to define IBAs. Expert drawing is preferable to not identifying conservation boundaries in areas of known species persistence, but this method may yield only moderately accurate overlap with the most biologically important areas (Cowling et al. 2003; Brown et al. 2004; O'Dea et al. 2006) and the results are not strictly repeatable by future researchers.

Through banding, satellite transmitters, or geolocators, extensive information has been collected on the distance that birds travel to foraging areas from their breeding colony. Lascelles (2008) summarized the available information for global seabird species into a foraging distance database. This information has been used to extend globally significant seabird colonies into the marine environment by buffering those colonies based on foraging distances of the species present (Yorio 2009; Thaxter et al. In press). This approach is useful as a starting point for defining a core area, followed by further refinement based on marine habitats or other information (BirdLife International 2010). However, even where data for a given species are extensive, the foraging distances are often highly variable between studies and regions, such that local information or pelagic survey data is often preferable, if available.

In study areas where satisfactory at-sea survey data exists, a number of other analytical techniques are available for identifying important areas for seabirds. Most often these data are analyzed to produce maps indicating the relative importance of locations for the species or species group. Kernel density estimation can be used to smooth survey data, or spatial interpolation (such as kriging) can be used to both smooth data and fill in data gaps in unsurveyed areas (Skov et al. 2007; Kober et al. 2010).

A popular and growing trend is to investigate seabird-environment interactions to produce predictive models of seabird use (Tremblay et al. 2009). These techniques use seabird survey or tracking data and relate locational information to associated environmental covariates to identify known and predicted hotspots on a species by species basis (Piatt and Springer 2003; Ford et al. 2004; Yen et al. 2005; Hyrenbach et al. 2006; Piatt et al. 2006; Suryan et al. 2006; Yen et al. 2006; Ainley et al. 2009; Louzao et al. 2009; Tremblay et al. 2009; Wakefield et al. 2009; Louzao et al. 2011; Nur et al. 2011; Montevecchi et al. In press). These data-intensive approaches work well when studying a limited number of species, in areas rich in marine habitat data and when implemented by ecologists and ornithologists who are knowledgeable about the local ecosystem in a particular area. These methods are, however, difficult to implement over a very large study area for numerous species.

Another method is to create models of multiple physical and biological attributes of the seascape, such as sea surface temperature (Etnoyer et al. 2004), salinity, prey distribution, bathymetry, chlorophyll, or sea surface height, and then analyze data to identify ecosystem-level hotspots. Those hotspots can then be explored for their significance to individual species or species groups (O'Hara et al. 2006; Palacios et al. 2006; Suryan et al. 2009; Tremblay et al. 2009).

Each of these approaches has contributed to the growing understanding of the areas and attributes that seabirds require but none have established a standardized method which could be applied globally for identification of IBAs.

1.2 The Challenges of Delineating Important Area Boundaries for Seabirds

Although there are specific criteria describing the number of birds required to establish an IBA, defining the area over which those birds might occur is ambiguous. Currently, IBA boundaries reflect geopolitical boundaries, physiographic boundaries, study area boundaries, or habitat-type boundaries. Boundaries within terrestrial IBAs are typically recognizable and relatively static. In the marine realm, however, a number of difficulties arise in trying to define the specific area that is important for conservation.

While we know that not all waters are uniformly valuable to birds, it is difficult to define boundaries on the water itself. First, the marine environment has greater ecological connectivity with fewer distinguishing surface features relative to the terrestrial landscape (Carr et al. 2003). Second, the marine realm can be highly variable. Food resources exploitable by seabirds are patchy and ephemeral, shifting between years, seasons, months, and even days (Hyrenbach et al. 2000; Gaston 2004; Palacios et al. 2006; Weimerskirch 2007). Third, seascapes are vast, and marine conservation areas may be orders of magnitude larger than terrestrial areas to encompass globally significant numbers of birds and the resources they are selecting for (Hyrenbach et al. 2000; Yorio 2009). Finally, because seabirds are dispersed over large areas, population estimates are based on accumulated extrapolations from sample densities measured using standard ship-board survey protocols (Tasker et al. 1984). At present, there are no guidelines for how intensive the sampling must be, or over what size area the sample can be extrapolated, to qualify an area as important.

Due to the complexities and error associated with ecological modeling and prediction (Guisan and Zimmermann 2000; Rocchini et al. 2011) for species conservation (Wilson et al. 2005), especially for a large group of species with very different ranges and abundances (Segurado and Araújo 2004), the optimal situation would be a complete census of species locations and abundances over the time period of interest. However, even if the ideal dataset were available, and species distribution maps were not accompanied by uncertainty, drawing conservation areas boundaries remains a challenge.

Few have focused on the methods for drawing boundary lines in the marine environment. Often, studies that have used spatial analysis or ecosystem models to produce continuous hotspot maps stop short of drawing conservation area boundaries from the results. This step is necessary for establishing IBAs or MPAs. A suitable method should be robust enough to accommodate multiple species, different foraging guilds (short- versus long-distance foragers), and concentrated or dispersed populations. It should identify vital habitats a seabird requires, including breeding (terrestrial) sites and foraging (marine) areas. Finally, the method should be as parsimonious as possible to meet these goals.

Our goal was to make methods for identifying marine IBAs objective, replicable, defensible, and transferable using survey data alone. We describe the problems we encountered, the options we explored, and the solutions we settled on. We hope to stimulate critical thinking and provide useful tools for identifying core areas and validating marine IBAs that others may adopt for their area of the world.

1.3 Study Area

Our study area was the US Exclusive Economic Zone (EEZ) surrounding the State of Alaska, which covers marine waters extending out to 200 nautical miles from the coast or to the international borders with Russia and Canada. The project covered 3.71 million km^2, about half the size of the US EEZ excluding Alaska. Our analysis included coastlines and islands where seabird colonies occur, nearshore zones used for migration, staging, and foraging by various waterbirds, and offshore areas frequented by pelagic seabirds.

The Alaska EEZ includes both the Pacific and Arctic oceans, from 47.9° to 74.7° north latitude, and from 130.5° west longitude, across the international dateline to 167.6° east longitude. The study area includes five large marine ecosystems: Gulf of Alaska, East Bering Sea, West Bering Sea, Chukchi Sea, and Beaufort Sea (Sherman et al. 2009). This includes temperate areas from the narrow fjords of Southeast Alaska's Inside Passage across the vast Gulf of Alaska; sub-Arctic areas from the very deep open ocean south of the Aleutian Islands north through the continental shelf and shelf edge waters of the Bering Sea; and into seasonally ice-covered Arctic waters north of the Bering Strait in the Chukchi and Beaufort seas.

2. METHODS

Globally significant IBAs are places that regularly hold more than 1% of the North American population of a congregatory waterbird species, or more than 1% of the global population of a congregatory seabird species, defined by BirdLife International as A4i and A4ii criteria, respectively (National Audubon Society 2012a). Because Alaska has such high numbers of seabirds, we only used the stringent A4 criteria for this project. Our analysis process was an exploration of many spatial-ecological questions and methods to identify the most beneficial and parsimonious workflow for delineating marine IBAs. Early on in the project we developed a list of key questions, and then used Geographic Information Systems (GIS) to explore solutions to those questions. Questions involved how to identify important breeding (colony) and foraging/resting (pelagic) areas; what concentration of birds spread across the water should indicate a core area (a potential IBA); how to draw a meaningful line in a marine environment to capture persistent, rather than ephemeral, high-density areas; how to avoid spatially overfitting boundaries to the available survey data; how to identify core areas of a size meaningful for conservation at the scale of Alaska; and how to make our methods globally applicable. We tried many approaches that were not part of our final process. Some of the noteworthy but unused methods are presented in Appendix A in the interest of documenting some alternative ideas for IBA identification, as well as the lessons learned.

Our final process used two methods for identifying globally important seabird areas: (1) using colony data to identify significant breeding locations, and (2) using at-sea survey data to identify important pelagic areas. We built the final steps into geoprocessing tools using ArcGIS Model Builder (ESRI 2011), Python (Python Software Foundation 2012), and R (R Development Core Team 2011) to automate IBA identification and nomination for all species, and to calculate IBA attributes such as ownership, number of WatchList species (Kirchhoff 2010), and threats to IBAs. We analyzed IBAs for loons, albatrosses, shearwaters, storm-petrels, cormorants, diving ducks, sandpipers, jaegers, gulls, terns, and alcids.

Our approach required making three assumptions. First, we assumed that the at-sea survey information we had access to constituted a reasonable representation of seabird densities. We acknowledge that there are data gaps in the coverage of the study area (some significant), but believe that the available data are informative for our study. Second, we assumed that the birds themselves indicated what areas were important by their presence. Third, because important areas may exist in places where survey coverage is lacking, we assumed failure to identify an IBA did not mean that particular area was not important (Rocchini et al. 2011). In addition to marine IBAs in pelagic waters, we also identified numerous colony IBAs for seabirds on land. This distinction between colony and pelagic IBAs is necessary because the spatial linkage among individual colonies and associated marine foraging areas is often poorly known. Moreover, the management prescriptions applied to terrestrial versus pelagic IBAs will naturally be different.

2.1 Colony IBAs

First we assessed important breeding areas for marine birds in Alaska by analyzing colony data.

Single Colonies

Colony data came from the Seabird Information Network's North Pacific Seabird Data Portal published online (World Seabird Union 2011). The abundance of each species present at each colony was recorded by surveyors counting the number of individuals, nests, or pairs. The database reports the best estimate made for that colony based on one or more site visits. We eliminated older (pre-1971), poor, or questionable records prior to beginning our analysis. The location of 1,640 seabird colonies used in our analysis is shown in Figure 2-1.

The analysis was performed on Alaskan seabird species for which colony and global population data were both available, and for which there was a sufficiently large number of birds represented in the database (>1% of the A4 population) to potentially generate IBAs (Table 2-1). Global population estimates were taken from the BirdLife International online database (BirdLife International 2012a). All colonies with at least one species meeting the 1% A4 population criteria qualified for global IBA status. Next, seabird colonies were further evaluated using the "meta-colony" approach described below.

Meta-colonies

Individual colonies were as close as 30 m apart, which raised the question of how to define a colony, and how nearby islets or cliff faces might be grouped into meta-colonies. We decided to combine significant colonies that were near one another before selecting those that met the 1% global abundance criterion. Doing so accomplishes multiple goals: 1) recognizes the relationship between nearby breeding populations of the same species, 2) identifies smaller colonies near larger, globally significant colonies, which will conserve spatially linked areas as individual colonies wax and wane, and 3) groups colonies into larger management units for simpler management so that, for example, discrete island complexes such as the Barren or Semidi islands would be nominated as a single IBA.

To identify meta-colonies, we ran a moving window analysis using the Focal Statistics tool in ArcGIS. First we converted colony locations into a raster map for each of the species analyzed. The tool visits each cell in the raster map and calculates the sum of all birds (repeated for each species) within the neighborhood (search radius) specified. We tested distances of 1, 5, 10, and 25 km before settling on 10 km as a reasonable neighborhood for clustering colonies. The next step was to draw a core area polygon around all raster cells meeting or exceeding the A4 (1%) threshold. We then used Zonal Statistics (ESRI 2011) to validate that the colonies within the polygon met the threshold to qualify as an IBA, and grouped all conspecific colonies into a single meta-colony IBA. We repeated this process for each species.

After selecting the colony point locations that qualified for IBA status, we calculated an estimated land area for each by selecting any coastline within 1 km of each colony, and buffering that coastline inland by 250 m. Colonies on small rocky outcrops that were not included in the state coastline file were assumed to have a land area of a 100-m radius circle.

We tried several other approaches for combining colonies before choosing the moving window method. Other methods that we tried but ultimately did not use are documented in Appendix A-1.

Combining Colony IBAs for Nomination

Where single-species meta-colony polygons overlapped spatially, boundaries were dissolved and all colony points for A4 species were joined into larger meta-colony IBAs. Combining overlapping IBAs reduces the number of IBA nominations, makes the product easier to communicate, and effectively groups important areas into larger management units.

Initially, we thought IBAs should be nominated only for those species which originally generated the IBAs. Later we decided that if an area is to be established as an IBA, the population numbers and trigger species associated with it should reflect the full suite of qualifying populations within. So we took one final step using the combined, multi-point colonies to test for A4 trigger populations for all species. This step does not add any new IBAs, but may add additional qualifying species to the IBA nomination, and may increase the reported abundance of previously qualifying species. This better reflects the total significance of the area nominated.

2.2 Pelagic IBAs

Next we turned our attention to identifying important pelagic foraging and resting areas used by globally significant congregations of waterbirds and seabirds. Seabird foraging areas are ephemeral and patchy yet somewhat predictable (Weimerskirch 2007). The term hotspot has been applied variously; similar to Piatt et al (2006), we defined marine bird hotspots as areas in which *significant aggregations* of a species *occur repeatedly*. We translated this hotspot definition into spatial analysis parameters to identify *areas of persistence* (i.e. repeated presence in an area in multiple years) and *major concentration areas* for seabirds. To identify hotspots for Alaskan seabirds, we completed six main steps: 1) accounting for survey effort, 2) filtering input data for persistence, 3) producing maps representing a gradient from low to high abundance, 4) drawing core area boundaries around major concentrations, 5) validating the results, and 6) combining overlapping single-species IBAs into multi-species IBAs.

Other published approaches required some level of prediction of important area boundaries to fill in missing information on species distributions. As an alternative, we used spatial pattern analysis to map hotspots directly (as suggested by Tremblay et al. 2009). The analysis was performed on Alaskan seabird species for which pelagic survey data were available, and for which there were sufficiently large numbers of birds represented throughout the EEZ (>1% of the population) to potentially generate IBAs (Table 2-1). We used at-sea survey data from the North Pacific Pelagic Seabird Database, version 2 (NPPSD v2) (Drew and Piatt 2011). NPPSD v2 is a compilation of seabird surveys covering the Northern Pacific Ocean, including data from Japan, Russia, the US, Canada, and Mexico. Survey emphasis is on Alaska, British Columbia, and the US West Coast. The database included 305,359 bird observation locations, of which 301,406 locations included seabird density data recorded on survey transects.

Prior to using at-sea survey data to identify core areas we tried buffering colonies based on documented seabird foraging distances (Lascelles 2008; Yorio 2009; Thaxter et al. In press), as recommended by BirdLife International in their Marine IBA Toolkit (BirdLife International 2010). Although we did not use this technique for our final set of IBAs, the methods we explored are documented in Appendix A-2.

Survey Effort

We removed off-transect observations (birds outside the survey area) and surveys covering an area less than 0.2 km^2, leaving 291,988 survey start locations, of which 125,683 were within the EEZ (Figure 2-2), collected between 1974 and 2009 (Figure 2-3). Next we split observations into breeding (May through September) and non-breeding (October through April) seasons, and summarized the data in 10 × 10 km blocks for all regularly occurring Alaskan species during that season. We tested blocks of various sizes and selected 10 km bins (100 km^2 cells) as a balance between covering a large enough area to capture multiple surveys for averaging survey densities, but small enough that extrapolating the average density across the block was not overinflating our abundance estimates.

For each block we calculated the number of surveys, number of different years surveyed, and average density of each species. We included zero values (null counts) in computing the average density for each species. Including zeros acknowledges the lack of use of an area during the season, which helps bring forth long-term foraging hotspots, rather than infrequent occurrences of transient birds. Figure 2-4 represents survey effort across the Alaska EEZ.

Filtering Input Data for Persistence and Adjacency

We eliminated blocks which were surveyed only during a single year so that IBAs could not result from a single high count of birds on the water. Taking this one step further, we only retained blocks with non-zero counts in two or more years for each species analyzed. Because a large proportion of the 10 × 10 km blocks were surveyed in only one year (51% during breeding season and 69% during non-breeding season), our persistence filter was leaving out a large pool of useful data, which hampered our ability to identify IBAs across much of the EEZ. Additionally, because oceanic conditions change, areas of persistent use shift within the local area (Gaston 2004; Reese and Brodeur 2006). Accordingly, we decided to use an adjacency filter to retain blocks that were spatially associated with the areas of persistence. We used the Expand Tool in ArcGIS to include areas within 3 blocks of the areas of persistent use. This step allowed us to use some single-year survey data and to include areas that were closely associated with areas of known persistent use, recognizing that hotspots regularly shift and that meaningful core area boundaries would account for that spatial variation.

When summarized in 10 km × 10 km blocks, the map did not approximate the coastline very well, as the nearshore blocks often included significant areas of land. To correct for this, we resampled our 10 × 10 km blocks to 1 km grid cells, each representing the average density value. Note that at a 1 km cell size, density (birds per km^2) and abundance values (birds within the cell) are equal, which allows easy translation between the two measures. We then removed cells from the resampled 1 km raster map that fell onto land, correcting a potential overestimate of the marine populations. Particularly for nearshore species, such as murrelets along the convoluted coastline of southeast Alaska, extrapolating survey densities onto land with large blocks would have introduced a substantial population overestimate.

Finally, we rounded abundance values down to the nearest integer so that data were expressed in whole birds rather than fractions of birds. The resulting 1 km raster map for each species was our final input layer for creating abundance gradient maps.

Abundance Gradient Maps

We used a moving window analysis (Dale et al. 2002) with the Focal Statistics tool in ArcGIS to draw abundance gradient maps (Figures 2-5a–b). This produced smoothed maps from the block data. The tool visits each cell in the raster map and calculates the sum of all birds within the neighborhood (search radius) specified, by species. We experimented with several search radii: 10, 25, 35, 50, 75, and 100 km. We chose 25 km because this distance produced boundaries conducive to drawing appropriately sized core area boundaries. That is, it provided a balance between not overfitting the boundaries to the survey transects (generality), and not losing important local-scale information (precision) (i.e. Guisan and Zimmermann 2000), and it fit our professional judgment of the appropriate scale (size and connectivity) of the resulting core areas. Using a set search radius avoided coming up with arbitrary borders by expanding an area until numbers within it reached 1% (Skov et al. 2007). A smaller search radius produced abundance gradient maps that were more reflective of survey tracks, while a larger radius produced results that were expansive and generalized when compared to our idea of how compact a core area should be.

