From: Dominika Phillips
To: Hornsea Project Three; Kay Sully; KJ Johansson
Cc: Andrew Guyton; Stuart Livesey
Subject: Hornsea Project Three (UK) Ltd response to Deadline 3 (Part 6)
Date: 14 December 2018 21:01:35
Attachments: image001.png
D3_HOW03_Appendix 9_McGregor 2018.pdf
D3_HOW03_Appendix 10_JNCC 2015.pdf
D3_HOW03_Appendix 11_JNCC 2014.pdf
D3_HOW03_Appendix 12_Band 2012.pdf
D3_HOW03_Appendix 13_Figures to the WQ1.2.46.pdf

Dear Kay, K-J

Please find attached the sixth instalment of documents.

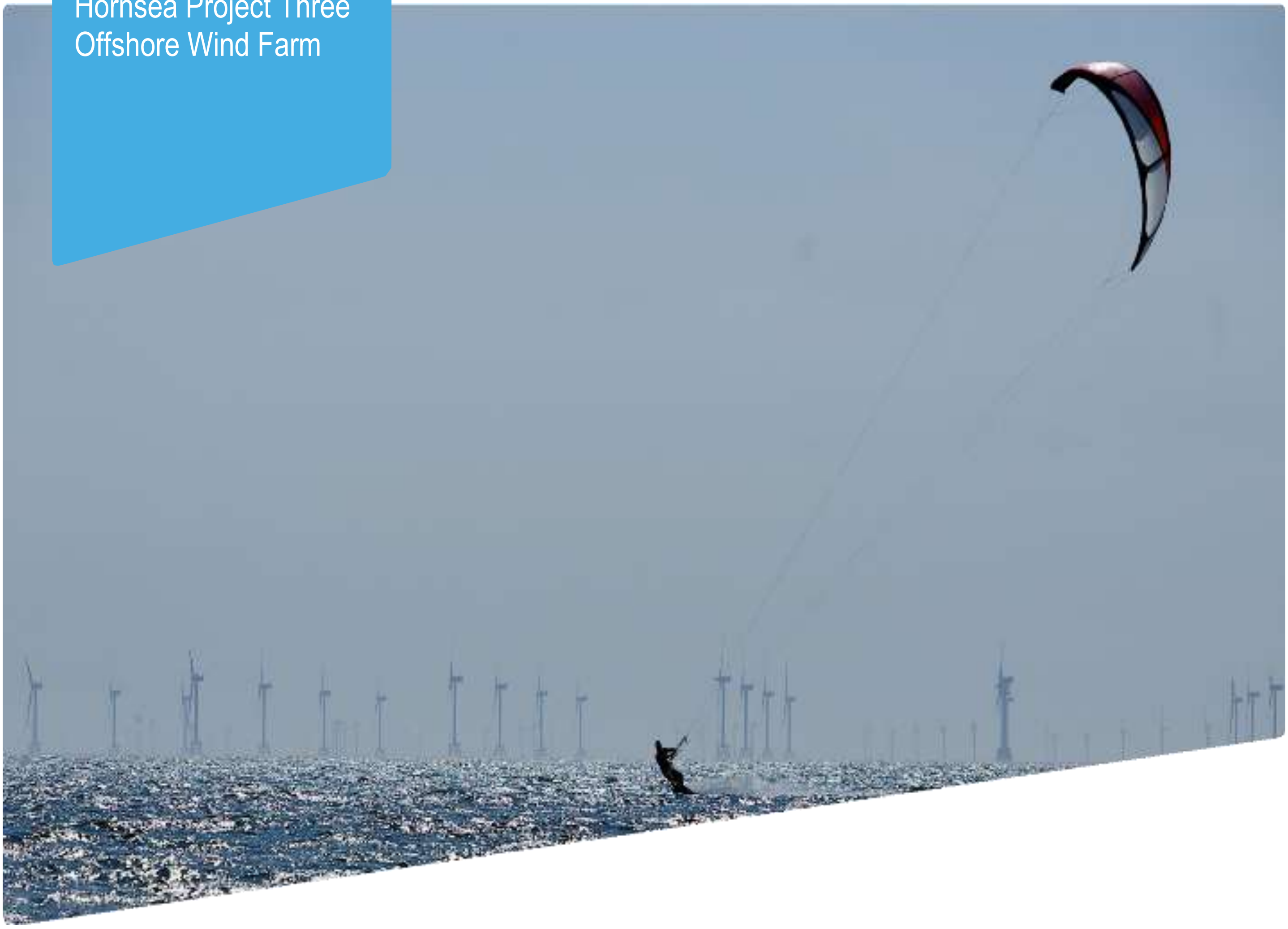
Best regards,
Dr Dominika Chalder PIEMA
Environment and Consent Manager

+44 (0) 7767 007 815

Environmental Management UK│ Wind Power
5 Howick Place │ London │ SW1P 1WG

Orsted

Hornsea Project Three
Offshore Wind Farm



Hornsea Project Three

Offshore Wind Farm

Appendix 11 to Deadline 3 Submission – JNCC Report no 500 – Wilson et al. 2014

Date: 14th December 2018

Hornsea 3
Offshore Wind Farm

Ørsted

Document Control	
Document Properties	
Organisation	Ørsted Hornsea Project Three
Author	Wilson L.J., et al.
Checked by	n/a
Approved by	n/a
Title	Appendix 11 to Deadline 3 Submission – JNCC Report no 500 – Wilson et al. 2014
PINS Document Number	n/a

Version History

Date	Version	Status	Description / Changes
14/12/2018	A	Final	Submitted at Deadline 3 (14/12/2018)

Ørsted

5 Howick Place,

London, SW1P 1WG

Front cover picture: Kite surfer near a UK offshore wind farm © Ørsted Hornsea Project Three (UK) Ltd., 2018.

JNCC Report No. 500

Quantifying usage of the marine environment by terns *Sterna* sp. around their breeding colony SPAs

Wilson L. J.[a], Black J.[a], Brewer, M. J.[b], Potts, J. M.[b], Kuepfer, A.[a], Win I.[a], Kober K.[a], Bingham C.[a,c]., Mavor R.[a] and Webb A.[a,d]

[a] Joint Nature Conservation Committee
[b] Currently Royal Society for the Protection of Birds
[c] Biomathematics and Statistics Scotland
[d] Currently HiDef Aerial Surveying Limited

September 2014

ISSN 0963 8901

For further information please contact:

Joint Nature Conservation Committee
Monkstone House
City Road
Peterborough PE1 1JY

www.jncc.defra.gov.uk

This report should be cited as:

Wilson L. J., Black J., Brewer, M. J., Potts, J. M., Kuepfer, A., Win I., Kober K., Bingham C., Mavor R. & Webb A. 2014. Quantifying usage of the marine environment by terns *Sterna* sp. around their breeding colony SPAs. JNCC Report No. 500

Acknowledgements:

This work was done on behalf of, and funded by, Natural Resources Wales (NRW), formerly Countryside Council for Wales (CCW); Natural England (NE); Northern Ireland Environment Agency (NIEA); Scottish Natural Heritage (SNH); and the Joint Nature Conservation Committee (JNCC). We would particularly like to thank Jim Reid, Lawrence Way, Sue O'Brien, Matt Parsons and Lorna Deppe (all JNCC); Nigel Buxton (SNH); Matty Murphy (NRW); Richard Caldow, Sarah Anthony, Joanna Redgwell and Peter Clement (all NE); and Gregor Watson, Neil McCulloch and Ian Enlander (all NIEA).

Fieldwork was carried out by: Dave Allen, Sophy Allen, Chris Bingham, Julie Black, Craig Bloomer, Toby Burrell, Richard Caldow, Peter Clement, Tim Dunn, Kerstin Kober, Kerry Leonard, Mark Lewis, Roddy Mavor, Clive Mellon, Matty Murphy, Sue O'Brien, Stuart Thomas, Andy Webb, Dennis Weir, Paul Welsh, Linda Wilson and Ilka Win. We are grateful for the support of RSPB for our survey work around the RSPB reserves (Coquet Island, Larne Lough, The Skerries, Papa Westray).

RIBs and skippers were provided by Coastal Connection, Environmental Research Institute, Explorer Fast Sea Charters, Farne Island Dive Charters, Farne Islands Divers, Highland RIBS, Marine Revolution, North Irish Divers and Waterline Boat Charters. We would particularly like to thank our skippers (Colin Barber, Peter Christian, Julian Dale, Sven van Sweeden, Graeme and Thomas Harrison, Ken Miles, Stewart Ryrie, William Simpson, Struan Smith, Peter Steele, Paul Turkentine, Paul Walker and Marcus Vile) and consultants (Allen & Mellon Environmental Ltd and Stuart Thomas) whose expertise, good humour and willingness to work long, hard hours were invaluable for this work.

We are grateful for the additional colony-based data provided by Therese Alampo, Alex Ash, Chris Bell, Clive Craik, Annabelle Drysdale, Simon Foster, Adrian Hibbert, Gemma Jennings, Laura Morris, Paul Morrison, Kevin Redgrave, Daryl Short, David Steele, Hugh Thurgate, Matthew Tickner and Chris Wynne. Gemma Jennings, Richard Bevan, Bob Furness, Kerry Leonard, Laura Morris, Paul Morrison, Chris Redfern and Zoe Tapping provided useful help, advice and colony-based support.

We are grateful to Martin Perrow (ECON Ecological Consultancy Ltd) for sharing his tern ecology expertise and providing advice on the use of the visual-tracking technique. ECON Ecological Consultancy Ltd kindly provided visual tracking data collected on behalf of Centrica Renewable Energy Ltd; we are grateful to Centrica Renewable Energy Ltd for permission for its use. ECON Ecological Consultancy Ltd also kindly provided visual tracking data collected on behalf of Crown Estate.

Additional statistical advice was gratefully received from Esther Lane (University of St. Andrews); Jason Matthiopoulos (University of Glasgow, formerly University of St. Andrews); and Ewan Wakefield (University of Leeds). We are grateful to two anonymous referees who carried out reviews of the first contract report of the model development work (Brewer *et al* 2013a). We are also grateful to two reviewers of an earlier version of this report, along with its annexes, whose comments greatly improved the report.

Summary

- There are five species of tern breeding in Great Britain: Arctic tern *Sterna paradisaea*, Sandwich tern *S. sandvicensis*, common tern *S. hirundo*, little tern *Sternula albifrons* and roseate tern *Sterna dougallii*. The latter two species are among the rarest seabirds breeding in Great Britain and all five species of tern are listed on Annex 1 of the EU Birds Directive.

- The EU Birds Directive requires Member States to classify Special Protection Areas (SPA) for birds listed on Annex I to the Directive and for regularly occurring migratory species. In the UK, there are currently 57 breeding colony SPAs for which at least one of the five species of tern is an interest feature; 41 of these have one or more of the larger tern *Sterna* species as a feature.

- This report describes work undertaken between 2009 and 2013 to quantify usage of the marine environment by the four larger tern *Sterna* species around their breeding colony SPAs in the UK where these remain regularly occupied (32 colony SPAs). Up to three years of targeted data collection were carried out (largely during chick rearing) around ten colony SPAs from 2009 to 2011 using visual tracking, a non-invasive method for quantifying the use of the marine environment by breeding terns of known provenance (colony of origin). Additional visual tracking data were also collated for two colony SPAs through a data-sharing agreement.

- For each study colony, the environmental characteristics at the foraging locations were compared with those for a control sample of locations across the maximum potential foraging range to quantify the habitat preferences of each species. Generalised Linear Models (GLMs, a type of regression technique), were used to model habitat preference relationships and to generate estimates of usage across the entire potential foraging range of each species around each SPA colony.

- Phase 1 of the project developed colony-specific models for each species for colonies where data were available. Selection of the final model was based on a standard approach which trades off model complexity with goodness-of-fit to the underlying data, but also incorporated measures of the repeatability of covariate selection and considerations of biological plausibility. We used cross-validation to test the ability of the models to predict validation data from different individuals and from different years and found that overall models performed well in their predictive ability.

- Phase 2 involved pooling data across colonies to generate a generic model for each species, which was applied to colonies where we had little or no data. Selection of the final model was based on cross-validation which assessed the ability of a model to correctly predict validation data from another colony, and confirmed that Phase 2 models performed well in their predictive ability.

- The resulting models were relatively simple, with most containing only two or three covariates and all except one containing distance to colony. There was high consistency in the covariates selected in the final models across SPAs both within and between species, with distance to colony, bathymetry and salinity in spring being selected in a third of Phase 1 models for all species.

- The outputs from this work may be used to inform conservation of terns in the marine environment, including the identification of marine SPAs, marine planning and environmental impact assessments. Parallel work to identify marine foraging areas for little terns will be reported separately.

Contents

1 Background and aims

There are five species of tern breeding in Great Britain (GB), all of which are colonial ground-nesters. In order of abundance they are: Arctic tern *Sterna paradisaea* (52,613 pairs), Sandwich tern *S. sandvicensis* (10,536 pairs), common tern *S. hirundo* (10,134 pairs), little tern *Sternula albifrons* (1,927 pairs) and roseate tern *Sterna dougallii* (52 pairs) (Mitchell *et al* 2004). The latter two species are among the rarest seabirds breeding in GB and all five species of tern are listed on Annex 1 of the EU Birds Directive (EU 2009). In terms of biogeographic context, GB hosts 2-7% of the European population of Arctic, common and roseate terns and 14-16% of the European population of Sandwich terns (Mitchell *et al* 2004). The EU Birds Directive requires Member States to classify Special Protection Areas (SPA) for birds listed on Annex I of the Directive and for regularly occurring migratory species. In the UK, there are currently 57 breeding colony SPAs for which at least one of the five species of tern is an interest feature (Stroud *et al* 2001); 41 of these have one or more of the larger tern *Sterna* species as a feature[1]. At the time of designation, the seaward boundaries of these colony SPAs ended at the mean low water mark[2,3].

JNCC has been working with the four Statutory Nature Conservation Bodies to identify important marine areas around the UK that may be suitable for designation as marine SPAs to complement the existing terrestrial suite. The aim of the work reported here was to provide evidence that could help support the identification of marine SPAs for terns. As such, this report describes work undertaken between 2009 and 2013 to quantify the use of the marine environment by the four larger tern *Sterna* species around their breeding colony SPAs in the UK, by studying their foraging distribution (mainly during the chick-rearing period). While the main aim of this work was to inform the identification of marine SPAs, the outputs from this work may also be used to inform conservation of terns in the marine environment more widely, such as marine planning and environmental impact assessments. Parallel work to identify marine foraging areas for little terns will be reported separately (Parsons *et al* in prep.) as the more restricted foraging ranges of little terns (Thaxter *et al* 2012) warrant a different approach. For completeness, little terns are included in the following review of tern ecology and conservation.

1.1 Tern ecology and conservation

Arctic terns breed mainly in coastal areas in the north and west of the GB with almost 80% of the population occurring in Shetland, Orkney and the Outer Hebrides. Common terns frequently nest inland, with small colonies occurring along the large river valleys of south-east and central England and also scattered along rivers in south-east Scotland and on islets in the freshwater loughs of Ireland. However, they also have a widespread coastal distribution around most of GB. Sandwich terns breed exclusively along the coast in relatively few, often large, colonies with an almost complete absence around Shetland, the west coast of Scotland and to the south-west of GB. Little terns occur around much of the coastline, but around 79% of the GB population breed on the east and south coasts of England (from Northumberland to Dorset), where low-lying sandy coastlines (their preferred habitat) predominate. Roseate tern breeding range is restricted to the coast of north-east England and south-east Scotland, with outlying pairs in Norfolk and Hampshire. Almost the entire GB population breeds on Coquet Island (Northumberland), with the remaining colonies

---

[1] This includes Copeland Islands SPA and Imperial Dock Lock SPA, which have been designated since Stroud *et al* 2001. In addition there are three SPAs for Sandwich terns during passage.

[2] Mean low water springs in Scotland.

[3] Note that seaward extensions of up to 4km into the marine environment have since been designated for some seabird colony SPAs, including some for which terns are interest features. The extensions were identified on the basis of capturing areas adjacent to the colony that are important for essential resting and maintenance activities for seabird species other than terns (see McSorley *et al* 2003; McSorley *et al* 2008). However all interest features, no matter their activity, benefit from the extended spatial protection.

being small and often ephemeral; the Republic of Ireland (particularly Rockabill, Co. Dublin) hosts 93% of Britain and Ireland's roseate tern population (Mitchell *et al* 2004).

Observations at selected colonies suggest that the GB populations of Arctic and common have declined since the last complete seabird census ('Seabird 2000', Mitchell *et al* 2004) was carried out between 1998 and 2002, while the population of roseate terns has increased (though almost entirely confined to Coquet Island, Northumberland), little terns have increased and Sandwich terns have changed little (JNCC 2013). A large proportion of terns nest on mainland beaches, spits or near-shore islets where they are vulnerable to mammalian/avian predation, human disturbance and flooding. Predation can cause complete breeding failure, and colonies will often be attacked in successive years until the terns abandon the site, causing a high occurrence of switching colony between (and sometimes within) years (Mitchell *et al* 2004).

Large gulls can compete for breeding space with terns (Thomas 1972; Kress *et al* 1983, Kress 1997) causing displacement and disturbance to nesting attempts, and prey upon the eggs and chicks (Fuchs 1977; Yorio & Quintana 1997). Inter-specific competition can cause population declines (Hannon *et al* 1997) and has also resulted in little terns nesting closer to the high water mark (Pickerel 2002). Nesting habitat or entire breeding sites can be lost to erosion or flooding by winter storms (Thomas 1982; Brown & McAvoy 1985; Visser & Peterson 1994) or become overgrown with rank herbage or scrub (Brown & McAvoy 1985; Brindley 1998).

Terns are long distance migrants, wintering along the coasts of West Africa, or in the case of Arctic tern, the oceans of Antarctica (Cramp 1985; Egevang 2010). Factors that affect survival in the wintering areas will also influence subsequent population trends observed in the UK. Such factors include food availability (Cramp 1985, Dunn & Mead 1982) and mortality, mainly of first year Sandwich, common and roseate terns captured for sport and food (Dunn & Mead 1982; Ntiamoa-Baidu *et al* 1992; Mead 1978; Ratcliffe & Merne 2002; Wendeln & Becker 1999).

Threats to terns in the marine environment largely stem from changes in prey availability. Arctic terns breeding in Orkney and Shetland are almost entirely dependent on sandeels during the breeding season, and their productivity is strongly affected by the size of the sandeel stock (Monaghan *et al* 1989; Suddaby & Ratcliffe 1997). Poor food availability, such as during the sandeel stock declines from 1983 to 1990 has been associated with breeding failure, reduced growth and survival of chicks for this species (Monaghan *et al* 1989; Monaghan *et al* 1992) but also had an indirect effect on common terns, which were heavily depredated by gulls and skuas that switched their diet from predominantly fish to seabirds (Uttley *et al* 1989). In addition, general food shortage can be exacerbated by black-headed gull *Chroicocephalus ridibundus* kleptoparasitism (Stienen & Brenninkmeijer 2002a, b). Another potential threat to terns in the marine environment comes from renewable developments, although direct evidence of this is limited given the relative infancy of the industry (though see Everaert & Stienen 2007 and Stienen *et al* 2008). Direct effects could occur through collision, displacement and disturbance while indirect effects on prey availability can potentially compromise survival (Huddleston 2010).

Terns lay a clutch of between one and four eggs and normally rear one brood per season from May to June. Incubation and chick rearing is performed by both parents who may spend up to 80% of their time foraging. The area over which breeding terns can forage is constrained by their need to return to the nest to relieve their mate or feed their chicks (i.e. they are central place foragers). Rate of chick provisioning varies among species but can be as high as 12 feeds per day for common terns (Becker *et al* 1993). The most recent published maximum foraging ranges are 11km (little tern); 30km (Arctic, common and roseate); and 54km (Sandwich tern) (Thaxter *et al* 2012).

Terns are specialist foragers largely dependent on dense shoals of clupeids and sandeel within foraging range of their colonies, although common terns have a more generalist diet compared with the other species (Stienen *et al* 2000; Cramp 1985; Gochfeld *et al* 1998; Shealer 1999, Fasola *et al* 2002). The smaller species also pick small aquatic and marine invertebrates from water surfaces in flight (Fasola *et al* 2002). Terns usually forage by plunge-diving after hovering and are shallow divers, catching prey close to, or at, the sea surface. More details can be found in a literature review of tern foraging ecology which was commissioned by JNCC as part of this project and is available as a separate contract report (Eglington & Perrow 2014).

2 Methods

The project relied primarily on data collected using visual tracking, a technique specifically developed by Perrow *et al* (2011) for quantifying the use of the marine environment by terns of known provenance (colony of origin). The alternatives of bird-borne radio-tags and GPS tracking devices were not feasible: the larger tern foraging ranges exceed the detectable range (from land) of the radio signal, and at the time the project started, GPS devices were unsuitable for terns (they are now available due to advances in the technology making the devices smaller)**.** Existing aerial and boat transect[4] data were collated and a small number of boat transect surveys were also carried out as part of the project but these are not included in this report. Data from those transect surveys did not allow the origin of individuals to be identified.

Logistics, resources and timescale of the project precluded surveying around all SPA colonies of interest and instead a habitat modelling approach was adopted incorporating surveys around selected colonies. Habitat modelling can establish statistical relationships of the environmental preferences of terns which, if applied spatially, not only provides a spatial surface of relative distributions within a surveyed area (i.e. interpolating, or filling in the gaps, between the recorded observations), but also allows predictions to be made by geographical extrapolation to unsurveyed areas (provided the required environmental information is available for the unsurveyed areas). For the modelling analysis aspect of the project, JNCC worked collaboratively with Biomathematics and Statistics Scotland (BioSS)[5].

The project was delivered in two phases, in accordance with data coverage: Phase 1 developed colony-specific models for each tern species of interest for colonies where surveys had been carried out and sufficient data had been obtained, while Phase 2 developed generic models using combined data across surveyed colonies which was then used to make geographically extrapolated predictions to unsurveyed colonies or data-poor colonies.

2.1 Data collection

Data collection to assess the foraging distribution of the large tern species was carried out or commissioned by JNCC over three years from 2009 to 2011 using visual tracking. The visual tracking method involved using an easily manoeuvrable boat capable of speeds up to 40 knots (such as a rigid-hulled inflatable boat (RIB)) to follow individual terns from their breeding colony out to sea and back. An on-board GPS recorded the boat's track, which was used to represent the track of the bird. The RIB was kept *c*.50-200m from the bird so that one observer could maintain constant visual contact with the bird and another observer could record behaviours, along with their associated timings. We took care to observe any

---

[4] Transects are lines across a survey area along which observations are recorded. If designed appropriately, transect surveys allow estimation of population sizes and their distributions.

[5] BioSS are one of the Main Research Providers for strategic research in environmental, agricultural and biological science funded by the Scottish Government's Rural and Environment Science and Analytical Services Division.

changes in behaviour, such as evasive flying, which might indicate an adverse reaction of the birds to the presence of the vessel and if so, increased the distance of the RIB from the bird. Behaviours were assigned to locations based on the common time field between observations and the GPS track log. Observers were given operational definitions of the different behaviours, which were categorised as continuous behaviours (different types of flight) and instantaneous behaviours (different types of foraging events) (see Table 1). In addition, any foraging associations with other individuals of the same or other species were recorded.

We could not confirm the breeding stage of any of the birds we followed[6]; this could only be implied from the date of data collection combined with timing-of-breeding information collected at the colony, the availability/quality of which varied between colonies. Timing of survey varied between colonies and years (see Results for details). In 2009, surveys were restricted to the chick-rearing period. In 2010 the feasibility of extending coverage to include incubation was piloted. However, surveying over the two periods stretched resources, such that fewer data were obtained within each period and overall i.e. data collection was less efficient. Continuing data collection across the two breeding periods risked compromising sample sizes so in 2011 the focus of data collection was again during chick-rearing. Thus overall, timing of survey was largely concentrated during chick-rearing. This period was prioritised for data collection as it is a highly demanding part of the life-cycle, with breeding adults required to make frequent foraging trips to provision their chicks as well as themselves; available foraging areas are likely to be more restricted than at other times in the life-cycle due to central-place foraging constraints (see Orians & Pearson 1979). Therefore, it is important to identify the foraging areas used during this period to inform any marine conservation management measures. This does not necessarily mean that vulnerability to threats during incubation is inconsequential, but our prioritisation was based on the more restricted ability of birds to buffer against any pressures experienced during chick-rearing.

Table 1. Definitions of various continuous or instantaneous behaviour categories applied by JNCC during visual tracking surveys from 2009-2011.

Behaviour category	**Continuous behaviour or instantaneous event**	**Description**
Direct flight	Continuous	Clear and consistent direction, usually fast, often adopted when flying back to the colony with a fish.
Transit search	Continuous	Slower than direct flight, direction can change but not erratically, head can be down, as though opportunistically searching while in transit. The usual flight type when not actively searching.
Active search	Continuous	Actively searching for food: head down, erratic flight course, lower flight speed, hovering, swooping and/or circling around; includes instantaneous foraging behaviours of diving and surface feeding.
Plunge dive	Instantaneous	Diving from a height, head first. All or mostly submerged.
Surface dip	Instantaneous	Diving from close to the water surface, sometimes ‘feet first’. Partially submerged.
Surface peck	Instantaneous	Picking item from the surface with bill, no submerging.

---

[6] There was the odd exception to this when observers were able to view the contents of the nest from which the individual was seen to depart.

2.1.1 Study colonies

Terns regularly move between different nesting sites from year to year and breeding success often varies markedly between colonies, and between years within colonies (Mitchell *et al* 2004)[7]. Several of the 41 colony SPAs for which one or more of the larger tern species are a feature currently have very low numbers (or in some cases none) of the relevant tern species, so we focussed on quantifying the use of the marine environment for the tern interest features which recently regularly occupied their colony SPAs. Recent regular occupation was defined as the mean of peak numbers over the five most recent years for which data are available being ≥25 Apparently Occupied Nests (AON). Count data were taken from JNCC's Seabird Monitoring Programme (SMP) database. A limit of five years was chosen to be consistent with the UK practice of using five year peak means to assess populations (e.g. Musgrove *et al* 2011) and data were collated spanning the period from 2000-2010[8] to ensure that at least five years of data were available. It has been the Statutory Nature Conservation Bodies' long-standing practice to require at least 50 individuals to be regularly present on a site before that area is considered for site selection (see Stroud *et al* 2001). Although this 'minimum 50 rule' has its origins in the context of wintering waterbirds, this provided a useful baseline against which an assessment could be made as to whether a tern colony SPA can be considered as still being occupied. The normal metric used to assess tern breeding population sizes is AON rather than individuals, thus the minimum number in this context would be 25 AONs, given that each nest is assumed to represent one pair. The tern interest features for the 32 SPA colonies deemed to be recently regularly occupied and for which analysis was undertaken are shown in Figure 1. Table 2 shows the 17 features within 17 SPAs which fell outwith the scope of the project due to no longer being recently regularly occupied**.** Note that the assessment of recent occupancy was only to allow prioritisation of survey effort and not to revisit the selection of colony SPAs.

Visual tracking was carried out or commissioned by JNCC at ten of these 32 colony SPAs. When choosing how to prioritise our survey resources there were several considerations. For selecting the survey colonies we aimed to maximise geographical coverage across each species' range, even if this meant only one year of survey was possible for some areas. This was based on the assumption that variation (in the relationships of tern foraging distribution with local environmental conditions) between colonies was likely to be greater than variation between years within a colony, and it would be important to capture this variation if we were to use data from more than one colony to make predictions to data-poor colonies. However, we also aimed to get two or three years of data from several colonies to allow investigation of consistency in environmental preferences between years. Other factors affecting allocation of survey resources included prioritising colonies that: had little or no existing data (e.g. from aerial surveys or other visual tracking studies); were logistically easier to work at; or maximised likely sample sizes (e.g. larger/multi-species colonies with recent successful breeding seasons). In addition to JNCC's surveys, visual tracking data were made available to the project for two colony SPAs via a data sharing agreement with ECON Ecological Consultancy Ltd. These data were for the North Norfolk Coast SPA, and Ynys Feurig, Cemlyn Bay and The Skerries SPA (see Perrow *et al* 2011 for methods).

---

[7] This was taken into account at the time the breeding colony SPAs were designated, such that a site where contemporary numbers were very low (below the qualifying threshold) could still be designated where there was a history of occupancy and/or where a site was known to be part of a large complex of nesting areas (Stroud *et al* 2001).

[8] The assessment of recent occupation was made in 2010.

