



Defining marine important bird areas: Testing the foraging radius approach



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ABSTRACT

Recent international initiatives have promoted a number of different approaches to identify marine Important Bird and biodiversity Areas (IBAs), which are important areas for foraging, migrating or over-wintering seabirds. The 'Foraging Radius Approach' is one of these and uses known foraging range and habitat preferences to predict the size and location of foraging areas around breeding colonies. Here we assess the performance of the Foraging Radius Approach using GPS tracking data from six seabird species with a variety of foraging modes. For each species we compared the population home-range areas of our six study species with the home-range areas defined using the Foraging Radius Approach. We also assessed whether basic information on depth preferences from tracking data could improve these home-range area estimates. Foraging Radius Approach home-range areas based on maximum foraging radii encompassed the entire population home-range of five out of six of our study species but overestimated the size of the population home-range area in every case. The mean maximum foraging radius overestimated the population home-range areas by a factor of 4–14 for five of the six species whilst the mean foraging radius overestimated the population home-range area for half of the species and underestimated for the rest. In the absence of other data, the Foraging Radius Approach appears to provide a reasonable basis for preliminary marine IBA identification. We suggest that using the mean value of all previously reported maximum foraging radii, informed by basic depth preferences provides the most appropriate prediction, balancing the needs of seabirds with efficient use of marine space.

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1. Introduction

In an effort to identify sites of most value to protect and conserve avian populations, BirdLife International has defined over 12,000 Important Bird and Biodiversity Areas (IBAs) worldwide (BirdLife International 2014). These are selected based on the following criteria: (i) sites holding globally threatened species on a regular basis; (ii)

sites holding a significant component of a group of species whose breeding distributions define an Endemic Bird Area; (iii) sites holding a significant component of a group of species whose distributions are largely or wholly confined to one biome; and (iv) important sites for congregatory species, holding more than 1% of a species' global or biogeographic population or exceeding specific thresholds set for waterbirds, seabirds or migratory species. Whilst the designation of an IBA has no legal standing, they have been used to both raise the profile of a site and to provide justification for protected area management by relevant local statutory authorities and NGOs (BirdLife International, 2010, Heath et al., 2000). The identification and subsequent management of marine IBAs has been recognised as a key tool for the conservation of seabirds. Seabirds are declining at a rate faster than any other avian group (Croxall et al., 2012), but do not receive adequate protection from terrestrial IBAs alone.

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BirdLife International's marine Important Bird and Biodiversity Area programme has provided guidance and protocols for identifying priority sites for seabird conservation in a consistent manner, and a number of countries have now compiled marine IBA inventories (BirdLife International, 2010). The recommended methodologies for identifying marine IBAs include: (1) **direct tracking**, for example, the BirdLife International Marine IBA atlas (<http://maps.birdlife.org/marineIBAs/default.html>) which applies a maximum foraging radius (based on the linear distance between the colony and the position located furthest away from the colony) around a globally important breeding colony when tracking data for that colony has been submitted to them. Similarly Lascelles et al. (2016) developed a methodological approach to use seabird tracking data to identify marine Important Bird Areas around globally important breeding colonies; (2) **boat or aerial surveys**; Smith et al. (2014) used at-sea survey data spanning 30 years to identify 59 pelagic sites important to breeding seabird populations in the waters of Alaska; and (3) **the 'Foraging Radius Approach'** whereby one or more foraging radii are drawn around a breeding colony based on (i) the maximum reported distance travelled on a single trip from the same species from a different breeding colony (maximum foraging radius); (ii) a mean of all maximum foraging radii from the same species from several colonies and (iii) a mean of the total distance of all foraging trips reported from other colonies. This method was first advocated by BirdLife International (2010) in their marine Important Bird Areas toolkit and then by Thaxter et al. (2012) who compiled a dataset representing the mean, mean maximum and maximum foraging ranges reported for 25 seabird species that breed in the UK. Data used by Thaxter et al. (2012) was derived from at-sea survey data and tracking datasets (where they existed) and the authors suggest the use of these previously reported foraging radii as a good basis for defining marine Important Bird Areas for seabird breeding colonies where tracking or at-sea survey data does not exist.

To provide even more robust and valuable predictions of important foraging areas the approaches detailed above are often used in combination with modelling frameworks to account for important habitat associations which can generate predictions of likely occurrence and abundance. For example, Opper et al. (2012) used ship-based survey data and 13 environmental variables to predict the distribution of the Balearic Shearwaters *Puffinus mauretanicus* in the Mediterranean. Grecian et al. (2012) state that the most comprehensive approach is to incorporate multiple data sources including foraging radius predictions, tracking data, habitat data, near-colony behaviour and prey data into a single modelling framework. The authors used this integrated approach for the Northern gannet *Morus bassunus* in the UK and predicted higher densities of birds closer to the breeding colonies and in areas of high copepod abundance (used as a likely indicator of prey abundance) (Grecian et al., 2012).