We tried other approaches for creating abundance or density gradient maps, including interpolation and kernel density methods, before choosing the moving window analysis. Other methods that we tried but ultimately did not use are documented in Appendix A-3.

Core Area Boundaries

Next we designed a method for drawing core area boundaries from the abundance gradient maps. We used the term core area to indicate a boundary drawn around a major concentration area for a seabird species; core areas are synonymous with potential IBAs (one step prior to completing final validation steps). We defined major concentrations as cells that met or exceeded the A4 threshold for that species, based on the moving window (focal statistics) sum of birds within 25 km of each raster cell. We used the GIS to draw contours around all major concentrations and converted the contour lines to core area polygons (Figure 2-5c).

We also came up with a method for drawing core area boundaries from kernel density maps, which was not used to produce our final set of IBAs, but is documented in the appendix, section A-4.

IBA Validation Steps

We analyzed the core areas for IBA status using three criteria. First, we checked for adequate abundance by summing the extrapolated abundance data within each core area to see if the enclosed population met the 1% abundance criteria. Small polygons that enclosed < 1% of the population were removed from further analysis. Second, we checked for sufficient survey effort; based on the raw NPPSD v2 data, we retained only those core areas that were surveyed five or more times. Third, we checked for good persistence by retaining only those core areas that had the species recorded on surveys in two or more different years. The core areas remaining after these validation steps became IBAs (Figure 2-5d).

A final visual inspection was conducted to compare pelagic IBAs abundances to nearby colony counts for the same species. This cross-check helped us to ensure that results from our two different methods and databases were reasonably well matched.

Combining Pelagic IBAs for Nomination

Single-species IBAs with spatial overlap were combined into multiple-species IBAs for nomination. To combine overlapping pelagic IBAs we initially dissolved boundaries between IBAs with any amount of spatial overlap. This approach yielded very large IBAs and combined IBAs across regions with different ecologies. Instead, we decided to combine IBAs only within the same marine ecoregion.

We collected two ecoregion datasets: Marine Ecoregions of the World (Spalding et al. 2007) and Marine Ecoregions of Alaska (Piatt and Springer 2007) and combined them into one spatial layer. The Marine Ecoregions of the World separated large geographic areas, such as the Beaufort, Chukchi, and Bering seas, and the Gulf of Alaska. The Marine Ecoregions of Alaska offered finer scale information based on physical and biological characteristics of Alaskan waters. We assigned each single-species IBA to the majority marine ecoregion in which it fell, and dissolved overlapping boundaries of IBAs within the same ecoregion. If an IBA fell wholly inside another larger IBA then we combined them based on the majority ecoregion of the larger polygon. These boundaries were then smoothed with a 50 km tolerance using the Smooth Polygon tool in ArcGIS.

This step results in a smaller number of larger, multi-species IBAs. Combining overlapping IBAs reduces the number of IBA nominations, makes the product easier to communicate, and effectively groups important areas into larger ecosystem-level management units. This step also results in areas where the edges of IBAs overlap from one marine ecoregion to the next. Because ocean conditions vary and seabirds do not congregate within firm lines, these overlaps indicate a blending of one ecologically important area into the next, comparable to a marine ecotone.

Although these areas were located using a single-species approach, we treated the larger combined polygons as ecosystem core areas. Whether an IBA was made up of a single core area or multiple species core areas dissolved together, we recalculated abundances within to test for global significance for all species present. Initially, we thought IBAs should be nominated only for those species which originally generated the IBAs. Later we decided that if an area is to be established as an IBA, the population numbers and trigger species associated with it should reflect the full suite of qualifying populations within. Recalculating total abundances for the larger IBA area may add additional qualifying species to the IBA nomination, and may increase the abundance of the original trigger species. This better reflects the total significance of the area nominated. Because the final boundaries were adjusted through smoothing to make better management units, some areas that qualified as just over the 1% threshold could potentially fall just under the 1% threshold and no longer qualify for IBA status.

2.3 Automated Processing of IBAs and Attributes

Throughout the design of our methods, we used the ArcGIS Model Builder to connect geoprocessing tools and scripts to automate the analysis since we were dealing with potentially hundreds of IBAs. This allowed us to easily add or remove steps and change parameters during development. The final processing steps are built into two models automating the identification of colony and pelagic A4 IBAs. Figure 2-6 is a conceptual diagram of the GIS processing steps for identifying pelagic IBAs.

We also created a geodatabase of attribute layers and used R scripting to populate attribute tables further describing the resulting IBAs. Attribute layers included species abundance and richness, land ownership, land use, bird conservation region, and threats. Global threat layers included fishing (demersal destructive, demersal non-destructive, and pelagic), shipping intensity, oil extraction, habitat fragmentation, natural events (ocean acidification, climate change), nutrient pollution, and water pollution, based on the National Center for Ecological Analysis and Synthesis (NCEAS) global map of human impact on marine ecosystems (Halpern et al. 2008). Threat values were binned into ten categories, and the maximum threat value (0–10) was reported for each IBA for each threat type.

The resulting tables were incorporated in a Microsoft Access 2010 database containing the full set of IBAs for nomination and all related attributes. We used R code to automatically generate site descriptions including information on trigger species and abundances, location and ecoregion, Alaska WatchList species present (Kirchhoff 2010) and its habitat, land use, and ownership characteristics.

Finally, we built a Python script to automate IBA nomination. The script accesses the National Audubon Society's IBA nomination website, and automatically fills all forms and fields based on the Access database of IBAs and attribute information.

RESULTS

3.1 Colony IBAs

Single Colonies

Alaska's seabird colonies are home to an estimated 29.2 million birds, based on all 35 recorded species plus birds identified only to genus or family. We assessed 25 species for global IBA status that had a population sum of at least 1% of the national or global population, according to the A4i or A4ii criteria. The total population of the assessed species in Alaska was 26.5 million. Of the 1,640 seabird colonies in Alaska, 52 colonies had over 100,000 birds present, and 5 colonies had over 1 million birds. Species with the largest congregations at a single colony were Least Auklet (2.6 million), Leach's Storm-Petrel (1.7 million), Fork-tailed Storm-Petrel (1.3 million), and Thick-billed

Murre (1.1 million). The largest colony in Alaska is the Buldir Island colony in the Bering Sea with 3.5 million birds (Table 3-1).

We identified 102 globally significant seabird colonies in Alaska for 21 of the 25 assessed seabird species (Figure 3-1). Many colonies met the A4i/A4ii (1% abundance) criteria for multiple species, with a maximum of 9 globally significant populations supported by the Buldir Island colony, and 8 populations at the St. George Island colony. Many colonies also supported populations well above the 1% abundance standard, with a maximum of ~75% of the global Red-legged Kittiwake population supported by the St. George Island colony. Tufted Puffins had the largest number of globally significant IBA colonies in Alaska (25), followed by Red-faced Cormorants (19), and Horned Puffins (14) (Table 3-2). The total sum of qualifying A4 populations in single colonies was 19.7 million and the total of all birds at these colonies was 24.3 million.

These single-colony results were not our final set of IBAs. We nominated IBAs identified through the meta-colony approach (below), which included these areas as well as significant nearby colonies.

Meta-colonies

Using the meta-colony approach, we identified 142 globally significant IBAs (including both single colonies and colony groups) for 22 of the 25 assessed seabird species (Figure 3-2). Again, the highest number of IBAs identified was for Tufted Puffins (17), followed by Red-faced Cormorant (15). This approach reduced the number of IBAs for many species by grouping nearby large colonies together into a single IBA nomination. For other species, such as Black-legged Kittiwake, Northern Fulmar, and Pelagic Cormorant, the approach increased the number of IBAs by grouping together colonies that would not otherwise qualify (Table 3-2). The largest decrease was for Tufted Puffins, where there were eight fewer IBAs through the metacolony approach compared with the single-colony approach; the largest increase was for Glaucous-winged Gulls, which gained three additional IBAs. The highest number of colonies included in a single meta-colony IBA was 11, at the Hegemeister Island and Ugamak Strait IBAs.

The sum of individual seabirds by qualifying A4 populations using the meta-colony approach was 25.8 million, a 31% increase over the single-colony approach. Note that 4.1 million of these birds occurred in a single location, Big Diomede Island in Russia, just 4 km from Alaska's Little Diomede Island, and part of the Diomede Islands Colonies IBA. The addition of this one colony accounts for a 21% increase, while all other meta-colony additions account for a 10% increase from the single colony approach. For the final meta-colony IBAs, <0.1% of the birds were in the Arctic Ocean, 81.9% were in the Bering Sea, and 18.0% were in the Gulf of Alaska. The total number of birds for all species in these IBAs was 32.2 million (6.1 million, or 19% of the total, accounted for by Big Diomede Island). The meta-colony IBAs capture 89% of the colonial birds in Alaska in 15% of the colonies.

Combined Meta-Colony IBAs for Nomination

We combined 142 single-species colony IBAs into multiple-species meta-colonies, resulting in 59 globally significant meta-colony nominations. We recalculated the A4 qualifying populations based on the combined IBA boundaries, which added no new species, but did add five A4 populations to the IBAs, for a total 147 globally significant populations within the 59 areas (Table 3-3).

3.2 Pelagic IBAs

Extrapolated average survey densities within the 10 × 10 km blocks resulted in a total pelagic population estimate of 78.7 million seabirds within the Alaska EEZ during the breeding season and 17.4 million during the non-breeding season. Hotspots were located in the Bering Strait region (also see Piatt and Springer 2003), along the Bering Sea and Gulf of Alaska shelf breaks, along the Aleutian chain, in lower Cook Inlet, and near Barrow Canyon. Summarized by geographic location, 8% of the breeding season birds were located in the Arctic Ocean, 64% in the Bering Sea, and 28% in the Gulf of Alaska.

Breeding Season Core Areas

An initial 185 pelagic core areas were identified for 38 of 52 assessed seabird species present during the breeding season. Of these, 123 core areas for 38 species had adequate abundance, 103 core areas for 36 species had sufficient survey effort and good persistence (having 5 or more surveys in 2 or more years), and 100 core areas remained above the 1% level after the final boundary smoothing. These 100 fully validated core areas became breeding-season pelagic IBAs (Table 3-4; Figure 3-3). These boundaries were later combined with non-breeding-season IBAs.

Non-breeding Season Core Areas

An initial 64 pelagic core areas were identified for 19 of 34 assessed seabird species present during the non-breeding season. Of these, 41 core areas for 14 species had adequate abundance, 36 core areas for 12 species had sufficient survey effort and good persistence (having 5 or more surveys in 2 or more years), and 34 core areas remained above the 1% level after the final boundary smoothing. These 34 fully validated core areas became non-breeding-season pelagic IBAs (Table 3-4; Figure 3-4), which were later combined with the breeding-season IBAs.

Combined Pelagic IBAs for Nomination

Overlapping breeding season and non-breeding-season IBAs within the same marine ecoregion were dissolved into multi-species IBAs. A total 134 single-species IBAs were reduced to 64 IBAs for single or multiple species (Figure 3-5). This final set of IBAs covered 246,400 km^2 with an average IBA area of 3,850 km^2 and a range from 655 km^2 (Marmot Bay) to 19,398 km^2 (Buldir & Near Islands Marine).

We recalculated the A4 qualifying populations based on the combined IBA boundaries, which added four new breeding-season species and ten new non-breeding-season species. We identified pelagic IBAs for 40 of the 52 assessed species during the breeding season and for 22 of the 34 assessed species during the non-breeding season, or a total 45 out of 57 pelagic species between the two seasons. Prince William Sound IBA had the highest number of qualifying species (18).

The Unimak & Akutan Passes IBA had the greatest species richness (58) based on all species in the database, and the highest total breeding season population for all species at 7 million. Six other IBAs included over 1 million total birds in the breeding season: Bering Sea Shelf Edge 166W55N (4.3 million), Kiska Island Marine (1.4 million), St. George Island Marine (1.3 million), Buldir & Near Islands Marine (1.1 million), Fenimore Pass & Atka Island (1.1 million), and Shumagin Islands Marine (1.1 million). Glaucous-winged Gulls had the most pelagic IBAs (27), followed by black-legged kittiwake (11). The Unimak & Akutan Passes IBA had the highest abundance of a single species, with 3.3 million Short-tailed Shearwaters.

In total, there were 18.4 million breeding birds of qualifying A4 species within pelagic IBAs, of which 7.4% were in the Arctic Ocean, 81.8% were in the Bering Sea, and 10.8% were in the Gulf of Alaska. There were an estimated 21.4 million birds of all species in these IBAs during the breeding season, and 3 million during the non-breeding season, or a total of 23 million between both seasons. This represents about 38% of Alaska's breeding-season pelagic birds, and 37% of the non-breeding-season birds, covering 6% of the Alaska EEZ.

Notably, Whiskered Auklet had the highest population percentage within IBAs, at well over 100%, suggesting that the global estimate for this species may be low. This is corroborated by colony count data from the US and Russia which estimated a population of 220,000 birds (World Seabird Union 2011), or 220% of the current global estimate. The IBAs also include approximately 100% of the Red-faced Cormorant and Horned Puffin populations, followed by Red-legged Kittiwake (79%), Tufted Puffin (74%), Glaucous-winged Gull (66%), Long-tailed Duck (61%), Parakeet Auklet (53%), and Kittlitz's Murrelet (50%). The final pelagic IBAs are listed in Table 3-5, including IBA name, marine ecoregion, A4 trigger species, total bird population, total species richness, and total area.

4. DISCUSSION

Our application of new, standardized method was successful at identifying globally significant IBAs for a variety of species. Our work suggests that these methods are broadly applicable across ecosystem types where appropriate data sets exist. We identified IBAs throughout Alaska, spanning 20 degrees of latitude and 56 degrees of longitude, in two different oceans, with climates ranging from temperate to polar. Our results also suggest these methods are broadly applicable across species guilds, including both short- and long-range foragers, and locally common to widely abundant species.

4.1 Standardized Methods

We used spatial tools to design standardized methods that are repeatable and transferable to other marine study areas with similar types of at-sea and/or colony survey data available. Decisions about tool parameters such as scale (block size), persistence, adjacency, neighborhood size (search radius), and boundary smoothing interact like a series of levers which drive the shape, location, size, and connectivity of the results. Our extensive testing led us to what seemed an appropriate balance between these parameters for our area of study. In applying these methods elsewhere, we suggest applying the parameter values used here, then testing scenarios and adjusting values based on the data availability and underlying ecological drivers of the study area.

This project yielded useful bird conservation information beyond the final IBA boundaries. Our multi-layered spatial databases provide information on species abundance and richness for all species present, as well as information on ownership, land use, and threats. We can look into spatial relationships between large colonies and associated foraging areas, or recognize core areas that did not qualify as a global IBA but are important for other reasons, such as total abundance of common species, or potential state or continental IBA status.

Because current standard IBA criteria only prescribe the species abundance that triggers IBA status, we suggest standard criteria for drawing boundaries around seabird concentrations should be established as well. These new tools step through the processes for accounting for variability in survey effort, averaging densities (by species), filtering for data in or adjacent to persistent hotspots, drawing boundaries around core areas, and validating IBAs. The availability of these tools to other researchers will aid in standardizing IBA methods, further contributing to our ability to use IBAs as a "global currency" for conservation.

Figure 4-1 shows all 123 final meta-colony and pelagic IBAs identified for 49 out of 58 total species. Table 4-1 summarizes the final meta-colony and pelagic IBAs by species and reports the percent of global population captured within the IBAs based on recalculated abundances using the combined boundaries. Since pelagic breeding and non-breeding populations and colony populations are made up of many of the same birds, we used the maximum value of the three to quantify the percent of A4 population within IBAs. The number reported, then, is actually the minimum value of birds included since there is not 100% overlap among the three abundance measures.

4.2 Advantages of This Approach

Given the size of our study area (one third of the United States EEZ), we required an empirical approach that could address the range and variety of seabirds present in an efficient manner. Our method did not require local/expert knowledge for the whole region, and did not require the analysis of environmental covariates and development of predictive models on a species-by-species basis. To test our model parameters and results we examined draft IBAs in areas where our team did have substantial local knowledge to judge IBA size, location, and trigger species. We felt, for example, that the Glacier Bay & Icy Strait IBA should be a separate boundary from the Glacier Bay Outer Coast IBA, as should the Kachemak Bay and Lower Cook Inlet IBAs. This helped us determine the appropriate size and connectivity of the core areas, and we parameterized and tested the spatial tools accordingly. This also led us to using marine ecoregions to combine or separate overlapping single-species IBAs. The identification of meta-colonies was useful for both ecological reasons and management considerations by allowing us to objectively group nearby large colonies into fewer and larger IBAs.

Overall, our approach to identifying important areas was conservative. In accordance with BirdLife International standards, we used only empirical data to validate IBAs. Besides our need for an efficient and broadly applicable method, this requirement discouraged us from using certain techniques such as interpolation or habitat suitability modeling for identifying core areas. Predictive habitat models could be used to suggest core area boundaries if at-sea observations were available to validate the areas, similar to IBAs identified in Spain by Arcos et al. (2012); however, employing such methods over 3.7 million sq. km for 58 species would not have been practical. By requiring that IBAs be in or adjacent to areas that were repeatedly measured and persistently occupied, we ensured that the areas identified are significant and founded on solid survey data. Our results are prone to an error of omission where data gaps exist, but there is a low probability that our method would identify areas as important that are not.

4.3 Research Needs

The pelagic analysis is biased toward locating foraging destinations more often than stop-over sites, because we averaged observations across several months (for both breeding and non-breeding seasons). Doing so meant that short time periods with high densities were "averaged-out" when combined with low or zero counts from other months. Had we not included zeros, used maximum density values, or conducted our analysis by month, our results could have better approximated migration stop-over or staging sites. We may return to such an analysis in the future.