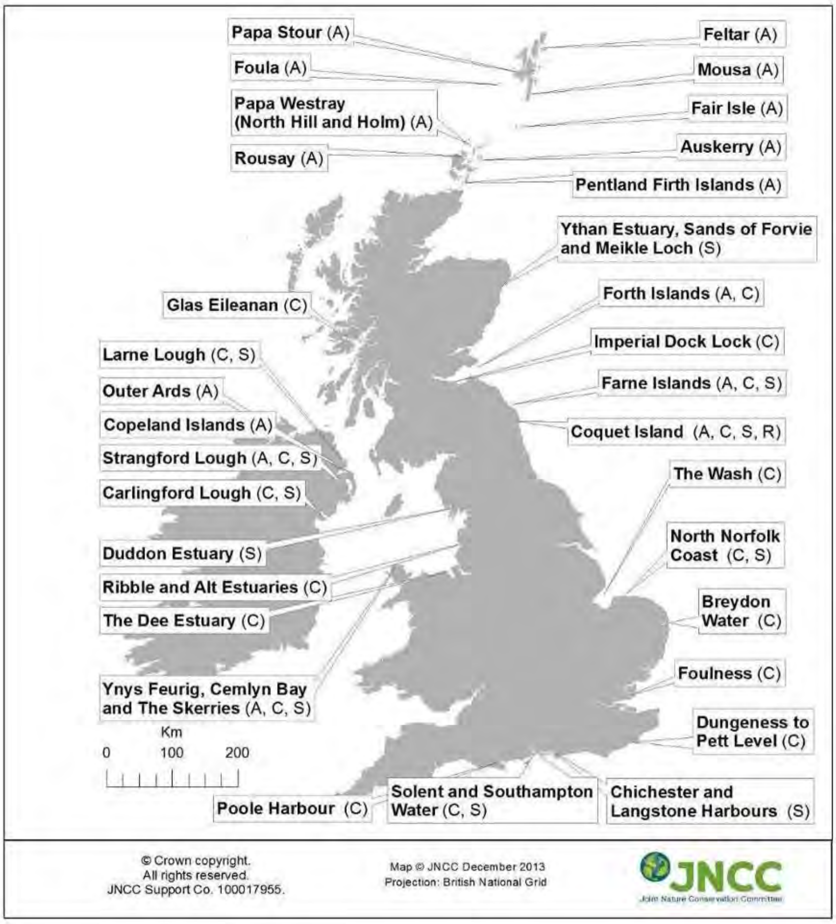


Figure 1. Tern colony SPAs and the relevant tern species (A = Arctic, C = common, R = roseate tern and S = Sandwich) which were considered within the project.

Table 2. The tern species within tern colony SPAs which were considered no longer regularly occupied and fell outwith the scope of the current project.

SPA name	Arctic	Common	Roseate	Sandwich
Alde–Ore Estuary				X
Morecambe Bay				X
Foulness (Mid-Essex Coast Phase 5)				X
Solent and Southampton Water			X	
Farne Islands			X	
North Norfolk Coast			X	
Firth of Forth Islands			X	X
Loch of Strathbeg				X
Monach Isles		X		
Sumburgh Head	X			
West Westray	X			
Cromarty Firth		X		
Inner Moray Firth		X		
Ythan Estuary, Sands of Forvie and Meikle Loch		X		
Lough Neagh and Lough Beg*		X		
Larne Lough			X	
Ynys Feurig, Cemlyn Bay and The Skerries			X	

*Recent data from www.loughneagh.com which is not in the SMP database suggests that *c*.50 pairs may be present. However, the SPA is well inland and not suitable for our modelling approach.

2.1.2 Collation of environmental covariates

Environmental data to use as predictor covariates in our habitat models were subsequently collated from various sources, rather than collected concurrently with the tern data. Data sets with coverage extending across the UK were required for the UK-wide application of generic models in Phase 2. Environmental covariates were chosen for their potential to explain the variation in our tern distribution data and based on this be used as predictors for foraging distribution. The most direct explanatory covariate is likely to be the distribution of prey. Unfortunately, our knowledge on the types and distribution of prey consumed by each tern species breeding at each colony of interest is limited, especially for prey consumed at sea by adults. Existing studies of terns in the UK show that they rely to varying extents on clupeids, zooplankton and, in particular, sandeels as their primary prey source (Cramp 1985). However, there was a lack of prey distribution data at a useful resolution or level of coverage for our project. Instead we aimed to inform models with a variety of other environmental covariates that could either act as proxies for prey distribution, or relate to the availability of prey to the terns.

The at-sea distributions of central-place foragers such as breeding seabirds, is known to be constrained by the energetic costs of travelling to a particular location from the central place (e.g. the breeding colony) (Gaston 2004). Therefore distance to the colony was offered to the models as a proxy for these energetic costs. Euclidean (straight-line) distance was used rather than biological distance *(*defined as the minimum path length required to get from one point to another while avoiding obstacles such as land, as per Matthiopoulos (2003)). This was because our own observations showed that although terns tended to fly along coastlines, they did not necessarily avoid flying over low-lying islands and peninsulas. Generating biological distances would therefore require case-by-case judgements on what constitutes a land barrier to a tern. For the most part we felt that our study sites generally did not present major land barriers and that Euclidean distance was, on the whole, sufficiently representative as a proxy for the energetic costs of travel.

The other candidate environmental covariates offered to the models were: depth; temperature stratification; chlorophyll concentration; sea surface temperature; sea surface salinity; sediment type; current energy; wave energy; probability of a front[9]; seabed slope and aspect (see Table A1.1 in Appendix 1 for more details)[10]. Some of these covariates are dynamic and their values may vary over time; where possible, we averaged data over time for the dynamic variables (see Appendix 1 for more details). For some areas, the chlorophyll concentration and sea surface temperature covariates had a much higher proportion of missing data than other covariates (as they are based on satellite data and satellites may have difficulties taking readings in coastal areas due to cloud cover), so for some colonies they were excluded altogether as candidate covariates. Distance to nearest shore was also offered as a covariate because this is likely to be correlated with missing environmental information which might drive tern foraging distributions.

---

[9] Earlier work also explored the use of the standard deviation of the probability of a front, but there was insufficient understanding on how this might explain variation in our data and was therefore removed

[10] Before analysis, extreme values of sea surface temperature were excluded (for April this is interpreted as less than 6°C, for May as less than 8°C, and for June as less than 9.3°C) and chlorophyll concentrations, slope and wave and current shear stresses were log-transformed. Where necessary, a small constant was added to variables prior to log transformation to avoid taking logs of zero values. Before making the final predictions data points with values of log chlorophyll greater than 2.5 were also excluded.

2.2 Data analysis

The project used logistic[11] regression analysis, a statistical process which estimates the relationship between a dependent or ‘response’ variable (e.g. density of foraging locations) and one or more independent or ‘predictor’ variables (environmental covariates). The logistic regression models were used to generate predicted foraging distributions on a data grid extending out to the maximum foraging range around the colonies of interest. The maximum foraging range was taken from Thaxter *et al* 2012 and was either 30km (Arctic, common and roseate terns) or 54km (Sandwich terns) [12,13]. Model predictions were made to the centre points of grid cells of 500m x 500m resolution. For analysis we used R (v. 2.15.2) and ArcGIS (v. 10.1).

Only the records of foraging locations (both active search and foraging events) were used for the analysis of habitat preference. We felt that data from commuting periods of flight might mask some of the habitat preference relationships; although terns may show directed travel along the track during commuting, we were unsure whether this would be linked with the underlying environmental covariates. Restricting the analysis to only foraging locations maximised the chances of identifying the habitat preference relationships from the response (tern case/control) data. Accordingly, tracks which did not contain any observations of foraging behaviours were not used in the analysis. All records of instantaneous foraging events were retained but for computational reasons, the continuous records of active search (one record per second) were thinned by 90% (using every 10th record) before analysis – this is equivalent to retaining one record for every ten seconds of active search so it is still very high resolution data (it was not necessary to thin data provided from ECON Ecological Consultancy Ltd as these were already summarised at one minute intervals).

2.2.1 Assessing sample size sufficiency

The modelling assumes that a representative sample of terns for each species/colony was tracked and that the outputs will be representative of the population as a whole. A separate analysis was commissioned to investigate the sufficiency of our sample sizes and is reported in Harwood & Perrow (2014).

2.2.2 Model development

The analysis included a model development phase, which is described in several contract reports (Brewer *et al* 2012a-c, Potts *et al* 2013a)[14]; here we describe the key points and refer the reader to the relevant report(s) for more detailed information. Model development was an iterative process but consisted broadly of three main steps (1) developing the application of a case-control approach, to allow comparison of the areas used with those which were available but not used for foraging (Section i); (2) Exploring different types of regression analysis to determine which was most suitable (Section ii) and (3) Investigating whether various additional complexities were required (Sections iii - v). The final approach was then applied separately to Phase 1 and 2, using appropriate model selection methods for each.

---

[11] Logistic regression is a type of non-parametric regression analysis used for predicting the outcome of a categorical (a variable that can take on a limited number of categories, in our case either 0 or 1) dependent variable based on one or more predictor variables.

[12] A 1km buffer was added to this because initially covariate values were averaged within a 1km x 1km grid; the buffer allowed this average to be calculated more accurately at the edge of the foraging range. A point approach was later adopted (where the actual value of the environment at the tern location point was extracted) but the 1km buffer was retained.

[13] Note that for earlier work (Brewer *et al* 2012a) a maximum of 60km had been used for Sandwich terns, based on an earlier draft of Thaxter *et al* (2012)

[14] Model development did not include data from ECON Ecological Consultancy Ltd.

i Case-control approach

Tracking data provides information about the locations of individual birds, but no explicit information about which areas are unused. Such presence-only data can be analysed using a case-control approach where the observed locations (cases) are matched with control points that are selected according to an appropriate null model (see below), and which represent locations which are available to the animal but where the animal was absent at that time (Aarts *et al* 2008). Control data were generated by relocating the observed 'case' tracks (foraging locations only) randomly throughout the maximum potential foraging range[15] from the colony for each species. Each control track was assigned its starting location based on a random distance and angle from the colony so that our null model assumed terns were central place foragers with no foraging location preference. Twelve control tracks were generated for each track; exploratory work found that this number was sufficient to ensure model stability (i.e. the estimates of the regression slope parameters are stable regardless of which random selection of the twelve control tracks was chosen).

By comparing the environmental characteristics between the observed and control locations, a logistic regression model can be used to quantify tern habitat preferences which are then adjusted to provide estimates of relative usage (see Box 1). The estimates of relative usage are equivalent to predicted relative densities of foraging locations (expressed as a proportion).

Box 1. Quantifying habitat preference and relative usage

<u>Estimating habitat preference</u>

Following Aarts *et al* (2008), we define habitat preference as the ratio of the use of a habitat over its availability, conditional on the availability of all habitats. If there was no preference for particular habitats, the odds ratio (which is a particular way of looking at relative probabilities of two mutually exclusive events, such as the probability of a presence or absence) would be equal to the ratio of the number of observations to the number of controls.

Logistic regression is used to model a response variable which takes the value 1 for the observations and 0 for the control (available environment) points. So in our case, the logistic regression approach models the probability that a point is a foraging location. Because the number of controls per observation is user-defined, this probability has no physical meaning and tends to zero as the number of control points increases; it is the intensity (or density) of the presences rather than the probability of occupancy that is of interest. It has been shown that the exponential function of the linear predictor (i.e. the odds ratio; *(probability / (1 - probability))* is proportional to the expected density of presences (Aarts *et al* 2008). Multiplying this by the number of controls per observation then accounts for the unequal number of cases and controls selected, and provides a valid estimate of preference. i.e.:

Preference = number of controls x (probability / (1 - probability))

<u>Estimating usage from preference</u>

The null model used to generate the controls assumed that the frequency distribution of control points was uniform with respect to distance to colony up to the maximum foraging range. However, due to the laws of geometry (i.e. the size of an area increasing as a

---

[15] Although all control 'start points' were generated within the maximum foraging range, it was possible that control points from the rest of the track could fall beyond the maximum foraging range. In practise this occurred relatively rarely but where it did occur, those points were deleted.

function of the circle's circumference), the density of control points per unit area is higher at distances close to the colony compared to further away. The null model can therefore be seen as making the assumption that accessibility declines with increasing distance from the colony (in a two dimensional sense), so the model outputs are estimates of preference and need to be adjusted to provide estimates of actual usage.

To make this adjustment, we need to know the density of control points at a particular distance; this depends on the circumference of a circle at that distance which is proportional to the radius. So the density of our control points is in proportion to 1/distance from the colony, coming from the equation for circumference of a circle (C=πd). To then convert the resulting preference outputs from the model into usage we multiply by 1/distance-to-colony. i.e.:

Usage = (probability/1-probability) x no. of controls / distance to colony

Since the model is based on a random sample of controls, the cumulative estimated usage over all space will usually deviate from unity and will need to be normalized (Aarts *et al* 2008). So the output was multiplied by a scale factor which ensures that the probabilities sum to one. This means that the final values, which we call 'relative usage', represent relative densities of foraging locations, expressed as a proportion.

Note that had we had generated controls with a (two dimensional) uniform distribution in space, so that the density of points was the same everywhere, this would mean that the model outputs would provide direct estimates of usage and no correction would have been needed to go from preference to usage.

Usage values were then multiplied by 1000 for mapping purposes (the value for each cell would otherwise be extremely small due to the need for them to sum to one across a very large number of cells). It would be possible to instead multiply by the number of birds at sea to obtain a bird density estimate. The number of birds at sea could be approximated based on the number of breeding pairs at the colony and the proportion of time they spend at the colony (to account for the fact that not all individuals forage at the same time). i.e.:

*Bird density = Usage * (pairs*2/(1-colony attendance))*

However, this would assume that (i) the density of foraging locations is proportional to the density of foraging birds and (ii) all birds at sea are foraging (as opposed to commuting). Coupled with this, there is relatively little information on colony attendance patterns and they are likely to vary between colonies and seasons. So we did not convert our usage estimates to bird densities as it would add a level of uncertainty into the estimate which would be difficult to quantify.

ii Type of regression

Two different types of regression were explored for modelling the data under Phase 1; Logistic Generalised Linear Models (GLMs, McCullagh & Nelder 1989) which only allow linear relationships between the response and predictor variables, and logistic Generalised Additive Models (GAMs, Hastie & Tibshirani 1990; Wood 2006) which also allow non-linear relationships. We explored three different methods of model selection on the basis of AIC (Akaike's Information Criterion); BIC (Bayesian Information Criterion); and significance of individual terms via likelihood ratio tests (LRTs) (see Brewer *et al* 2012a for more details). The exploratory analysis showed that most relationships were linear (only eight out of the 40 relationships in the GAM models were non-linear and all were simple, broadly linear relationships). Thus the added complexity of GAMs was unwarranted and GLMs were used for the final Phase 1 models. For Phase 2, we only considered GLMs as we wanted to avoid complex models when making geographical extrapolations.

iii Assessing effects of year and breeding period

As part of the model development phase, we checked for consistency of the environmental covariate effects across different years for those species/colony SPAs for which we had more than one year of data (n=8). This was done by fitting year as an interaction term within the GLM model and concluding effects were not temporally consistent if the interaction is significant. We found that covariate effects were consistent between years for all datasets except one, where the effect was only just significant at p=0.049. On the basis of these results, and to maintain a consistent approach across all of our datasets, data from all years were combined for the final models.

Although we were unable to confirm the breeding status of most of the birds tracked, our surveys were timed to focus on breeding birds largely during the chick-rearing period, so the proportion of ‘likely incubators’ was small. This very uneven split was not conducive to modelling the effects of breeding stage; logistic models tend to need larger datasets overall to add in fixed effects, especially when they include several covariates. Thus, there were insufficient data to include an interaction term within the model, or model distributions separately, for different breeding periods. In the absence of being able to confirm breeding status for a large proportion of the data, we felt that combining data offered the best solution.

iv Addressing repeated measures and between-individual variation

The modelling needs to take account of the fact that locations along a given track are not independent (i.e. they are repeated measures[16]), as birds generally move only a short distance from one observation to the next. As the time, and therefore the distance, between successive foraging locations can be short, and as the environmental covariates are spatially auto-correlated (values closer together in space are more similar to each other than with those further away), foraging locations from the same track tend to occur in similar environmental conditions. Failure to account for the lack of independence between foraging locations within a track (a form of pseudoreplication) leads to underestimation of the variance of parameter estimates and might therefore result in some environmental covariates being wrongly regarded as significant. The simplest way to deal with this is to weight each foraging location by the reciprocal of the length of the observed track. This has the effect of treating each track as a single sampling unit, instead of treating the individual observation as the sampling unit. In addition, the weighting process avoids biasing the results towards the longer tracks (another form of pseudoreplication) and ensured the results were not dictated by a small number of data-rich individuals.

Existing methodological approaches fit mixed effects models (e.g. GLMM or GAMM) to account for between-individual variation. However, it is non-trivial to deal with the control points when specifying the random effects as it is unclear what the analogue is for the tracks in the case data (see Brewer *et al* 2012a). We considered several approaches but felt that none were appropriate, essentially because our data set consisted of only one (known) track recorded per individual. Multiple tracks per bird would be needed to investigate differences in individual preferences between birds, in which case mixed models would then be appropriate. Thus we report results using fixed effects-only models, and we combined data across all individuals for analysis.

---

[16] They are also auto-correlated; this is addressed in Section 2.2.2.v

v Accounting for residual autocorrelation

We explored whether environmental covariate selection in the models was biased by any residual spatial autocorrelation (i.e. the remaining autocorrelation after the effect of the environmental covariates has been accounted for). Not accounting for this autocorrelation can lead to underestimation of the standard errors for parameter estimates, and this in turn implies some variables may wrongly be declared significant as a consequence; for more detail see Beale *et al* (2010).

We applied a Bayesian modelling approach using Integrated Nested Laplace Approximation (INLA, Rue *et al* 2009) to fit full spatial models which accounted for spatial autocorrelation. The approach fits a weighted regression model as before, but allows for dependence between the residuals. This residual dependence structure is defined via a 'mesh' (or 'network'), itself estimated by the procedure, which encapsulates the spatial autocorrelation structure based on the locations of the observations; one observation is linked via the mesh to a small number of its closest neighbours, and the modelling is able to relate the correlation between residuals to these between-neighbour distances; a longer link in the mesh corresponds to a lower correlation, and vice versa. The key here is that the mesh provides a computationally efficient (but complex) way of encoding the spatial autocorrelation. We compared the results from these models with those which did not account for residual autocorrelation to explore the extent to which covariates may have been selected as a consequence of residual autocorrelation (see Brewer *et al* 2012a). We found that residual autocorrelation led to only a small amount of bias in covariate selection in the models; of the five (out of twelve) model comparisons which identified issues, these were limited to seven out of a total of 48 covariates across the models; as a result we decided to use results from the (far simpler) weighted GLM analyses. Although the effect of not accounting for residual autocorrelation was only investigated using the GAM models, it is unlikely that the scale of this would substantially differ from the GLM models given all relationships were broadly linear.

vi Cross-correlated covariates

High correlation[17] between covariates affects parameter estimates and standard errors, and therefore estimates of statistical significance. If model selection is based on significance testing then some variables may be excluded when they are actually important predictors. Although its presence affects the ability of a model to explain distributions (identifying statistically significant associations), it is unlikely to be a serious issue for making predictions at the colony for which the model was built (Schmueli 2010). However, cross-correlation may pose problems if the model is used to make predictions at other colonies, where the correlations between covariates may differ. In such cases, if a model has been based on covariates which are not causally related to the response variable, it is not likely to perform well outside the sample on which it is based. However, in the absence of knowledge of the true causal relationships, it then falls to judgement as to which variables to omit or include. Instead of making such judgements, we selected the covariates in the models used for geographic extrapolation based on their predictive performance at new colonies (see ii). We also incorporated existing biological knowledge within our model selection methods thus reducing the potential for including spurious relationships caused by cross correlations between covariates.

---

[17] e.g. pair wise correlations with r >c.0.8 (A. Zuur, Highland Statistics, *pers. com.*), although there is no agreed level

2.2.3 Phase 1: generating site-specific models

In Phase 1 of the project, colony-specific models for each species were generated for each colony where data were available. Following the model development phase (Section 2.2.2), the final models applied to the case-control data were weighted binomial GLMs. Model selection (identifying which explanatory environmental covariates to retain in the model) for Phase 1 was based on a stepwise search for the model which minimised the AIC. The AIC value (lower is better) offers a relative estimate of model quality by looking at the trade-off between model complexity and goodness-of-fit to the underlying data (Burnham & Anderson 2002). Often, a search for the model which minimises AIC identifies a number of models with very similar AIC values close to the minimum and a rule of thumb is that two models are essentially indistinguishable if the difference in their AIC value is less than two (Burnham & Anderson, 2002). So there is merit in choosing an essentially equivalent model (∂AIC ≤ 2) to the minimum AIC model if there is reason to believe it is more robust and/or biologically meaningful.

We investigated how robust our models were by using a bootstrapping approach (resampling the dataset with replacement) to quantify the repeatability of covariate selection within the models. For each species/colony, the stepwise model selection procedure was repeated 100 times with the case-control dataset being sampled with replacement (i.e. bootstrapping). By counting the number of times each variable was selected across the resulting 100 minimum AIC models, this allowed us to assess how consistently covariates were selected, indicating their robustness to the influence of individual bird's preferences.

We recognised that some environmental covariates may be more useful to predict foraging tern distributions than others. This could be due to a number of reasons relating to the degree to which the proposed biological mechanism is realistic and of direct importance in governing the birds' use of the habitat, and also depending on the quality of our covariate data. We therefore ranked our covariates based on the biological meaningfulness of the proposed biological mechanism, while taking account of how good the data may be for making predictions (e.g. quality of data measurement, predictability of the variable, its resolution and coverage) (see Appendix 1).

For the final model we used the model with the lowest AIC[18], but where this contained covariates that were selected in less than half of the 100 models derived from the bootstrapping and / or ranked low on biological mechanism or data measurement quality (corresponding to a biological ranking >5), we investigated whether removal of these covariates provided an equivalent (∂AIC ≤ 2) model. If so we used the equivalent, but more robust and/or biologically meaningful, model.

i Assessing model performance

We used cross-validation to assess the performance of the final Phase 1 models. Cross-validation involves omitting a sub-set of data (the validation set), and refitting the chosen model to the training set (the remaining data). Predictions based on each training set are then compared with the validation set. Comparisons can be done by various scoring methods; we used three to avoid reliance on a single method (see Box 2). The validation process was performed several times to ensure all data points were omitted at some stage during the process. We assessed Phase 1 model performance in two ways by investigating

---

[18] In cases where sea surface temperature or chlorophyll concentration were available as candidate covariates but were not selected in the potential lowest AIC models, the stepwise search was rerun with the exclusion of these variables to ensure a more reliable AIC statistic (more reliable because covariates which are unable to make predictions to some grid cells due to incomplete datasets are excluded). By excluding these covariates, additional grid cells can be included in the analysis: the dataset is not identical to that for a model where those grid cells have been excluded to allow inclusion of these covariates, and therefore the AIC score may differ.

how well the model predicted (i) validation data for individuals and (ii) validation data for years.

Model performance in predicting validation data for individuals

This analysis was carried out for any species/colonies with at least 50 tracks. For each colony and species we formed 100 bootstrap samples for each of 10, 20 or 30 tracks in the training set. In each case we held back 30 tracks sampled randomly without replacement for use as a test set and then sampled 10, 20, or 30 tracks randomly with replacement from the training set, together with the corresponding control tracks. The covariates that were included in the final model were used to fit a model to the training set samples and model performance assessed with the test set. More details are available in Potts and Brewer 2013.

Model performance in predicting validation data for years

This analysis was carried out for any species/colonies with more than one year of data with at least five tracks in each. The test set comprised an individual year of data and the corresponding controls, with the remaining year(s) forming the training sets. A model was fitted containing the covariates that were included in the final model to each training set and model performance assessed with the test set. This process is repeated with a different year of data used as the test set, until all years of data had been used as a test set once.

2.2.4 Phase 2: Generating models for geographic extrapolation

i Determining input datasets for model building

When generating models for use in geographical extrapolation, an important consideration is which colony datasets to include in the models, to ensure that the data used are as representative as possible for the unsurveyed area. One option is to use all available data for that species to generate a single, broadly applicable model that aims to overcome site-specific factors and identify over-arching habitat preferences. Another option is to use a sub-set of available data that might be considered more representative of the area to which predictions will be made. We considered sub-setting the data based on ecological groupings, for example there might be variation between colonies in terms of the type of prey consumed, and therefore environmental preferences might differ. However, there is a lack of information to inform such ecological groupings so instead we used judgements based on geographic similarities (e.g. whether the colony was on an island or within a sheltered inlet) or regional groupings (e.g. colonies bordering the Irish Sea). In addition, we explored sub-setting the data based on similarities in the covariate data, between the colony to which models are being extrapolated and the colonies for which data are available to the model. We compared the covariate data between colonies in two ways: (i) comparing simple boxplot summaries for each environmental covariate in turn; (ii) using a principal component analysis (PCA) to study the combination of information from all covariates simultaneously. PCA takes a set of variables and replaces them with a smaller number of new variables (the principal components) in such a way that as much as possible of the information in the original variables is retained in the new ones. This allows us to plot the data in a concise way, for example by plotting the second principal component (PC2) against the first principal component (PC1). Colonies which are close together in this plot will be similar in terms of the original set of environmental covariates. These exploratory analyses informed the selection of suitable subsets of colonies which shared environmental, geographic or regional similarities.

To determine which grouping (all colonies or the various sub-sets of colonies identified) was likely to be most appropriate for making geographically extrapolated predictions to each unsurveyed area, we compared the predictive abilities of models generated from each grouping using cross-validation. This involved omitting data from each colony in the grouping in turn to assess the ability of a model built using data from the remaining colonies in that group to predict to the colony omitted. The results of the cross-validation exercise (Brewer *et al* 2013b) showed that model performance was generally better when data from all available colonies for that species are combined.

Therefore, for the final Phase 2 models, we pooled data across all available colonies for each species. As with Phase 1, a weighted binomial GLM was applied. For extrapolating to new colonies, we aimed to identify relationships which were consistent across colonies and which were most biologically plausible. So for the final Phase 2 models, for each species we limited the candidate covariates to those which were selected in at least one third of all Phase 1 models for that species, and which had a biological ranking of ≤5 (see Appendix 1) (recognising that model selection may then further reduce the covariates within the models). Boxplots were used to compare the range of values for the shortlisted candidate covariates at the colonies for which predictions were required with those for which data were available, to confirm that there was overlap in these values between the colonies in Phase 1 and 2; this is important for extrapolation purposes.

ii Model selection and assessing model performance

Our main concern for Phase 2 was ensuring the models performed well when extrapolated to new areas. Therefore model selection for Phase 2 was based on the ability of models to predict data from new colonies. The predictive ability of models consisting of all combinations of the candidate covariates was tested using cross-validation, by omitting each colony in turn and developing a model using data from the remaining colonies. Three scores were used to compare the predictive ability of the models in the cross-validation (see Box 2). For each scoring method, the scores omitting each colony in turn were then averaged to give an overall score. For common and Sandwich terns, the cross-validation exercise was repeated excluding the salinity in spring covariate so that North Norfolk tern data could be included (salinity in spring data were not available for this area). The covariates chosen for the final model (which would be built using data from all colonies) were those contained within the model was that supported by two of the three scoring methods (based on the average score from each), except where there were extrapolation issues (see Results), in which case the next best model was chosen. As well as providing a tool for model selection, the cross-validation exercise provided an indication of the predictive ability of the final model chosen, and therefore our confidence in its performance.

Box 2. The three scores used for cross-validation exercises to assess predictive ability of each model.

(1) The Brier score or mean squared error $\frac{1}{n}\sum(y_i - p_i)^2$
where *y* is the binary variable indicating foraging behaviour and *p* is the predicted probability.
This represents the mean squared difference between the actual outcome (1 for presence or 0 for a control point) and the predicted probability of presence; lower values indicate a better model.

(2) A logarithmic score related to the log-likelihood $= \frac{1}{n}\sum(y_i \log(p_i) + (1-y_i)\log(1-p_i))$
This score means that the best model is the one which gives the highest predicted probability to the data; higher values of this score indicate a better model.

(3) The area under the curve (AUC), representing the area under the receiving operating

characteristic (ROC) curve. This is equivalent to the Wilcoxon signed-ranked test (Mason & Graham 2002) and was calculated by this method using the function roc.area in the R package 'verification'. If the model provided a perfect separation of the presences from the control points the AUC score would be 1, whereas it is 0.5 for a model with no discriminatory power.

The AUC is a widely used statistic for assessing species distribution models, but has been criticised for a number of reasons, including the fact that it is insensitive to transformations of the predicted probabilities that preserve their ranks (Lobo *et al*, 2008; Jiménez-Valverde 2012) and reliance on AUC as a single measure of model performance has therefore been questioned (Austin 2007). The Brier and logarithmic scores have similar properties but there is no clear criterion for preferring one over the other (Machete 2013).

2.2.5 Application of Phase 1 and 2 models

The intention is to use the model outputs from this project as part of the evidence base for any possible marine SPAs for the larger tern species. As such, further analyses (not reported here) are being undertaken using the maximum curvature technique (O'Brien *et al* 2012) to delineate possible boundaries based on the intensity with which foraging terns are predicted to be using the marine environment. For two of the Phase 1 colony-specific models (Sandwich terns at Farne Islands SPA and Larne Lough SPA) these analyses failed to find a point of maximum curvature, most likely due to the predicted output values containing a very high proportion of very small values. As an alternative, we applied generic models (under Phase 2), which were amenable to maximum curvature analysis. It is these Phase 2 models which are presented here for these two particular cases.

