STATISTICAL TOOL TO ATTRIBUTE SEABIRDS AT SEA TO THEIR BREEDING COLONIES

BLACK GUILLEMOT
Photo: Mark Peck

BLACK-LEGGED KITTIWAKE
Photo: Becky Matsubara

RAZORBILL
Photo: Gary Howells
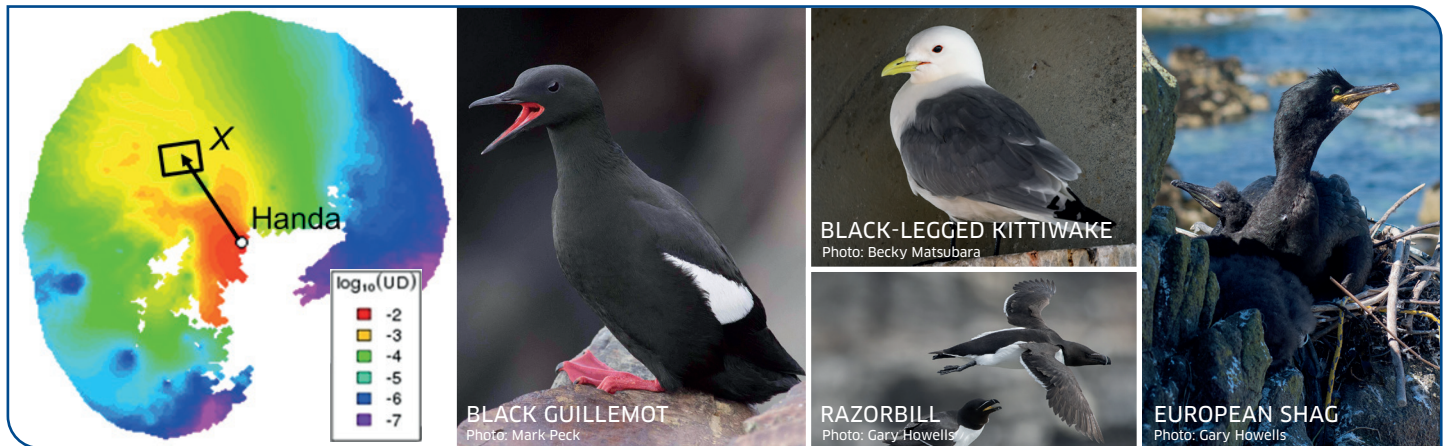
EUROPEAN SHAG
Photo: Gary Howells

FIGURE 1.
PREDICTED LOCAL FORAGING DISTRIBUTIONS (UDS) FOR KITTIWAKE FROM HANDA ISLAND SPA. HIGHER UD VALUES AND THE CORRESPONDING COLOURS INDICATE HIGHER NUMBERS OF BIRDS IN AN AREA THAT ORIGINATE FROM THE COLONY.

Background

Offshore renewables, such as wind farms, have an important role in helping to tackle climate change by contributing to the Scottish Government's ambitious emissions reduction and energy strategy. However, these developments also have the potential to impact the marine environment. Therefore, any new development must be assessed to inform decision makers so that Marine Scotland can effectively manage Scotland's seas for prosperity and environmental sustainability.

Scotland is home to many important seabird populations and breeding colonies, and a network of Marine Special Protected Areas (SPAs) have been establish to protect these globally iconic and valuable birds. However, offshore wind farms have the potential to impact these seabird populations primarily through collisions, displacement from favoured habitats, or by acting as barriers to movement. It is therefore vital to understand both how seabirds interact with these developments, and how potential impacts translate to breeding colony trends at SPA sites to ensure site integrity.

For a development such as a proposed offshore wind farm, collision and displacement mortality are usually calculated based on the number of birds observed at sea during baseline surveys. However, at sea surveys are not able to identify the breeding colony the bird has come from. For example, at wind farm X (*see* Figure 1) what proportion of kittiwake at risk from collision mortality originates from Handa SPA? Therefore, estimates are made through modelling approaches to identify a bird's breeding colony: this is termed apportioning.