This approach is sensitive to data gaps, and, as previously explained, we did not use interpolation or modeling techniques to fill those gaps. As a result, there are some areas where we know IBAs should have been identified but were not. Examples include areas of critical habitat for Spectacled Eiders in Ledyard Bay, Norton Sound, and south of St. Lawrence Island. For Marbled Murrelets, Port Snettisham was not identified. In these places very large congregations occur but survey data were not integrated into the NPPSD. The majority of the Chukchi and Beaufort Sea ecoregions have been relatively lightly surveyed, so density estimates may be more prone to error due to data gaps, and IBAs may be missing, especially in unsurveyed areas farther offshore. We plan to augment the marine IBA network in these and other areas, prioritizing spatial analysis as a means of boundary drawing in areas with adequate data, and using expert-drawn boundaries where sufficient aspatial survey data exist to indicate an IBA.

Several other standard criteria may be used to establish an IBA that were not addressed by our study. In addition to the A4 global IBA criteria that requires 1% of the population be present, the A1 criterion requires a "significant number" of species of global conservation concern. These numbers are significantly lower than 1%, and can even be as low as a single bird. Additionally, the National Audubon Society (2012a) also has standard criteria for continental and state level IBAs. The number of birds needed to trigger an A1, continental, or state IBA is lower than what is needed for an A4 IBA. The methods used here do not work well when applied to very low abundance triggers, and would not be suitable for A1 IBAs without additional steps to keep the resulting boundaries from expanding to approximate a distribution map, rather than core areas. One potential technique suggested by Skov et al. (2007) is to prioritize areas with 1% of the biogeographic population of a species concentrated in an area with a density exceeding four times the average regional density. Another option is using the top quantile from kernel density maps to restrict boundaries (Sydeman et al. 2012). We explored other similar solutions during our method development (see Section A-4) and found that 1) comparing density values to the regional average or using quantile maps to define core areas requires somewhat subjectively defining a region boundary; 2) a boundary-free analysis (such as the moving window) is ideal because core areas based on comparative densities or quantiles are very sensitive to the region boundary; 3) because these measures are relative, they also are sensitive to gaps in survey coverage; 4) when assessing highly concentrated species, using the top quantile or 4× density restricts boundaries to only the highest of already high abundance areas, thereby missing some important places; and 5) when assessing highly dispersed species, this type of boundary drawing expands to include the highest of low abundance areas, producing boundaries which can be overly inclusive. Our moving window (focal statistics) analysis is free of these problems when using the 1% (A4) global criteria, but as abundance triggers approach lower thresholds (e.g. one-tenth of 1% of global abundance), boundaries could be drawn using a combination of focal statistics, density thresholds, and quantiles to produce reasonably sized core areas.

Alaska's IBAs are potentially threatened by a variety of industrial uses, including pelagic and demersal fisheries, global shipping routes, and offshore energy development. These areas also face human-influenced ecological changes such as climate change, ocean acidification, and pollution. Based on data from Halpern et al.'s (2008) assessment of human impacts to the world's oceans, Alaska's marine IBAs have very low to very high impact, with an average score indicating medium-high impact. Impact scores are very low to medium in the Arctic Ocean, and low to very high in the Gulf of Alaska and the Bering Sea, with the greatest impact concentrated on the Bering Sea shelf.

The next steps in this project will include a comprehensive assessment of threat levels and risks for Alaska's IBAs, and a prioritization of conservation efforts.

4.4 Looking Forward

We aimed to draw IBA boundaries that represent meaningful conservation units. Global oceans are experiencing increased pressure from human uses and stand to benefit from appropriately sited oceanic reserves (Hyrenbach et al. 2000; Etnoyer et al. 2004; Game et al. 2009; Ronconi et al. In press). As acknowledged by others around the globe, seabird core areas translate well into MPAs (Louzao et al. 2011; Nur et al. 2011; Lascelles et al. In press; Montevecchi et al. In press; Ronconi et al. In press), and are often indicative of biodiversity hotspots which are important for other species (Piatt and Springer 2003; Ainley et al. 2009; Suryan et al. 2009). Similar to findings by Alpine and Hobday (2007), our IBAs covered 24% of Alaska's coastline and 6% of the Alaska EEZ, suggesting that an effective reserve network for conservation of Alaska's seabirds would not require excessively large ocean expanses.

These methods will not fit all data types, foremost those areas without adequate survey data where researchers use best professional judgment to draw boundaries. We suggest that standardized methods can, and should, be articulated for other situations, including expert opinion-based boundaries (Brown et al. 2004), colony buffers (BirdLife International 2010; Thaxter et al. In press), IBAs using tracking data (BirdLife International 2009; Montevecchi et al. In press), and predictive modeling to draw boundaries (which must be validated with observed data) (Amorim et al. 2009; Nur et al. 2011; Arcos et al. 2012). Ultimately, the global marine IBA network will be a blend of a few techniques, and will greatly benefit from increased transparency, repeatability, and objectivity in the process.

Our project was made possible through the sharing of two large data compilations (Drew and Piatt 2011; World Seabird Union 2011) and we encourage others to collaborate and share data compilations for the sake of conservation (see Hatch 2010). Using GIS to analyze important areas for birds is advantageous because it allows us to continue exploring other conservation research questions using the compiled information. Using a repeatable and objective method to identify IBAs enables us to update the IBA network as new information becomes available, and to look for changes in bird distribution among different points in time. We can easily make changes to input parameters, include new data, test different methods, and share tools with others. We hope that the lessons we learned while exploring common challenges for identifying important marine areas will help other analysts and biologists identify globally significant areas for conservation.

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Table 2-1. Species codes, common names, potential Important Bird Area (IBA) type and threshold for 58 Alaskan waterbird and seabird species assessed.

Species Code	Common Name	Criteria[1]	IBA Threshold	IBA Type Analyzed[2]
ALTE	Aleutian Tern	A4i	160	Colony, Pelagic (B)
ANMU	Ancient Murrelet	A4ii	10,000	Colony, Pelagic (B)
ARTE	Arctic Tern	A4i	10,000	Colony, Pelagic (B)
BAGO	Barrow's Goldeneye	A4i	2,300	Pelagic (NB)
BFAL	Black-footed Albatross	A4ii	1,100	Pelagic (B)
BLKI	Black-legged Kittiwake	A4i	21,500	Colony, Pelagic (B, NB)
BLOY	Black Oystercatcher	A4i	100	Colony (B)
BLSC	Black Scoter	A4i	3,300	Pelagic (NB)
BOGU	Bonaparte's Gull	A4i	3,900	Pelagic (B)
BRAN	Brant	A4i	3,500	Pelagic (B)
CAAU	Cassin's Auklet	A4ii	37,500	Colony, Pelagic (B)
COEI	Common Eider	A4i	13,000	Pelagic (B)
COGO	Common Goldeneye	A4i	10,000	Pelagic (NB)
COME	Common Merganser	A4i	16,500	Pelagic (B, NB)
COMU	Common Murre	A4ii	180,000	Colony, Pelagic (B, NB)
CRAU	Crested Auklet	A4ii	82,000	Colony, Pelagic (B, NB)
FTSP	Fork-tailed Storm-petrel	A4ii	60,000	Colony, Pelagic (B, NB)
GLGU	Glaucous Gull	A4i	5,700	Colony, Pelagic (B, NB)
GWGU	Glaucous-winged Gull	A4i	5,700	Colony, Pelagic (B, NB)
HADU	Harlequin Duck	A4i	2,100	Pelagic (B, NB)
HEGU	Herring Gull	A4i	3,700	Pelagic (B, NB)
HOGR	Horned Grebe	A4i	5,000	Pelagic (NB)
HOPU	Horned Puffin	A4ii	8,000	Colony, Pelagic (B, NB)
KIEI	King Eider	A4i	4,600	Pelagic (B, NB)
KIMU	Kittlitz's Murrelet	A4ii	240	Pelagic (B, NB)
LAAL	Laysan Albatross	A4ii	8,700	Pelagic (B, NB)
LEAU	Least Auklet	A4ii	240,000	Colony, Pelagic (B)
LESP	Leach's Storm-petrel	A4ii	80,000	Colony, Pelagic (B)
LTDU	Long-tailed Duck	A4i	10,000	Pelagic (B, NB)
LTJA	Long-tailed Jaeger	A4ii	3,000	Pelagic (B)
MAMU	Marbled Murrelet	A4ii	6,200	Pelagic (B, NB)
MEGU	Mew Gull	A4i	3,000	Colony, Pelagic (B, NB)
MOPE	Mottled Petrel	A4ii	15,000	Pelagic (B)
NOFU	Northern Fulmar	A4ii	200,000	Colony, Pelagic (B, NB)
PAAU	Parakeet Auklet	A4ii	8,000	Colony, Pelagic (B, NB)
PAJA	Parasitic Jaeger	A4ii	7,500	Pelagic (B)
PALO	Pacific Loon	A4i	12,000	Pelagic (B)
PECO	Pelagic Cormorant	A4i	1,000	Colony, Pelagic (B, NB)
PIGU	Pigeon Guillemot	A4ii	4,700	Colony, Pelagic (B, NB)
POJA	Pomerine Jaeger	A4ii	750	Pelagic (B)
RBME	Red-breasted Merganser	A4i	2,500	Pelagic (B, NB)
REPH	Red Phalarope	A4i	12,500	Pelagic (B)
RFCO	Red-faced Cormorant	A4i	750	Colony, Pelagic (B, NB)
RHAU	Rhinoceros Auklet	A4ii	8,000	Colony, Pelagic (B)
RLKI	Red-legged Kittiwake	A4i	2,600	Colony, Pelagic (B, NB)
RNGR	Red-necked Grebe	A4i	450	Pelagic (B, NB)
RNPH	Red-necked Phalarope	A4i	25,000	Pelagic (B)

Species Code	**Common Name**	**Criteria[1]**	**IBA Threshold**	**IBA Type Analyzed[2]**
RTLO	Red-throated Loon	A4i	400	Pelagic (B)
SAGU	Sabine's Gull	A4i	5,100	Pelagic (B)
SOSH	Sooty Shearwater	A4ii	200,000	Pelagic (B)
SPEI	Spectacled Eider	A4i	1,800	Pelagic (B)
STEI	Steller's Eider	A4i	930	Pelagic (NB)
STSH	Short-tailed Shearwater	A4ii	300,000	Pelagic (B)
SUSC	Surf Scoter	A4i	7,000	Pelagic (B, NB)
TBMU	Thick-billed Murre	A4ii	220,000	Colony, Pelagic (B, NB)
TUPU	Tufted Puffin	A4ii	24,000	Colony, Pelagic (B, NB)
WHAU	Whiskered Auklet	A4ii	1,000	Colony, Pelagic (B, NB)
WWSC	White-winged Scoter	A4i	5,000	Pelagic (B, NB)

[1] A4i = IBA status triggered by 1% or more of the North American waterbird population; A4ii = IBA status triggered by 1% or more of the global seabird population.

[2] B = assessed for pelagic breeding season IBAs, NB = assessed for pelagic non-breeding season IBAs.

Table 3-1. Top 20 seabird colonies in Alaska, ranked by total abundance, with the top five species listed. Based on the Seabird Information Network (World Seabird Union 2011).

IBA Name	Location Name	Total Abundance	Top 5 Species[1]
Buldir Island Colony	Buldir Island	3,548,450	LESP, FTSP, CRAU, LEAU, BLKI
Kiska Island Colonies	Kiska Island (Sirius Pt)	3,297,126	LEAU, CRAU, PAAU, TUPU, RFCO
St. George Island Colony	St. George Island	2,077,991	TBMU, LEAU, COMU, RLKI, PAAU
Southwest Cape Colonies	Ivekan Mountain	1,213,196	CRAU, LEAU, COMU, TBMU, BLKI
St. Matthew & Hall Islands Colonies	Hall Island	1,021,170	LEAU, TBMU, NOFU, COMU, CRAU
Savoonga Colonies	Cape Myaughee	824,054	LEAU, CRAU, TBMU, COMU, BLKI
Forrester Island Colonies	Petrel Island	713,619	LESP, FTSP, CAAU, COMU, TUPU
Gareloi Island Colony	Gareloi I.(S.E. Side)	644,227	LEAU, CRAU, PAAU, TUPU, UNCO
Semidi Islands Colonies	Suklik Island	611,286	HOPU, FTSP, FTSP, FTSP, UNMU
Diomede Islands Colonies	Little Diomede Island	543,273	CRAU, LEAU, BLKI, UNMU, PAAU
Segula & Davidof Islands Colonies	Segula Island	525,001	LEAU, CRAU, PAAU, HOPU, TUPU
Semidi Islands Colonies	Aghiyuk Island	517,558	UNMU, NOFU, BLKI, HOPU, UNCO
Northwest Cape Colony	Sevuokuk Mountain	511,985	LEAU, CRAU, HOPU, PIGU, TUPU
St. Matthew & Hall Islands Colonies	N.W. Colony	453,228	LEAU, NOFU, TBMU, CRAU, COMU
Amagat & Umga Island Colonies	Amagat Island	451,140	FTSP, HOPU, TUPU, GWGU, PECO
Baby Islands & Akutan Passes Colonies	Egg Island	435,527	FTSP, TUPU, LESP, GWGU, RFCO
Savoonga Colonies	Singikpo Cape	422,120	LEAU, CRAU, TBMU, BLKI, PIGU
St. Lazaria Island Colony	St. Lazaria Island	404,024	LESP, FTSP, TUPU, COMU, RHAU
Semidi Islands Colonies	Chowiet Island	384,210	UNMU, NOFU, HOPU, BLKI, PAAU
Cape Pierce & Cape Newenham Colonies	Bird Rock	316,785	UNMU, COMU, BLKI, TUPU, GWGU

[1]See Table 2-1 for species codes; UNCO = unidentified cormorant; UNMU = unidentified murre.

Table 3-2. Colony and meta-colony Important Bird Area (IBA) statistics for 25 species analyzed. Numbers represent meta-colony counts before combining into multi-species IBAs and recalculating abundances. Based on analysis of the Seabird Information Network (World Seabird Union 2011).

Species Code[1]	Num. Colonies	Pop. in All Colonies	Num. Single-Colony IBAs	Pop. in Single-Colony IBAs	Num. Meta-colony[2] IBAs	Pop. in Meta-colony IBAs[3]
ALTE	53	9,501	11	7,634	8	7,854
ANMU	45	95,628	4	60,000	4	60,000
ARTE	201	12,642	0	0	0	0
BLKI	370	1,233,005	12	474,084	13	619,166
BLOY	452	3,770	0	0	1	151
CAAU	31	370,490	4	286,000	4	290,400
COMU	141	1,566,686	1	201,913	1	201,913
CRAU	38	3,257,539	11	2,937,089	8	3,503,043
FTSP	54	2,682,817	8	2,402,070	8	2,435,070
GLGU	128	9,084	0	0	0	0
GWGU	758	257,327	6	53,736	7	61,584
HOPU	576	917,305	14	743,999	11	778,895
LEAU	33	6,968,471	10	5,943,999	9	9,868,501
LESP	55	3,038,944	6	2,740,004	6	2,754,004
MEGU	90	22,183	2	11,875	1	11,875
NOFU	37	924,402	1	224,000	2	617,000
PAAU	168	398,986	10	350,200	9	423,100
PECO	414	56,270	11	23,681	12	28,871
PIGU	809	47,265	0	0	0	0
RFCO	237	58,457	19	38,770	15	43,935
RHAU	15	118,917	1	108,000	1	108,030
RLKI	8	208,854	2	206,610	2	206,610
TBMU	70	1,932,029	2	1,333,200	2	1,357,350
TUPU	631	2,317,360	25	1,556,916	17	1,734,846
WHAU	29	4,241	1	3,000	1	3,000

[1] See Table 2-1 for species codes and thresholds.

[2] Meta-colonies resulted from grouping nearby significant colonies using a 10-km moving window analysis.

[3] Note that meta-colony populations include birds at Big Diomede Island in Russia, which is part of the Diomede Islands Colonies IBA.

Table 3-3. Meta-colony Important Bird Areas (IBAs) nominated for global A4 status. IBAs are listed alphabetically within each terrestrial ecoregion.