3 Results

3.1 Data coverage overview

Visual tracking proved to be a successful non-invasive data collection technique across all four larger tern species and to our knowledge this is the first time it has been undertaken on roseate terns. It is important that the behaviour and welfare of sampled birds is not adversely affected by the survey method and we found that birds appeared to generally ignore the presence of the vessel with observers recording very few instances of birds visibly reacting to the RIB, consistent with Perrow *et al* (2011). However, one of the difficulties with visual tracking is that it can be difficult to maintain constant visual contact with a bird and around 63% of terns tracked were lost before they completed their foraging trip (Table 3), for example because they flew faster than the RIB could follow; they were lost within flocks; or tracking had to cease due to safety issues such as areas of shallow reef.

The total number of tracks obtained was 1005 including 55 (6%) for roseate tern (2 SPAs), 184 (18%) for Arctic tern (6 SPAs, 1 non-SPA), 381 (38%) for common tern (7 SPAs, 1 non-SPA) and 385 (38%) for Sandwich tern (5 SPAs, 1 non-SPA), with multiple years of data collected at five of the ten JNCC study colony SPAs. In addition, visual tracking data were obtained through a data-sharing agreement with ECON Ecological Consultancy Ltd for two SPAs: Ynys Feurig, Cemlyn Bay and The Skerries SPA (136 Sandwich, 2 common and 1 Arctic tern track, all collected in 2009) and North Norfolk Coast SPA (108 Sandwich and 24 common tern tracks collected 2006-2008). This gives a total of 1276 tracks available to the project, although not all data were used in the modelling (see below). An overview of sample sizes obtained for each colony is given in Figure 2. The raw tracking data and analyses outputs for each colony SPA are detailed in the relevant colony SPA sections below. The vast majority of the data (*c*. 95%) were collected during a period timed to coincide with the chick-rearing period. The maximum foraging ranges that we recorded for each species at each colony are given in Table 4 along with the mean maximum across colonies. The most recent published mean maximum estimates available (Thaxter *et al* 2012, also shown in Table 4) fell within the range of mean maximum values we recorded, though it is important to note that the Thaxter *et al* 2012 estimates are largely based on data collected using methods other than visual-tracking.

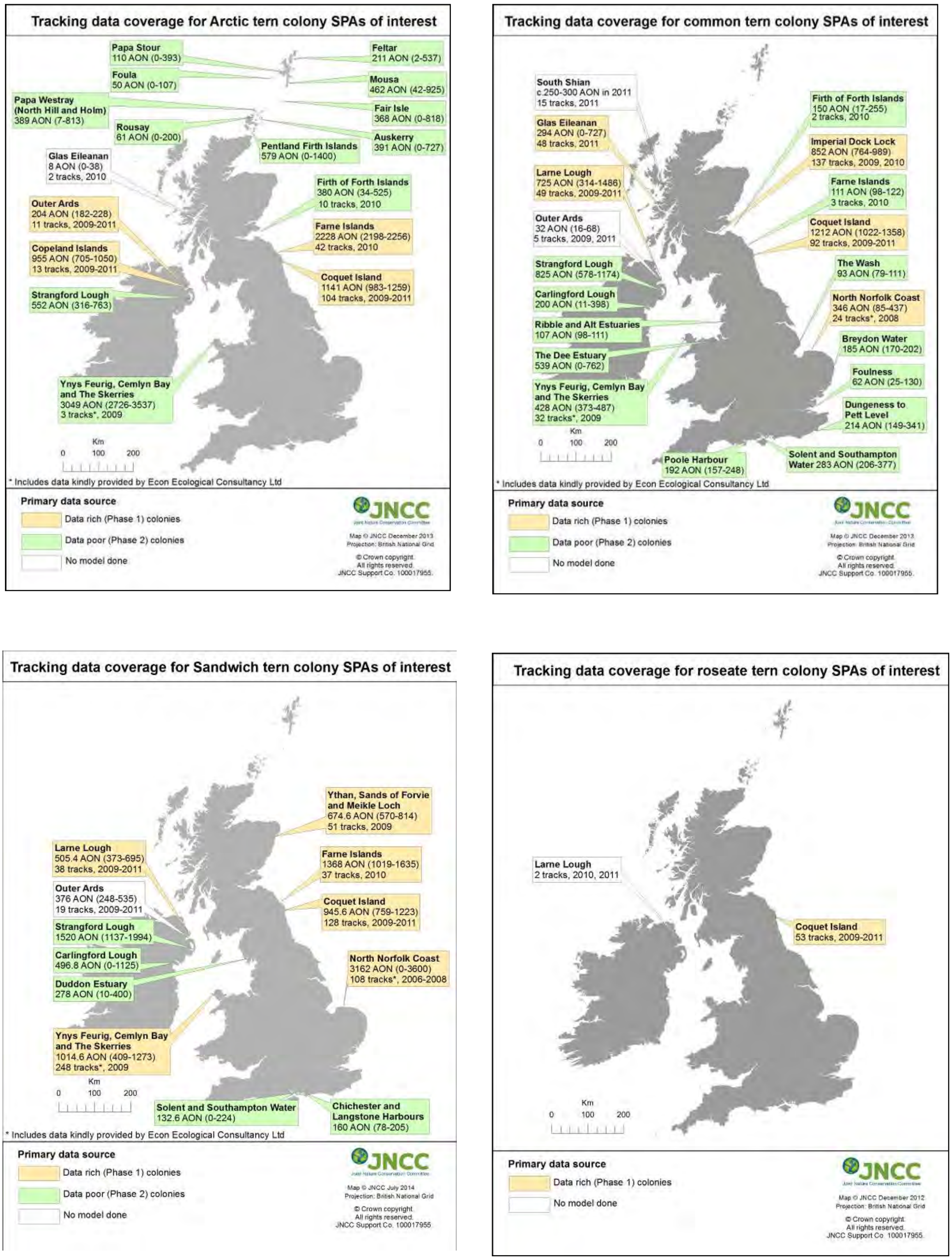


Figure 2. Data coverage and sample sizes for the relevant colony SPAs of interest, for each of the four larger tern species. The mean number (and range) of Apparently Occupied Nests (AON) are given as calculated using JNCC's Seabird Monitoring Programme database in 2010 (see Methods), except for South Shian and Glas Eileanan where data were kindly provided by C. Craik. Boxes are colour-coded according to whether models were developed under Phase 1 (site-specific) or Phase 2 (generic). Note that some data were collected that were not used in the modelling (see Results).

Table 3. The number and percentage of complete tracks compared to the total number (complete and incomplete), for each tern species per SPA per year, for data collected by JNCC.

SPA	**Total no. of tracks**	**complete tracks**		**Total no. of tracks**	**complete tracks**		**Total no. of tracks**	**complete tracks**		**Total no. of tracks**	**complete tracks**	
		n	**%**		**n**	**%**		**n**	**%**		**n**	**%**
2009												
	Arctic tern			**common tern**			**roseate tern**			**Sandwich tern**		
Ynys Feurig, Cemlyn Bay and The Skerries	2	1	50	30	9	30	0	0	-	112	25	22
Copeland Islands	1	0	0	0	0	-	0	0	-	0	0	-
Coquet Island	47	13	32	37	10	27	21	8	38	49	16	33
Imperial Dock Lock	0	0	-	114	48	42	0	0	-	0	0	-
Larne Lough	0	0	-	18	9	50	0	0	-	10	4	40
Outer Ards	6	5	83	4	2	50	0	0	-	9	2	22
2010												
	Arctic tern			**common tern**			**roseate tern**			**Sandwich tern**		
Copeland Islands	2	0	0	0	0	-	0	0	-	0	0	-
Coquet Island	14	7	50	13	8	50	1	0	0	8	2	25
Farne Islands	42	20	48	3	0	0	0	0	-	37	11	30
Imperial Dock Lock	0	0	-	23	7	30	0	0	-	0	0	-
Larne Lough	0	0	-	2	1	50	1	0	0	13	7	54
Outer Ards	1	1	100	0	0	-	0	0	-	8	1	13
Forth Islands	10	5	50	2	1	50	0	0	-	0	0	-
2011												
	Arctic tern			**common tern**			**roseate tern**			**Sandwich tern**		
Copeland Islands	10	6	60	0	0	-	0	0	-	0	0	-
Coquet Island	49	22	45	42	18	43	31	15	48	71	12	17
Larne Lough	0	0	-	29	13	45	1	0	0	15	7	47
Mull, Glas Eileanan	2	0	100	48	29	60	0	0	-	0	0	-
Mull, South Shian	0	0	-	15	0	0	0	0	-	0	0	-
Outer Ards	4	1	25	1	0	0	0	0	-	2	2	100
Sands of Forvie	0	0	-	0	0	-	0	0	-	51	26	51

Table 4. Maximum foraging ranges recorded (regardless of whether the track was complete or incomplete) for each species at each colony and the mean maximum across all colonies.

	Maximum foraging range (km) recorded			
Colony	**Arctic**	**Common**	**Roseate**	**Sandwich**
Blakeney Point, North Norfolk		12.29 (n=24)		42.5 (n=58)
Cemlyn Bay		12.18 (n=31)		34.75 (n=248)
Cockle Island, Outer Ards	46.01 (n=11)	19.88 (n=5)		36.89 (n=19)
Copeland Islands	39.56 (n=13)			
Coquet Island	22.8 (n=104)	17.89 (n=92)	18.68 (n=53)	27.61 (n=124)
Farne Islands	20.66 (n=42)			20.23 (n=37)
Glas Eileanan		13.68 (n=48)		
Larne Lough (Blue Circle Island and Swan Island)		30.38 (n=49)		17.25 (n=38)
Imperial Dock Lock		21.04 (n=137)		
Sands of Forvie				22.89 (n=51)
Scolt Head, North Norfolk				54 (n=48)
South Shian		21.55 (15)		
Mean Maximum Foraging Range	**32.26 (n=4)**	**18.61 (n=8)**	**18.68 (n=1)**	**32.02(n=8)**
Mean Maximum from Thaxter *et al* (2012)	24.2 (4)	15.2 (6)	16.6 (6)	49 (2)

The number of tracks for each colony/species is given in parenthesis. Data considered potentially unrepresentative were excluded (Firth of Forth data; datasets with fewer than five tracks; any tracks where birds were picked up offshore rather than adjacent to the colony as was the case for some of the ECON Ecological Consultancy Ltd data) The most recent published mean maximum estimates available (Thaxter *et al* 2012) are shown for comparison.

3.2 Model results overview

The results from the model development phase of the project are available in the relevant contract reports (Brewer *et al* 2012a, c and Potts *et al* 2013a for Phase 1, and Brewer *et al* 2012b for Phase 2) and are not repeated here. Instead we focus here on the final models applied in the project (described in Potts *et al* 2013b, c and Potts & Brewer 2014). Table 5 summarises the final Phase 1 models for each species and colony, along with the sample sizes of the data underlying the models; model selection details can be found in Appendix 2 and the final model equations can be found in Appendix 3.

For Phase 2, the candidate covariates that were short-listed for input into model building were those which were selected in at least one third of the Phase 1 models and had a biological ranking ≤5 (see Appendix 1). These are shown in Table 6. Model selection using cross-validation was then carried out on models containing different combinations of these covariates. The detailed results of the cross-validation using the three different scoring methods (see Methods) are given in Potts *et al* (2013c) and summarised in Table 7. For Arctic terns the preferred model involved distance to colony and bathymetry and was supported by all three scoring methods (Table 6). Boxplots showed that there were no extrapolation issues for bathymetry (i.e. there was overlap in the range of values at the colonies for which predictions were required with those for which data are available) (see Potts *et al* 2013c). For common terns the preferred model involved distance to colony, distance to shore and bathymetry. This model was chosen by all three scores except by the AUC score when applied to models using the full candidate covariate dataset (i.e. excluding Blakeney Point tern data but including salinity, see Methods); in the latter case the preferred model involved only distance to colony (Table 6). As with Arctic terns, there were no extrapolation issues for bathymetry. For Sandwich terns three different models were each supported twice across the six evaluation methods applied (Table 6). When North Norfolk data are excluded (to allow salinity in spring to be included, see Methods), the best model according to the likelihood score is one involving distance to colony, distance to shore and bathymetry, while the best model according to the other two scores is one involving distance to colony, distance to shore and salinity in spring. When North Norfolk data are included the model involving distance to colony, distance to shore and bathymetry is again selected, this time by the mean squared error score, although the model that involves just distance to colony and bathymetry is selected by the other two scores. As there are extrapolation issues with salinity in spring (due to the different ranges that this variable takes at different colonies and because this variable is not available for the Greater Wash area), the recommended model is therefore one involving distance to colony, distance to shore and bathymetry; these covariates were consistently selected across the short-list of models identified by the different evaluation methods.

Table 8 shows the covariates selected in the final models for each species under Phase 2, along with the sample sizes for the data underlying the models, and the list of colonies to which predictions were made with the models. The final model equations can be found in Appendix 3.

Table 5. Covariates selected in the final models for each species and colony under Phase 1, along with the sample sizes for the data underlying the models. Only tracks containing foraging records were used in the modelling.

Species	SPA	No. tracks available	No. tracks used in model	No. years of data	Covariates in the final Phase 1 model
Arctic tern	Farne Islands	42	32	1	Distance to colony, salinity in spring
	Coquet Island	104	91	3	Distance to colony, chlorophyll concentration in June, bathymetry
	Outer Ards[a]	11	24	3	Distance to colony, shear stress current
	Copeland Islands[a]	13			
Common tern	Coquet Island	90	75	3	Distance to colony, chlorophyll concentration in June, bathymetry, sea surface temperature in April
	North Norfolk Coast	24[b]	20	1	Distance to colony, shear stress wave
	Ynys Feurig, Cemlyn Bay and The Skerries	32[b]	19	1	Distance to colony, salinity in spring
	Larne Lough	49	32	3	Distance to colony, distance to shore, bathymetry, slope
	Imperial Dock Lock	137	118	2	Distance to colony, slope, salinity in spring, distance to shore, bathymetry
	Glas Eileanan	63[c]	49	1	Distance to colony, distance to shore, slope
Roseate tern	Coquet Island	53	40	3	Distance to colony, sea surface temperature in May, chlorophyll concentration in June
Sandwich tern	Coquet Island	127	90	3	Distance to colony, distance to shore
	North Norfolk Coast	108 [b]	88	3	Distance to colony, distance to shore, shear stress wave, bathymetry
	Ynys Feurig, Cemlyn Bay and The Skerries	248 [b]	72	1	Distance to colony, distance to shore, salinity in spring
	Ythan Estuary, Sands of Forvie and Meikle Loch	51	51	1	bathymetry, stratified temperature

[a] Data from Outer Ards and Copeland Islands were combined to build a single model which was then applied separately to each SPA

[b] includes data kindly provided by ECON Ecological Consultancy Ltd

[c] includes data from South Shian

Table 6. The short-list of candidate covariates for each species for input into the Phase 2 models.

Species	**Candidate covariates used for Phase 2 model building**
Arctic tern	distance to colony, bathymetry, salinity in spring, chlorophyll concentration in June
Common tern	distance to colony, bathymetry, salinity in spring, distance to shore
Sandwich tern	distance to colony, bathymetry, salinity in spring, distance to shore

Table 7. The summary results of model selection for Phase 2 using cross-validation. The models shown are those which were optimal according to each of the three different cross-validation scores (see methods). For common and Sandwich terns, cross-validation was carried out separately, both including and excluding salinity in spring (see Methods). The final model chosen is shown in bold.

		Optimal model according to different cross-validation scores					
Species	**Model**	**Likelihood**	**MSE**	**AUC**	**Likelihood**	**MSE**	**AUC**
Arctic tern	**Distance to colony, bathymetry**	✓	✓	✓			
		Including salinity			Excluding salinity		
Common tern	**Distance to colony, distance to shore, bathymetry**	✓	✓		✓	✓	✓
	Distance to colony			✓			
Sandwich tern	**Distance to colony, distance to shore, bathymetry**	✓				✓	
	Distance to colony, distance to shore, salinity in spring		✓	✓			
	Distance to colony, bathymetry				✓		✓

Table 8. Covariates selected in the final models for each species under Phase 2, along with the sample sizes for the data underlying the models, and the list of colonies to which predictions were made with the models. Only tracks containing foraging records were used in the modelling.

Species	SPAs (and track sample sizes) used to build model	Model	SPAs to which predictions were made
Arctic tern	Farne Islands (n = 32)	Distance to colony, bathymetry	Ynys Feurig, Cemlyn Bay and The Skerries; Strangford Lough; Fetlar; Mousa; Papa Stour; Foula; Fair Isle; Auskerry; Papa Westray; Rousay; Pentland Firth Islands; Firth of Forth Islands
	Coquet Island (n = 91)		
	Outer Ards (n = 11)		
	Copeland Islands (n = 13)		
Common tern	Coquet Island (n = 75)	Distance to colony, distance to shore, bathymetry	Firth of Forth Islands; Farne Islands; The Wash; Breydon Water; Foulness; Dungeness to Pett Level; Solent and Southampton Water; Poole Harbour; Ynys Feurig, Cemlyn Bay and The Skerries; The Dee Estuary; Ribble & Alt Estuaries; Carlingford Lough; Strangford Lough
	North Norfolk Coast (n = 20)		
	Larne Lough (n = 32)		
	Imperial Dock Lock (n = 118)		
	Glas Eileanan (n = 49[a])		
	Farne Islands (n = 3)		
Sandwich tern	Coquet Island (n = 90)	Distance to colony, distance to shore, bathymetry	Duddon Estuary; Carlingford Lough; Strangford Lough; Farne Islands; Larne Lough; Solent and Southampton Water; Chichester and Langstone Harbours
	Ynys Feurig, Cemlyn Bay and The Skerries (n = 72)		
	Larne Lough (n = 30)		
	Ythan Estuary, Sands of Forvie and Meikle Loch (n = 51)		
	Farne Islands (n=34)		

[a] Includes data from South Shian

3.3 Results by colony SPA

The final Phase 1 and 2 models documented above were used to make predictions for each species around all the colonies of interest which are shown as mapped outputs of relative usage (see Box 1, Section 2.2.2.i) in the following sections for each colony SPA. The spatial extent of the usage predictions around each colony is defined by a radius equal to the species-specific global maximum foraging range (see Section 2.2). The usage values displayed in the maps represent predicted relative densities of foraging locations and are not absolute values. Mapping of quantities, such as relative distributions or densities, can look very different depending on how the data are grouped (binned). The bin categories used for the model outputs presented here were based on natural groupings inherent in the data (‘natural jenks’). These were determined automatically in ArcMap, which identified break points that best grouped similar values and maximized the differences between classes. The bin category colours therefore cannot be compared on a like for like basis between species and between colonies.

As usage values are expressed as proportions which sum to one across the maximum foraging range, the values for each grid cell could potentially become very small due to the fine resolution (500m x 500m) of our spatial grid (i.e. large numbers of grid cells). Hence, for mapping purposes, usage values were multiplied by 1000.

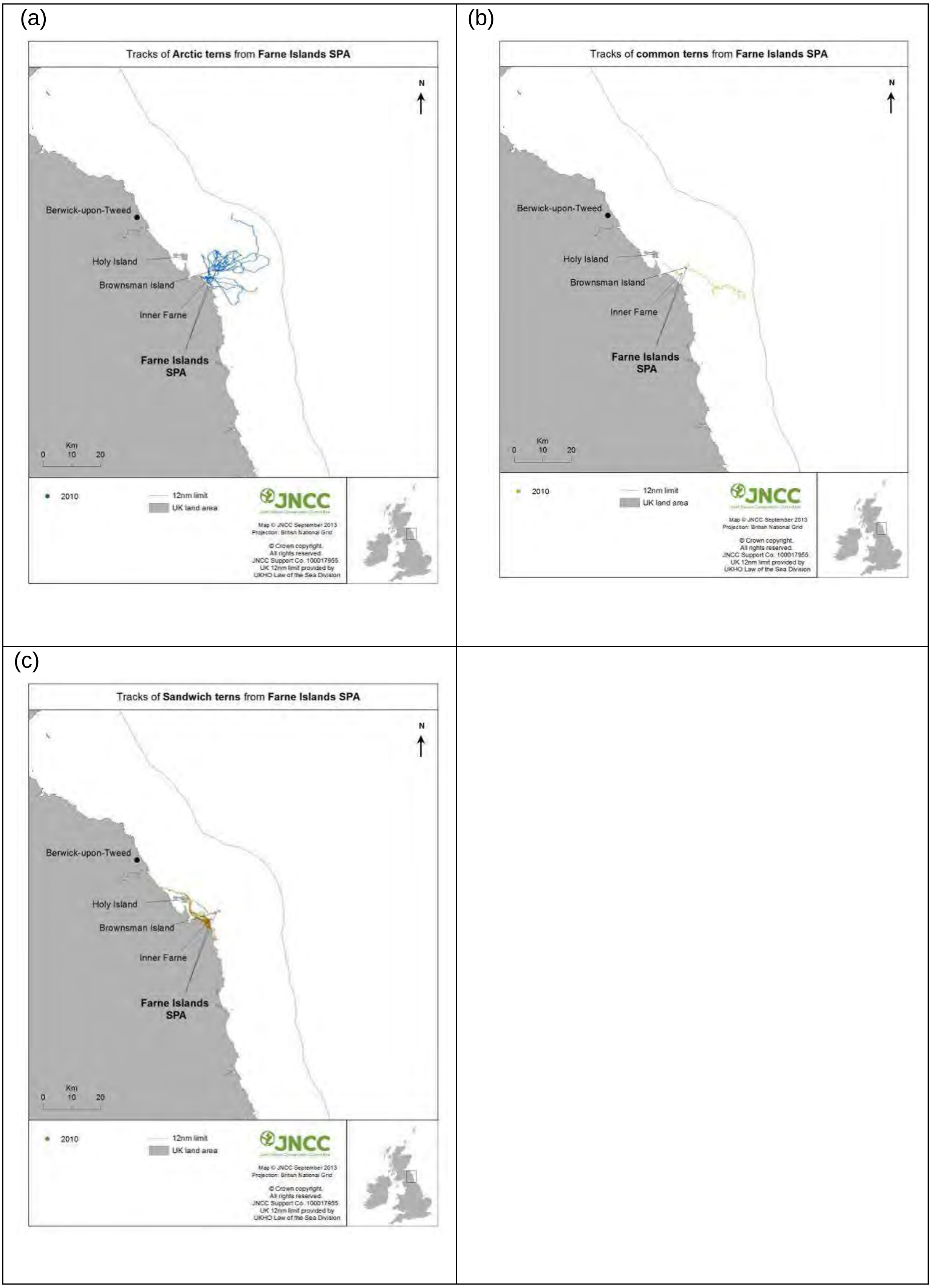
3.4 English colony SPAs

3.4.1 Farne Islands SPA

For the Farne Islands SPA, the species of interest for the project were Arctic, common and Sandwich terns. A total of 81 tern tracks was obtained for these species over a single survey season in 2010, with two separate periods of tracking carried out timed to coincide with incubation (mid May) and chick-rearing (mid June) (Table 9); these are shown in Figure 3. The distribution of Arctic tern tracks tended to radiate out to the northeast, east and southeast from the islands. Only three common terns were tracked from the Farnes Islands (one of which was lost soon after leaving Inner Farne). Sandwich terns tracked from Inner Farne all headed towards the coast (with some then heading up or down the coast); one of these headed north to Holy Island before it turned back and went to Brownsman Island within the Outer Farnes group (rather than return to Inner Farne). Only one Sandwich tern was tracked from the Outer Farnes group.

Table 9. Sample sizes of tracks obtained for tern species breeding at Farne Islands SPA.

Species	**No. of tracks 2010 (Inner Farne)**		**No. of tracks 2010 (Outer Farnes)**		**Total**
	16-23 May	**15-22 June**	**16-23 May**	**15-22 June**	
Arctic tern	5	15	11	11	42
Common tern	1	1	1	0	3
Sandwich tern	18	18	0	1	37
Total	**23**	**32**	**12**	**14**	**81**


(a) Tracks of **Arctic terns** from **Farne Islands SPA**

(b) Tracks of **common terns** from **Farne Islands SPA**

(c) Tracks of **Sandwich terns** from **Farne Islands SPA**

Figure 3. Tracks of (a) Arctic, (b) common and (c) Sandwich terns tracked from the Farne Islands SPA during 2010.

A site-specific model (under Phase 1) was generated for Arctic terns but due to the very low sample size of tracks, no site-specific model was generated for common terns and instead a generic model (under Phase 2) was used. Initially we generated a site specific model for Sandwich terns (under Phase 1) but this was not amenable to the further analyses (not reported here) we wished to apply to delineate possible SPA boundaries. As an alternative, we applied a generic model (under Phase 2) which is reported here (see Methods, Section 2.2.5).

For Arctic terns the results of the bootstrapping and the model selection process are given in Appendix 2. Details of model selection for the Phase 2 models for common and Sandwich terns are given in Potts *et al* 2013c. The final models selected are shown in Table 10. Distributions of predicted usage were made for Inner Farne and the Outer Farnes Group (centred on Brownsman Island) (Figure 4). These closely matched the underlying data for Arctic tern, while for Sandwich tern the predicted usage closely matched the underlying data around Inner Farne and also identified a hotspot around the Outer Farnes from where we were only able to track a single individual. As there were only data for three tracks for common terns, we do not compare this with the modelled prediction.

Table 10. The final models selected for each species for the Farne Islands SPA.

