Tern marine SPA identification:
Tracking data collection and analysis

For questions on the document, please contact:
seabirds@jncc.gov.uk

For further information on marine SPAs visit: http://jncc.defra.gov.uk/page-1414

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1. Background and overview

All five species of tern that breed in the UK (Arctic *Sterna paradisaea*, common *S. hirundo,* Sandwich *S. sandvicensis,* roseate *S. dougallii* and little tern *Sternula albifrons*) are listed as rare and vulnerable on Annex I of the EC Birds Directive and thus are subject to special conservation measures including the classification of Special Protection Areas (SPAs). Within the UK there are currently 57 breeding colony SPAs for which at least one species of tern is protected. However, additional important areas for terns at sea have yet to be identified and classified as marine SPAs to complement the existing terrestrial suite. Since 2007, the JNCC has been working with the four Statutory Nature Conservation Bodies (SNCBs) towards the identification of such areas.

The work described here aimed to detect and characterise marine feeding areas used by larger terns breeding within colony SPAs. Since resource and time constraints prevented detailed surveys at all 57 colony SPAs across the UK, a statistical modelling approach was taken which used data collected from a sub-sample of colonies to a) characterise the types of marine environment that is used by foraging terns, and b) use this information to identify potential feeding areas around all colony SPAs.

This summary document gives an overview of the surveys and analytical work carried out between 2009 and 2013 for the four larger tern species (*Sterna* species). A full and detailed description of the analysis can be found in JNCC report 500. A different approach was deemed appropriate for little terns as they search for food in a much more restricted area closer to the coast and to the breeding colony. This is described in JNCC report 548.

2. Data collection

To acquire information on the at-sea foraging distributions of breeding terns, three years of targeted data collection have been carried out or commissioned by JNCC around selected tern colonies from 2009 to 2011, using the visual-tracking technique[1] (see BOX 1 for details). The majority of the data were collected during the chick-rearing period (June to early July), a highly demanding period for breeding adult terns due to food gathering and chick feeding. The need to regularly return to the colony results in a higher number of foraging trips within a generally more restricted foraging range. Accordingly, areas used during this period are considered as crucial for overall survival and are thus high priority for site-based conservation.

Information on habitat conditions was subsequently gathered from various sources to be fed into the habitat models as so-called 'environmental covariates'. Such environmental covariates were chosen for their potential to explain the observed tern distribution data. Due to a lack of information on actual prey distributions (e.g. sandeels, clupeids such as herring and sardine, zooplankton), environmental covariates which could relate to the occurrence or availability of these prey species such as water depth, temperature, salinity, current and wave energy, frontal features, chlorophyll concentrations, seabed slope and type of sediment as well as distance to colony (as a proxy for energetic costs) were used instead.

[1] PERROW, M. R., SKEATE, E. R. and GILROY, J. J. (2011). Visual tracking from a rigid-hulled inflatable boat to determine foraging movements of breeding terns. *Journal of Field Ornithology*, 82(1), 68-79.

Box 1: Visual-tracking technique

Observers onboard a rigid-hulled inflatable boat (RIB) followed individual terns during their foraging trips. An on-board GPS recorded the boat's track, which was used to represent the track of the bird. Observations commenced immediately adjacent to the SPA colony. The actual starting position was varied to capture the full range of departure directions of the birds. Observers maintained constant visual contact with the bird (by maintaining the RIB c.50-200m from the bird*) and recorded any incidence of foraging behaviours, along with their associated timings. Behaviours could then be assigned to a distinct location within the GPS track by matching the timings.

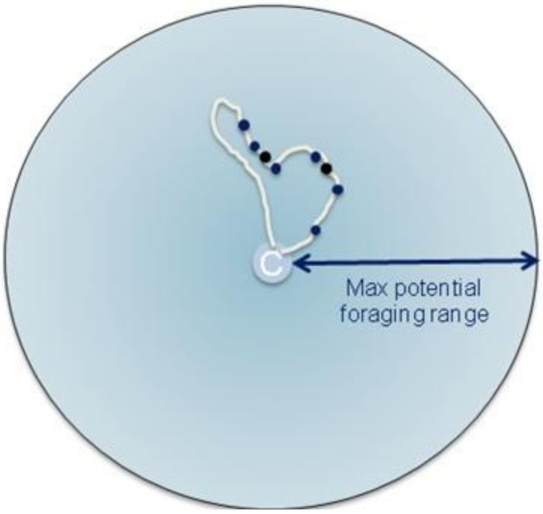
* This distance was found to be optimal in terms of maintaining visual contact whilst minimising disturbance to the bird.