IBA Name	Terrestrial Ecoregion	A4 Trigger Species[1]	Total Pop. for All Species	Species Richness	Num. Colonies
Cape Peirce & Cape Newenham Colonies	Ahklun Mountains	BLKI; COMU; TUPU	835,448	11	5
Crooked Island Colony	Ahklun Mountains	PECO	40,106	8	1
Goodnews Bay Colony	Ahklun Mountains	ALTE	350	2	1
Hegemeister Island Colonies	Ahklun Mountains	BLKI; PECO	73,094	9	11
Round Island Colony	Ahklun Mountains	BLKI	227,756	12	1
Amagat & Umga Island Colonies	Alaska Peninsula	CAAU; FTSP; GWGU; HOPU; PECO; RFCO; TUPU	557,306	10	3
Amak Island Colony	Alaska Peninsula	RFCO	23,146	7	2
Amalik Bay Colonies	Alaska Peninsula	RFCO	2,768	10	3
Bird Island Colony	Alaska Peninsula	GWGU	22,613	7	1
Castle Rock Colonies	Alaska Peninsula	ANMU; BLKI; CAAU; HOPU; PAAU; TUPU	286,508	18	2
Cherni Island Complex Colonies	Alaska Peninsula	ANMU; BLOY; CAAU; HOPU; LESP; RFCO; TUPU	301,019	16	6
Entrance Point Colony	Alaska Peninsula	ALTE	1,200	2	1
Koniuji-Shumagin Islands Colonies	Alaska Peninsula	HOPU	122,078	14	5
Near Island Colony	Alaska Peninsula	HOPU	27,040	8	1
Nelson Lagoon Colonies	Alaska Peninsula	ALTE; GWGU	15,101	7	2
Semidi Islands Colonies	Alaska Peninsula	BLKI; FTSP; HOPU; LESP; NOFU; PAAU; TUPU	2,407,910	15	9
Spitz Island Colony	Alaska Peninsula	BLKI	40,216	7	1
Ugaiushak Island Colonies	Alaska Peninsula	HOPU; RFCO; TUPU	71,776	14	4
Tuxedni Island Colony	Alaska Range	BLKI	36,000	3	1
Agattu Island Colonies	Aleutian Islands	GWGU; PECO; RFCO; TUPU	118,891	15	9
Akun Strait Colonies	Aleutian Islands	RFCO; TUPU	171,869	12	10

IBA Name	Terrestrial Ecoregion	A4 Trigger Species[1]	Total Pop. for All Species	Species Richness	Num. Colonies
Amchitka Island Colony	Aleutian Islands	PECO; RFCO	4,000	2	1
Attu Island Colony	Aleutian Islands	GWGU; PECO; RFCO	72,419	10	1
Baby Islands & Akutan Pass Colonies	Aleutian Islands	FTSP; RFCO; TUPU	609,206	16	8
Buldir Island Colony	Aleutian Islands	ANMU; BLKI; CRAU; FTSP; HOPU; LESP; PAAU; RLKI; WHAU	3,548,450	20	1
Chagulak Island Colony	Aleutian Islands	TUPU	90,186	12	1
Gareloi Island Colony	Aleutian Islands	CRAU; LEAU; PAAU	652,046	13	1
Kigul Islets Colonies	Aleutian Islands	BLOY; TUPU	220,229	16	7
Kiska Island Colonies	Aleutian Islands	CRAU; GWGU; LEAU; PECO; RFCO	3,333,960	14	6
Koniuji-Atka Island Colony	Aleutian Islands	ANMU; FTSP	288,263	13	1
Ogangen Island Colonies	Aleutian Islands	TUPU	38,102	8	2
Segula & Davidof Islands Colonies	Aleutian Islands	HOPU; LEAU	563,067	16	1
Semichi Islands Colonies	Aleutian Islands	PECO; RFCO	24,213	10	5
Semisopochnoi Island Colonies	Aleutian Islands	RFCO	111,868	12	2
Ugamak Strait Colonies	Aleutian Islands	GWGU; TUPU	401,544	15	11
Unimak Pass Colonies	Aleutian Islands	LESP; TUPU	169,895	10	2
Forrester Island Colonies	Alexander Archipelago	CAAU; FTSP; LESP; RHAU	884,221	12	2
St. Lazaria Island Colony	Alexander Archipelago	FTSP; LESP	406,583	12	1
Diomede Islands Colonies	Bering Sea Islands	BLKI; CRAU; LEAU; PAAU	6,688,820	11	2
King Island Colony	Bering Sea Islands	PAAU	245,910	11	1
Northwest Cape Colony	Bering Sea Islands	CRAU; LEAU	511,991	7	1
Pinnacle Island Colony	Bering Sea Islands	BLKI	181,540	6	1
Savoonga Colonies	Bering Sea Islands	CRAU; LEAU	1,482,260	13	6
Southwest Cape Colonies	Bering Sea Islands	BLKI; CRAU; LEAU; PECO	1,718,940	12	3

IBA Name	Terrestrial Ecoregion	A4 Trigger Species[1]	Total Pop. for All Species	Species Richness	Num. Colonies
St. George Island Colony	Bering Sea Islands	BLKI; COMU; HOPU; LEAU; PAAU; RFCO; RLKI; TBMU	2,077,990	11	1
St. Matthew & Hall Islands Colonies	Bering Sea Islands	BLKI; CRAU; LEAU; NOFU; PAAU; PECO; TBMU	1,636,510	12	4
St. Paul Island Colony	Bering Sea Islands	PAAU; RFCO	182,023	11	1
Susitna Flats Colonies	Cook Inlet Basin	MEGU	12,604	4	4
Barren Islands Colonies	Gulf of Alaska Coast	BLKI; FTSP; GWGU; PECO; TUPU	401,308	14	6
Blacksand Spit Colony	Gulf of Alaska Coast	ALTE	2,433	2	1
East Copper River Delta Colonies	Gulf of Alaska Coast	ALTE	7,138	4	10
Egg Island Colonies	Gulf of Alaska Coast	GWGU	11,260	3	2
Middleton Island Colony	Gulf of Alaska Coast	PECO	44,212	9	1
Riou Spit Colony	Gulf of Alaska Coast	ALTE	1,076	4	1
Tiedeman Slough Colony	Gulf of Alaska Coast	ALTE	2,428	1	1
Flat Island Colony	Kodiak Island	TUPU	31,153	5	1
Marmot Bay Colonies	Kodiak Island	TUPU	108,472	12	8
Chamisso Island Colonies	Kotzebue Sound Lowlands	HOPU	27,651	7	6
Noatak River Delta Colony	Kotzebue Sound Lowlands	ALTE	180	1	1

[1] See Table 2-1 for species codes.

Table 3-4. Pelagic breeding and non-breeding season Important Bird Area (IBA) statistics. Numbers represent abundances in single-species IBAs before combining into multi-species IBAs and recalculating abundances. Based on analysis of the North Pacific Pelagic Seabird Database, version 2 (Drew and Piatt 2011).

Species Code[1]	Num. Breeding-season IBAs[2]	Est. Breeding-season Pop. in IBA(s)	Num. Non-breeding-season IBAs	Est. Non-breeding-season Pop in IBA(s)
ALTE	1	312	NA	NA
ANMU	4	120,038	NA	NA
ARTE	1	42,123	NA	NA
BAGO	NA	NA	2	94,503
BFAL	1	1,381	NA	NA
BLKI	5	312,419	0	0
BLSC	NA	NA	3	16,759
BOGU	0	0	NA	NA
BRAN	0	0	NA	NA
CAAU	1	108,520	NA	NA
COEI	0	0	NA	NA
COGO	NA	NA	0	0
COME	0	0	0	0
COMU	1	183,218	0	0
CRAU	3	450,662	1	375,758
FTSP	3	313,284	0	0
GLGU	5	144,377	2	110,096
GWGU	10	127,644	16	300,859
HADU	1	30,953	1	51,959
HEGU	1	5,006	0	0
HOGR	NA	NA	0	0
HOPU	6	266,993	0	0
KIEI	1	102,000	0	0
KIMU	6	8,064	1	293
LAAL	0	0	0	0
LEAU	2	1,519,326	NA	NA
LESP	0	0	NA	NA
LTDU	4	556,558	0	0
LTJA	0	0	NA	NA
MAMU	4	66,274	0	0
MEGU	0	0	0	0
MOPE	0	0	NA	NA
NOFU	3	1,097,308	2	708,310
PAAU	5	91,549	0	0
PAJA	0	0	NA	NA
PALO	0	0	NA	NA
PECO	3	11,377	2	6,936
PIGU	1	9,656	0	0
POJA	4	8,129	NA	NA
RBME	0	0	0	0
REPH	2	124,247	NA	NA
RFCO	1	80,730	0	0
RHAU	1	154,189	NA	NA
RLKI	1	48,675	1	7,348

RNGR	0	0	0	0
RNPH	0	0	NA	NA
RTLO	0	0	NA	NA
SAGU	2	16,881	NA	NA
SOSH	2	1,328,523	NA	NA
SPEI	1	11,359	NA	NA
STEI	NA	NA	0	0
STSH	1	3,273,340	NA	NA
SUSC	1	14,681	0	0
TBMU	0	0	0	0
TUPU	4	421,757	0	0
WHAU	9	302,029	1	11,432
WWSC	2	15,446	4	65,168

[1] See Table 2-1 for species codes and thresholds.

[2] NA = not assessed.

Table 3-5. Pelagic Important Bird Areas (IBAs) nominated for global A4 status. IBAs are listed alphabetically within each marine ecoregion.

IBA Name	Marine Ecoregion	A4 Trigger Species[1]	Total Breeding Season Pop. For All Species	Total Species Richness	Total Area (km²)
Amchitka Pass 180W51N	Aleutian Islands	WHAU	110,689	15	3,167
Buldir & Near Islands Marine	Aleutian Islands	ANMU; BLKI; CRAU; FTSP; GWGU; HOPU; LAAL; PAAU; RFCO; TUPU; WHAU	1,128,226	45	19,398
Cape Tanak Marine	Aleutian Islands	GWGU	127,812	28	1,552
Chagulak Island Marine	Aleutian Islands	NOFU	486,923	28	2,841
Fenimore Pass & Atka Island Marine	Aleutian Islands	ANMU; CRAU; GWGU; HOPU; PAAU; PECO; PIGU; TUPU; WHAU	1,109,571	42	12,156
Gareloi Island Marine	Aleutian Islands	CRAU; LEAU; PAAU; WHAU	912,678	32	3,955
Kagamil Island Marine	Aleutian Islands	GWGU; WHAU	442,602	31	5,515
Kiska Island Marine	Aleutian Islands	CRAU; GWGU; LEAU; WHAU	1,389,265	34	4,680
Seguam Island Marine	Aleutian Islands	NOFU; WHAU	345,325	21	2,959
Unimak & Akutan Passes	Aleutian Islands	ANMU; BLKI; CRAU; GWGU; KIMU; NOFU; REPH; SOSH; STSH; TUPU; WHAU	7,023,266	58	11,286
Barrow Canyon & Smith Bay	Beaufort Sea	ARTE; BLKI; GLGU; KIEI; LTDU; POJA; REPH; RTLO; SAGU	725,467	38	11,861
Beaufort Sea Nearshore	Beaufort Sea	ARTE; BRAN; GLGU; KIEI; LTDU; RTLO	447,037	29	13,842
Beaufort Sea Shelf Edge 152W71N	Beaufort Sea	GLGU; POJA	35,281	15	2,645
Colville River Delta Marine	Beaufort Sea	GLGU	23,738	11	887
Chukchi Sea Nearshore	Chukchi Sea	ARTE; BLKI; GLGU; LTDU; POJA; REPH; SAGU	698,091	33	7,951
Icy Cape Marine	Chukchi Sea	BLKI; GLGU; POJA	185,449	32	3,576
Kotzebue Sound 163W66N	Chukchi Sea	LTDU	35,051	17	1,790
Lisburne Peninsula Marine	Chukchi Sea	BLKI	104,504	33	1,292
Point Lay Marine	Chukchi Sea	LTDU	32,088	24	953

IBA Name	Marine Ecoregion	A4 Trigger Species[1]	Total Breeding Season Pop. For All Species	Total Species Richness	Total Area (km²)
Bering Sea Shelf 163W56N	Eastern Bering Sea	GWGU	36,071	25	2,116
Bering Sea Shelf 165W56N	Eastern Bering Sea	GWGU	52,423	21	1,584
Bering Sea Shelf 166W56N	Eastern Bering Sea	GWGU	153,805	33	3,729
Bering Sea Shelf 166W57N	Eastern Bering Sea	GWGU	38,069	27	2,686
Bering Sea Shelf 168W62N	Eastern Bering Sea	POJA	22,847	15	2,295
Bering Sea Shelf 169W60N	Eastern Bering Sea	POJA	42,377	20	2,747
Bering Sea Shelf 170W58N	Eastern Bering Sea	GLGU	34,915	26	2,684
Bering Sea Shelf Edge 166W55N	Eastern Bering Sea	BLKI; GWGU; NOFU; SOSH; STSH; TUPU; WHAU	4,279,426	47	12,164
Bering Sea Shelf Edge 168W56N	Eastern Bering Sea	GWGU; RLKI	149,655	30	4,408
Bering Sea Shelf Edge 169W55N	Eastern Bering Sea	GWGU	23,431	18	1,818
Bering Sea Shelf Edge 173W58N	Eastern Bering Sea	FTSP	208,527	19	2,130
Bering Sea Shelf Edge 174W59N	Eastern Bering Sea	GLGU; NOFU	630,356	26	5,219
Bering Sea Shelf Edge 178W61N	Eastern Bering Sea	CRAU; FTSP; REPH	615,790	25	4,536
Bering Strait	Eastern Bering Sea	PAAU	630,767	20	1,998
Cinder River Marine	Eastern Bering Sea	GWGU	66,941	11	1,020
Ilnik Marine	Eastern Bering Sea	BLKI; GWGU; WWSC	411,140	38	4,548
Izembek Refuge Marine	Eastern Bering Sea	BLKI	160,277	22	1,175
St. George Island Marine	Eastern Bering Sea	PECO	113,731	42	14,029
St. Matthew Island Marine	Eastern Bering Sea	CRAU; PAAU; SPEI	292,769	22	1,257
Western St. Lawrence Island Marine	Eastern Bering Sea	TUPU	804,342	28	2,602
Barren Islands Marine	Gulf of Alaska	ALTE; BLSC; HADU; KIEI; POJA; RNGR; WWSC	179,496	35	2,193
Chirikof Island Marine	Gulf of Alaska	GWGU	273,714	26	1,713
Eastern Kodiak Island Marine	Gulf of Alaska	HEGU	33,215	56	2,123

IBA Name	Marine Ecoregion	A4 Trigger Species[1]	Total Breeding Season Pop. For All Species	Total Species Richness	Total Area (km²)
Glacier Bay Outer Coast Marine	Gulf of Alaska	BFAL	17,390	36	2,575
Gulf of Alaska Shelf 151W58N	Gulf of Alaska	GWGU	103,722	26	1,585
Gulf of Alaska Shelf 155W57N	Gulf of Alaska	BLSC; GWGU; KIMU; MAMU; PECO; WWSC	116,577	20	2,063
Gulf of Alaska Shelf Edge 143W60N	Gulf of Alaska	GWGU	57,825	14	1,013
Gulf of Alaska Shelf Edge 148W59N	Gulf of Alaska	GWGU	45,306	22	1,309
Gulf of Alaska Shelf Edge 163W54N	Gulf of Alaska	BLSC	37,707	25	1,646
Kachemak Bay	Gulf of Alaska	GWGU; HOPU; RFCO	61,626	50	2,571
Kamishak Bay	Gulf of Alaska	ARTE; BAGO; BLKI; BLSC; COGO; GWGU; HADU; HOGR; KIMU; MAMU; MEGU; PECO; PIGU; RBME; RNGR; SUSC; TUPU; WWSC	388,179	30	1,731
Kenai Fjords	Gulf of Alaska	GWGU; HOPU	71,162	42	1,765
Lower Cook Inlet 153W59N	Gulf of Alaska	GWGU; HOPU; PAAU	426,091	26	1,548
Marmot Bay	Gulf of Alaska	ANMU; CAAU; FTSP; GWGU; HOPU; PAAU; SOSH; TUPU	1,083,777	49	655
Morzhovoi Bay	Gulf of Alaska	PECO; PIGU	111,379	30	1,609
Prince William Sound	Gulf of Alaska	KIMU	44,094	52	9,775
Seal Cape Marine	Gulf of Alaska	ANMU	37,614	24	1,666
Semidi Islands Marine	Gulf of Alaska	BAGO; GWGU; HADU; KIMU; MAMU; PECO; PIGU; SUSC; WWSC	158,293	30	2,236
Shumagin Islands Marine	Gulf of Alaska	RHAU	381,663	36	6,062
Southwestern Kenai Peninsula Marine	Gulf of Alaska	MAMU	80,307	36	1,237
Yakutat Bay	Gulf of Alaska	WHAU	110,689	30	2,250
Dixon Entrance 132W54N	Pacific Fijordland	ANMU; BLKI; CRAU; FTSP; GWGU; HOPU; LAAL; PAAU; RFCO; TUPU; WHAU	1,128,226	13	1,693

IBA Name	Marine Ecoregion	A4 Trigger Species[1]	Total Breeding Season Pop. For All Species	Total Species Richness	Total Area (km²)
Glacier Bay & Icy Strait	Pacific Fijordland	GWGU	127,812	47	3,600
Outer Islands Marine	Pacific Fijordland	NOFU	486,923	19	3,267
Stephens Passage & Tracy-Endicott Arms	Pacific Fijordland	ANMU; CRAU; GWGU; HOPU; PAAU; PECO; PIGU; TUPU; WHAU	1,109,571	19	1,467

[1] See Table 2-1 for species codes.

Table 4-1. Summary of results for pelagic and meta-colony Important Bird Areas (IBAs) for 58 assessed species. Numbers reflect combining into multi-species IBAs and recalculating abundances for all species. Based on analysis of the Seabird Information Network (World Seabird Union 2011) and the North Pacific Pelagic Seabird Database, version 2 (Drew and Piatt 2011).