Limitations in capacity, logistics, data and finances mean that it is not always possible to undertake approaches (1) and (2) for all globally important seabird populations or the integrated approach recommended by Grecian et al. (2012). In the absence of such site specific data, the third "Foraging Radius Approach" is recommended as a simple, easier to apply method for defining marine Important Bird Areas with further refinement, if possible, using habitat and oceanographic preferences (BirdLife, 2010; Thaxter et al., 2012). However, when predicting the location of marine IBAs using this Foraging Radius Approach it is important to note the potential limitations. These may include an inability to account for the size of the colony, or the social aspects of seabird foraging behaviour both of which are known to affect foraging range (Gremillet et al., 2004; Wakefield et al., 2013). Furthermore the predicted foraging radii may often be too large to be easily used as a management unit in marine spatial planning and further refinement using oceanographic features such as benthic habitat and prey abundance has its complications, particularly in many parts of the world where this data does not exist or is inaccessible or hard to analyse. In addition

the Foraging Radius Approach may be more suitable/accurate for coastal rather than pelagic foragers (BirdLife, 2010).

Here we investigate the home-range areas of six seabird species representing different families and modes of foraging: (1) the European shag (*Phalacrocorax aristotelis*); (2) black-legged kittiwake (*Rissa tridactyla*); (3) masked booby (*Sula dactylactra*); (4) razorbill (*Alca torda*); (5) little penguin (*Eudyptula minor*), and (6) short-tailed shearwater (*Puffinus tenuirostris*) (Table 1). Our aim was to use these six species as test cases to assess how well the Foraging Radius Approach compares with the predicted foraging distributions derived from tracking data. To do this, sample home-range areas identified from the foraging tracks of our six study species, were combined with colony size to make population-specific predictions of home-range area. We then examined how well these estimates of population home-range area for each species fitted to the extent of areas predicted by the Foraging Radius Approach home-range areas. We also assessed whether basic information on depth preferences from tracking data could improve the foraging radius home-range area estimates.

2. Methods

2.1. Collection of tracking data

GPS tracking data was collected from European shags and black-legged kittiwakes (2010) and razorbills (2012), breeding on Puffin Island, UK (53.3°N, 4.0°W) (Soanes et al., 2013, 2014), from masked boobies (2014) breeding on Sombrero, Anguilla (Lesser Antilles) (18.6°N 63.4°W); and from little penguins (2011) and short-tailed shearwaters (2012) breeding on Gabo Island, Australia (37.55°S, 149.91°E). Birds were caught at their nests using a hand-held net or crooked pole (European shag, razorbills, masked booby, little penguin, and short-tailed shearwater) or noose pole (black-legged kittiwake and razorbills). I-gotU gt120 GPS loggers (Mobile Action Technology, Taiwan) were attached to the tail feathers (masked booby) or back feathers (all other species) using Tesa tape (Wilson et al., 1997). Loggers were set to record a location every two minutes (shags, kittiwakes, boobies and penguins), five minutes (shearwaters) or 100 s (razorbills). Differences in recording interval was due to this data being collected originally as part of other studies. Loggers were retrieved 2–10 days after deployment.

2.2. Tracking data analysis

The first three trips made by European shags, black-legged kittiwakes and masked boobies were included in the analysis to ensure that no individual was under- or over-represented in the analysis, whilst one trip per individual was used for razorbills, little penguins and short-tailed shearwaters, due to shorter logger deployment periods and fewer foraging trips recorded for these species. The GPS devices did not always record a position as programmed to do. This may provide a biased sample of the spatial distribution of foraging activity (McLeay et al., 2010), and so all GPS fixes were interpolated to every 10 s using the R statistical package *adehabitatLT* (Calenge, 2007; R Core Team, 2014). This process and interval ensured that all areas likely to have been flown over or swum through by birds were included in the spatial analysis. Tracking data used in this study were collected from chick-rearing individuals only, and compared to previously reported foraging radii from birds that were also tracked while chick-rearing. For short-tailed shearwaters which are reported to make short (1–2 day) and long trips (≥ 3 day) trips (Cleeland et al., 2014; Einoder et al., 2011) we used data from short trips only, and applied foraging radii around the colony determined from previous studies of short trips only. Long-foraging trips were not analysed in this study as there are relatively few existing data reporting the long-trips of this species, though we acknowledge that they are still an important consideration for

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