3. Data preparation and analysis

Prior to analysis within the habitat models, data had to be prepared and processed into a suitable format. As data from commuting periods (i.e. parts of the bird track where no foraging behaviour[2] was recorded) had the potential to mask the habitat relationships we aimed to identify for foraging terns, analysis was restricted to observed foraging locations only. In order to identify the preferred type of area used for feeding, the environmental conditions found at foraging locations had to be compared with conditions found at locations which were not used for foraging. The analysis therefore compared observed foraging presence locations with foraging absence locations (see Box 2 for more detail on how these were defined) to characterise the kind of environment used for foraging by the terns.

Box 2: Comparing observed foraging presence locations with foraging absence locations

Given that the data is collected by tracking individual birds rather than from transect surveys, we do not have a comprehensive picture of where the terns did not forage, but instead we do know where a particular bird did forage throughout a feeding trip. During that trip, it did not feed anywhere else. There is an infinite number of possible 'non-foraging locations' so to provide something meaningful for the analysis, we took a sample of non-foraging locations from within the maximum published foraging range of each species.



In this case, 'absence' locations represented areas available to the foraging bird but where the bird was absent at the time of recording. Absence locations were generated at random within the maximum published foraging range of each species[1], based on the number and spatial structure of observed foraging locations within the birds track. The figure shows an example of observed foraging locations (blue) along a bird track and matching sets of absence locations (red) distributed at random within the foraging range. Subsequently, the resulting data sets to be used in the habitat models consisted of both 'foraging' and 'absence' points for each individual foraging trip, as well as respective X and Y co-ordinates and values of the environmental covariates associated with each point.

[2] Foraging behaviour was defined as an instance of circling slowly actively searching for food in the water below, diving into the water, or dipping into the water surface.

Once the environment that the terns use for foraging has been characterised by the analysis, we can then 'reverse' the analysis to search for similar environmental conditions or habitats around important tern colonies. In other words, based on the analysis of observed tern foraging locations, we predict areas that other terns at the same colony, and terns at other colonies, are likely to use for foraging, as shown in Figure 1. More details on the modelling of tern distributions can be found in Box 3.

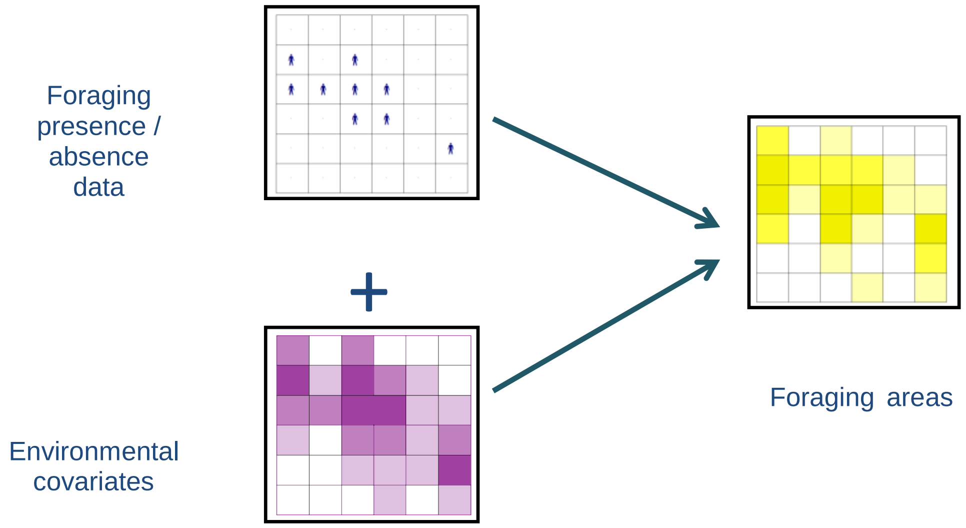


Figure 1: Process of modelling distributions based on environmental information, using a single covariate distribution map in the example.

Box 3: Generalised Linear Models to predict tern relative foraging densities

Extensive investigative analysis showed that logistic Generalised Linear Models (GLMs) were the appropriate statistical tool to identify habitat preferences of foraging terns based on observational data, and to generate predicted foraging distributions around colonies where data were missing. GLMs quantify the relationship between environmental covariates and tern foraging locations within a defined area, and by simply reversing this relationship, they are able to calculate the relative likelihood of a tern foraging (or not) at any location based on the values of the environmental covariates at that location.

As part of the development of the final GLMs used in the analysis, we ascertained that the relationship between tern foraging usage and environmental covariates was consistent between years, warranting the combination of data from all years of the study in the final models. Moreover, environmental covariates were ranked based on their biological meaningfulness, while also taking into account of the suitability and robustness of the data sets for making predictions of foraging use. Selection of which environmental covariates were included in the final model was based on this ranking combined with a standard statistical approach which trades off model complexity with goodness-of-fit to the underlying data.