Species Code[1]	Pelagic Breeding-season IBAs[2]	Pelagic Est. Breeding Abundance in IBA(s)	Pelagic Non-breeding-season IBAs	Pelagic Est. Non-breeding Abundance in IBA(s)	Num. Meta-colony IBAs	Meta-colony Abundance in IBA(s)[3]	Total IBAs	Total A4 Pop.[3,4]
ALTE	1	299	NA	0	8	7,854	9	49%
ANMU	5	195,539	NA	0	4	60,000	9	20%
ARTE	4	110,533	NA	0	0	0	4	11%
BAGO	NA	0	2	94,723	NA	0	2	41%
BFAL	1	1,517	NA	0	NA	0	1	1%
BLKI	11	671,410	2	78,245	14	682,287	25	32%
BLOY	NA	0	NA	0	2	293	2	3%
BLSC	NA	0	4	26,422	NA	0	4	8%
BOGU	0	0	NA	0	NA	0	0	0%
BRAN	1	5,527	NA	0	NA	0	1	2%
CAAU	2	150,779	NA	0	4	313,740	6	8%
COEI	2	150,779	NA	0	NA	0	0	12%
COGO	NA	0	1	12,753	NA	0	1	1%
COME	0	0	0	0	NA	0	0	0%
COMU	0	0	0	0	2	490,503	2	3%
CRAU	6	836,965	1	406,391	8	3,533,043	15	43%
FTSP	5	672,624	0	0	8	2,472,270	13	41%
GLGU	6	203,567	2	110,748	0	0	8	36%
GWGU	12	231,229	19	378,840	9	75,272	36	66%
HADU	2	38,081	3	60,399	NA	0	3	29%
HEGU	1	3,746	0	0	NA	0	1	1%
HOGR	NA	0	1	5,600	NA	0	1	1%
HOPU	8	302,917	0	0	11	784,048	19	98%
KIEI	2	109,282	1	4,905	NA	0	3	24%
KIMU	7	11,986	1	632	NA	0	7	50%
LAAL	1	13,895	0	0	NA	0	1	2%
LEAU	2	1,492,276	NA	0	9	9,886,315	11	41%
LESP	0	0	NA	0	6	2,774,904	6	35%
LTDU	5	610,278	0	0	NA	0	5	61%
LTJA	0	0	NA	0	NA	0	0	0%
MAMU	6	125,843	1	13,851	NA	0	6	20%
MEGU	1	6,497	1	7,130	1	11,875	2	4%
MOPE	0	0	NA	0	NA	0	0	0%
NOFU	6	1,961,907	2	759,847	2	731,550	8	10%
PAAU	8	136,897	0	0	9	425,400	17	53%
PAJA	0	0	NA	0	NA	0	0	0%
PALO	0	0	NA	0	NA	0	0	0%
PECO	7	18,080	4	16,772	12	29,817	20	30%
PIGU	4	38,662	1	5,407	0	0	4	8%
POJA	7	13,376	NA	0	NA	0	7	18%
RBME	0	0	1	5,213	NA	0	1	2%
REPH	4	179,170	NA	0	NA	0	4	14%

Species Code[1]	Pelagic Breeding-season IBAs[2]	Pelagic Est. Breeding Abundance in IBA(s)	Pelagic Non-breeding-season IBAs	Pelagic Est. Non-breeding Abundance in IBA(s)	Num. Meta-colony IBAs	Meta-colony Abundance in IBA(s)[3]	Total IBAs	Total A4 Pop.[3 4]
RFCO	2	83,512	0	0	15	45,467	17	111%
RHAU	1	151,947	NA	0	1	108,030	2	19%
RLKI	2	58,190	1	13,287	2	206,610	4	79%
RNGR	0	0	2	4,338	NA	0	2	10%
RNPH	0	0	NA	0	NA	0	0	0%
RTLO	2	1,291	NA	0	NA	0	2	3%
SAGU	2	26,762	NA	0	NA	0	2	5%
SOSH	3	1,754,624	NA	0	NA	0	3	9%
SPEI	1	11,405	NA	0	NA	0	1	6%
STEI	NA	0	0	0	NA	0	0	0%
STSH	2	5,859,330	NA	0	NA	0	2	20%
SUSC	1	19,724	2	27,963	NA	0	2	4%
TBMU	0	0	0	0	2	1,407,375	2	6%
TUPU	7	675,688	0	0	17	1,781,794	24	74%
WHAU	9	313,725	1	12,079	1	3,000	10	314%[5]
WWSC	2	23,927	5	77,969	NA	0	6	16%

[1] See Table 2-1 for species codes and thresholds.

[2] NA = not assessed.

[3] Note that meta-colony populations include birds at Big Diomede Island in Russia, which is part of the Diomede Islands Colonies IBA.

[4] Represents percent of the North American waterbird population or global seabird population for each species.

[5] Our results suggest that the WHAU global estimate may be low. This is corroborated by colony count data from the US and Russia estimating 220% of the current global estimate (World Seabird Union 2011).

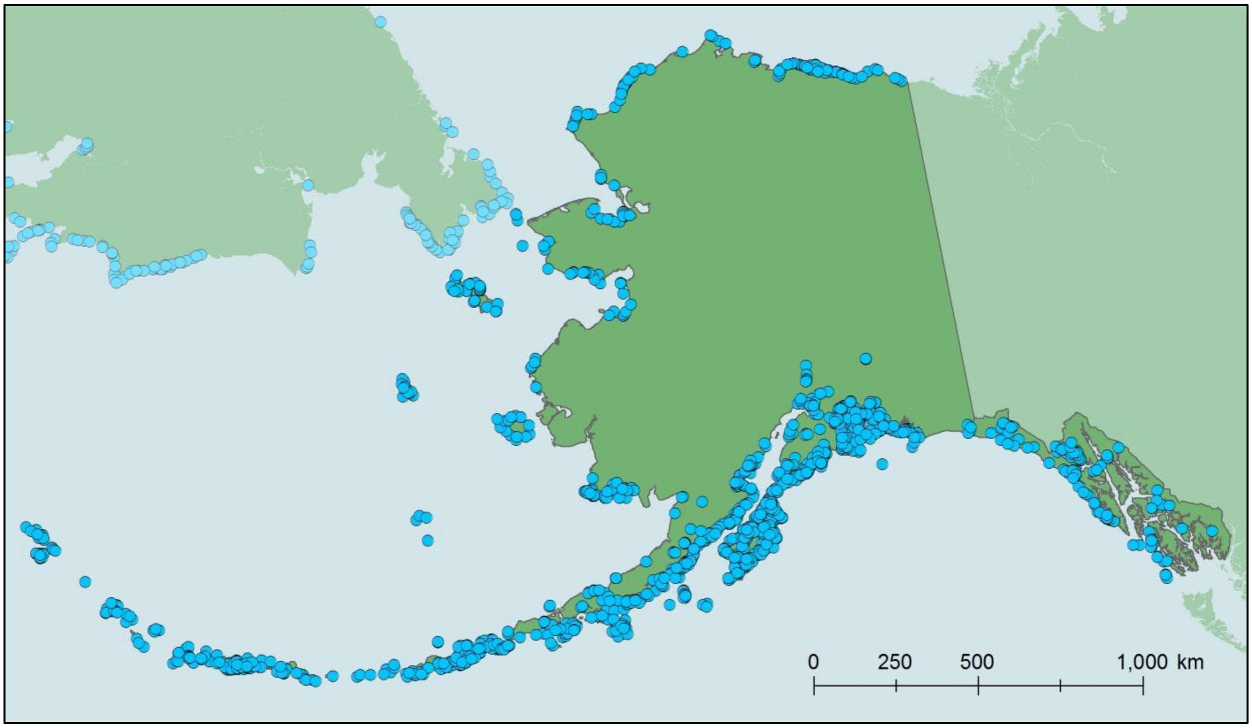

Figure 2-1. The spatial distribution of seabird colonies used for global Important Bird Area (IBA) analysis (Alaska count = 1,640 colonies). Based on the Seabird Information Network (World Seabird Union 2011).

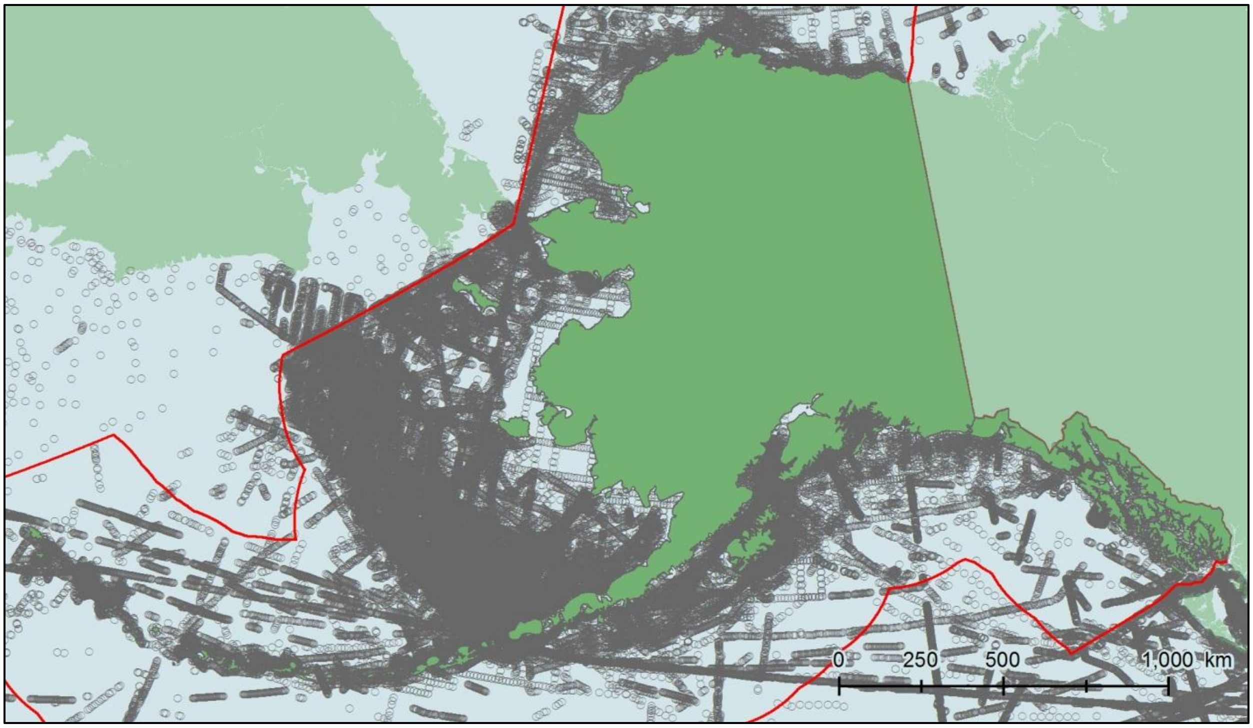

Figure 2-2. The distribution of transect starting points in the Alaska Exclusive Economic Zone (EEZ) with sample areas >0.2 km² (n = 125,683 within the EEZ). Based on the North Pacific Pelagic Seabird Database, version 2 (Drew and Piatt 2011).

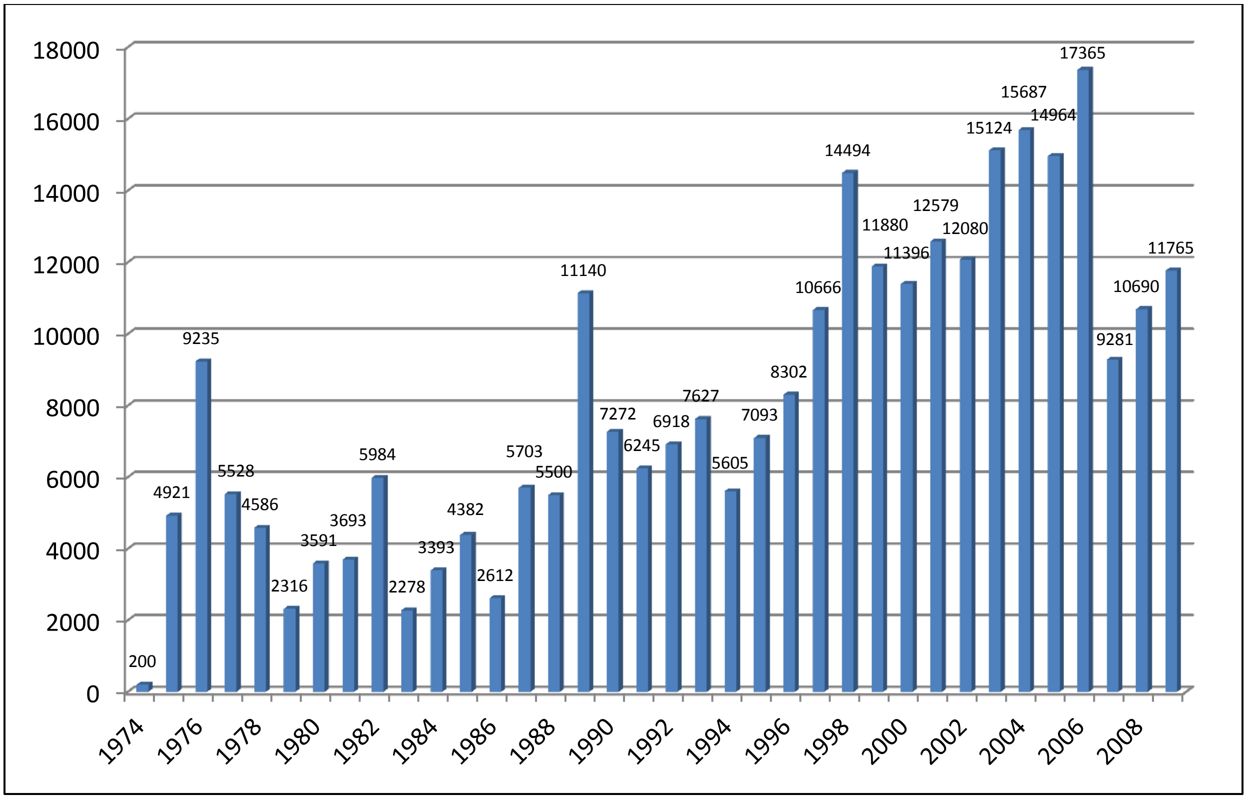

Figure 2-3. Number of survey transects, by year, used in the analysis of pelagic Important Bird Areas. Based on the North Pacific Pelagic Seabird Database, version 2 (Drew and Piatt 2011).

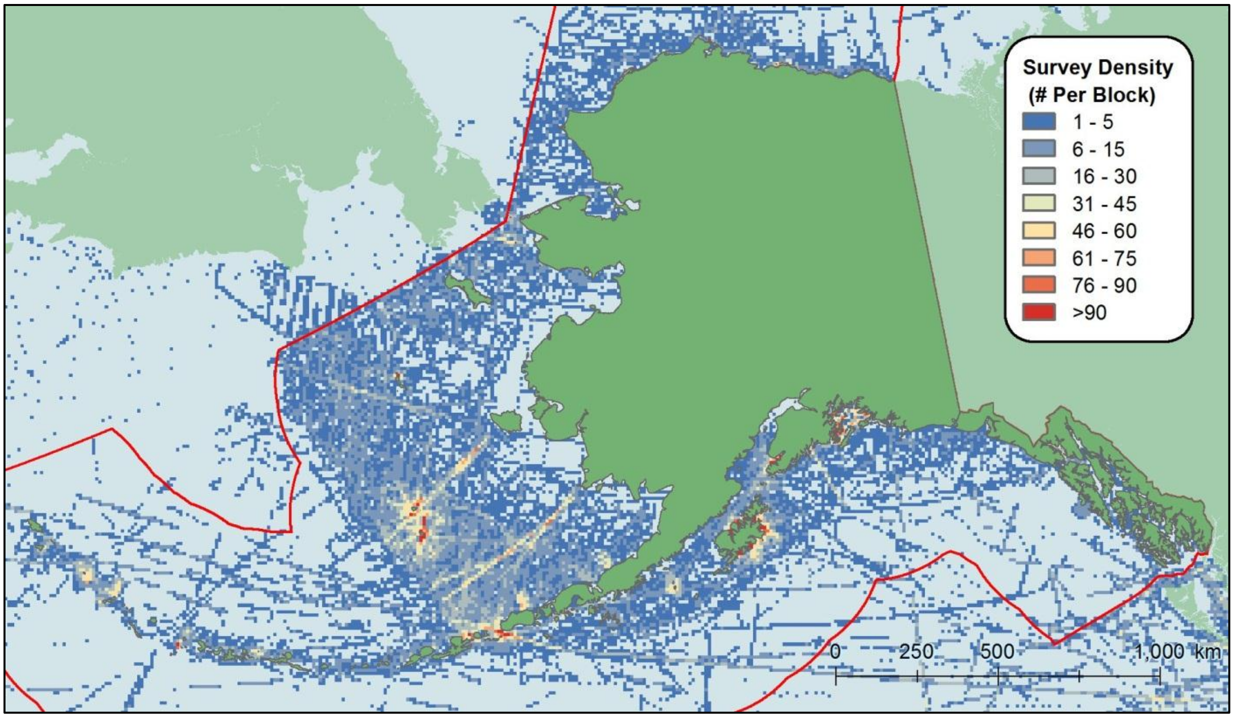

Figure 2-4. Survey effort, measured by the count of survey transects start locations within 10 × 10 km blocks. Based on the North Pacific Pelagic Seabird Database, version 2 (Drew and Piatt 2011).

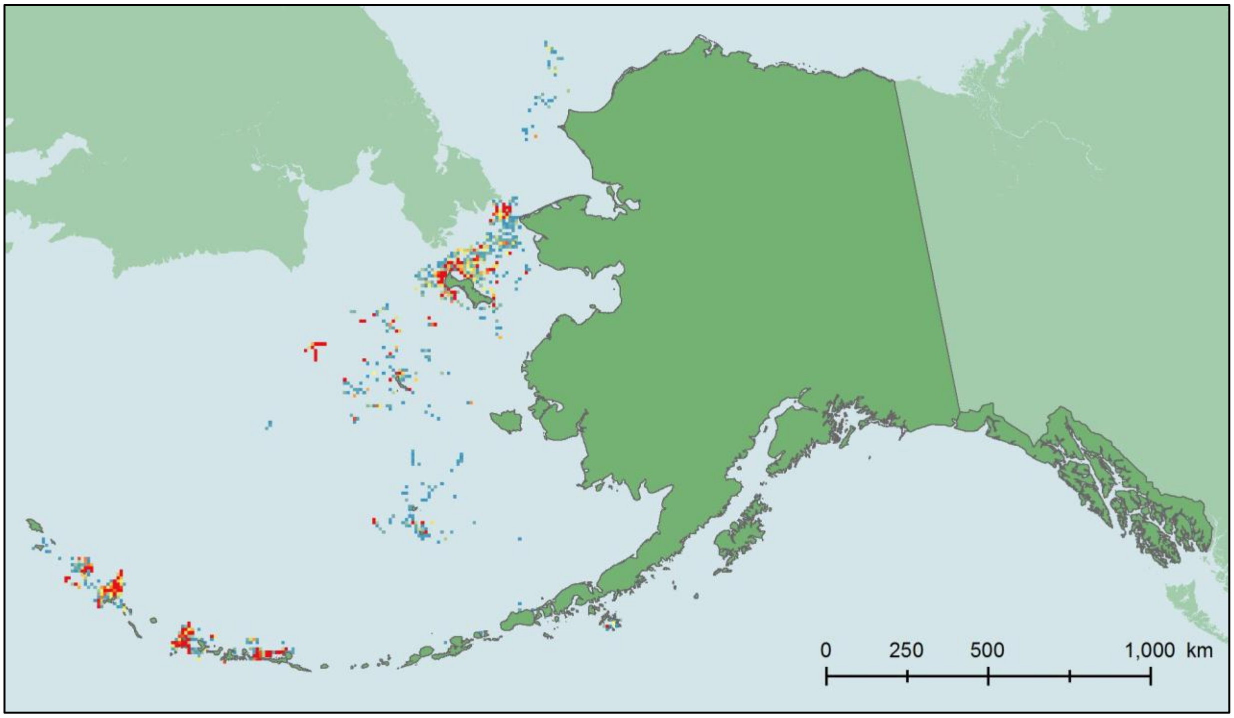

Figure 2-5a. Abundance data for Crested Auklet, summarized in 10 × 10 km blocks, used as input for a moving window analysis to create an abundance gradient map.