The standard calculation used for apportioning is based on the distance to each colony and the size of each colony. It assumes that foraging ranges of neighbouring colonies overlap, with birds from adjacent colonies feeding in these overlap zones. However, segregation of birds from different colonies may occur because some birds choose to forage close to their own colony, either to save energy or to avoid competing with birds from other colonies. By assuming overlap
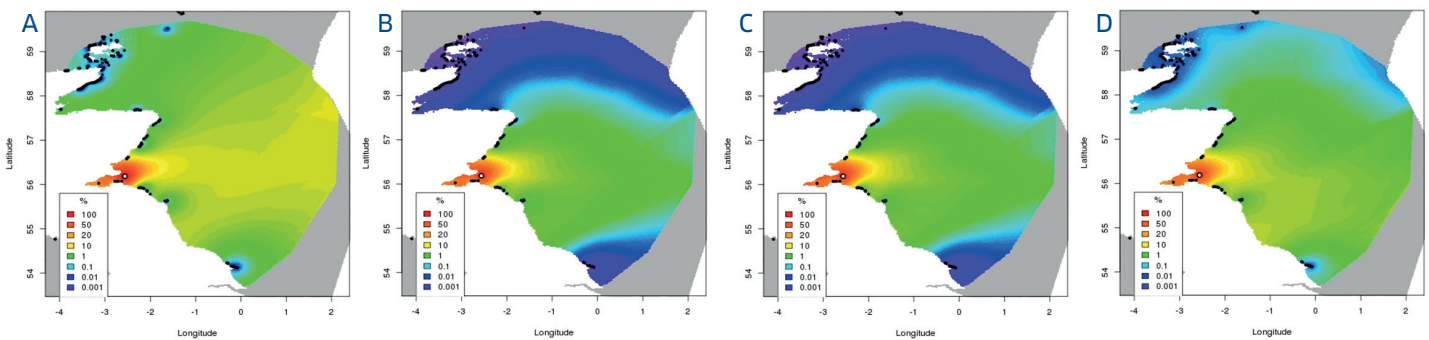
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FIGURE 2.
SPATIAL DISTRIBUTION OF APPORTIONING PERCENTAGES FOR GUILLEMOTS ASSOCIATED WITH THE ISLE OF MAY BASED ON A) THE ORIGINAL APPORTIONING METHOD, B) THE ORIGINAL RSPB METHOD, C) THE RSPB METHOD WITH UPDATED COLONY SIZES AND D) THE RSPB METHOD MODIFIED TO INCLUDE NON-BREEDERS. GREY DENOTES AREAS WITH AN APPORTIONING PERCENTAGE OF LESS THAN 0.001%.

zones, the current approach for apportioning birds to colonies may oversimplify the situation, adding a source of uncertainty in assessments and risk to decision makers. To address this uncertainty, Marine Scotland commissioned The UK Centre for Ecology and Hydrology (UKCEH) and Biomathematics and Statistics Scotland (BioSS) to develop a more accurate analytical tool to apportion seabirds. This project was funded by Scottish Government's Contract Research Fund.

Apportioning tool design process

To build the tool, CEH implemented and compared four different statistical methods: the standard apportioning method and three novel statistical approaches.

The first novel approach is based on a model developed by the RSPB, which uses GPS tracking data and information on colony size from the Seabird 2000 census. This model estimates the areas in which individual breeding birds from four species (common guillemot, black-legged kittiwake, razorbill, European shag) are found around each colony in UK waters during the breeding season. Unlike the standard apportioning approach, this method accounts for observed patterns of seabird segregation and aggregation, and

can quantify the uncertainty associated with this apportioning. The code for this model was streamlined by CEH to reduce computational time.

The second and third approaches modify the RSPB model in two ways. One modification used more recent colony counts than Seabird 2000, and one used spatial survey data (both at-sea and aerial) to estimate the distribution of non-breeding as well as breeding birds, thereby calculating the apportioning percentages associated with all birds.

After comparing the four methods across a randomly selected set of locations, results suggested in general a broad agreement in apportioning percentages between them all. However, at some locations there were relatively substantial differences between the original method and the three novel methods (e.g. *see* Figure 2). The report recommends using the original RSPB model for the apportioning tool.

These results suggest that the original tool can, in some situations, yield results that differ substantially from those obtained using more ecologically informed methods (Figure 2), and that alternatives to the original tool (i.e. novel approaches) should be considered for these species. This new tool produces more accurate estimates for apportioning birds to colonies during the breeding season, and is available online.

UK Centre for Ecology & Hydrology

BioSS