Species	**Model**	**Terms**
Arctic tern	Site-specific	distance to colony, salinity in spring
Common tern	Generic	distance to colony, distance to shore and bathymetry
Sandwich tern	Generic	distance to colony, distance to shore and bathymetry

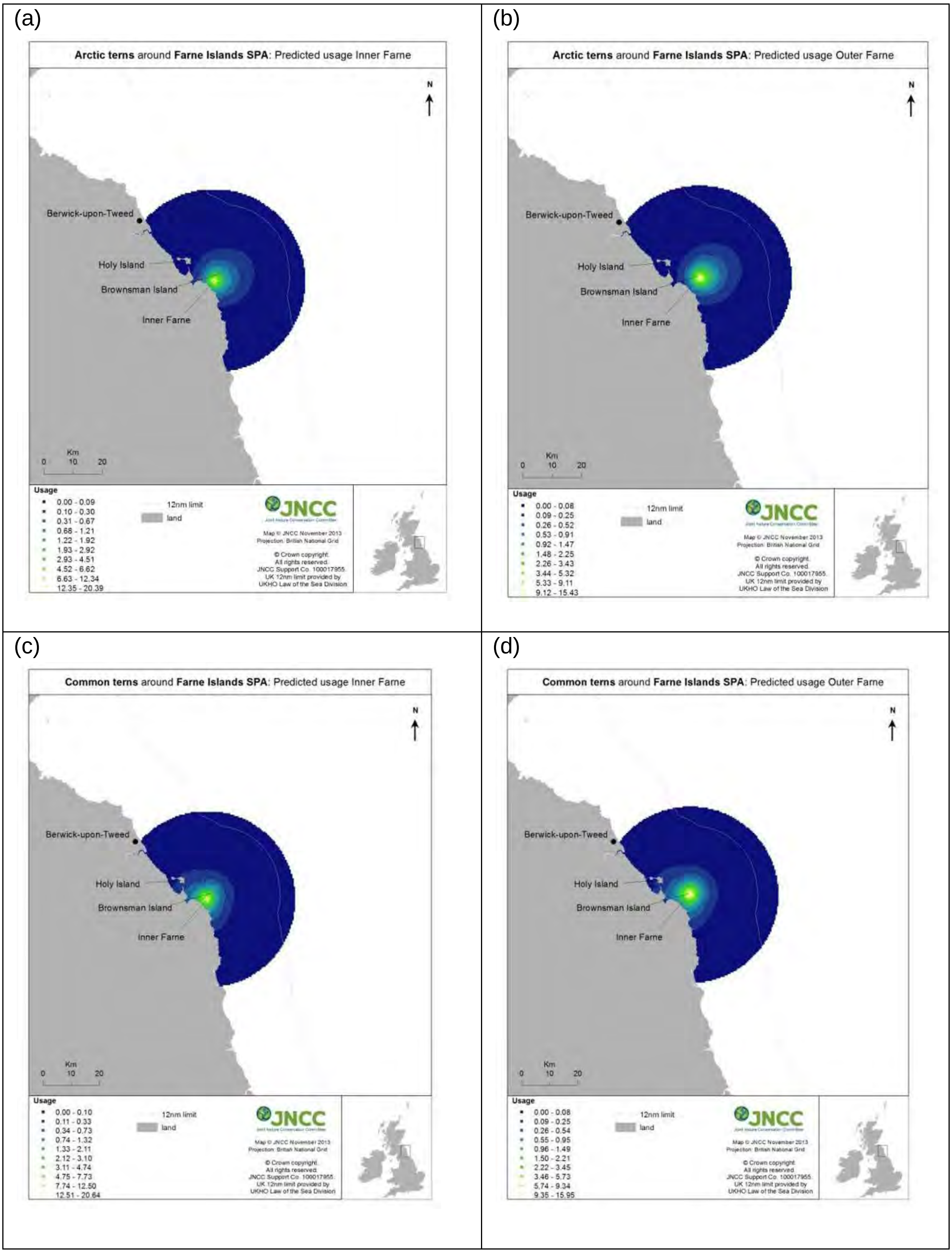


Figure 4. Predicted relative usage of the waters around Inner and Outer Farne Islands for Arctic (a, b) and common terns (c, d). Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

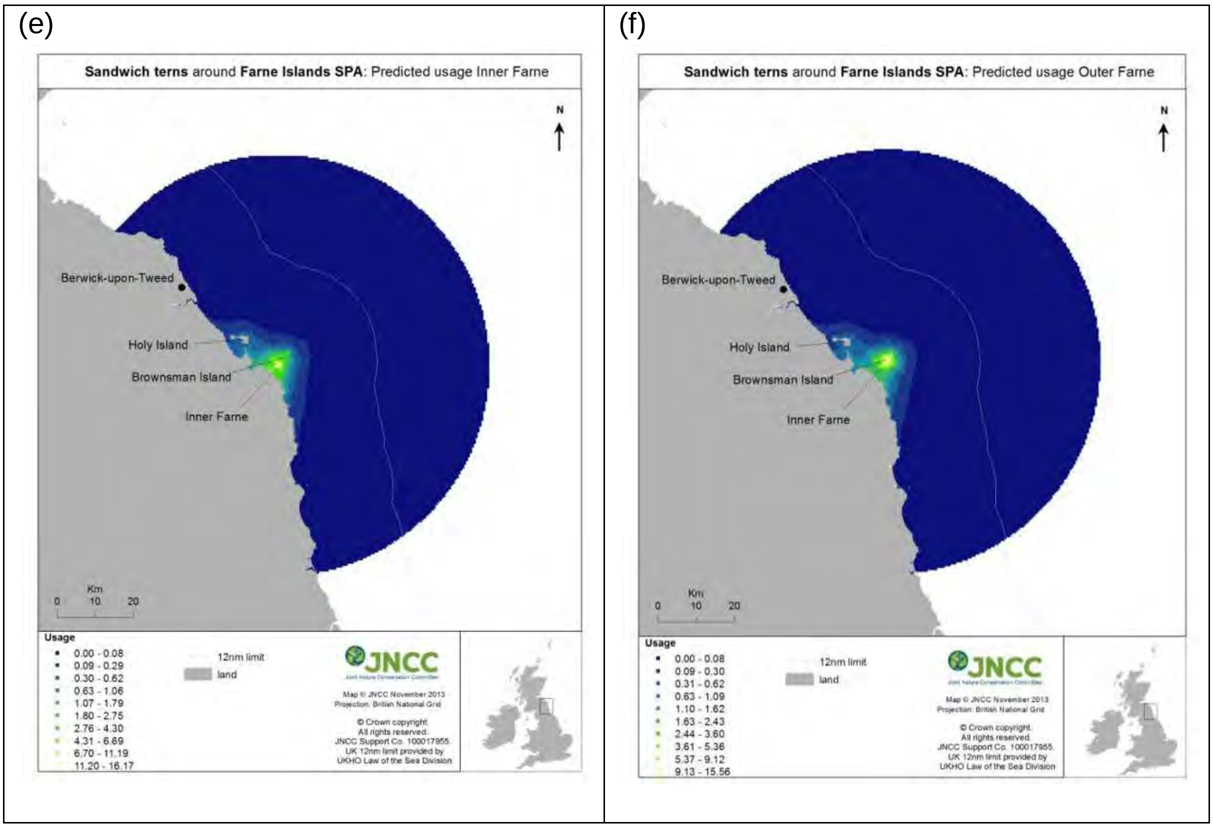


Figure 4 (cont). Predicted relative usage of the waters around the Inner (e) and Outer Farne Islands (f) for Sandwich tern. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.2 Coquet Island SPA

For Coquet Island SPA, the species of interest for the project were Arctic, common, roseate and Sandwich terns. A total of 374 tern tracks was obtained for these species over three survey seasons from 2009-2011 (Table 11). Tracking work was timed to coincide with the chick-rearing season, except in 2010 when data were also collected during the incubation period in May. The distribution of Arctic and common tern tracks tended to radiate out in all directions from the colony, while those for roseate terns tended to be confined to Alnmouth Bay northeast of Coquet Island, and those for Sandwich terns were concentrated in a coastal strip from just north of Alnmouth Bay down to Druridge Bay (Figure 5).

Table 11. Sample sizes of tracks obtained for the four tern species breeding at Coquet Island SPA.

Species	No. of tracks			
	2009 (3-26 June)	2010 (19-21 May; 17-23 June)	2011 (7 June- 1July)	Total
Arctic tern	41	14	49	104
Common tern	35	13	42	90
Roseate tern	21	1	31	53
Sandwich tern	48	8	71	127

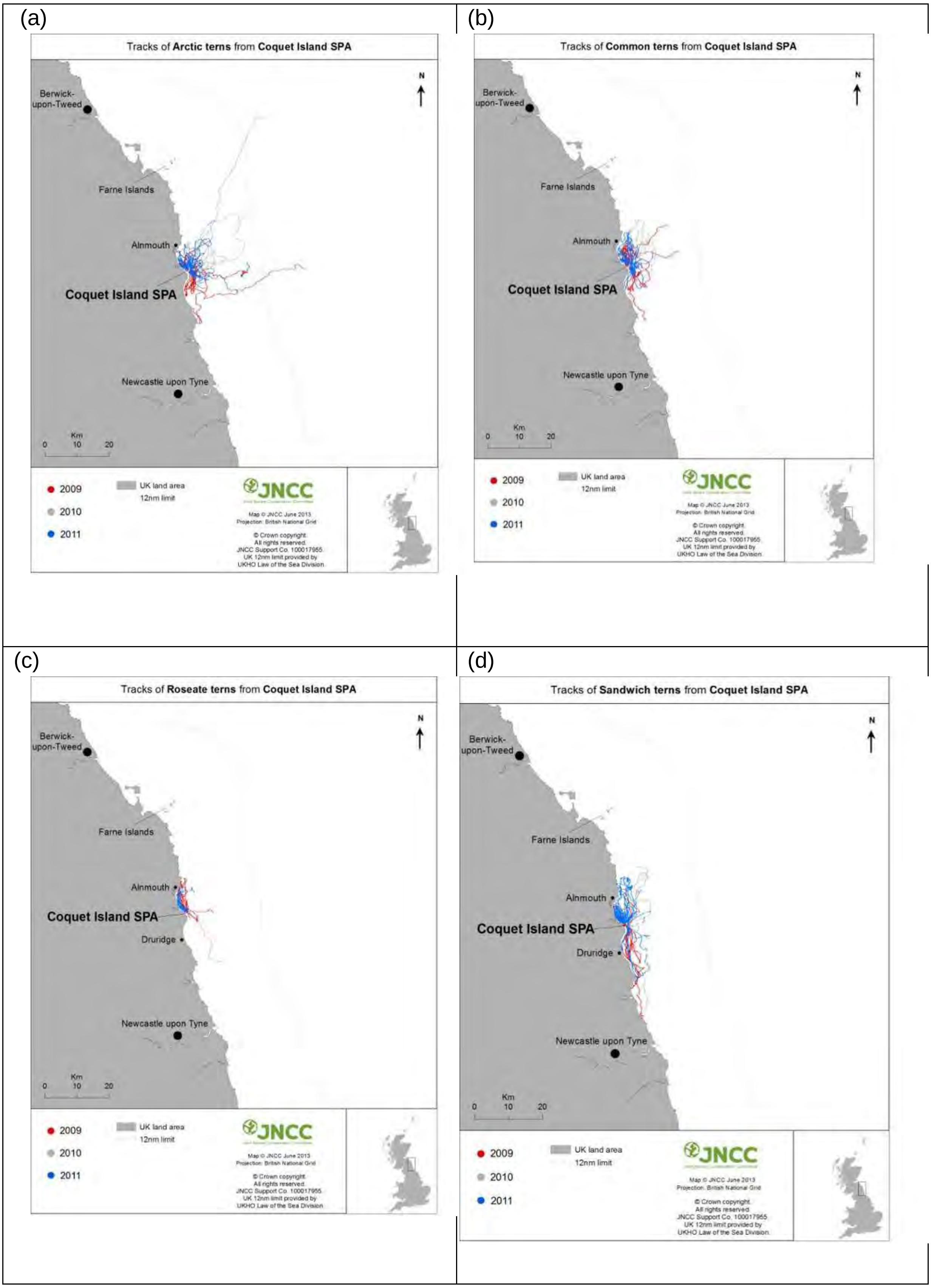


Figure 5. Tracks of (a) Arctic, (b) common, (c) roseate and (d) Sandwich terns tracked from Coquet Island SPA from 2009-2011.

The results of the bootstrapping and model selection process are given in Appendix 2. The final models selected are shown in Table 12. Distributions of predicted relative usage closely matched the underlying data and are shown in Figure 6. The exception to this is that the predicted distribution for roseate terns was more widespread than the recorded observations from visual tracking. It was not possible to generate predictions for many of the grid cells which were between *c*.1-2km adjacent to the coast for Arctic or common terns. This is due to missing data in one or more of the covariates selected in the final model. Missing values close to the coast are common for the chlorophyll concentration and sea surface temperature covariates as these are derived from satellite imagery, which is prone to inaccurate measurement close to the coast due to cloud cover.

Table 12. The final models selected for each species for Coquet Island SPA.

Species	Model	Terms
Arctic tern	Site specific	distance to colony, chlorophyll concentration in June, depth
Common tern	Site specific	distance to colony, chlorophyll concentration in June, depth, sea surface temperature in April
Roseate tern	Site specific	distance to colony, temperature stratification
Sandwich tern	Site specific	distance to colony, distance to shore

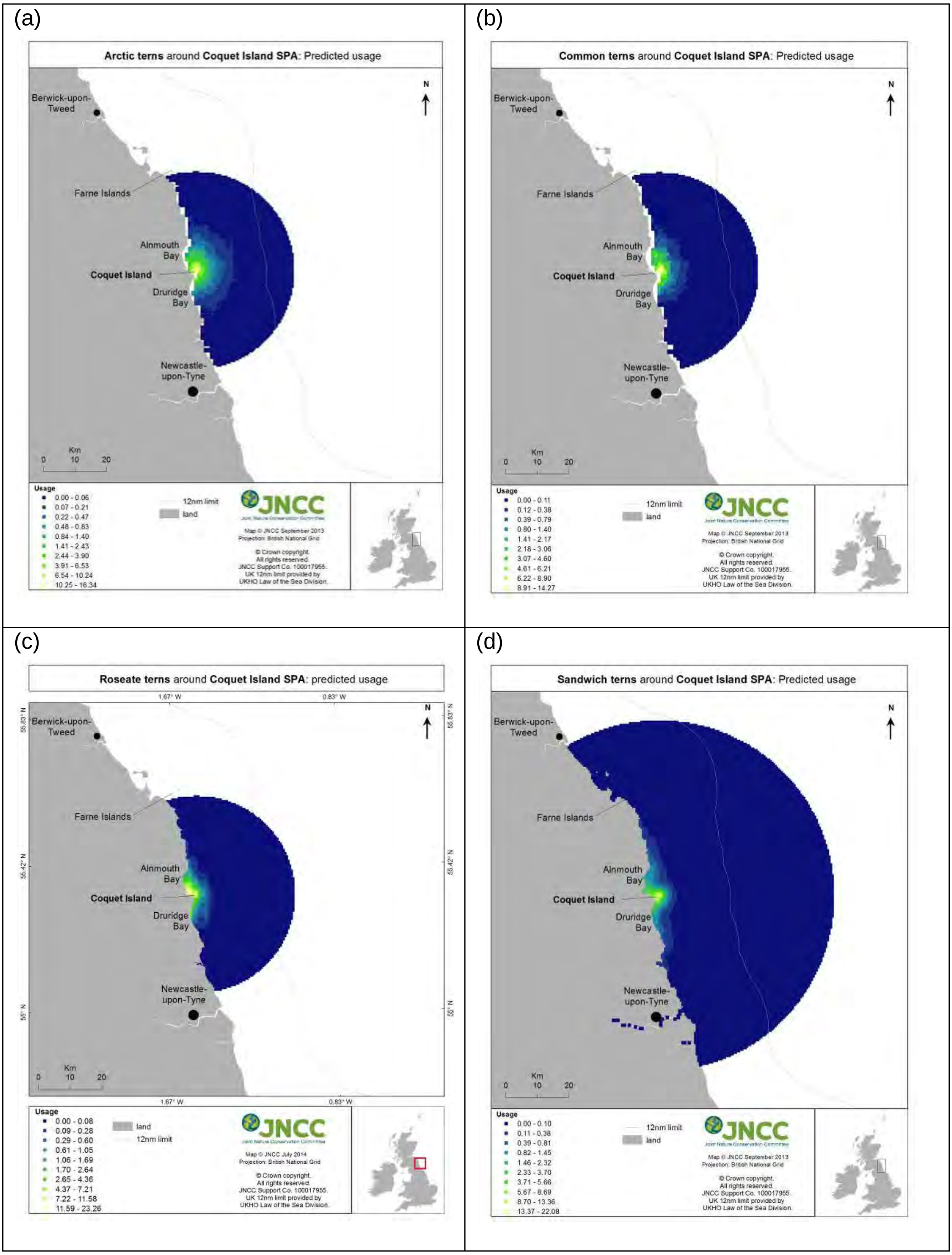


Figure 6. Predicted relative usage of the waters around Coquet Island for (a) Arctic, (b) common, (c) roseate and (d) Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.3 The Wash SPA

For The Wash SPA the species of interest for the project was common tern. No visual tracking data were available so a generic model was applied (Table 13). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Predictions of relative usage were made around Freiston Shore and Snettisham, the only two notable common tern colonies within The Wash SPA (the only other common tern colony in within The Wash SPA is Frampton Marsh, with a mean of 10 AON between 2009-2013). These are shown in Figure 7. The predicted distributions were highest around each colony and decreased with distance from each colony; the foraging areas of birds from each colony did not tend to overlap.

Table 13. The final model selected for The Wash SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry

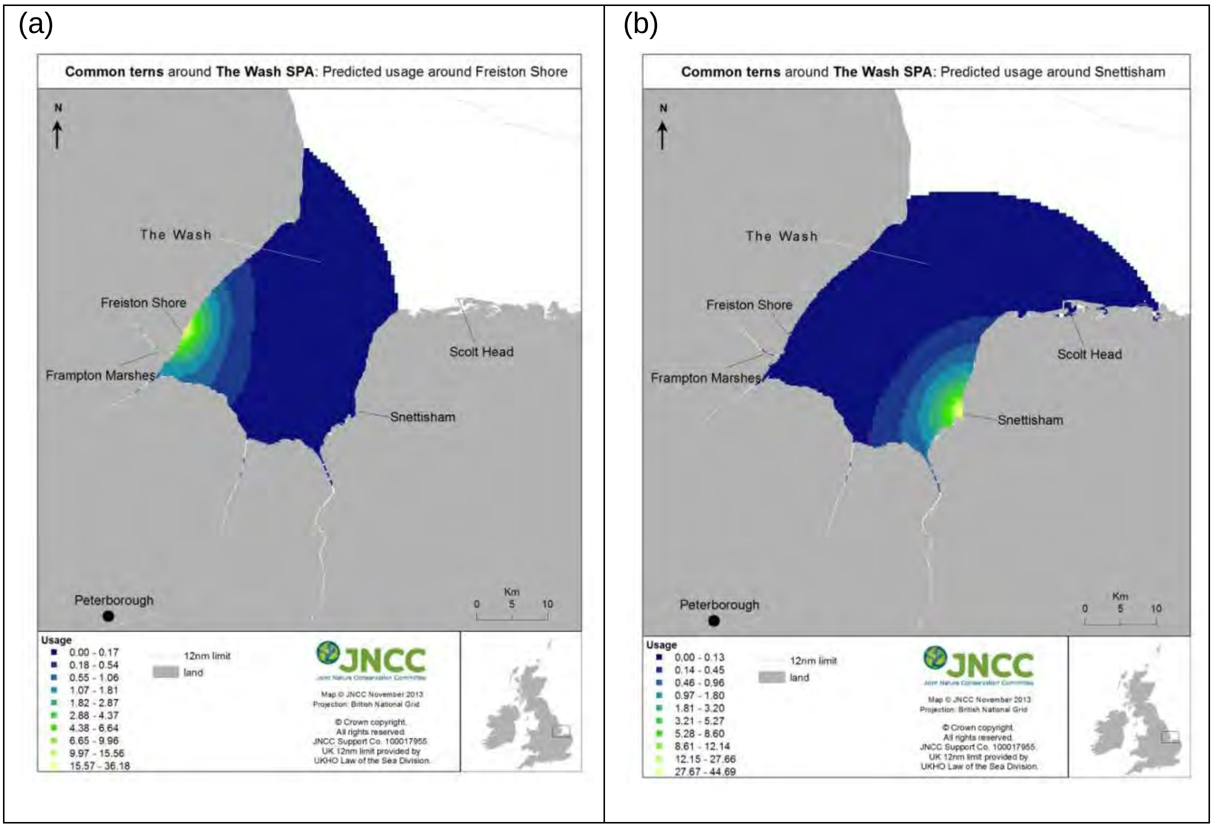


Figure 7. Predicted relative usage of the waters around Freiston Shore (a) and Snettisham (b) within The Wash SPA for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.4 North Norfolk Coast

For the North Norfolk Coast SPA, the species of interest for the project were common and Sandwich terns. Data were kindly provided to the project by Econ Ecological Consultancy Ltd. A total of 132 tern tracks were available for the two species; Sandwich terns were tracked from both Scolt Head and Blakeney Point over three survey seasons from 2006 to 2008 while common terns were tracked from Blakeney point during 2008 (Table 14). Tracking work was generally timed to coincide with the chick-rearing season, except in 2007 when data were also collected during the incubation period in May. The distribution of Sandwich tern tracks tended to radiate out to sea in all directions out to sea from both Scolt

Head and Blakeney Point, while those for common terns tended to be confined in a coastal strip just north and north-east from Blakeney Point (Figure 8).

Table 14. Sample sizes of tracks obtained for North Norfolk Coast SPA.

Species	No. of tracks				
	Scolt Head	Blakeney Point	Scolt Head	Blakeney Point	Total
	2006 (2-17 June; 2-25 July)	2007 (17 May; 12-18 June; 9-10 July)	2007 (13-19 June; 12-23 July)	2008 (4-14 July)	
Common tern	-	-		24	24
Sandwich tern	32	34	16	26	108

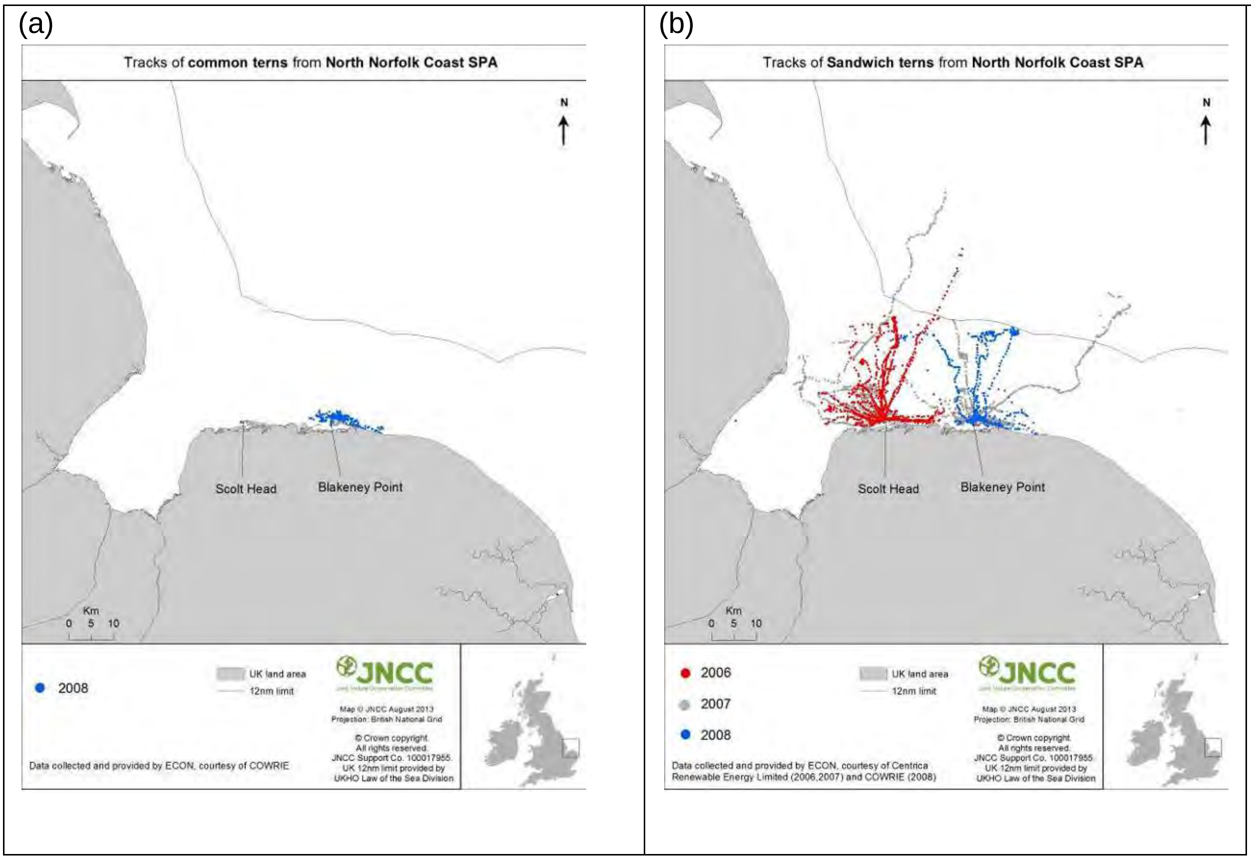


Figure 8. Tracks of (a) common and (b) Sandwich terns tracked from North Norfolk Coast SPA from 2006-2008. Common terns were only tracked from Blakeney Point, while Sandwich terns were tracked from both Scolt Head and Blakeney Point.

The result of the bootstrapping and model selection process are given in Appendix 2. The final models selected are shown in Table 15. Common terns were only tracked from Blakeney Point so we used the common tern model generated from Blakeney Point data to extrapolate usage predictions to Scolt Head (around 20km along the coast). Common terns at Scolt Head were treated this way rather than being considered under Phase 2 because the Scolt Head colony is within the same SPA complex as Blakeney Point. Predictions of relative usage were made around both Blakeney Point and Scolt Head and are shown in Figure 9. Predicted usage was highest around the colony, generally decreasing with distance from the colony. However both common tern and Sandwich tern predicted usage from Scolt Head show a particular section of the usage surface to the north west of the colony where predicted usage does not change in the smooth pattern seen elsewhere. This is attributable to the underlying shear stress wave data, which forms one of the covariates of both these models. At that particular section, the shear stress wave values change abruptly.

Table 15. The final models selected for North Norfolk Coast SPA.

Species	Model	Terms
Common tern	Site specific	distance to colony, shear stress wave
Sandwich tern	Site specific	distance to colony, distance to shore, shear stress wave, bathymetry

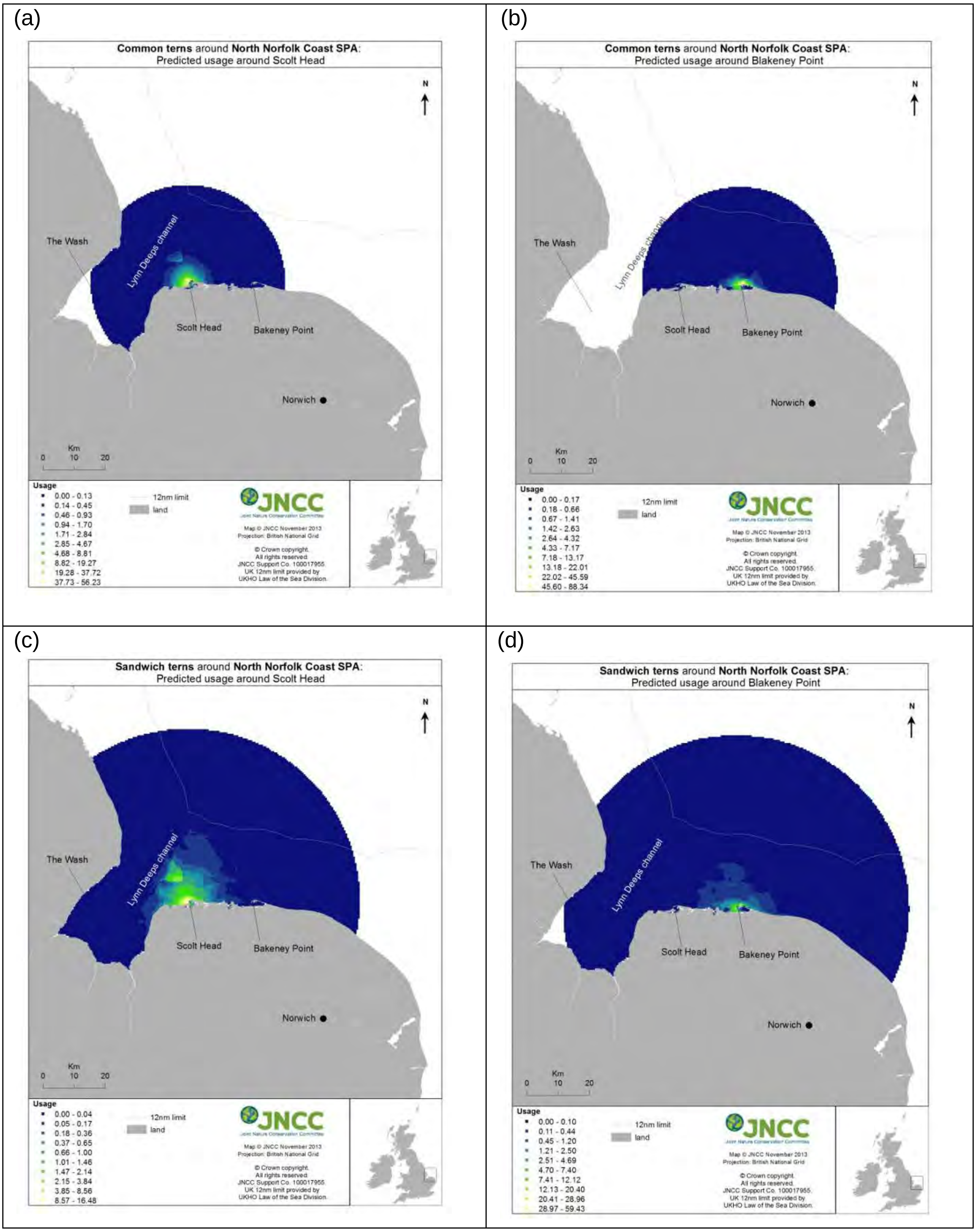


Figure 9. Predicted relative usage of the waters around North Norfolk Coast SPA for common terns around Scolt Head(a) and Blakeney Point (b) and for Sandwich terns around Scolt Head (c) and Blakeney Point (d). Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.5 Breydon Water

For Breydon Water SPA the species of interest for the project was common tern. No visual tracking data were available so a generic model was applied (Table 16). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage (Figure 10) radiated out from the colony, generally declining with distance to colony and shore.

Table 16. The final model selected for Breydon Water.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry

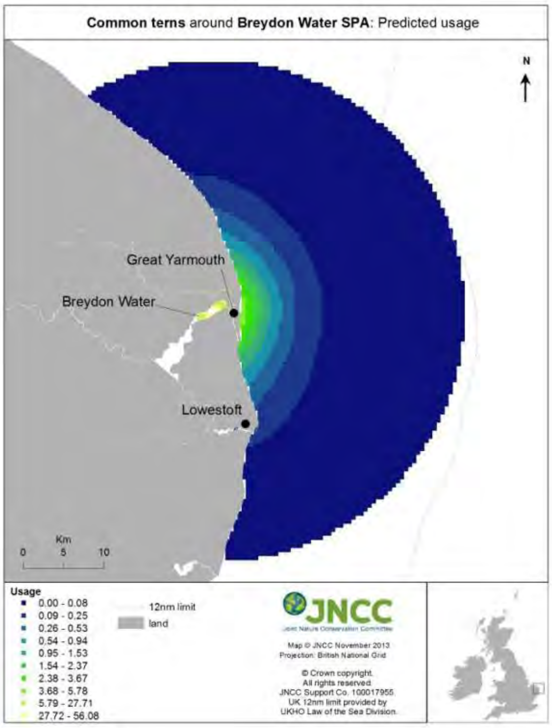


Figure 10. Predicted relative usage of the waters around Breydon Water for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.6 Foulness (Mid-Essex Coast Phase 5)

For Foulness (Mid-Essex Coast Phase 5) SPA the species of interest for the project was common tern. No visual tracking data were available so a generic model was applied (Table 17). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage (Figure 11) radiated out from the colony, generally declining with distance to colony.