In order to make a smoothed map of predicted foraging distribution, a 500m by 500m grid was created to cover the published foraging range for each colony of interest. Predictions of foraging likelihood were then made to each grid-cell based on the environmental conditions at the centre points of each cell. These predictions were then rescaled to provide a measure of relative foraging density within each grid-cell.

For each species of tern, there were two types of analysis: for colonies where we had collected sufficient data, the data from that colony only was used in the analysis, providing a colony-specific relative foraging density map (phase 1 analysis in Figure 2).

For colonies where we had insufficient data to produce a colony-specific relative foraging density map, all data for that species was combined to produce a UK wide analysis which could be used to produce foraging density maps around any tern colony in the UK, based on the environment and habitat conditions around those colonies (phase 2 analysis in Figure 2).

The process of analysis involves creating a statistical model, and it is this model which characterises the environment that the terns use for foraging.

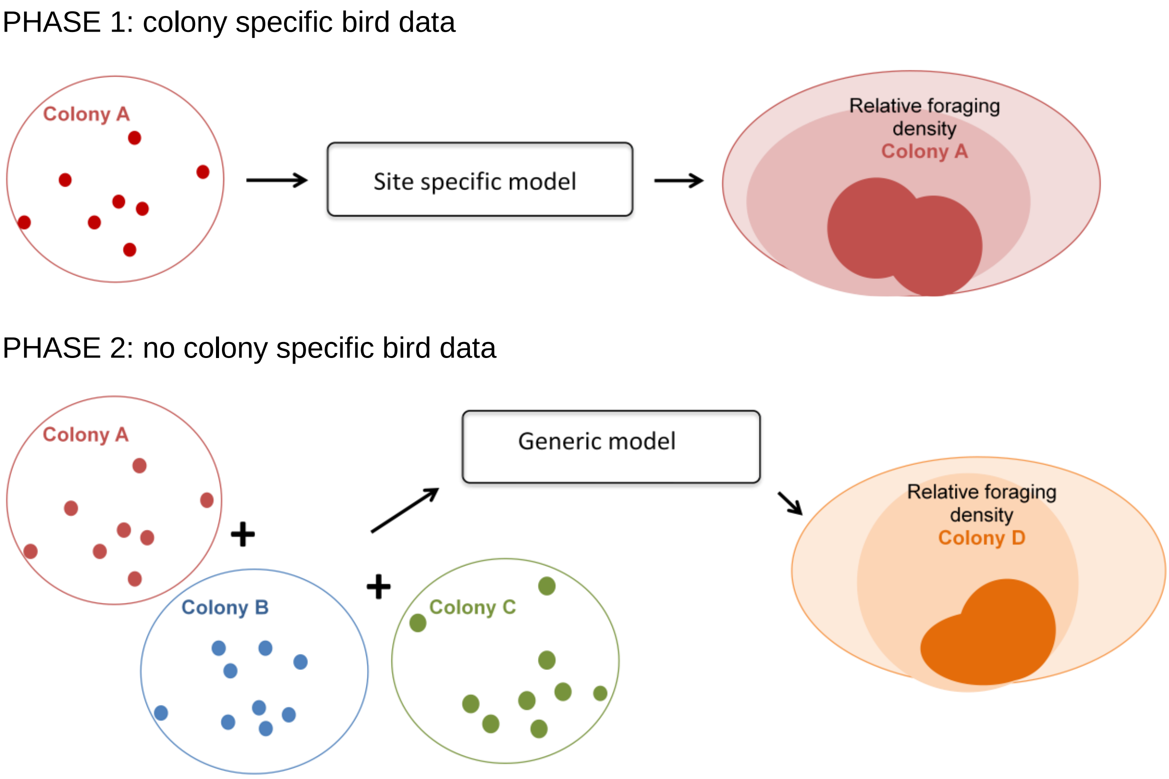


Figure 2: Process for production of relative foraging density maps for phase 1 and phase 2 analyses.

For each model produced, we assessed how good this model would be at making predictions of tern foraging around the same colony (for colony specific analysis) or around other colonies (for UK wide analysis). This assessment was made using a technique called cross-validation. Using a UK wide analysis based on data from three tern colonies (such as that in Figure 2b) as an example: The cross validation analysis is undertaken, creating a model of tern foraging, based on data from only two of the three colonies, which is then used to make predictions of tern foraging around the third colony. Those predictions are compared with the data that was actually collected around the third colony to see how similar they are; how well does the prediction match what the data tells us. This process is repeated with all possible combinations of two colonies going into the analysis, and testing the output on the third, or ‘left-out’, colony, to give an overall estimate of how well the model performs when making predictions to a ‘new’ colony (see Figure 3).