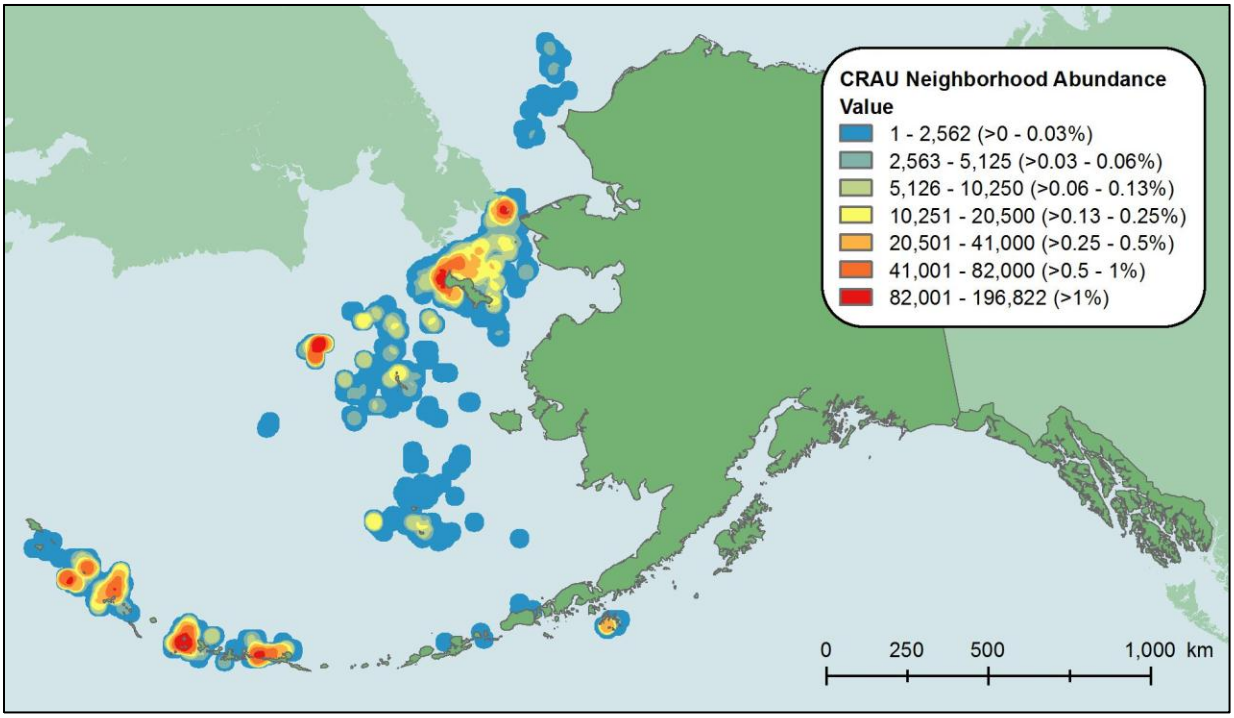

Figure 2-5b. Results of a moving window analysis for Crested Auklets indicating the total abundance within the specified neighborhood (i.e. number of birds within a 25-km radius of each cell), compared to the 1% global abundance threshold of 82,000 birds.

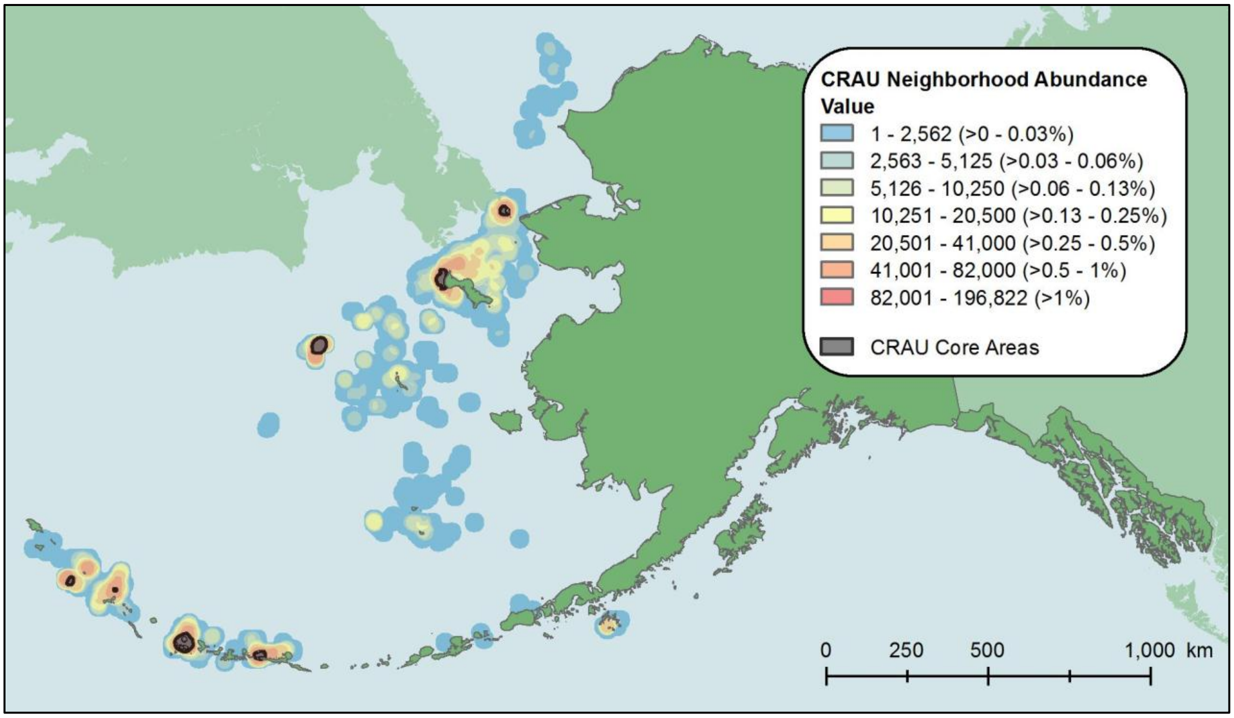

Figure 2-5c. Core area boundaries drawn around major concentrations of Crested Auklets. Major concentrations were defined as cells with more than 1% of the global population within a 25-km radius, based on a moving window analysis.

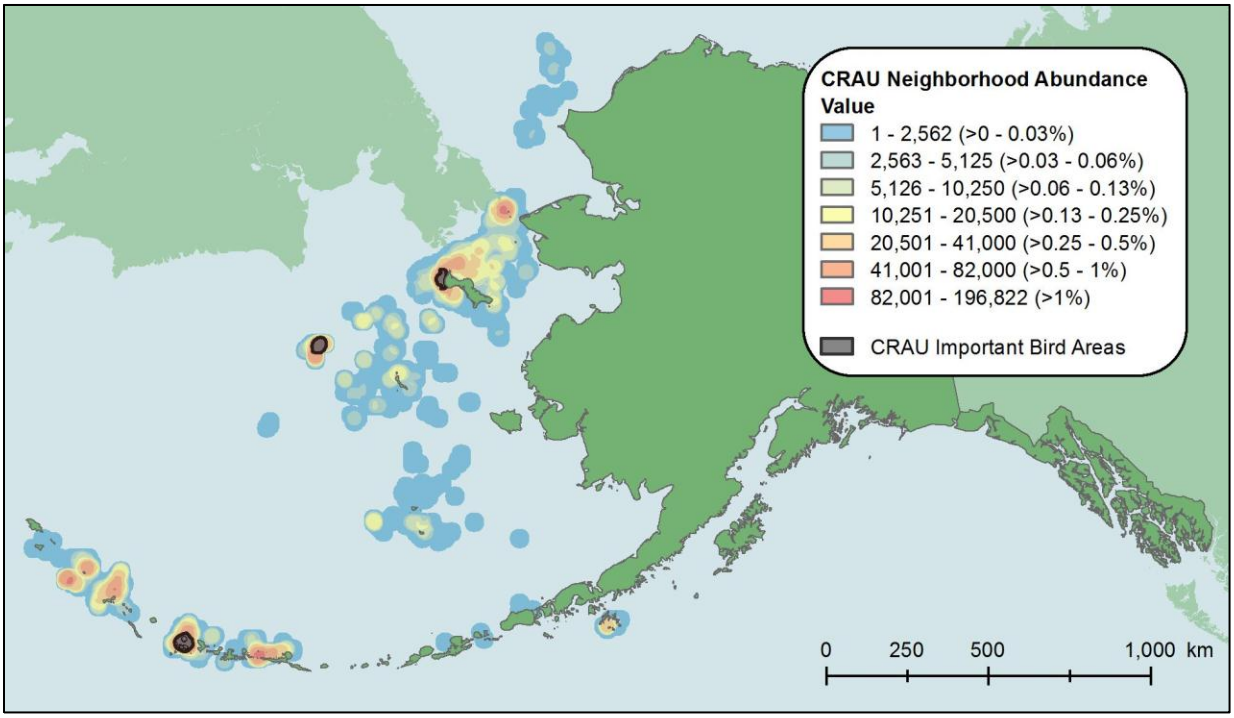

Figure 2-5d. Final IBA boundaries for Crested Auklets. IBAs are a subset of core areas which met validation criteria for adequate abundance, sufficient survey effort, and good persistence.

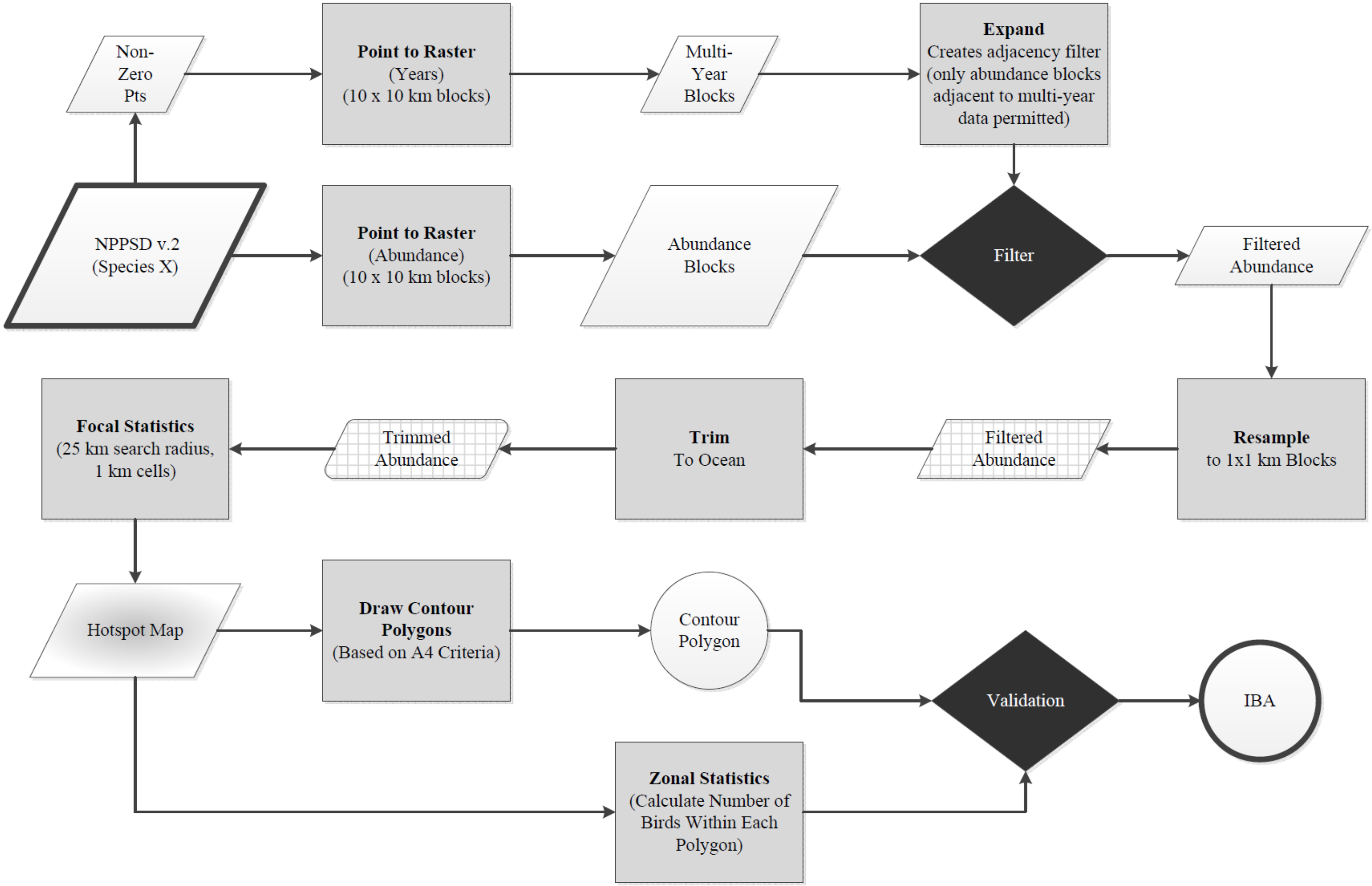

Figure 2-6. Conceptual diagram of processing steps for identifying pelagic Important Bird Areas using GIS analysis.

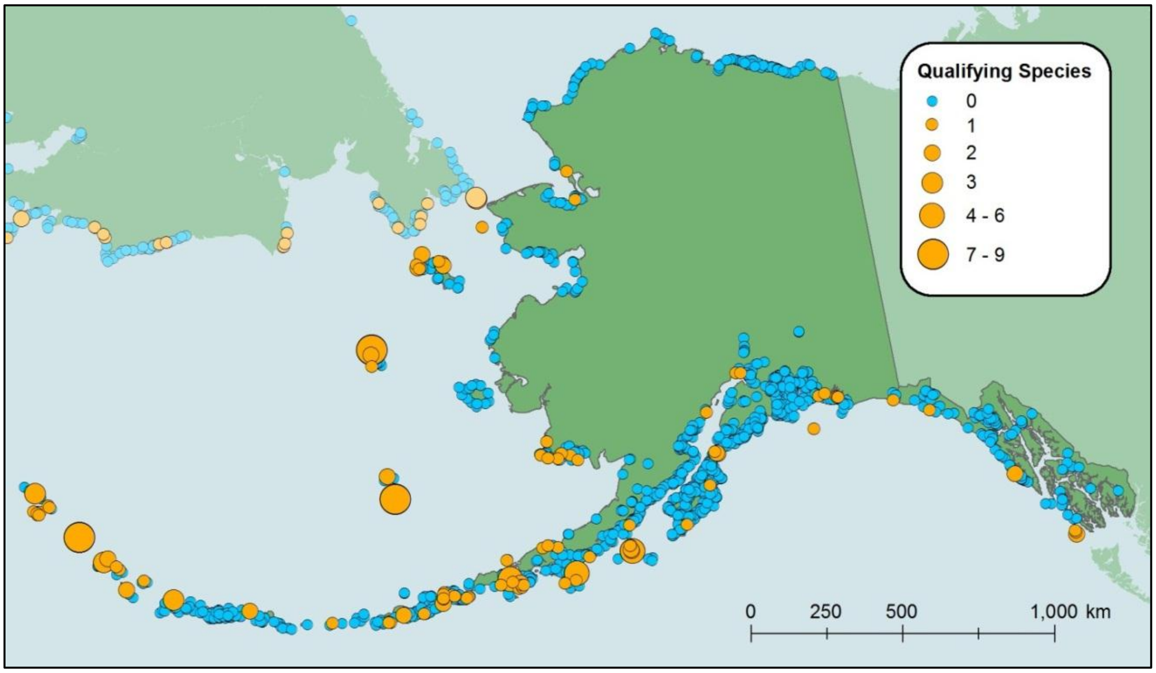

Figure 3-1. Potential seabird colony Important Bird Areas (IBAs), shown in orange, support more than 1% of the global seabird or North American waterbird population for one or more species; non-qualifying colonies are shown in blue (21 qualifying species; 102 qualifying colonies; 161 qualifying populations). Based on the Seabird Information Network (World Seabird Union 2011).