Table 17. The final model selected for each species at Foulness (Mid-Essex Coast Phase 5) SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry

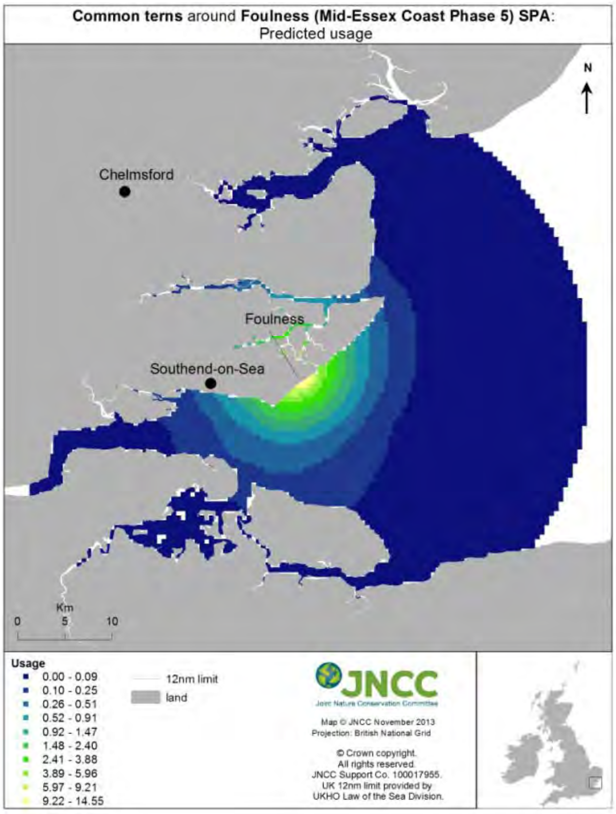


Figure 11. Predicted relative usage of the waters around Foulness for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.7 Dungeness to Pett Level

For Dungeness to Pett Level SPA the species of interest for the project was common tern. No visual tracking data were available so a generic model was applied (Table 18). The details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Predictions of relative usage were made around the colony at Rye Harbour and are shown in Figure 12. Predicted distributions were highest around the colony, generally declining with distance to colony.

Table 18. The final model selected for Dungeness to Pett Level SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry

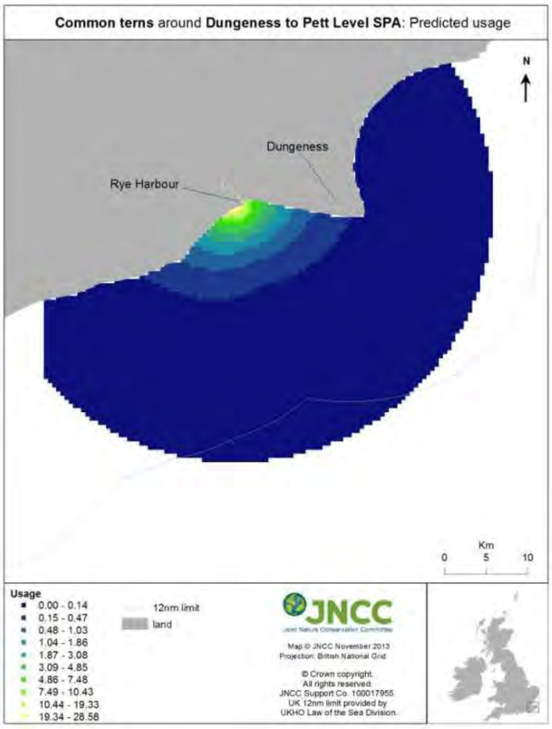


Figure 12. Predicted relative usage of the waters around Rye Harbour within Dungeness to Pett Level SPA for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.8 Chichester and Langstone Harbour

For Chichester and Langstone Harbours SPA, the species of interest for the project was Sandwich tern. No visual tracking data were available so a generic model was applied (Table 19). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Predictions of relative usage were made separately to Chichester Harbour and Langstone Harbour and are shown in Figure 13. Predicted distributions radiated out from each colony, generally declining with distance to each colony. The pattern of predicted usage extended towards the north eastern coastline of the Isle of Wight.

Table 19. The final model selected for Chichester and Langstone Harbours SPA.

Species	Model	Terms
Sandwich tern	Generic	Distance to colony, distance to shore, bathymetry

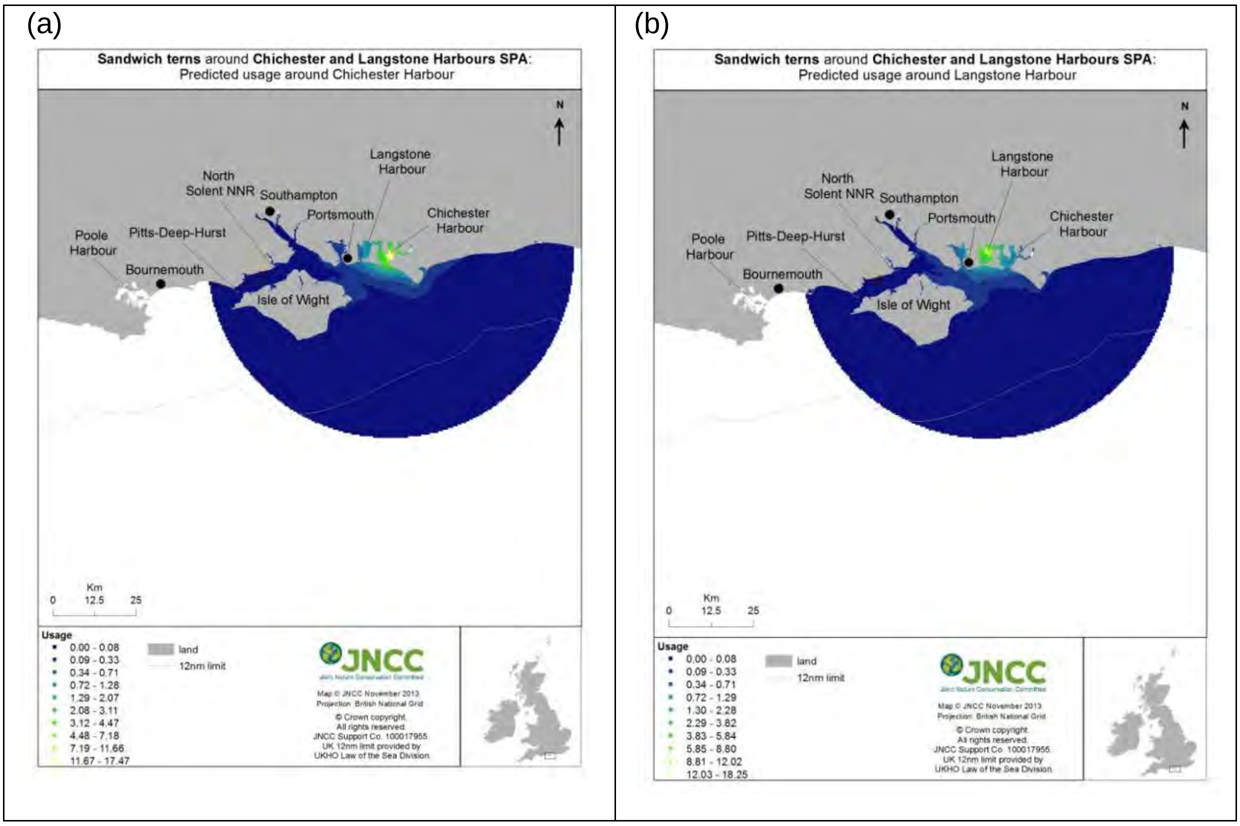


Figure 13. Predicted relative usage of the waters around (a) Chichester Harbour and (b) Langstone Harbour for Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.9 Solent and Southampton Water

For Solent and Southampton Water SPA the species of interest for the project were common and Sandwich terns. No visual tracking data were available so generic models were applied (Table 20). Details of model selection for these Phase 2 models for common and Sandwich terns are given in Potts *et al* 2013c. Predictions of relative usage were made to North Solent NNR and to Pitts-Deep-Hurst for Sandwich tern, and to Pitts-Deep-Hurst for common tern (Figure 14). Predicted distributions were highest around each colony, generally decreasing with distance from each colony.

Table 20. The final model selected for each species at Solent and Southampton Water SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry
Sandwich tern	Generic	Distance to colony, distance to shore, bathymetry

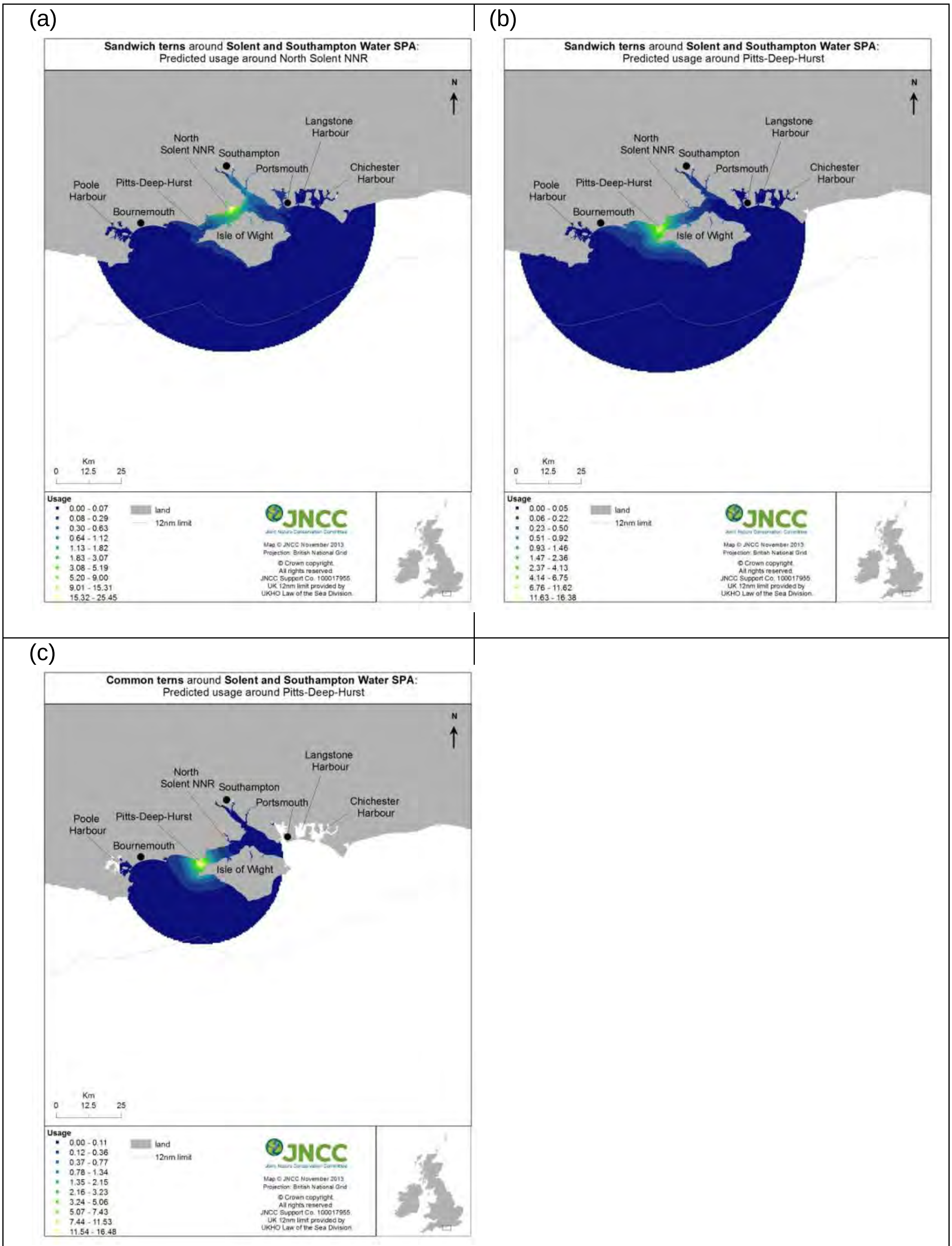


Figure 14. Predicted relative usage of the waters around (a) North Solent NNR and (b) Pitts-Deep-Hurst for Sandwich terns and around Pitts-Deep-Hurst (c) for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.10 Poole Harbour

For Poole Harbour SPA the species of interest for the project was common tern. No visual tracking data were available so a generic model was applied (Table 21). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 15. The predicted distributions were highest around the colony and decreased with distance from the colony.

Table 21. The final model selected for each species at Poole Harbour SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry

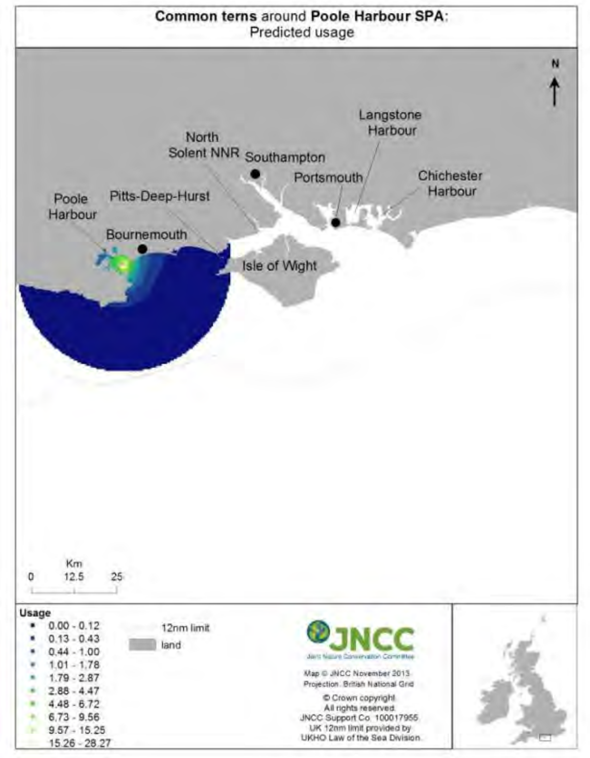


Figure 15. Predicted relative usage of the waters around Poole Harbour for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.11 Ribble and Alt Estuaries

For Ribble and Alt Estuaries SPA the species of interest for the project was common tern. No visual tracking data were available so a generic model was applied (Table 22). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Predictions of relative usage were made to the colony at Ribble Marshes and are shown in Figure 16. Predicted distributions were highest around the colony, decreasing with distance from the colony.

Table 22. The final model selected for each species at Ribble and Alt Estuaries SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry

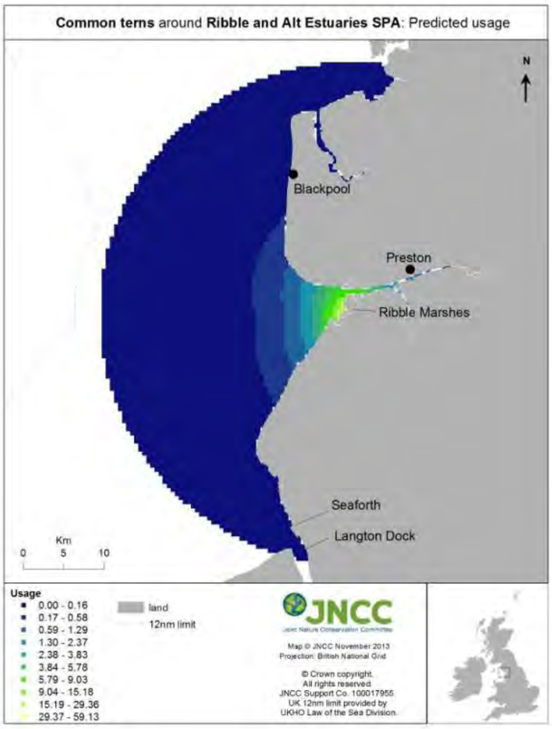


Figure 16. Predicted relative usage of the waters around Ribble Marshes for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.4.12 Duddon Estuary

For Duddon Estuary SPA the species of interest for the project was Sandwich tern. No visual tracking data were available so a generic model was applied (Table 23). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 17. Predicted distributions were highest around the colony, decreasing with distance from the colony and from the shore.

Table 23. The final model selected for each species at Duddon Estuary SPA.

Species	Model	Terms
Sandwich tern	Generic	Distance to colony, distance to shore, bathymetry

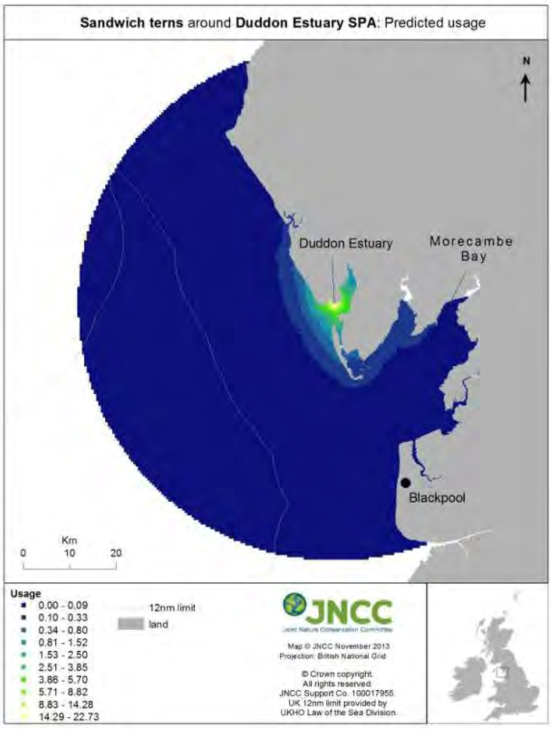


Figure 17. Predicted relative usage of the waters around Duddon Estuary for Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.5 English/Welsh colony SPAs

3.5.1 The Dee Estuary

For The Dee Estuary SPA the species of interest for the project was common tern. No visual tracking data were available so a generic model was applied (Table 24). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Predictions of relative usage were made to the colony at Shotton Pools are shown in Figure 18. Predicted distributions were highest around the colony, decreasing with distance from the colony. The predicted areas of usage did not extend beyond The Dee Estuary SPA.

Table 24. The final model selected for each species at The Dee Estuary SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry

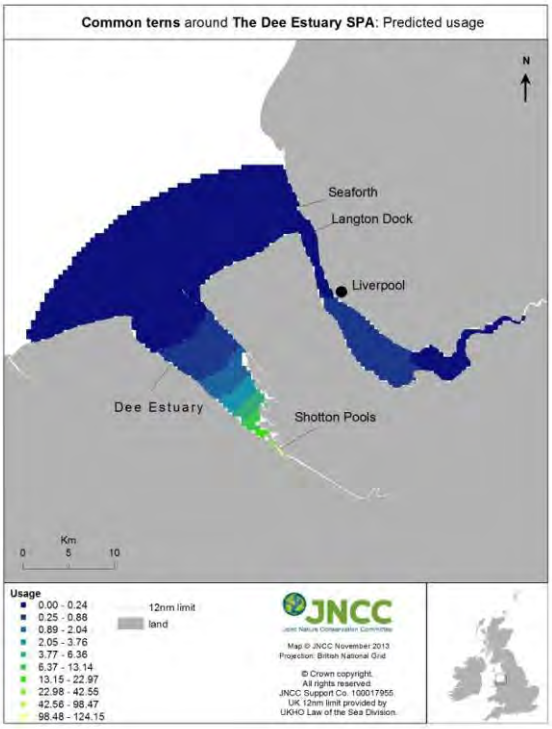


Figure 18. Predicted relative usage of the waters around Shotton Pools for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.6 Welsh colony SPAs

3.6.1 Ynys Feurig, Cemlyn Bay and The Skerries

For Ynys Feurig, Cemlyn Bay and The Skerries SPA, the species of interest for the project were Arctic, common and Sandwich terns. A total of 157 tern tracks was obtained, all collected for birds located at the colony at Cemlyn Bay (Table 25). Data were collected over a single survey season in 2009 (Table 11) and were timed to coincide with the chick-rearing period. The distribution of common tracks radiated northwards from Cemlyn Bay, whereas Sandwich tern tracks tended to radiate mainly to the north and north-east out from the colony at Cemlyn Bay, predominantly running eastwards along the northern coast of Anglesey, with multiple tracks running as far as the east coast of Anglesey (Figure 19). Only three Arctic terns were tracked (Figure 19).

Table 25. Sample sizes of tracks obtained for Ynys Feurig, Cemlyn Bay and The Skerries SPA. All data were collected at Cemlyn Bay.

Species	**No. of tracks**		
	Collected by JNCC (9 June – 6 July 2009)	**Collected by Econ Ecological Consultancy Ltd (28-29 May; 10-11, 24 & 26 June; 9-10 July 2009)**	**Total**
Arctic tern	2	1	3
Common tern	30	2	32
Sandwich tern	112	136	248

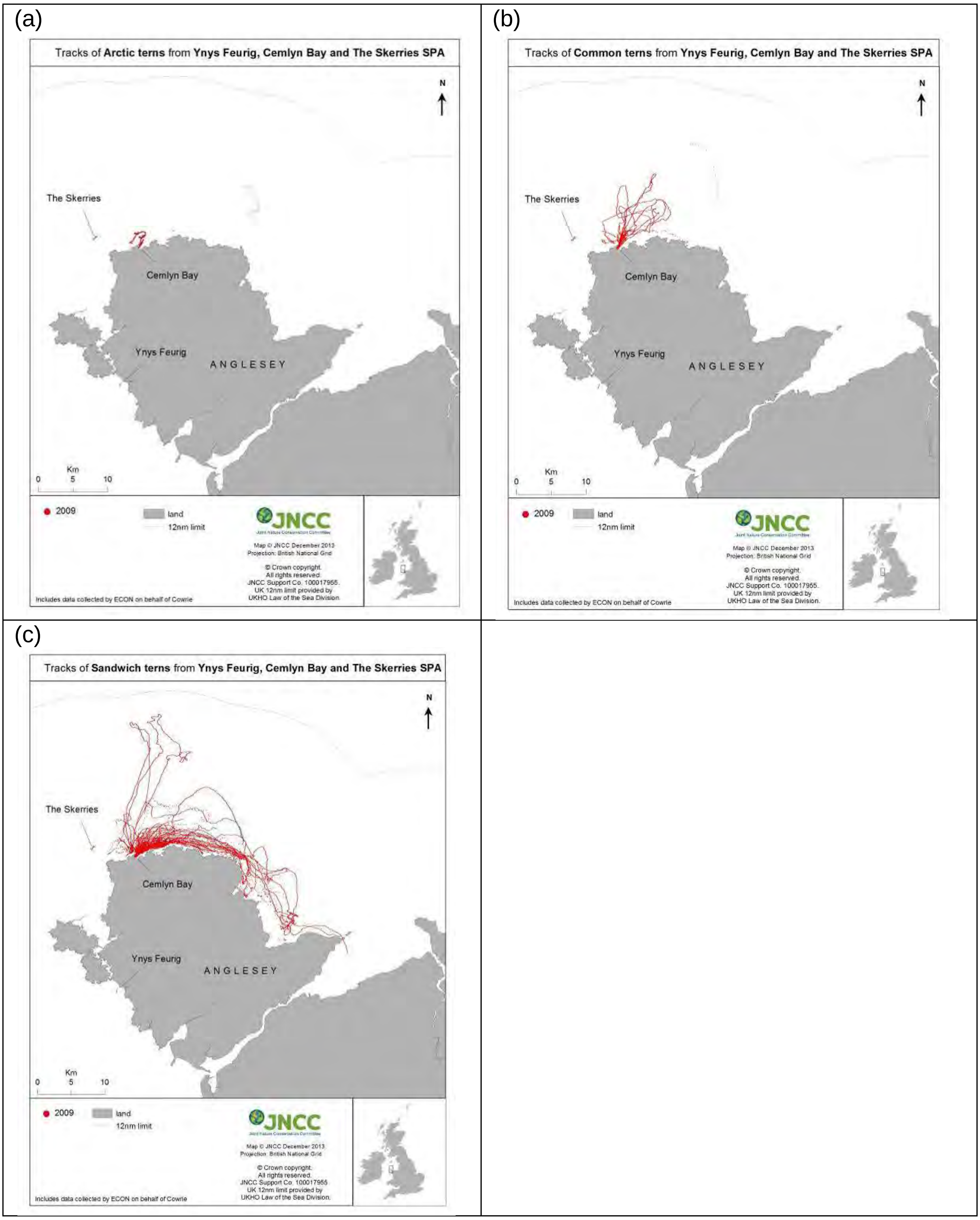


Figure 19. Tracks of (a) Arctic, (b) common and (c) Sandwich terns tracked from Ynys Feurig, Cemlyn Bay and The Skerries SPA from 2009. Includes data kindly provided by Econ Ecological Consultancy Ltd. All birds were tracked from Cemlyn Bay, except for one Arctic and one common tern tracked by ECON Ecological Consultancy Ltd which were tracked from further offshore.

The results of the bootstrapping and model selection process are given in Appendix 2 for the Phase 1 models generated and applied to Cemlyn Bay for common and Sandwich terns. Due to the low sample size for Arctic terns, a Phase 2 model was used for this species at Cemlyn Bay. Phase 2 models were applied to the other two colonies within the SPA for which no data were available for common and Arctic terns (Ynys Feurig and The Skerries).

Sandwich terns do not regularly occupy either Ynys Feurig or The Skerries so no models were applied in these cases. Details of model selection for the Phase 2 models are given in Potts *et al* 2013c. The final models selected are shown in Table 26. Distributions of predicted relative usage are shown in Figure 20 and closely matched the underlying data where data were available. Predicted distributions for Arctic terns were highest around each colony, decreasing with distance from each colony. A similar pattern was predicted for common terns at The Skerries and Ynys Feurig (using generic models). The distributions of common terns predicted around Cemlyn Bay, using the site-specific model, again predicted highest usage around the colony which decreased with distance from the colony, but this decline with distance to colony was more gradual to the east of the colony. Predicted distributions for Sandwich terns around Cemlyn Bay (using the site specific model) showed highest usage around the colony, declining with distance from colony but extending eastwards along the northern coast of Anglesey.

Table 26. The final models selected for each species for Ynys Feurig, Cemlyn Bay and The Skerries SPA. See Appendix 2 for details on the model selection.