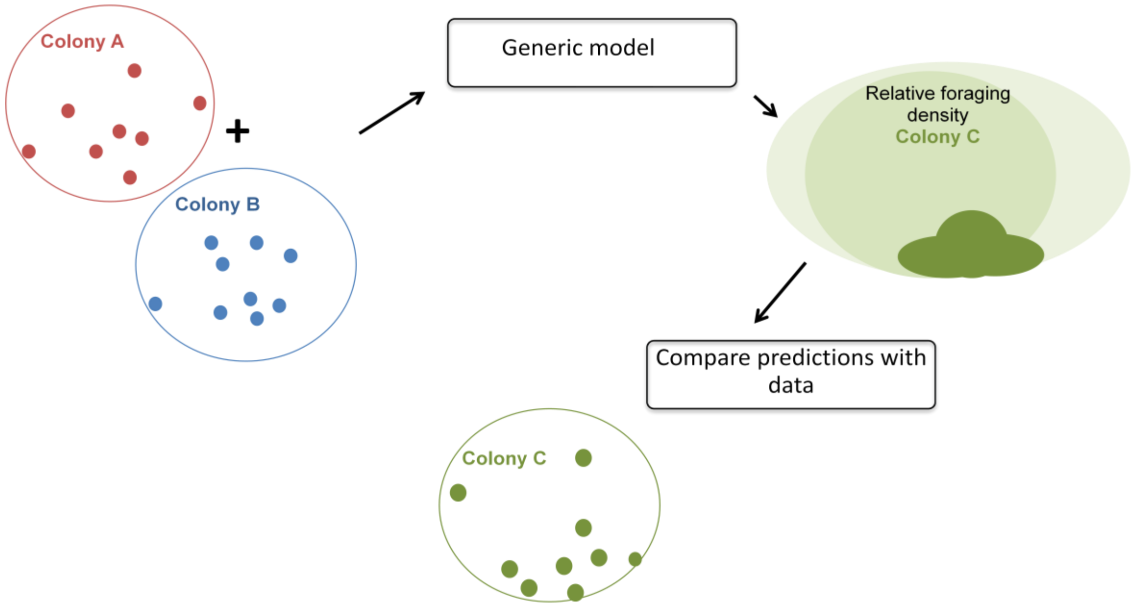


Figure 3: Cross-validation process, using an example where we have data for three colonies.

4. Boundary Delineation

The maps created from outputs of the GLM models in Phases 1 and 2 are essentially a series of grid squares, each with an associated measure of relative foraging density, indicating how likely the area within that square is to be used by feeding terns compared to other squares. There is no clear threshold in these relative density values to distinguish between 'important' and 'not important'. This kind of problem occurs in most of the marine SPA analysis JNCC has undertaken and details on how we solved this problem can be found in 'Defining SPA boundaries at sea'. In order to identify important foraging areas for terns and draw a boundary around them, a cut-off or threshold value had to be found and only those grid squares with a usage value above this cut-off would be included within an SPA boundary. An objective and repeatable method called maximum curvature, identifies such a threshold value. It indicates at what point disproportionately large areas would have to be included within the boundary to accommodate any more increase in foraging tern numbers. As the maximum curvature technique is sensitive to the size of the area it gets applied to, the analysis was based on a common area unit for each species. A species-specific mean maximum foraging range (i.e. the furthest that an average individual forages) was determined using all available data[3], resulting in 30km for Arctic, 20km for common, 32km for Sandwich and 21km for roseate tern. Any points outside the mean maximum foraging ranges were excluded prior to maximum curvature analysis.

[3] The global mean maximum foraging range was calculated using all available tracking data (those collated for Thaxter *et al*. 2012, JNCC's tern project data, and data collected by Econ Ecological Consultancy Ltd). THAXTER, C.B., LASCELLES, B., SUGAR, K., COOK, A.S.C.P., ROOS, S., BOLTON, M., LANGSTON, R.H.W. & BURTON, N.H.K. 2012. Seabird foraging ranges as a preliminary tool for identifying candidate Marine Protected Areas. *Biological Conservation*. **156**: 53-61.

Finally, boundaries were then drawn around the cells exceeding the maximum curvature threshold. In many cases, draft SPAs will be composite sites where the most suitable territories for foraging terns have been combined into an area which is also important for other bird species, e.g. little tern or red-throated divers for example.