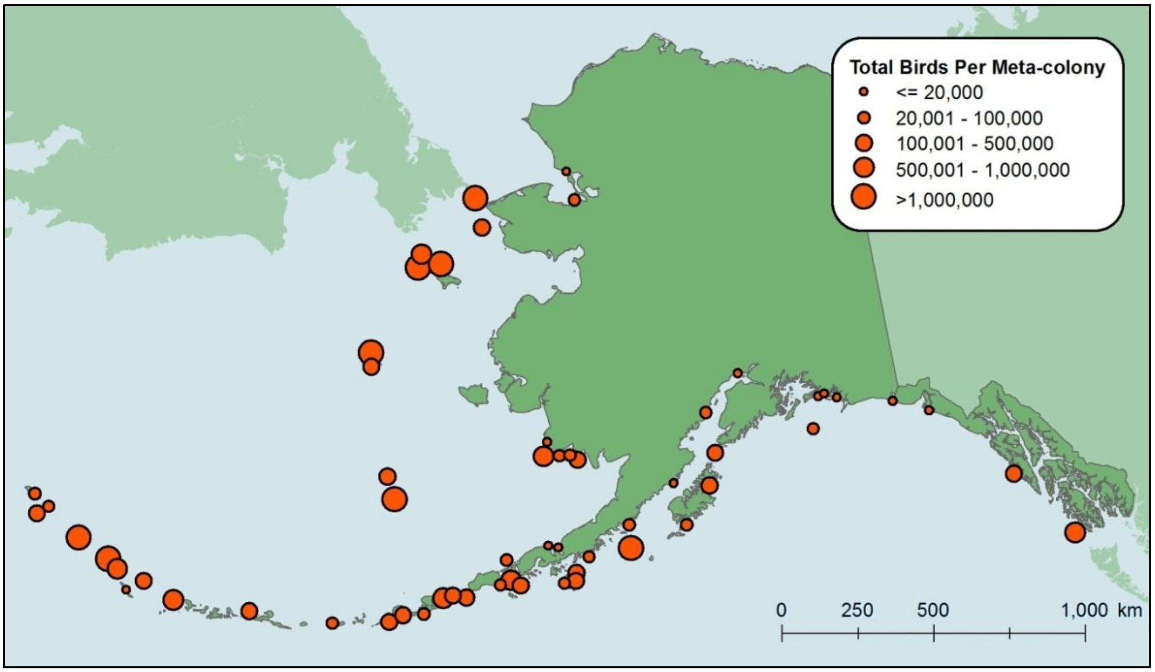

Figure 3-2. Total abundance of all seabirds at meta-colony Important Bird Areas (IBAs) (22 qualifying species; 59 qualifying meta-colonies; 147 qualifying populations). Based on the Seabird Information Network (World Seabird Union 2011).

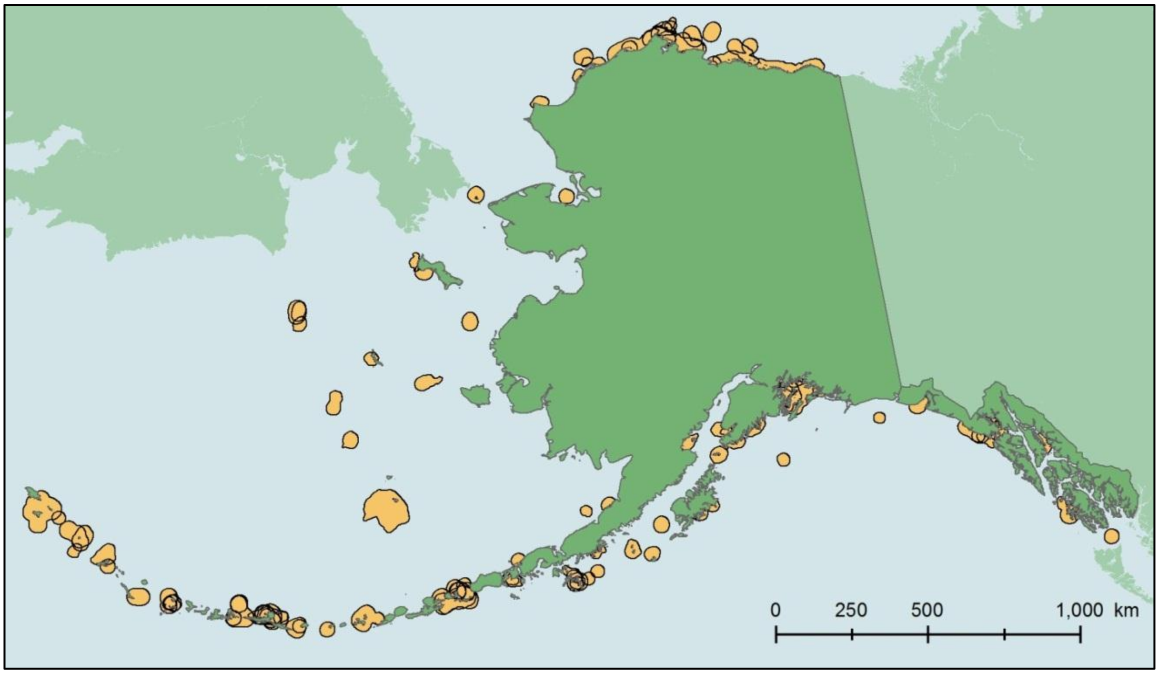

Figure 3-3. Validated single-species, breeding-season pelagic Important Bird Areas (IBAs) (May through September; n = 100; total area = 201,507 km²).

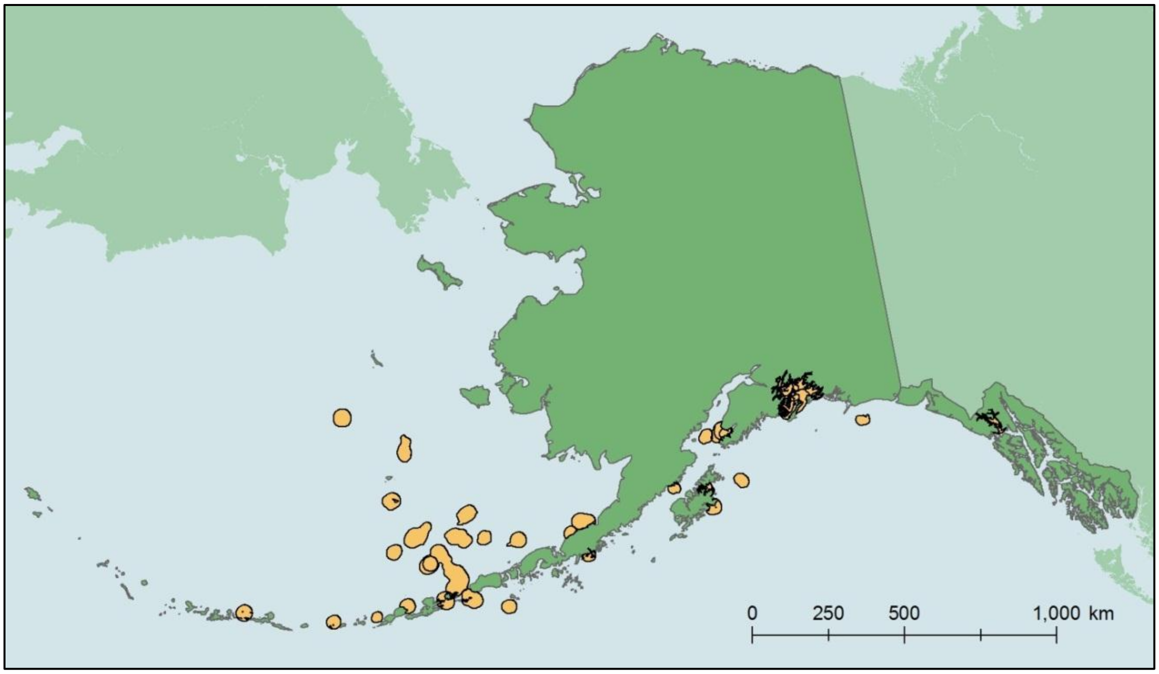

Figure 3-4. Validated single-species, non-breeding-season pelagic Important Bird Areas (IBAs) (October through April; n = 34; total area = 76,088 km²).

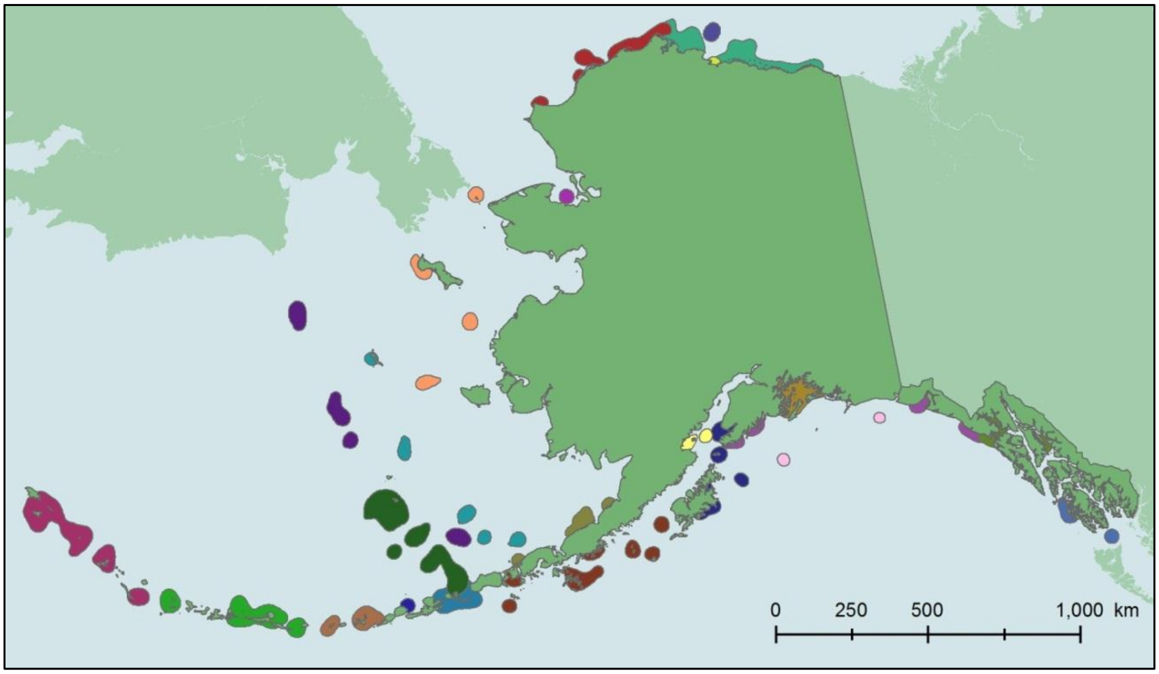

Figure 3-5. Validated multi-species pelagic Important Bird Areas (IBAs) colored by majority marine ecoregion (Piatt and Springer 2007; Spalding et al. 2007). IBAs were identified for 45 of the total 57 pelagic seabird species assessed (IBAs = 64; enclosed A4 population = 18.4 million birds; total area = 239,700 km²).

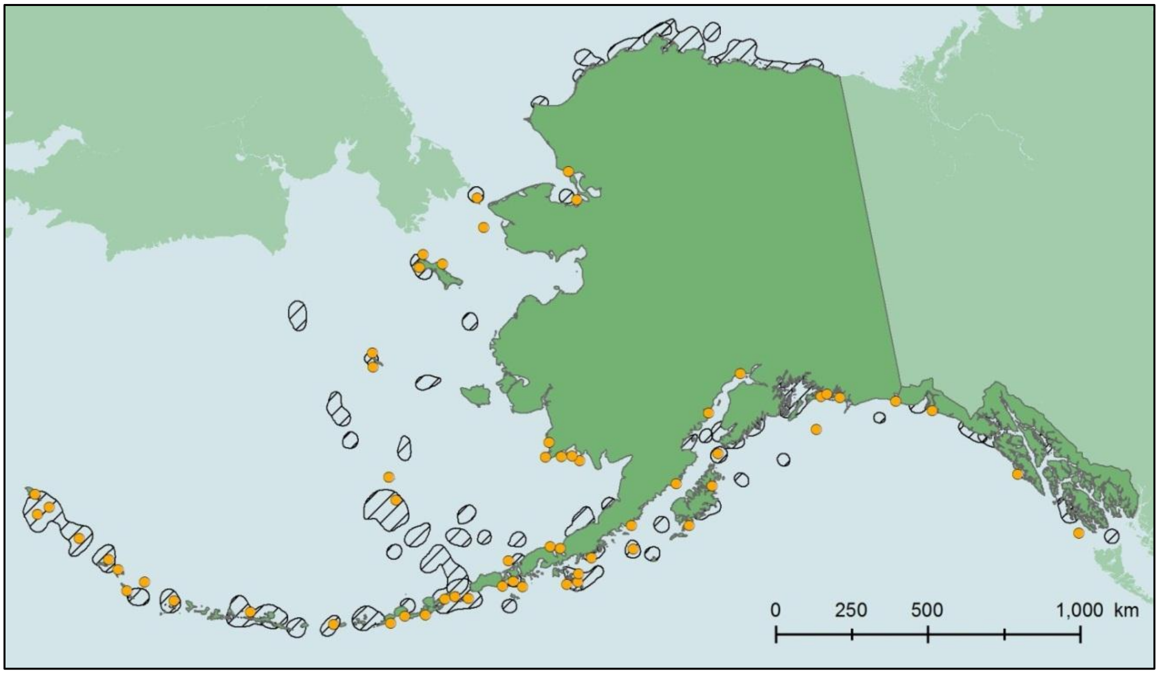

Figure 4-1. Alaska's new globally significant meta-colony and pelagic areas for 49 of 58 species assessed in 123 IBAs.

Appendix A

Other Approaches Not Used in Our Final Analysis

This supplementary section describes some of the other analytical approaches we tried while developing our methods for global IBA identification. This is not a full documentation of alternatives we explored. We have included this information to relay the more noteworthy approaches, and the insights and obstacles encountered along the way. This also serves as supporting information for why we ultimately chose the methods described in the report.

A-1 Clustering Meta-colony IBAs

We tried the following approaches for grouping meta-colonies that were not used in our final analysis: (1) joining colonies which occur on the same island; (2) grouping and summing colony points within a specified distance (e.g. 1, 5, and 10 km); (3) buffering colonies by a distance proportional to the species abundance at each point; and (4) using kernel density analysis to spatially summarize and select core areas. Each approach is described below.

(1) Joining colonies on the same island worked well for small and/or isolated islands, but also required making decisions about the maximum-sized island that would operate as a meta-colony. For example, combining all colonies on the 2.3 million acre Kodiak Island would have produced unsatisfactory results. Finding no recommendations in the published literature for such an approach, we opted not to make a subjective decision about grouping colonies this way.

(2) Grouping and summing colony points within a specified distance was too simplistic an approach in areas where numerous, small nearby colonies with insignificant, low counts would create a chain many kilometers long. The resulting IBAs might qualify as significant due to covering a vast area and summing together many colonies, rather than focusing in on an area of a couple of very large nearby colonies.

(3) Building on the previous approach, we tested scenarios where larger colonies (measured by species abundance) would have a proportionally larger buffer than smaller colonies. The results of this exercise were more similar to the type of output we wanted to achieve but still required making subjective decisions about buffer distances that were not documented in the literature.

(4) Next, we used a kernel density estimator in ArcGIS with a 10 km search radius to smooth the colony point data and to identify core areas. The Kernel Density tool searches some specified distance from each point, and sums the total abundance of a species occurring within that search area, giving more weight to the count at the center. The kernel function provided by the software is based on the quadratic kernel function (Silverman 1986). The tool returned density values as birds per square kilometer. We then converted our 1% abundance threshold to a 1% density threshold by simply dividing 1% of the global species population by the search area used in the density analysis:

1% Species Density Threshold = 1% Global Species Population / Search Area

Search Area = 314.16 km^2 (10 km radius circle)

We drew contours around all areas meeting or exceeding the 1% density threshold, by species, and grouped all colony points within those contours into a single meta-colony IBA. We felt that this method did achieve the right results, but was cumbersome to explain. We abandoned this approach in favor of a very similar, yet simpler, moving window summarization process.

A-2 IBAs Using Foraging Distance Buffers

Our first method for estimating important pelagic areas used foraging distance data to map a buffer around globally significant colonies. This method is described below, but was ultimately replaced by an analysis of at-sea survey data to identify core area boundaries independent of, but often in proximity to, globally significant colonies.

Initially we used the foraging distance database provided by BirdLife International (Lascelles 2008) to delineate pelagic areas of global significance by extending globally important colonies to include the foraging areas of the birds within those colonies. A series of species-specific foraging radii were calculated for each species in the database by interpreting textual database entries into average and maximum foraging distance values (Table A-1).

The foraging distance database, based on a comprehensive review and collation of the published information on seabird foraging ranges, provides as much of the following information as possible: date and location of the study, stage of the breeding season, foraging distance, trip duration, dive depth, habitat associations, data quality, and survey methods. The purpose of the database is to provide an authoritative global dataset to be used in the delineation of marine IBAs and the identification of areas requiring future research.

This method required the calculation of a foraging distance for each species in the database. The database generally reports the foraging distance of each species as a mixed list of maximums, averages, and ranges, which means the foraging distance utilized in IBA delineation can be estimated as an average of the average values, an average of the maximum values, or a maximum of the maximum values. We were obligated to make some difficult, if not arbitrary, decisions. For example, does a range, such as “30–50km”, imply an average of 40km and a maximum of 50 km? Does “75% within 15 km” represent an average, a maximum, or something else? After inferring the meaning of the foraging distance for each entry in the database, the average of averages, the average of maximums, and the maximum of maximums were calculated for each species with foraging data available.

We analyzed foraging distance data from 23 Alaskan seabird species for which data were available (Table A-2). There were insufficient data to calculate the average foraging distance for Ivory Gulls, Long-tailed Ducks, and Red-throated Loons, the average maximum foraging distance for King Eiders, Parakeet Auklets, and Pelagic Cormorants, or the maximum foraging distance for Parakeet Auklets and Pelagic Cormorants. Many of these foraging distance metrics were calculated using only a single database entry, and oftentimes this entry would be from a study conducted outside Alaska. Common Murre foraging distance metrics were calculated using the largest sample sizes: 38 database entries for the average foraging distance and 30 database entries for maximum foraging distances. The Short-tailed Shearwater exhibited the largest foraging range with average, average maximum, and maximum foraging distances of 968, 2,134, and 3,468 km respectively. The Steller's Eider, on the other hand, exhibited the smallest foraging range with a maximum foraging distance of 0.2 km.

The resulting values were a blend of foraging distances from studies around the globe. Another caution with using non-local estimates is that often the foraging distance is reflective of the distance to nearby oceanographic hotspots, and does not necessarily reflect the true mean trip distance for each species independent of local conditions. The results of using average foraging distances to buffer globally significant colonies, based on the BirdLife International database, is presented in Figure A-2. These results were not used to nominate IBAs.