Species	Colonies	Model	Terms
Arctic tern	Ynys Feurig	Generic	Distance to colony, bathymetry
	The Skerries	Generic	Distance to colony, bathymetry
	Cemlyn Bay	Generic	Distance to colony, bathymetry
Common tern	Ynys Feurig	Generic	Distance to colony, distance to shore, bathymetry
	The Skerries	Generic	Distance to colony, distance to shore, bathymetry
	Cemlyn Bay	Site specific	Distance to colony, salinity in spring
Sandwich tern	Cemlyn Bay	Site specific	Distance to colony, distance to shore, salinity in spring

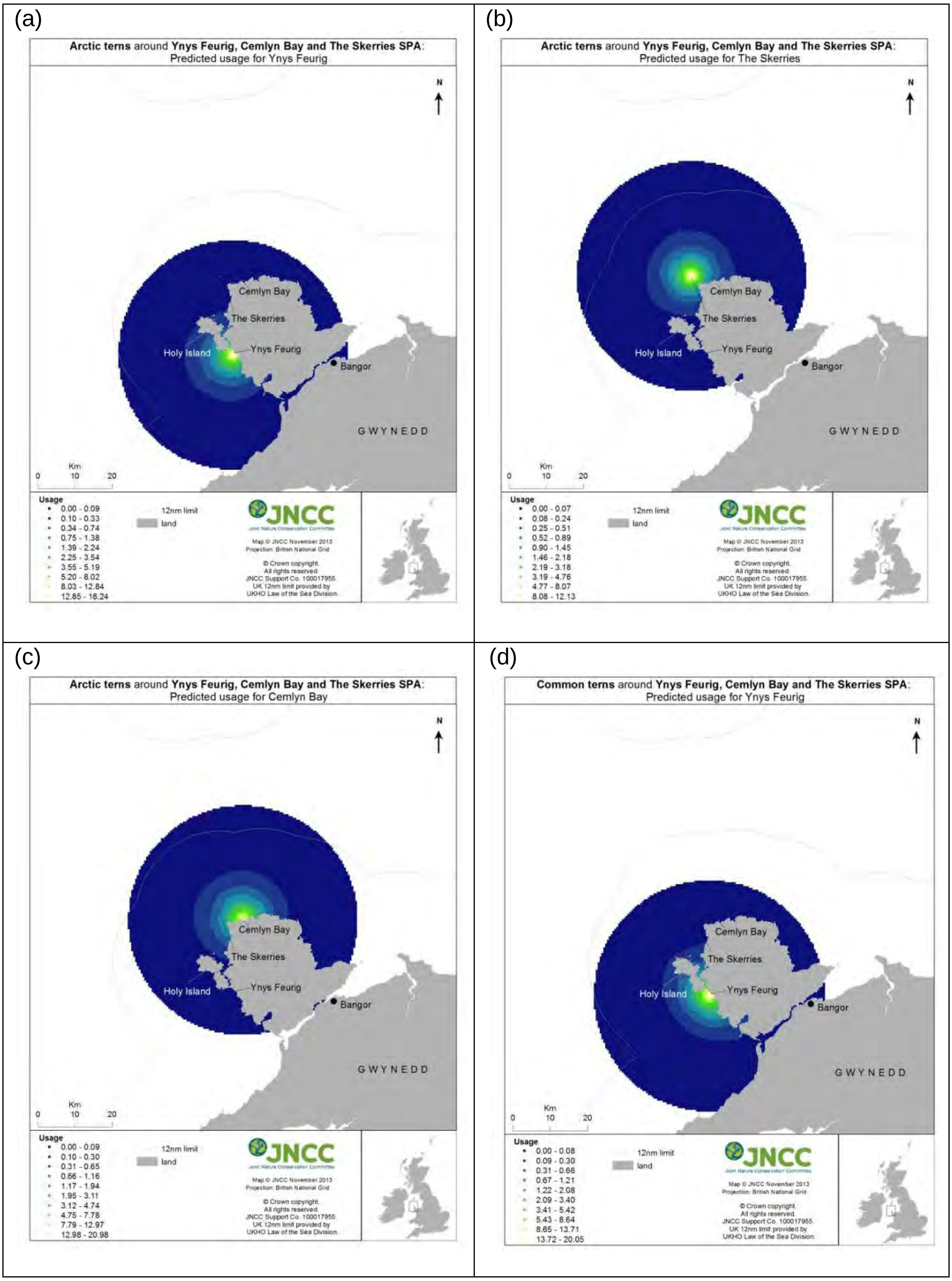


Figure 20. Predicted relative usage of the waters around (a) Ynys Feurig, (b) The Skerries and (c) Cemlyn Bay for Arctic terns; and around (d) Ynys Feurig for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

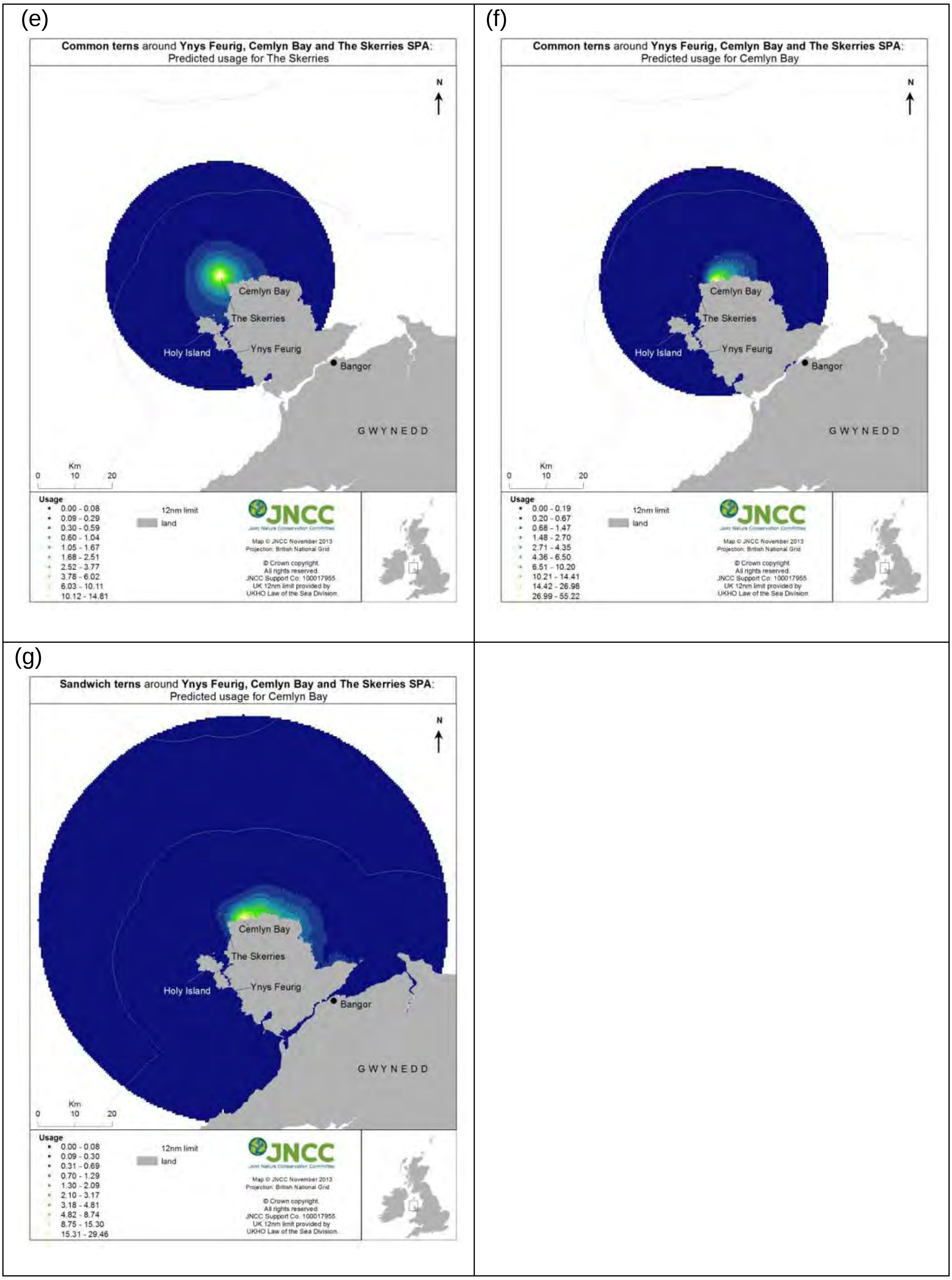


Figure 20 (cont). Predicted relative usage of the waters around (e) The Skerries and (f) Cemlyn Bay for common terns; and around (g) Cemlyn Bay for Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.7 Northern Ireland colony SPAs

3.7.1 Larne Lough

For Larne Lough SPA, the species of interest for the project were common and Sandwich terns. A total of 87 tern tracks was obtained for these species over the three survey seasons from 2009-2011 with the vast majority of tracks obtained from Blue Circle Island (Table 27). Two tracks were also obtained for roseate terns. Tracking work was timed largely to coincide with the chick-rearing season, although four Sandwich terns and one roseate tern tracked on 2 June in 2010 were thought to be incubating. The distribution of common tern tracks tended to largely concentrate immediately north-east of Larne Lough, although in 2009, two tracks also radiated out eastwards, and another one southwards of Larne Lough, whilst in 2011, birds also showed distribution inside the Lough itself and as far out as 20km northeast of the colony (Figure 21). In contrast, Sandwich tern tracks were concentrated along a coastal strip north and south of the colony, and within Larne Lough itself (Figure 21). Of the two tracks of roseate terns, one track went north of the colony, whilst the other remained within the Lough itself (Figure 21).

Table 27. Sample sizes of tracks obtained for Larne Lough SPA.

Species	**No. of tracks**					
	Swan Island		**Blue Circle Island**			**Total**
	2009 (26 June)	**2011 (27 June)**	**2009 (2 June-16 July)**	**2010 2 June; 9 July)**	**2011 (2 June-1 July)**	
Common tern	0	1	18	2	28	49
Sandwich tern	2	0	8	13	15	38
Roseate tern	0	0	0	1	1	2

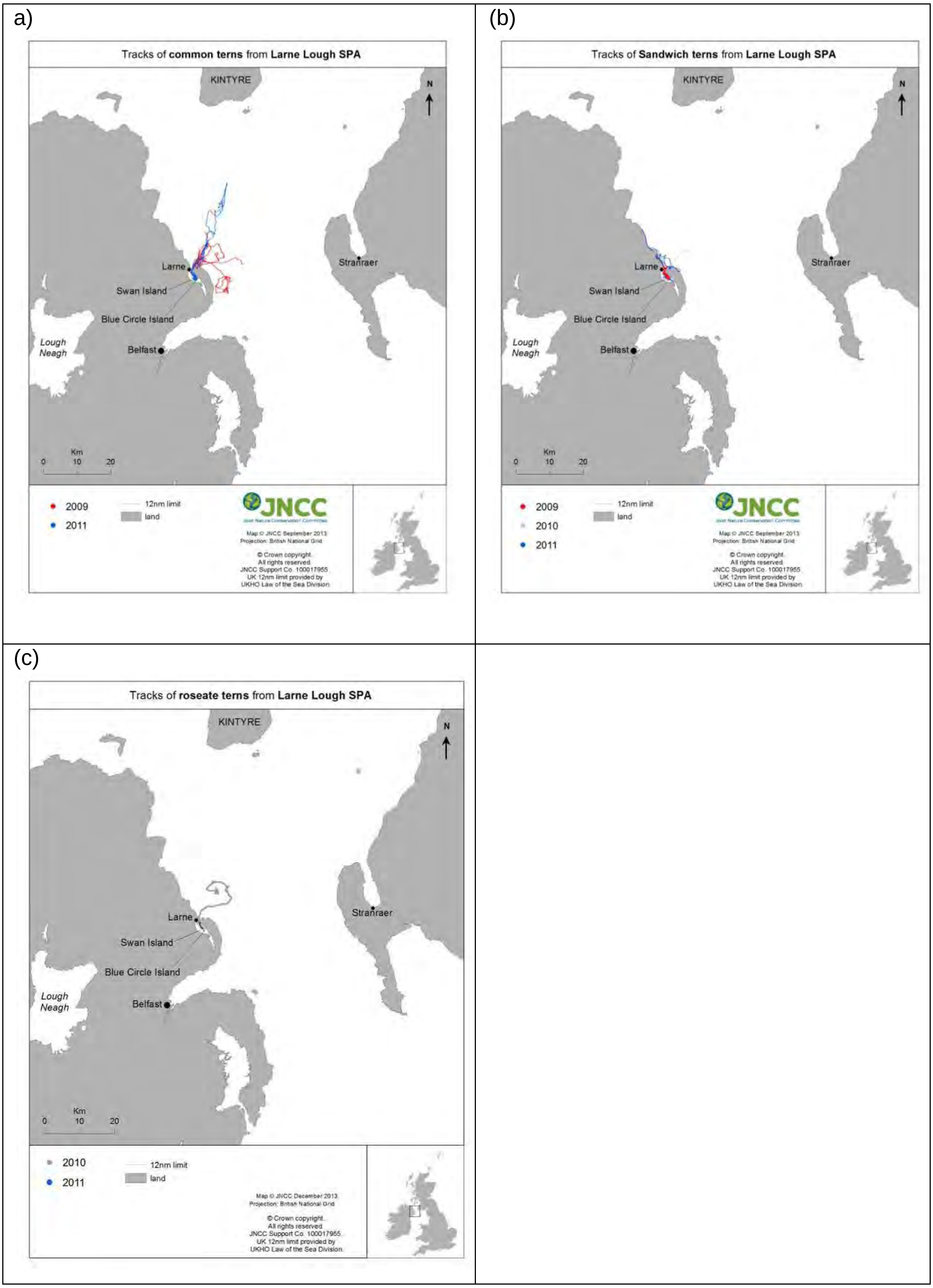


Figure 21. Tracks of (a) common, (b) Sandwich and (c) roseate terns tracked from Larne Lough SPA from 2009-2011.

Data from Swan Island and Blue Circle Island (a few hundred metres apart) were pooled to generate a single model for Larne Lough for each species of interest (common and

Sandwich terns). Predictions were made using Blue Circle Island as the colony location. Initially we generated a site specific model for Sandwich terns (under Phase 1) but this was not amenable to the further analyses (not reported here) we wished to apply to delineate possible SPA boundaries. As an alternative, we applied a generic model (under Phase 2) which is reported here (see Methods, Section 2.2.5).

The results of the bootstrapping and model selection process for the Phase 1 common tern model is given in Appendix 2. Details of model selection for the Phase 2 model are given in Potts *et al* 2013c. The final models selected are shown in Table 28. Relative distribution of both common and Sandwich terns (Figure 22) matched the underlying data well, although for Sandwich terns predicted usage extended into Belfast Lough, where no birds were tracked. Due to the absence of underlying environmental data, usage predictions could not be generated for the most southern part of Larne Lough.

Table 28. The final models selected for Larne Lough SPA. See Appendix 2 for details on the model selection.

Species	Model	Terms
Common tern	Site specific	Distance to colony, distance to shore, bathymetry, slope
Sandwich tern	Generic	Distance to colony, distance to shore, bathymetry

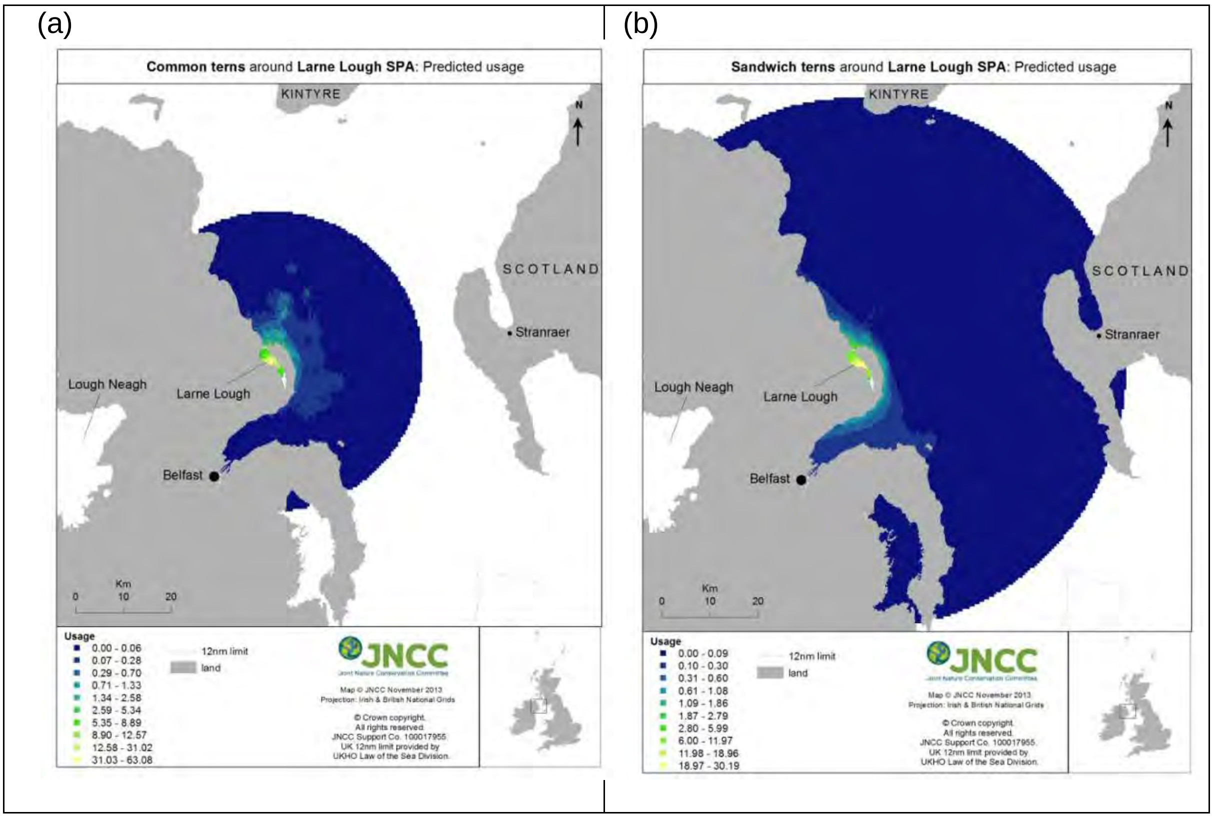


Figure 22. Predicted relative usage of the waters around Larne Lough for (a) common and (b) Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.7.2 Outer Ards SPA

For Outer Ards SPA, the species of interest for the project was Arctic tern. A total of 11 Arctic tern tracks was obtained over three survey seasons from 2009-2011; visual tracking data were also collected for common and Sandwich terns (Table 29). All data were collected from Cockle Island. Tracking work was generally timed to coincide with the chick-rearing season, but three Sandwich terns and one Arctic tern tracked on 16 June 2010; and two Sandwich terns and one Arctic tern tracked on 21 June 2011 were thought to be incubating.

The distribution of Arctic tern tracks tended to radiate out in a north/north-eastern direction, with a single track in 2011 also running eastwards, across the Irish Sea to near the southern coast of the Rhins peninsula, Scotland, where the bird was lost (Fi). The common tern tracks showed a northern direction distribution, whilst the Sandwich tern tracks radiated out westwards into Belfast Lough, as well as in a north/north-easterly direction. For Sandwich terns, tracks from multiple years went across to the Rhins peninsula, Scotland, and a single track in 2010 was found to go southwards along the Ards coastline, but the bird was lost before its return (Fi).

Table 29. Sample sizes of tracks obtained for Outer Ards SPA. All birds tracked were from Cockle Island.

Species	**No of tracks**			
	2009 (22 June-15 July)	**2010 (16 June; 20 July)**	**2011 (20-21 June)**	**Total**
Arctic tern	6	1	4	11
Sandwich tern	9	8	2	19
Common tern	4	0	1	5

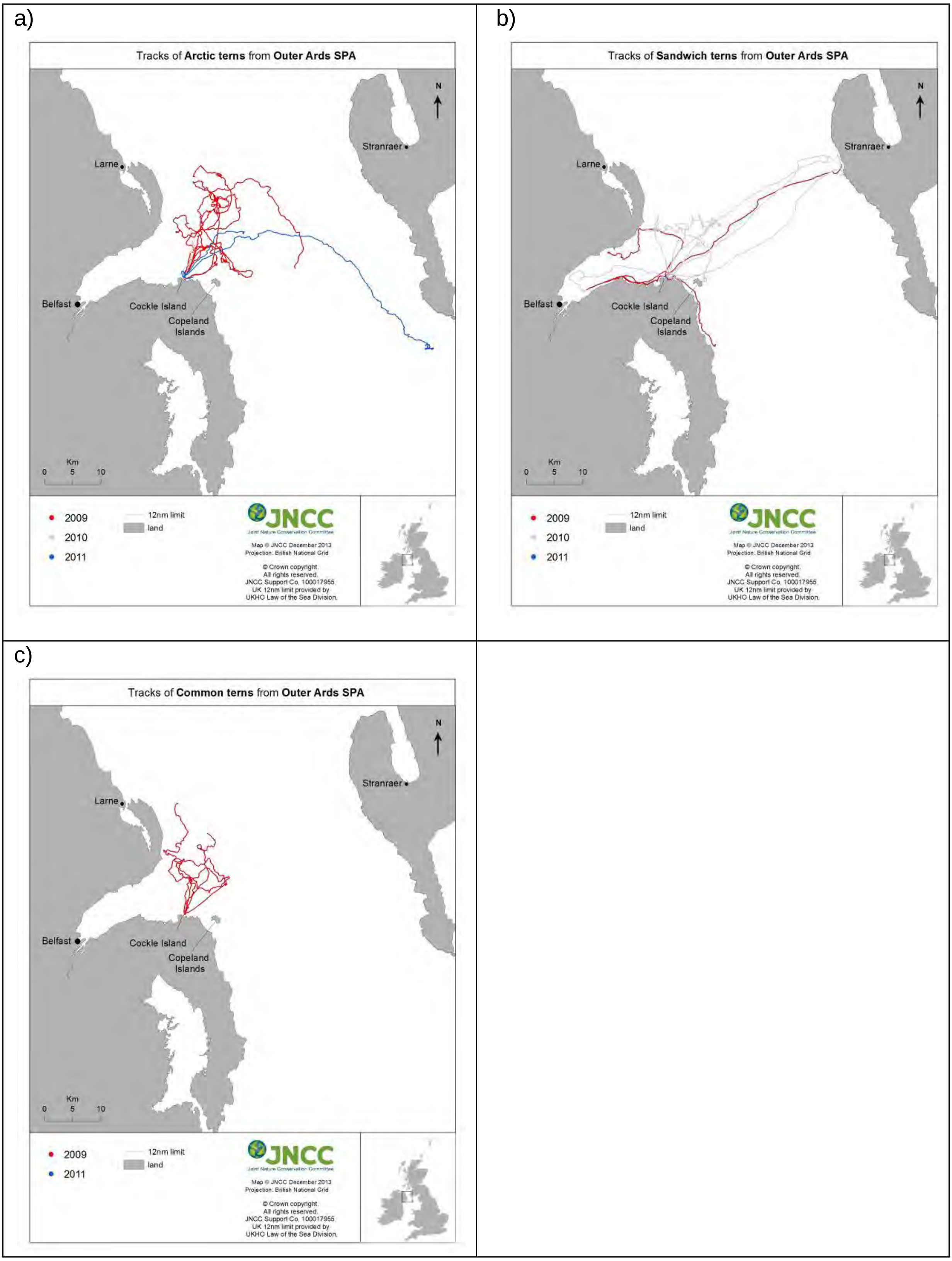


Figure 23. Tracks of a) Arctic, b) Sandwich and c) common terns tracked from Cockle Island within Outer Ards SPA from 2009-2011.

The data for Arctic terns was combined with those collected from Copeland Islands SPA (see section 3.3.17) to develop a single model which was then applied separately to both Outer Ards SPA and Copeland Island SPA. This approach increased the number of samples available to the model and was deemed appropriate due to the very close proximity of the two colonies from the two SPAs, with tracks from the two SPAs showing substantial overlap. The results of the bootstrapping and model selection process are given in Appendix 2. The final model selected is shown in Table 30. Distributions of predicted relative usage identified hotspots around both Cockle Island and the Copeland Islands, with predicted usage generally declining with distance from these colonies (Figure 24). Although the model has been applied to Cockle Island, it identifies a hotspot around the Copeland Islands due to high values of the shear stress current covariate in that area. It was not possible to generate predictions for many of the grid cells which lay between *c*.1-3km from the coast and most grid cells within Larne Lough, due to missing data of shear stress current in that area.

Table 30. The final model selected for Outer Ards SPA. See Appendix 2 for details on the model selection.

Species	Model	Terms
Arctic tern	Site specific (using data from both Outer Ards SPA and Copeland Islands SPA)	Distance to colony, shear stress current

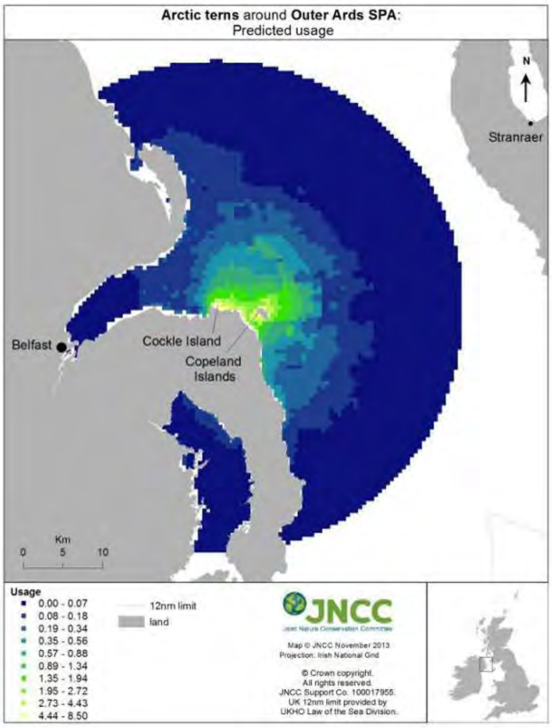


Figure 24. Predicted relative usage of the waters around Outer Ards SPA for Arctic terns from Cockle Island. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.7.3 Copeland Islands SPA

For Copeland Island SPA, the species of interest for the project was Arctic tern. A total of 13 tracks was obtained over the three survey seasons from 2009-2011 (Table 31). Tracking work was generally timed to coincide with the chick-rearing season, but one Arctic tern tracked on 21 June 2011 was thought to be incubating. Similar to track distributions from the Outer Ards SPA, Arctic tern tracks from Copeland Islands SPA tended to radiate out in a north/north-eastern direction, with a single track in 2011 also running eastwards, across the

Irish sea to near the southern coast of the Rhins peninsula, Scotland, where the bird was lost (Figure 25).

Table 31. Sample sizes of tracks obtained for Copeland Islands SPA.

Species	**No of tracks**			
	2009 (23 June)	**2010 (16 June)**	**2011 (20-21 June)**	**Total**
Arctic tern	1	2	10	13

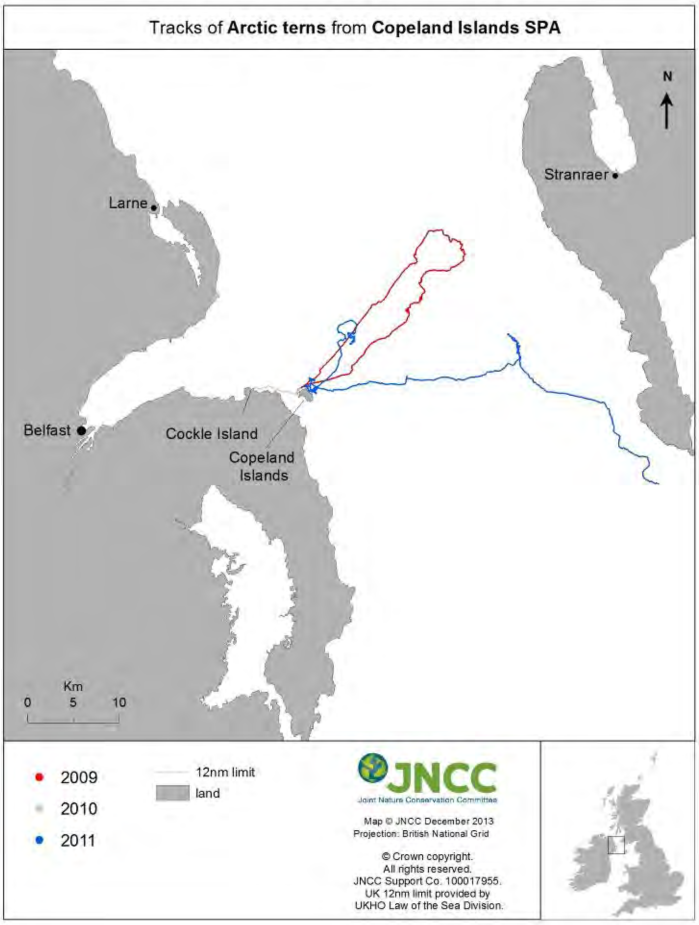


Figure 25. Tracks of Arctic terns tracked from Copeland Islands SPA from 2009-2011.

The data for Arctic terns was combined with those collected from Outer Ards SPA (see section 3.3.16) to develop a single model which was then applied separately to both Outer Ards SPA and Copeland Island SPA. This approach increased the number of samples available to the model and was deemed appropriate due to the very close proximity of the two colonies from the two SPAs, with tracks from the two SPAs showing substantial overlap. The results of the bootstrapping and model selection process are given in Appendix 2. The final model selected is shown in Table 32. Predicted usage was highest around the colony, decreasing with distance from the colony (Figure 26). It was not possible to generate predictions for many of the grid cells which lay between *c*.1-3km from the coast and most grid cells within Larne Lough, due to missing data of shear stress current in that area.

Table 32. The final model selected for Copeland Islands SPA. See Appendix 2 for details on the model selection.

Species	Model	Terms
Arctic tern	Site specific (using data from both Outer Ards SPA and Copeland Islands SPA)	Distance to colony, shear stress current

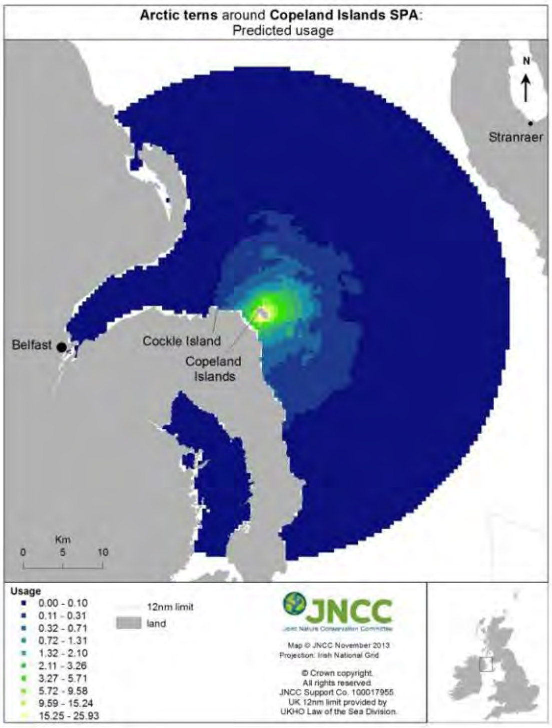


Figure 26. Predicted relative usage of the waters around Copeland Island SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.7.4 Strangford Lough

For Strangford Lough SPA the species of interest for the project were Arctic, common and Sandwich terns. No visual tracking data were available so generic models were applied (Table 33). Details of model selection for these Phase 2 models are given in Potts *et al* 2013c. Predictions of relative usage were made to the colony at Dunsy Rock and are shown in Figure 27. Predicted usage was highest around the colony, decreasing with distance from the colony for all three species. For common and Sandwich terns predicted usage extended beyond the peninsula.

Table 33. The final model selected for each species at Strangford Lough SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry
Common tern	Generic	Distance to colony, distance to shore, bathymetry
Sandwich tern	Generic	Distance to colony, distance to shore, bathymetry

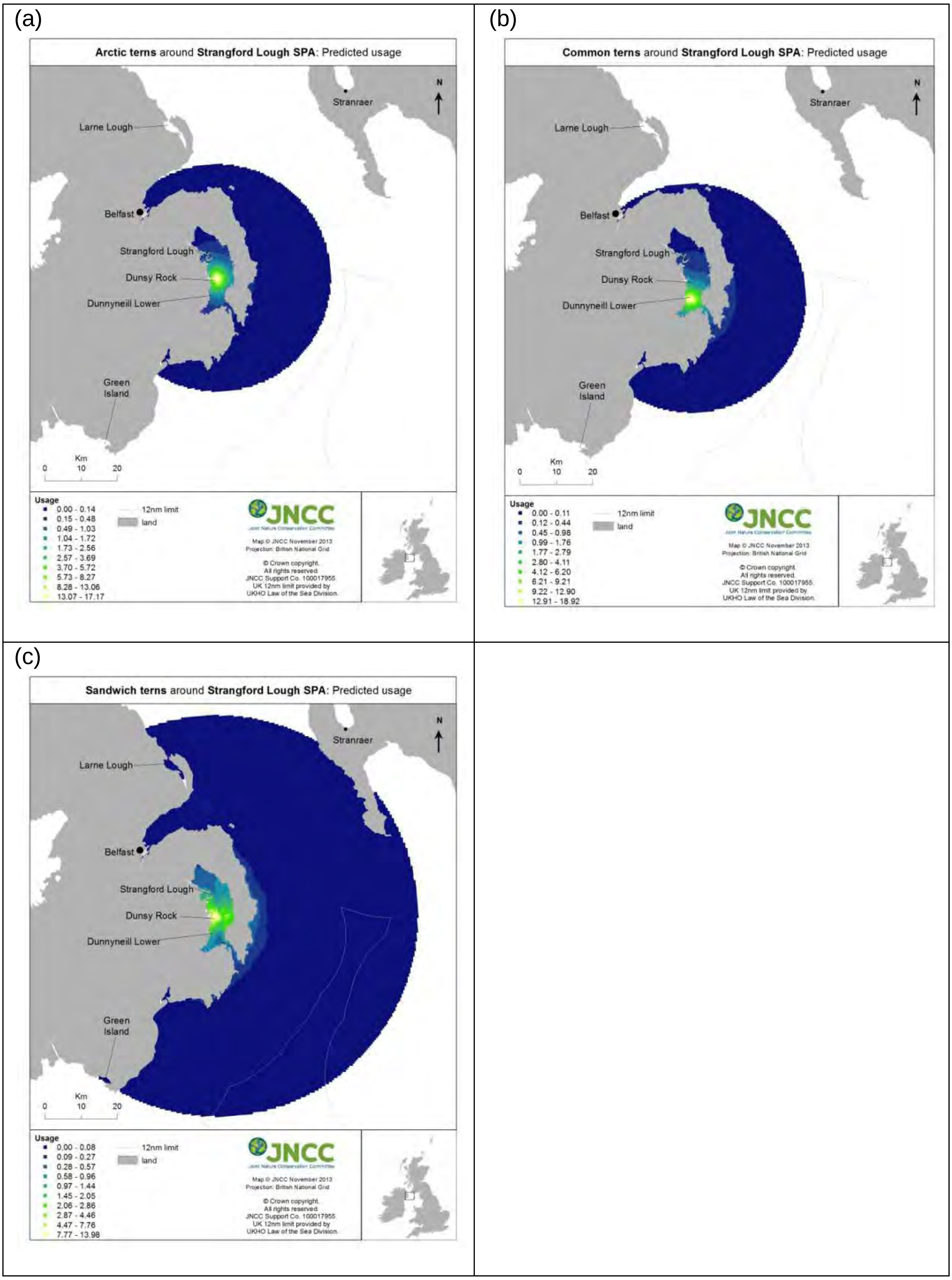


Figure 27. Predicted relative usage of the waters around Dunsy Rock within Strangford Lough SPA for (a) Arctic, (b) common and (c) Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.7.5 Carlingford Lough

For Carlingford Lough SPA the species of interest for the project were common and Sandwich terns. No visual tracking data were available so generic models were applied (Table 34). Details of model selection for these Phase 2 models are given in Potts *et al* 2013c. Predictions of relative usage were made to the colony at Green Island and are shown in Figure 28. Predicted usage was highest around the colony, decreasing with distance from the colony for both species.

Table 34. The final model selected for each species at Carlingford Lough SPA.

Species	Model	Terms
Common tern	Generic	Distance to colony, distance to shore, bathymetry
Sandwich tern	Generic	Distance to colony, distance to shore, bathymetry

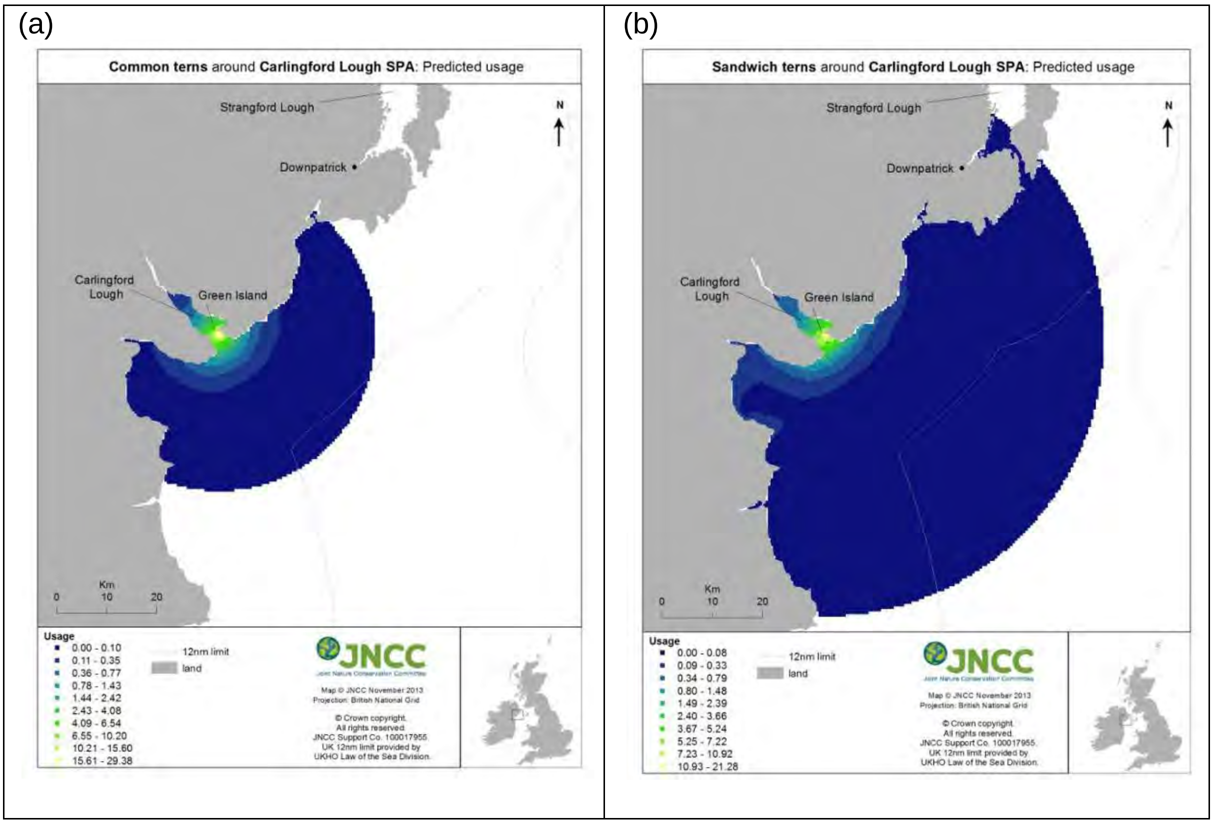


Figure 28. Predicted relative usage of the waters around Green Island within Carlingford Lough SPA for (a) common and (b) Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8 Scottish colony SPAs

3.8.1 Fetlar

For Fetlar SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 35). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 29. Predicted usage was highest around the colony, decreasing with distance from the colony.

Table 35. The final model selected for Fetlar SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

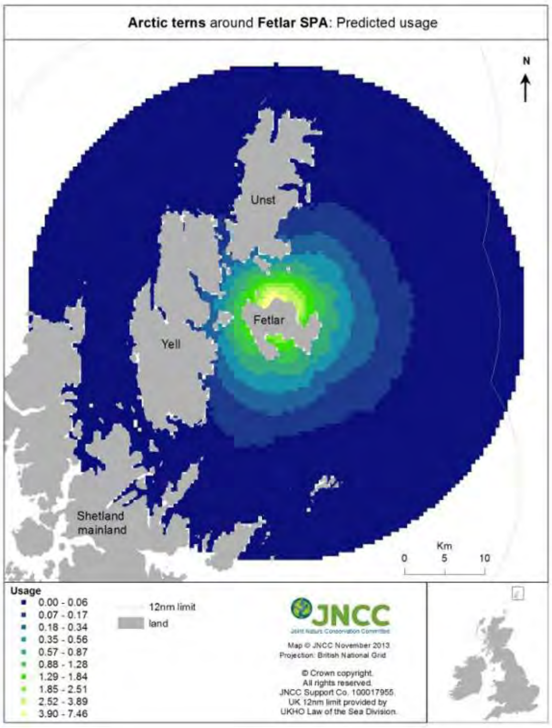


Figure 29. Predicted relative usage of the waters around Fetlar SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.2 Mousa

For Mousa SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 36). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 30. Predicted usage was highest around the colony, decreasing with distance from the colony and extended over to the west coastline of Shetland mainland.

Table 36. The final model selected for Mousa SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

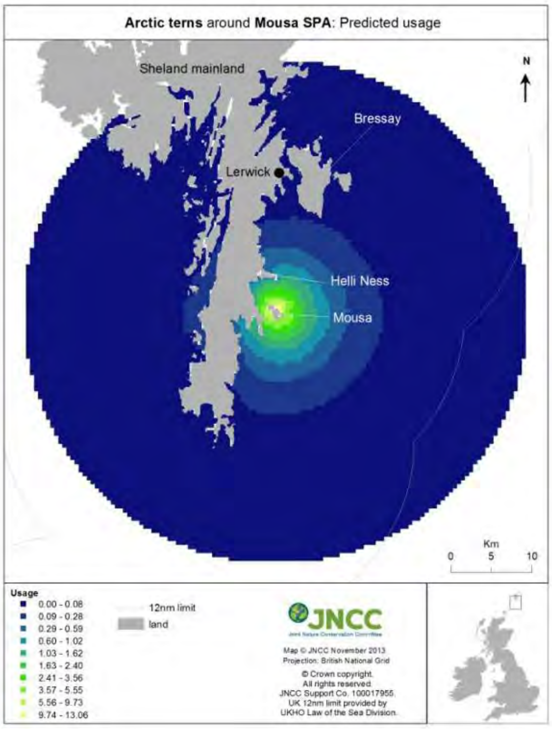


Figure 30. Predicted relative usage of the waters around Mousa SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.3 Papa Stour

For Papa Stour SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 37). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 31. Predicted usage was highest around the colony, decreasing with distance from the colony.

Table 37. The final model selected for Papa Stour SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

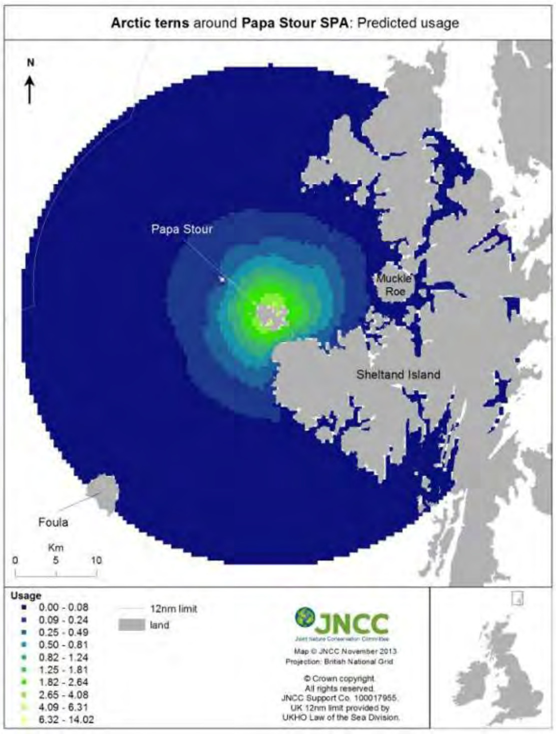


Figure 31. Predicted relative usage of the waters around Papa Stour SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.4 Foula

For Foula SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 38). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 32. Predicted usage was highest around the colony, decreasing with distance from the colony.

Table 38. The final model selected for Foula SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

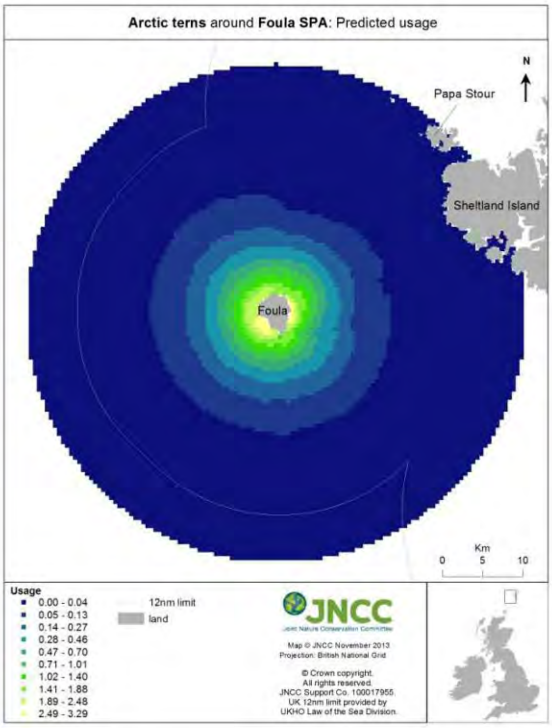


Figure 32. Predicted relative usage of the waters around Foula SPA for Arctic terns. Usage values are binned relative and using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.5 Fair Isle

For Fair Isle SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 39). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 33. Predicted usage was highest around the colony, decreasing with distance from the colony.

Table 39. The final model selected for Fair Isle SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

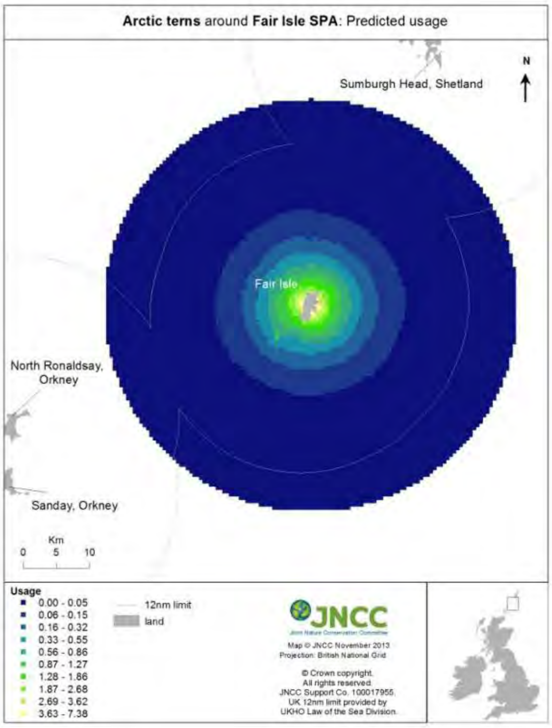


Figure 33. Predicted relative usage of the waters around Fair Isle SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.6 Auskerry

For Auskerry SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 40). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 34. Predicted usage was highest around the colony, decreasing with distance from the colony.

Table 40. The final model selected for Auskerry SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

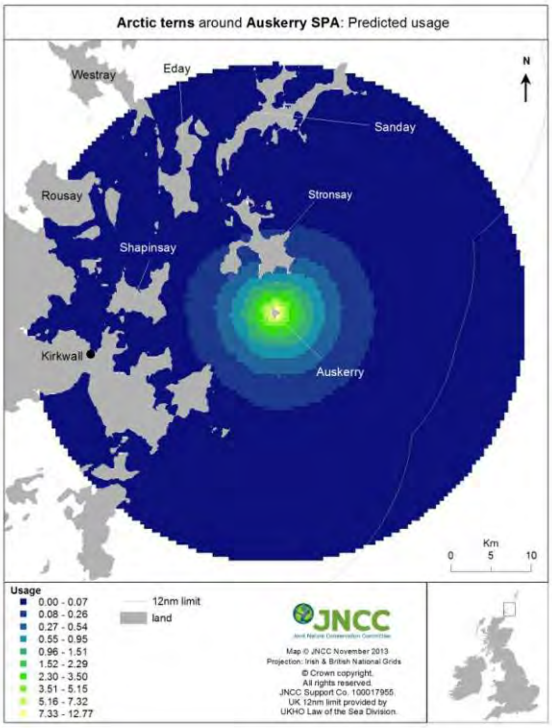


Figure 34. Predicted relative usage of the waters around Auskerry SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.7 Papa Westray (North Hill and Holm)

For Papa Westray (North Hill and Holm) SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 41). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Predictions of relative usage were made to the colonies at North Hill on Papa Westray and to Holm of Papay and are shown in Figure 35. Predicted usage for both colonies was highest around the colony, decreasing with distance from the colony, with overlap in the predicted areas used by birds from each colony.

Table 41. The final model selected for Papa Westray (North Hill and Holm) SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

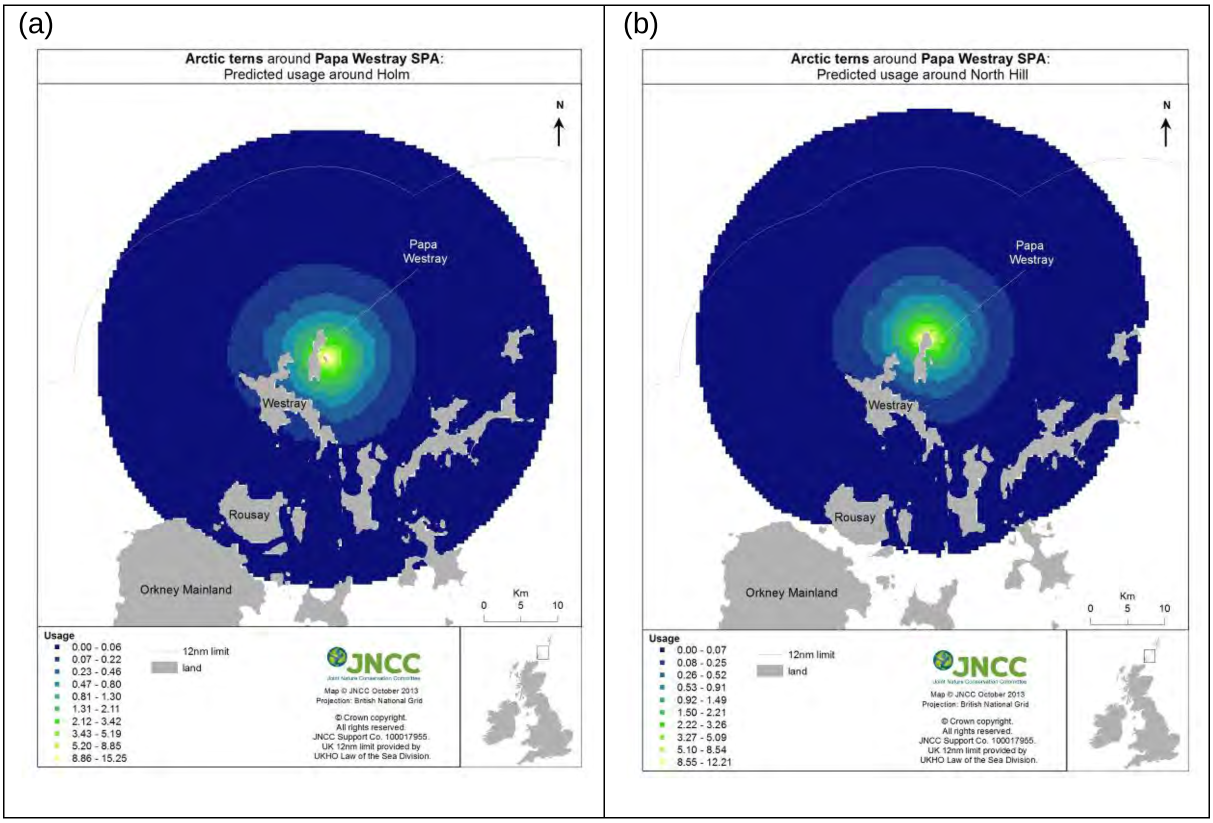


Figure 35. Predicted relative usage of the waters around (a) Holm of Papay and (b) North Hill, Papa Westray for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.8 Rousay

For Rousay SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 42). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 36. Predicted usage was highest around the colony, decreasing with distance from the colony.

Table 42. The final model selected for Rousay SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

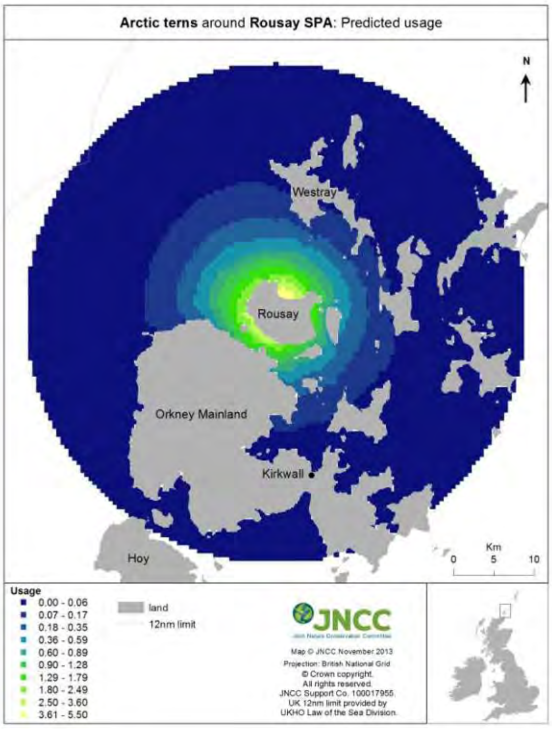


Figure 36. Predicted relative usage of the waters around Rousay SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.9 Pentland Firth Islands

For Pentland Firth Islands SPA the species of interest for the project was Arctic tern. No visual tracking data were available so a generic model was applied (Table 43). Details of model selection for this Phase 2 model are given in Potts *et al* 2013c. Predictions of relative usage were made to Muckle Skerry and to Swona and are shown in Figure 37. Predicted usage was highest around the colony, decreasing with distance from the colony, with overlap in the predicted areas used by birds from each colony.

Table 43. The final model selected for Pentland Firth Islands SPA.

Species	Model	Terms
Arctic tern	Generic	Distance to colony, bathymetry

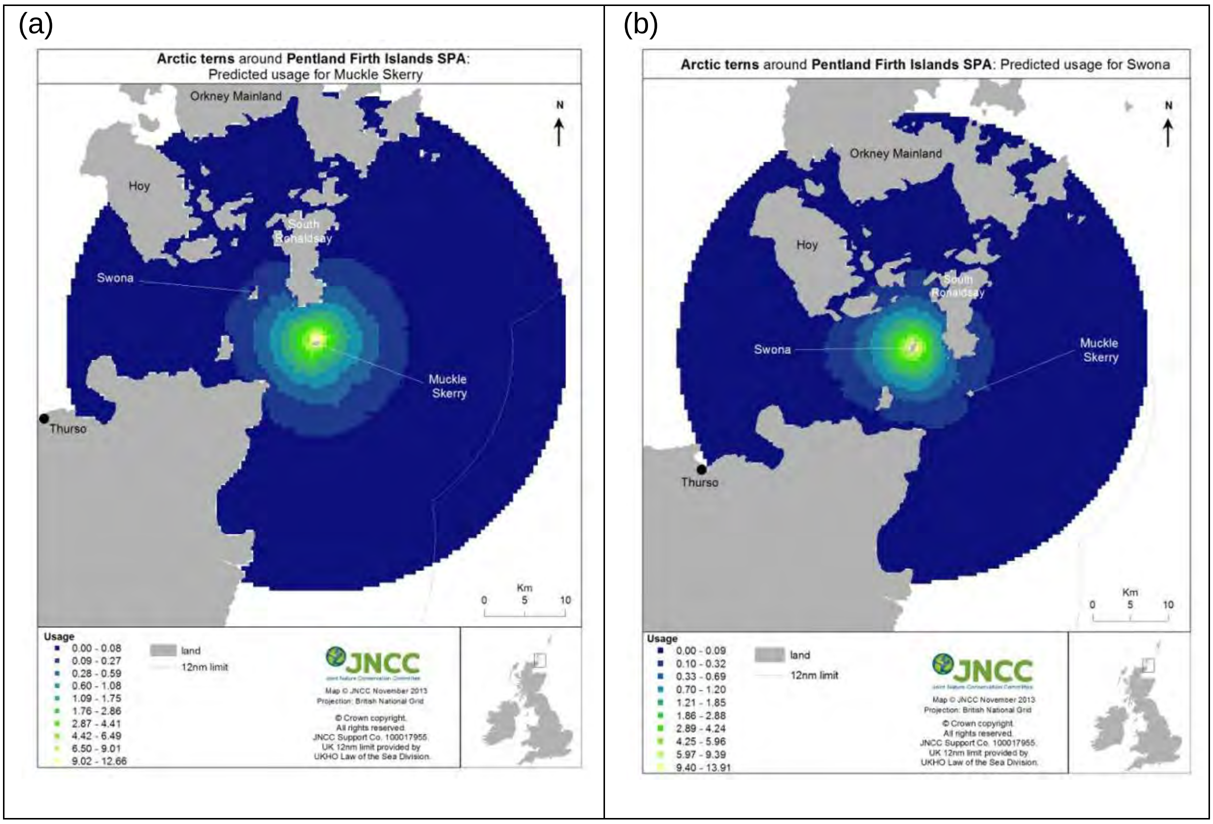


Figure 37. Predicted relative usage of the waters around (a) Muckle Skerry and (b) Swona within Pentland Firth Islands SPA for Arctic terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.10 Ythan Estuary, Sands of Forvie and Meikle Loch

For Ythan Estuary, Sands of Forvie and Meikle Loch SPA, the species of interest for the project was Sandwich terns. A total of 51 tracks was obtained over a single survey season in 2011 (Table 44). Birds were tracked from the Sands of Forvie colony, at the mouth of the Ythan Estuary. Tracking work was timed to coincide with the chick-rearing season. The distribution of Sandwich tern tracks tended to be confined to coastal waters from Aberdeen Bay north to Cruden Bay (Figure 38).

Table 44. Sample sizes of tracks obtained for Ythan Estuary, Sands of Forvie and Meikle Loch SPA. Birds were tracked from Sands of Forvie.

Species	No. of tracks	
	2011 (6-30 June)	Total
Sandwich tern	51	51

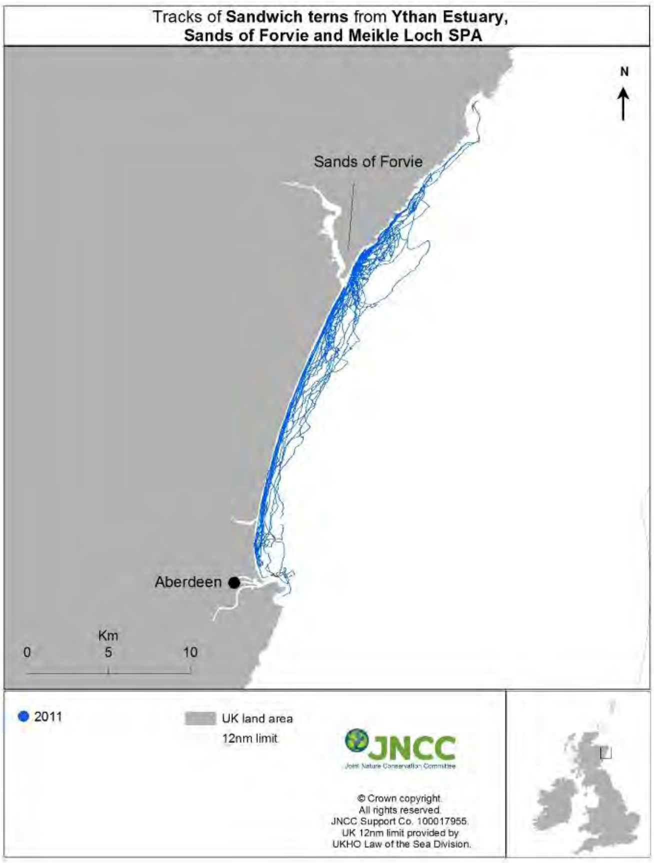


Figure 38. Tracks of Sandwich terns from Ythan Estuary, Sands of Forvie and Meikle Loch SPA from 2010. Birds were tracked from Sands of Forvie.