As an alternative, we computed values specific to Alaskan marine waters by conducting a nearest neighbor analysis using colony locations and at-sea survey data. We used observations from the North Pacific Pelagic Seabird Database version 1 (NPPSD v1) (Drew and Piatt 2005) to calculate the distance from birds on the water to the nearest conspecific colony for each species in the colony database. An average foraging distance was calculated by weighting the calculated distances by the abundance of each species at every observation. We then repeated foraging distance buffer mapping using these derived values.

A total of 5,185 NPPSD v1 survey points were used in the calculation of the average Horned Puffin foraging distance using the nearest colony analysis (Figure A-1). In comparison, seven database entries were used in the calculation of the average Horned Puffin foraging distance using the BirdLife International database. NPPSD v1 Horned Puffin observations were, on average, 31.90 +/- 0.55 km, from the nearest conspecific colonies, with a minimum separation of 0.22 km, and a maximum separation of 402.7 km. About 65% of Horned Puffins were observed within the average foraging distance, 31.9 km, from the nearest Horned Puffin colony. This result is compared with an average foraging distance of 75.9 +/- 21.2 based on the BirdLife International database. The advantage of this approach is the vastly larger sample size using local data, but the disadvantage is the assumption that birds are returning to the nearest colony, which could only be sorted out through tagging or tracking information such as presented in the BirdLife International database.

Had we chosen to proceed with the foraging buffer method, the nearest colony distance approach would have been preferred; we did not analyze nearest colony distances for additional species. Ultimately, we disconnected the identification of important colonies from important at-sea areas, using independent databases and methods to locate colony and pelagic IBAs.

A-3 Pelagic Density Gradient Maps

We tried multiple approaches for creating density gradient maps from the filtered pelagic data before settling on a moving window analysis. Two alternate approaches—interpolation and kernel density—are described below.

(1) We first explored the use of interpolation for drawing density gradient maps, using inverse distance weighted, natural neighbor, and kriging techniques. Due to the irregular survey effort within the NPPSD, accuracy of the results was highly variable, and produced questionable, jagged output maps, especially in areas with little survey effort or detection. We chose not to further explore and refine these techniques due to the requirement that IBAs be based on summarizing observed data rather than modeled data (i.e. using techniques to fill in knowledge gaps).

(2) Next we used a kernel density estimator in ArcGIS to calculate a density distribution from the filtered NPPSD points for each species, with a search radius (i.e. bandwidth) of 25 km. Density distribution calculations are sensitive to the user-defined search radius because this parameter determines the degree to which the population of a specific point is smoothed over neighboring cells. This smoothing step is converting an abundance measured at a point location to an equivalent density spread across the area of the search radius. We experimented with several search radii: 10, 25, 35, 50, 75, and 100 km, as well as variable search radii by species, which were equal to the foraging distance buffer. We chose a 25 km search radius because it provided a balance between not overfitting boundaries to the spatial locations, and not losing important local-scale information. A smaller search radius produced density gradient maps that were more reflective of survey tracks, while a larger radius produced areas that were expansive and generalized when compared to our idea of how compact an IBA should be. Because values were expressed in densities, we had to convert A4 abundance thresholds to density thresholds, which are dependent on the search radius chosen. Like the meta-colony analysis, explaining and drawing boundaries based on this method was complicated. We eventually dismissed this approach in favor of a very similar, yet simpler, moving window summarization process.

A-4 Variable Thresholds for Drawing IBA Boundaries

Before deciding to use a moving window analysis, we designed a method for drawing core area boundaries from kernel density gradient maps which used a variable threshold for drawing boundaries. The kernel density tool returned values in birds per square kilometer. Like the meta-colony analysis (described in A-1 #4 above), we converted our 1% abundance threshold to a 1% density threshold by simply dividing 1% of the global species population by the search area used in the density analysis:

$$\text{1\% Species Density Threshold} = \text{1\% Global Species Population} \,/\, \text{Search Area} \qquad (1)$$

$$\text{Search Area} = 1{,}963.50\ \text{km}^2\ \text{(25 km radius circle)} \qquad (2)$$

Initially we applied the 1% density threshold for all species. We used the GIS to draw contours around all areas that met or exceeded the threshold and converted the contour lines to potential IBA polygons. We then summed the cells within each polygon to test whether the enclosed population met the 1% abundance criteria.

The results from this exercise were satisfactory for many species but not for all. Clustered species with a large population percentage were producing IBAs that we felt were unnecessarily large. Dispersed species with a lower population percentage were not producing IBAs. The method worked well for the "mid-range" species. We manually explored different threshold standards: raising the bar to 2% density (a 2:1 ratio) for some clustered species, and lowering the bar to 0.5% density (a 1:2 ratio) for some dispersed species.

To obtain the threshold standards objectively we analyzed metrics describing species abundance, density, dispersal, and spatial variability. Ultimately two simple factors effectively described species distribution: (1) percent of range occupied and (2) percent of global/North American A4 population represented. Range size was measured by counting the number of 1 km^2 cells in which the species was present, then dividing by the area of the Alaska EEZ. Percent of global population was measured by summing each species map within the EEZ, and dividing the total by the A4 population estimate. If the population sum exceeded the global population estimate it was capped at 100%.

We plotted these two factors, percent population on the x-axis and percent range on the y-axis and then used a simple calculation to bin the data into threshold categories. We subtracted the percent population value from the percent range value and ranked those numbers. With the aid of a k-means classifier we identified breakpoints in the data (-30, 30, and 60) and assigned thresholds (Figure A-3). For most cases, we used 1% as the threshold. For dispersed species we used 0.5%, for moderately aggregated species we used 2%, and for the most highly aggregated species we used a 4% threshold. We then drew density contours, summed abundances, and removed invalid IBAs as previously described.

This approach worked well, but was difficult to communicate, and harder to calculate. Additionally, as we thought more about this, we decided that highly dispersed species (which would be assigned the 0.5% threshold) are probably more resilient to threats, and that it may not be necessary to lower the bar to identify IBAs. Conversely, the more concentrated species (which would be assigned the 2 or 4% threshold) are potentially more sensitive to threats, and it may be wise to allow more expansive IBAs rather than constraining the boundary. Ultimately we abandoned the variable threshold approach for boundary drawing after deciding to create abundance gradient maps using the moving window approach.

Table A-1. Example entries from the BirdLife Seabird Foraging Database (Lascelles 2008) for Thick-billed Murre and summarization of textual descriptions into empirical values for foraging distance calculations.

Country	Site Name	Foraging Radius	Avg. (km)	Avg. Max. (km)	Max. (km)
Iceland	Latrabjarg	max 168 km	–	168	168
Greenland	Hakluyt Island	max 50 km, avg 20–25 km	22.5	50	50
Greenland	Hakluyt Island	within 50 km	–	50	50
Norway	Western Spitsbergen	approx. 85 km	85	–	–
–	–	30–50 km, max 100 km	40	100	100
US	Alaska	8–104 km	56	104	104
US	Pribilof Islands, Alaska	up to 110 km	–	110	110
Canada	Prince Leopold Island	avg. 80 km, max 150–175 km	80	162.5	175
Canada	Coats Island	100 km	100	–	–
Atlantic	–	normal 2–25 km, max 75 km	13.5	75	75

Table A-2. The average, average maximum, and maximum foraging distance for all Alaskan seabirds with foraging data available in the BirdLife International Seabird Foraging Database (Lascelles 2008).

Species Code[1]	Average +/- se[2] (km)	Sample Size	Avg. Max. +/- se[1] (km)	Maximum (km)	Sample Size
ARTE	9.9 +/- 2.3	7	18.8 +/- 2.6	50	8
BLGU	5.8 +/- 2.5	18	9.7 +/- 3	55	17
BLKI	28.5 +/- 5.5	17	70.9 +/- 11.3	200	16
COEI	18.0 +/- 0.0	1	20.0 +/- 0.0	20	1
COMU	33.0 +/- 5.1	38	67.6 +/- 11.1	200	30
CRAU	56.4 +/- 16.1	6	94.0 +/- 18.1	150	5
HOPU	75.9 +/- 21.2	7	94.3 +/- 25.8	180	6
IVGU	–	0	72.0 +/- 0.0	72	1
KIEI	614.0 +/- 0.0	1	–	1499	0
KIMU	7.0 +/- 6.7	4	61.0 +/- 33.8	120	3
LEAU	44.8 +/- 9.7	9	70.7 +/- 13.7	150	7
LTDU	–	0	30.0 +/- 0.0	30	1
NOFU	186.8 +/- 78.2	16	273.1 +/- 70.9	1000	8
PAAU	26.8 +/- 23.3	2	–	–	0
PECO	10.0 +/- 0.0	2	–	–	0
RNPH	35.0 +/- 0.0	1	102.5 +/- 52.5	195	2
RTLO	–	0	2.8 +/- 2.3	5	3
SAGU	101.6 +/- 27.2	5	96.4 +/- 24.9	200	5
SPEI	102.5 +/- 0.0	1	145.0 +/- 0.0	145	1
STSH	968.8 +/- 311.8	4	2,134.0 +/- 1,334.0	3468	2
STEI	0.2 +/- 0.0	1	0.2 +/- 0.0	0.2	2
TBMU	58.3 +/- 10.6	15	106.4 +/- 13.0	200	20
TUPU	47.5 +/- 25.9	4	100.0 +/- 50.0	150	2

[1]See Table 2-1 for species codes.

[2]se = standard error.

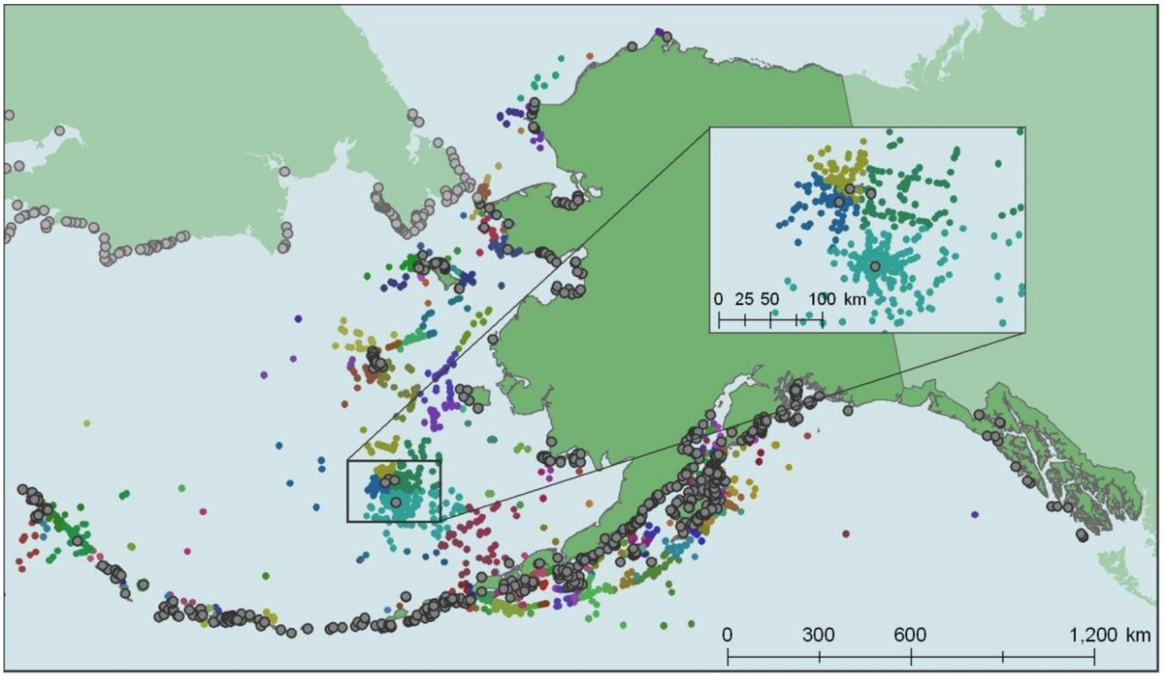

Figure A-1. An illustration of the nearest colony analysis performed on breeding-season Horned Puffin observations to calculate an Alaska-specific average foraging radius. Observations of the same color share a nearest colony (n = 5,185 survey points; average = 31.90 $^{+}$/- 0.55 km; range = 0.22 – 402.70 km). Based on the North Pacific Pelagic Seabird Database, version 1 (Drew and Piatt 2005).

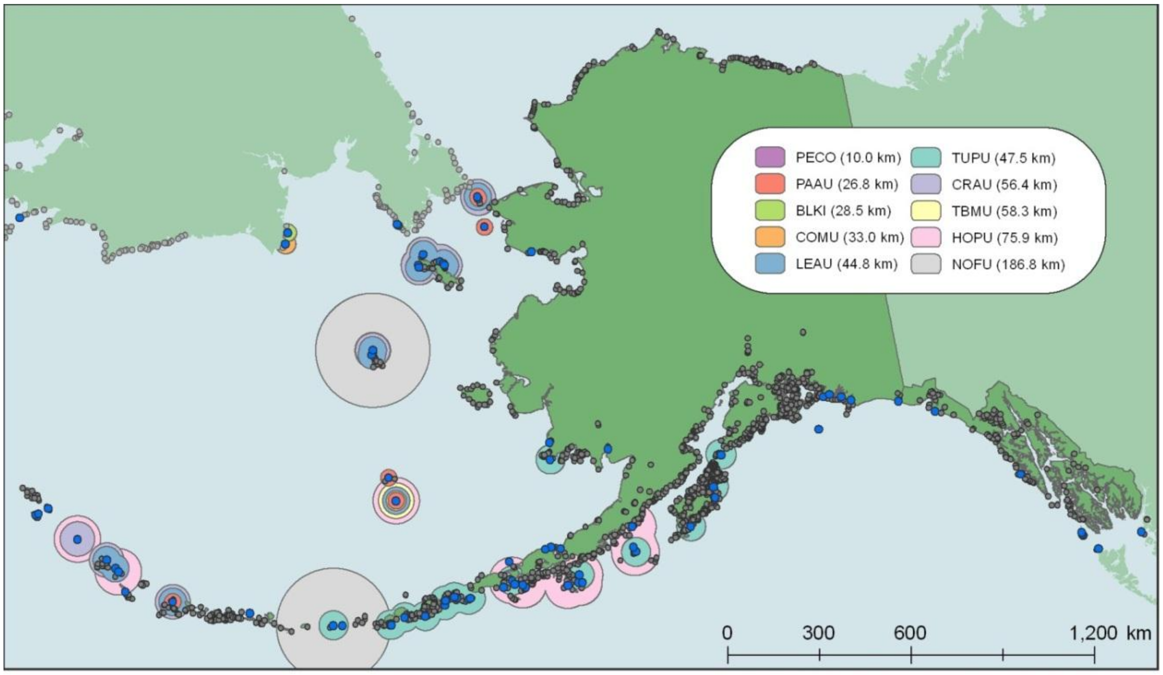

Figure A-2. The delineation of colony buffers for Alaska seabird species (average foraging distance listed in the map legend) (41 core areas; 284,700.46 km^2). Based on the BirdLife International Foraging Seabird Database (Lascelles 2008).

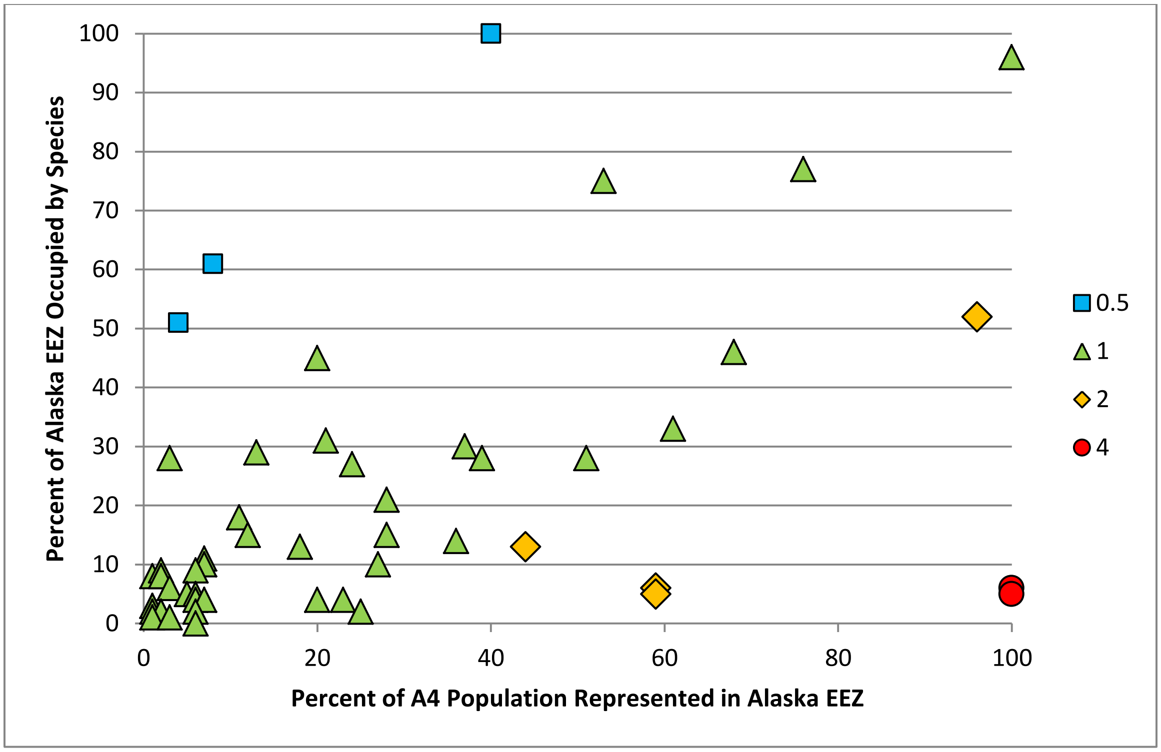

Figure A-3. Scatterplot of percent of A4 population represented and percent of range occupied within the Alaska Exclusive Economic Zone for assessed species during the breeding season. Colors represent different density thresholds (0.5%, 1%, 2%, and 4%) for drawing IBA boundaries from kernel density maps.