The results of the bootstrapping and model selection process are given in Appendix 2. The final model selected is shown in Table 45. This is the only model in the project which does not contain distance to colony; this might be because in this area stratified temperature is highly correlated ($r^2 = 0.86$) with distance to colony. Distributions of predicted relative usage closely matched the underlying data, with distributions confined to coastal waters and are shown in Figure 39. It was not possible to generate predictions for a few of the grid cells which were between *c*.1-2km adjacent to the coast for Sandwich terns. This is due to missing data in one or more of the covariates selected in the final model.

Table 45. The final model selected for Ythan Estuary, Sands of Forvie and Meikle Loch SPA.

Species	Model	Terms
Sandwich tern	Site specific	bathymetry, stratified temperature

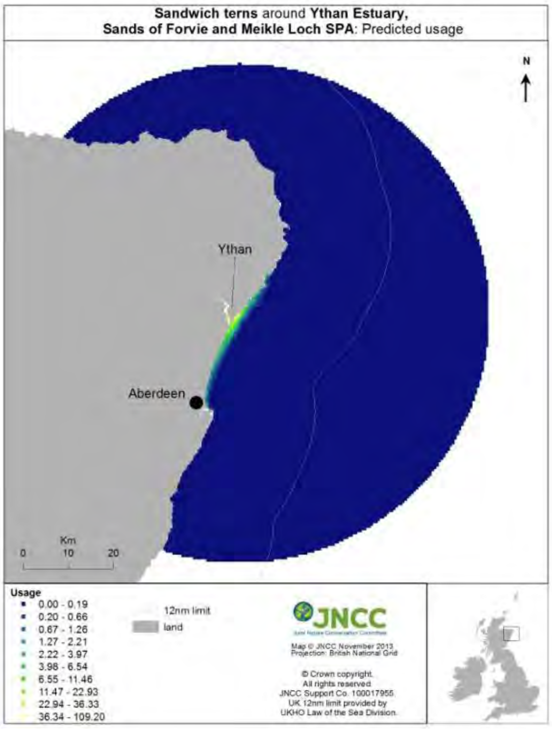


Figure 39. Predicted relative usage of the waters around Ythan Estuary, Sands of Forvie and Meikle Loch SPA for Sandwich terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.11 Imperial Dock Lock

For Imperial Dock Lock SPA, the species of interest for the project was common tern. A total of 137 tracks were obtained over two survey seasons from 2009 to 2010 (Table 46). Tracking work was timed to coincide with the chick-rearing season, except in 2010 when data were also collected during the incubation period in May. The distribution of common tern tracks tended to radiate out in all seaward directions from the colony, with concentrations of tracks within this area in a wide band stretching north of the colony up to the Fife coastline from Kinghorn to Kirkcaldy and south-east from the colony along the coastal waters down to Portobello (Figure 40).

Table 46. Sample sizes of tracks obtained for common tern species breeding at Imperial Dock Lock SPA.

Species	No. of tracks		
	2009 (16 June – 10 July)	**2010 (26/31 May; 25/26 June; 13 July)**	**Total**
Common tern	114	23	137

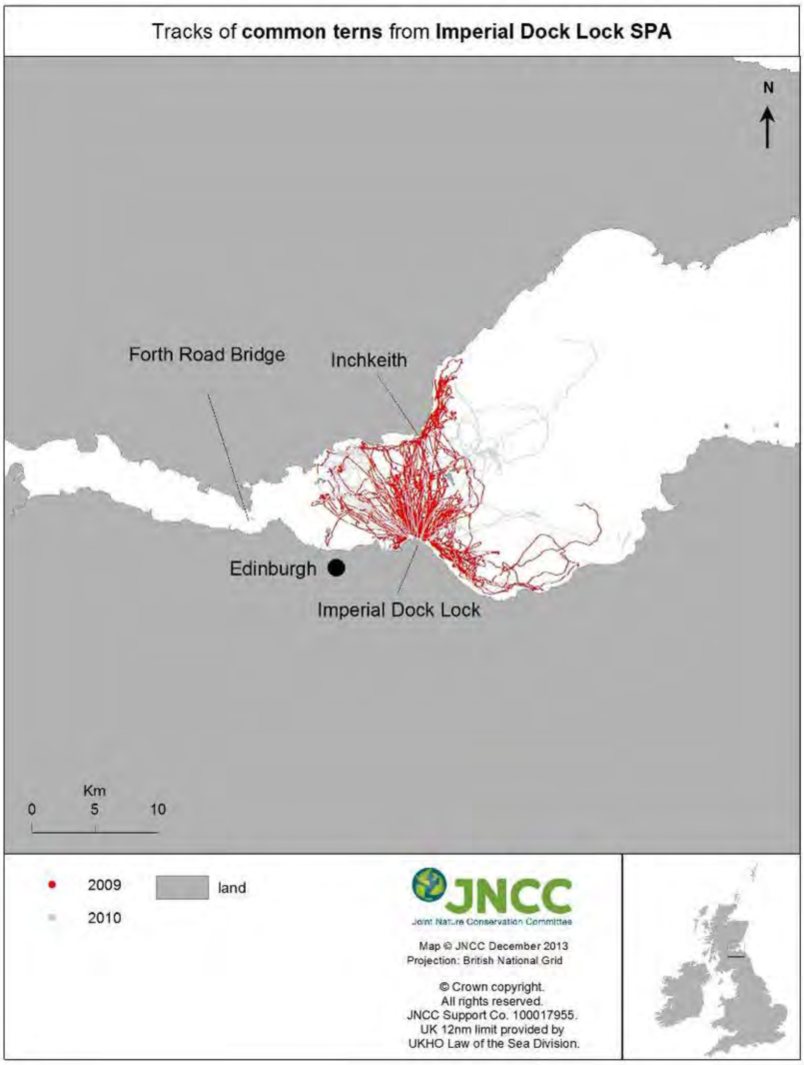


Figure 40. Tracks of common terns tracked from Imperial Dock Lock SPA from 2009 to 2010.

The results of the bootstrapping and model selection process are given in Appendix 2. The final model selected is shown in Table 47. Distributions of predicted relative usage closely matched the underlying data, with usage being highest around the colony and generally decreasing with distance from the colony (Figure 41). However there is a particular section of the usage surface to the north of the colony where predicted usage does not change in the smooth pattern seen elsewhere. This is attributable to the underlying salinity in spring data, which forms one of the covariates in this model. At that particular section, the salinity in spring values change abruptly along a line running east-west.

Table 47. The final model selected for common terns.

Species	Model	Terms
Common tern	Site specific	distance to colony, seabed slope, sea surface salinity in spring, distance to shore, bathymetry

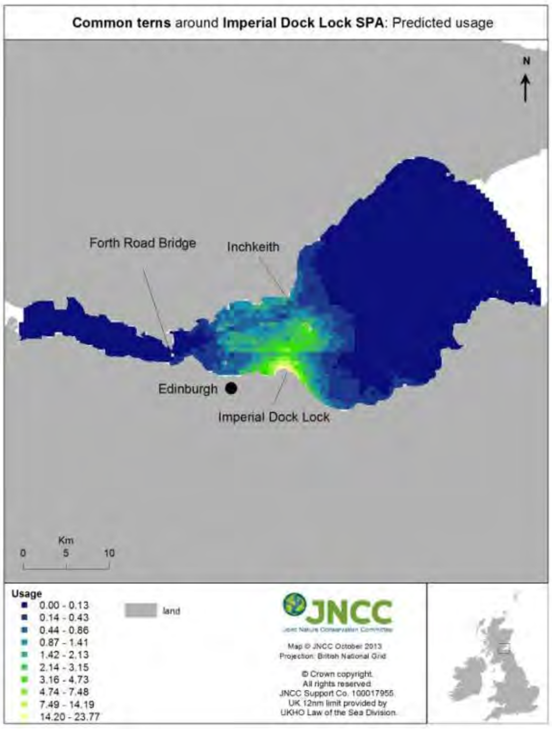


Figure 41. Predicted relative usage of the waters around the Imperial Dock Lock SPA for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.12 Forth Islands

Forth Islands SPA consists of a series of islands supporting the main seabird colonies in the Firth of Forth and include the islands of Inchmickery, Isle of May, Fidra and Long Craig. For the Forth Islands SPA the species of interest for the project were Arctic terns (Isle of May) and common terns (Isle of May and Long Craig). A total of 12 tracks was obtained from the Isle of May over a single survey season in 2010 (Table 48, Figure 42) with two separate periods of tracking carried out timed to coincide with incubation (early June) and chick-rearing (late June). Terns on the Isle of May had a very poor season in 2010, with few birds attempting to breed (seven common terns incubating by end of May, rising to 52 pairs by the last week of June, equally split between common and Arctic terns) and chicks suffered gull predation soon after hatching. We felt that the likelihood that our tracked individuals were non-breeders or failed breeders was very high compared to our other study colonies, and considered the data potentially unrepresentative. Therefore those data were discarded and instead, a generic model was applied for Forth Islands SPA (Table 49). Details of model selection for these Phase 2 models are given in Potts *et al* 2013c. Distributions of predicted relative usage are shown in Figure 43. For both species, predicted usage was highest around the colony, decreasing with distance from the colony.

Table 48. Sample sizes of tracks obtained for tern species breeding at Isle of May colony. Note that these data were not used in the modelling analysis as they were considered unrepresentative.

Species	**No. of tracks 2010 (1-3 June; 26 June)**
Arctic tern	10
Common tern	2

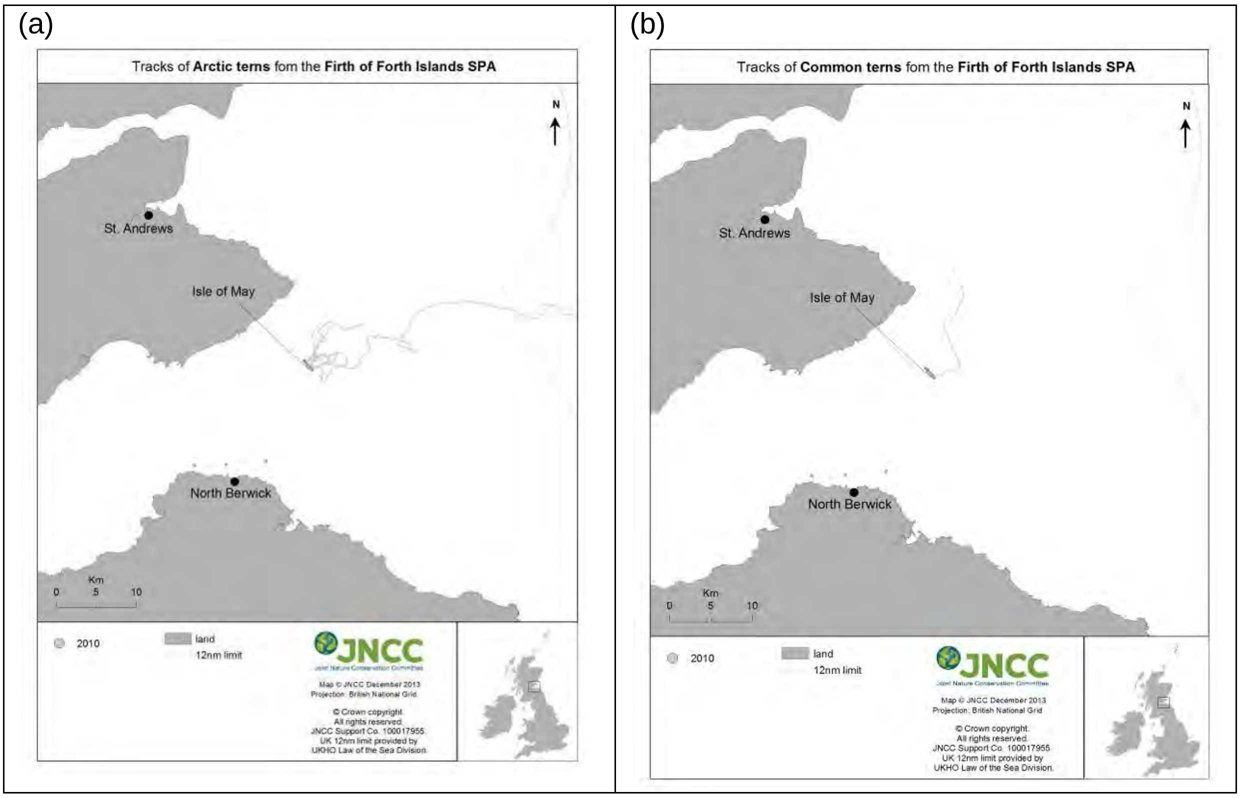


Figure 42. Tracks of (a) Arctic and (b) common terns tracked from the Isle of May within the Forth Islands SPA in 2010.

Table 49. The final models selected for Forth Islands SPA.

Species	**Model**	**Terms**
Arctic tern	Generic	Distance to colony, bathymetry
Common tern	Generic	Distance to colony, distance to shore, bathymetry

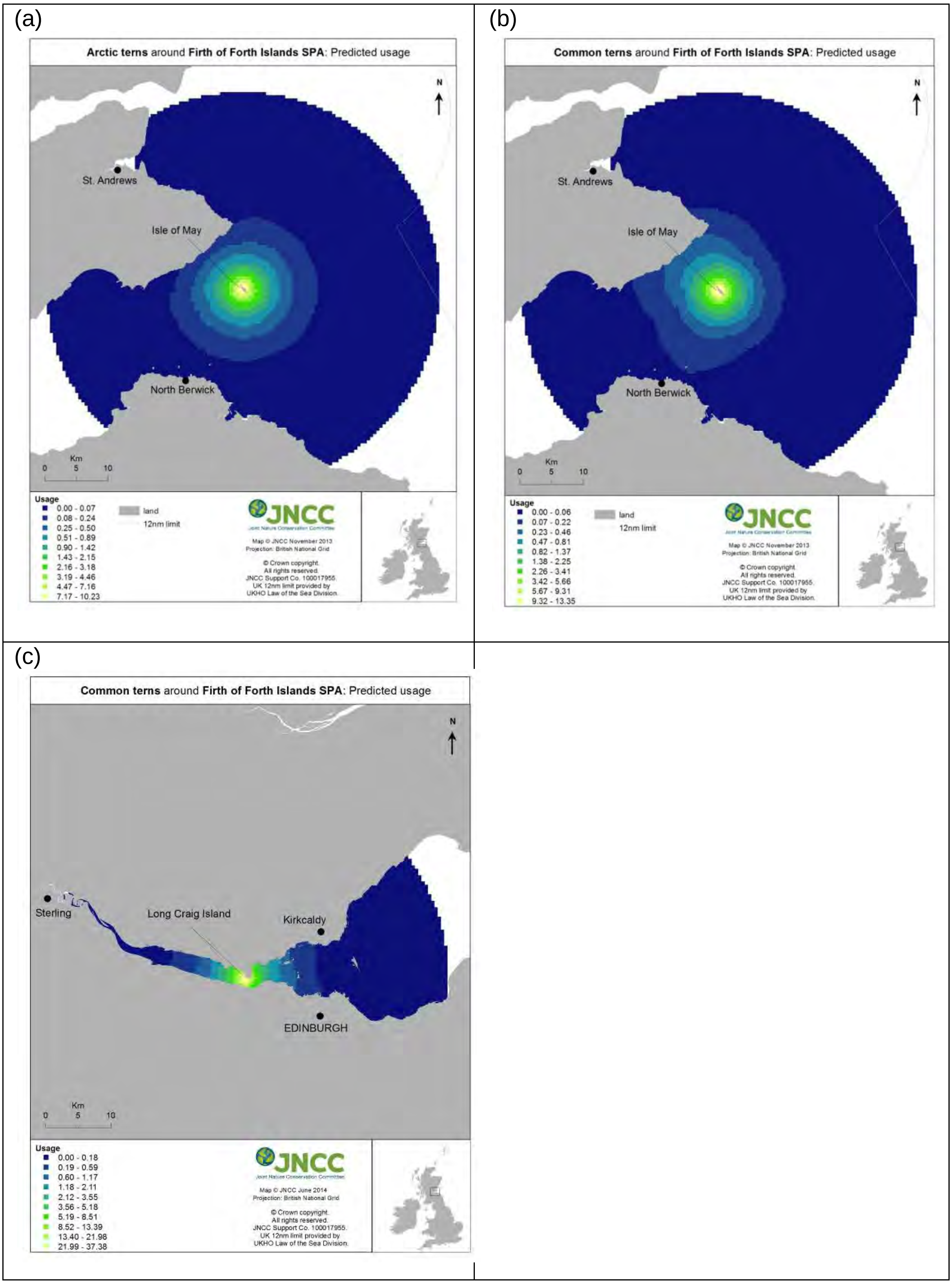


Figure 43. Predicted relative usage of the waters for (a) Arctic and (b) common terns around the Isle of May and for (c) for common terns around Long Craig. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

3.8.13 Glas Eileanan

For Glas Eileanan SPA, the species of interest for the project was common tern. A total of 63 common tern tracks was obtained over a single survey season in 2011, and two Arctic terns were also tracked (Table 50). Tracking work was timed to coincide with the chick-rearing season. Birds were tracked from both Glas Eileanan itself, and South Shian around 20km to the east where birds breed on artificial rafts. There is some evidence from ringed birds that there has been some movement of birds between these two colonies (C. Craik, *pers.com*.). The distribution of common tern tracks radiated out into the Sound of Mull, Firth of Lorne and into Loch Linnhe around Lismore. The two tracked Arctic terns remained within the Sound of Mull, eastwards of the colony (Figure 44).

Table 50. Sample sizes of tracks obtained for the four tern species breeding at Glas Eileanan SPA.

Species	**No. of tracks**		
	Glas Eileanan	**South Shian**	**Total**
	2011 (20-29 June)	**2011 (24-28 June)**	
Common tern	48	15	63
Arctic tern	2	0	2

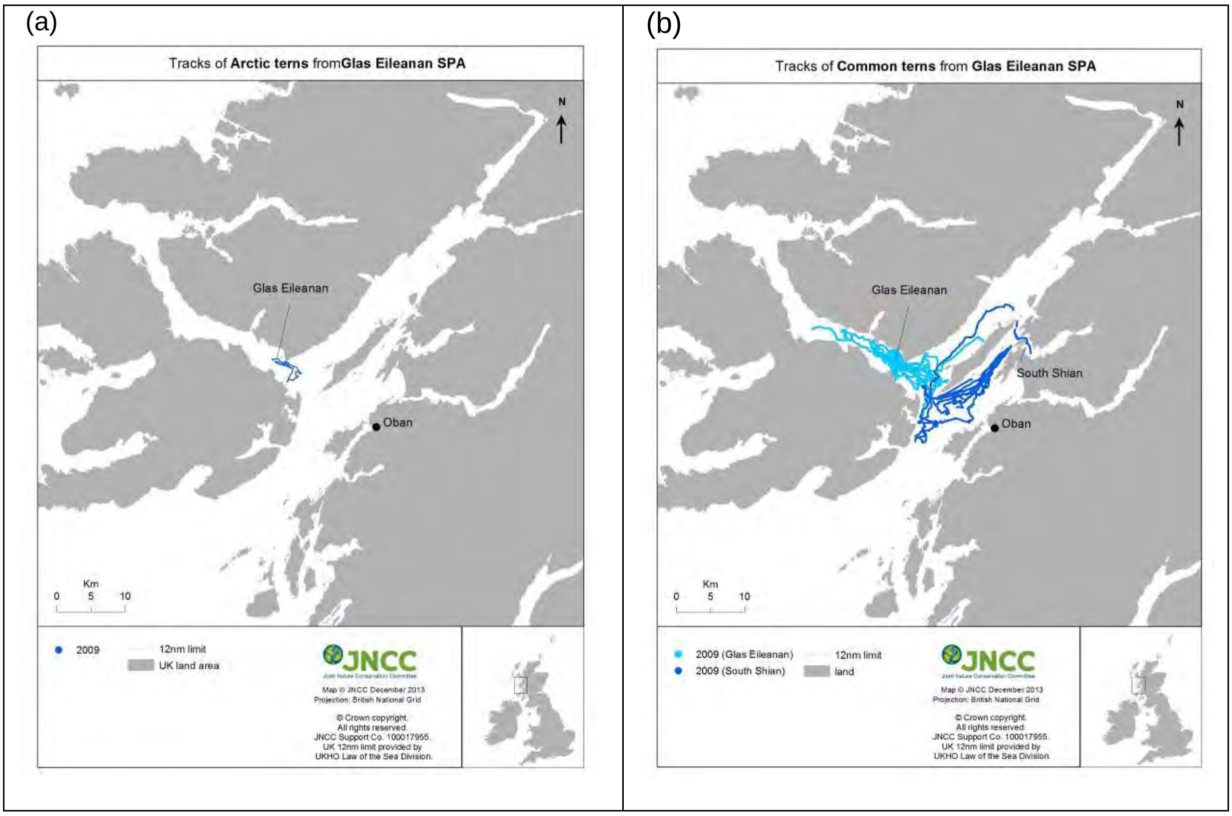


Figure 44. Tracks of (a) Arctic terns tracked from Glas Eileanan SPA and (b) common terns tracked from Glas Eileanan SPA and South Shian.

The results of the bootstrapping and model selection process are given in Appendix 2. The final model selected is shown in Table 51. Distribution of predicted usage for common terns matched the underlying data from Glas Eileanan reasonably well, although it failed to predict the high observed usage along the south coast of Lismore and overestimated the use off the east coast of Mull (Figure 45). It was not possible to generate predictions for a small number of the grid cells which lay between *c*.1-2km from the coast and for most of the grid cells within Loch Stunart, due to missing data for the seabed covariate in that area.

Table 51. The final model selected for Glas Eileanan SPA.

Species	**Model**	**Terms**
Common tern	Site specific	Distance to colony, distance to shore, slope

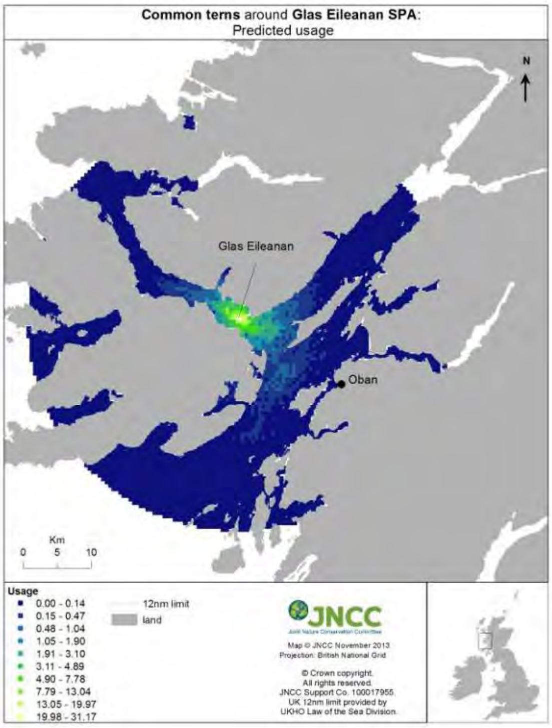


Figure 45. Predicted relative usage of the waters around Glas Eileanan for common terns. Usage values are relative and binned using natural groupings inherent in the data (natural jenks, which reduce the variance within classes and maximize the variance between classes, determined within ArcMap v10.1).

4 Assessing model performance

The cross-validation results for testing the ability of the Phase 1 models to predict validation data from individuals are shown in Table 52, while the results for testing the ability of the models to predict validation data from other years are shown in Table 53. The likelihood and mean square error scores are only relative to the other models in the test set, but the AUC score represents the discriminatory ability of a model as follows: >0.9, excellent; 0.8-0.9, good; 0.7-0.8, moderate; 0.6-0.7, poor; and 0.5-0.6, unsuccessful (Swets 1988). Of the Phase 1 models tested, five models performed moderately well, seven were good and nine were excellent in their ability to predict validation data for individuals (Table 52). Of those tested for their ability to predict validation data for years, based on the average AUC score, one performed poorly, two performed moderately well, three were good and two were excellent (Table 53). The cross-validation results for the Phase 2 models are summarised in Table 54. They showed that, when predicting data from new colonies, the final Arctic tern generic model performed moderately well, the common tern generic model was good, and the Sandwich tern generic model was excellent. For all species, the final Phase 2 models performed better than simple models containing only distance to colony, but only marginally so.

Table 52. The results of cross-validation, testing the ability of the models to predict validation data from individuals. Three scores of cross-validation were used. The average score for each for the bootstrap samples of 10, 20 or 30 tracks (see Methods) are shown.

SPA Colony	Bootstrap Sample Size	Average Likelihood Score	Average Mean Squared Error Score	Average AUC
Arctic tern				
Coquet Island	10	-0.225	0.056	0.791
	20	-0.213	0.055	0.801
	30	-0.213	0.056	0.795
Common tern				
Coquet Island	10	-0.232	0.059	0.838
	20	-0.197	0.056	0.848
	30	-0.193	0.056	0.849
Imperial Dock Lock	10	-0.305	0.086	0.734
	20	-0.294	0.084	0.744
	30	-0.291	0.084	0.744
Sandwich tern				
Coquet Island	10	-0.213	0.059	0.915
	20	-0.192	0.059	0.913
	30	-0.193	0.059	0.917
North Norfolk	10	-0.215	0.053	0.883
	20	-0.199	0.052	0.886
	30	-0.201	0.053	0.884
Ynys Feurig, Cemlyn Bay and The Skerries	10	-0.205	0.055	0.934
	20	-0.193	0.053	0.940
	30	-0.176	0.051	0.943
Ythan Estuary, Sands of Forvie and Meikle Loch	10	-0.104	0.030	0.989
	20	-0.085	0.027	0.990
	30	-0.082	0.026	0.991

Table 53. The results of cross-validation, testing the ability of the models to predict validation data from a different year of survey. Three scores of cross-validation were used (see Methods).

SPA colony	Test Year (no. tracks)	Training years (no. tracks)	Like-lihood	Mean squared error	AUC	Average AUC
Arctic tern						
Coquet Island	2009 (36)	2010 (13)	-0.45	0.11	0.62	0.71
	2009 (36)	2010, 2011 (55)	-0.2052	0.055	0.816	
	2009 (36)	2011 (42)	-0.43	0.11	0.59	
	2010 (13)	2009 (36)	-0.35	0.1	0.59	
	2010 (13)	2009, 2011 (78)	-0.2472	0.0692	0.7947	
	2010 (13)	2011 (42)	-0.69	0.16	0.45	
	2011 (42)	2009 (36)	-0.18	0.05	0.84	
	2011 (42)	2009, 2010 (49)	-0.1594	0.0418	0.8227	
	2011 (42)	2010 (13)	-0.16	0.04	0.84	
Outer Ards	2009 (7)	2010, 2011 (17)	-0.3814	0.1015	0.604	0.72
	2009 (7)	2011 (14)	-0.43	0.11	0.59	
	2011 (14)	2009 (7)	-0.18	0.05	0.84	
	2011 (14)	2009, 2010 (10)	-0.2009	0.053	0.8343	
Common tern						
Coquet Island	2009 (29)	2010 (13)	-0.21	0.06	0.87	0.84
	2009 (29)	2010, 2011 (46)	-0.2085	0.0626	0.8647	
	2009 (29)	2011 (33)	-0.21	0.63	0.86	
	2010 (13)	2009 (29)	-0.26	0.08	0.79	
	2010 (13)	2009, 2011 (62)	-0.2651	0.0777	0.7632	
	2010 (13)	2011 (33)	-0.28	0.08	0.74	
	2011 (33)	2009 (29)	-0.16	0.05	0.89	
	2011 (33)	2009, 2010 (42)	-0.1587	0.0478	0.8919	
	2011 (33)	2010 (13)	-0.17	0.05	0.89	
Imperial Dock Lock	2009 (97)	2010 (21)	-0.2922	0.086	0.7315	0.68
	2010 (21)	2009 (97)	-0.3318	0.0898	0.624	
Larne Lough	2009 (12)	2011 (19)	-0.21	0.06	0.89	0.87
	2011 (19)	2009 (12)	-0.24	0.07	0.84	
	2009 (12)	2010, 2011 (20)	-0.2116	0.0575	0.8885	
	2011 (19)	2009, 2010 (13)	-0.2251	0.0628	0.8465	
Roseate tern[19]						
Coquet	2009 (14)	2010, 2011 (26)	-0.182	0.050	0.919	0.90
	2011 (25)	2009, 2010 (15)	-0.342	0.073	0.882	

---

[19] The cross-validation analysis for Roseate terns was carried out by BioSS (see Potts & Brewer 2014)

SPA colony	Test Year (no. tracks)	Training years (no. tracks)	Like-lihood	Mean squared error	AUC	Average AUC
Sandwich tern						
Coquet	2009 (36)	2010 (8)	-0.14	0.04	0.92	0.92
	2009 (36)	2010, 2011 (54)	-0.1683	0.0552	0.9184	
	2009 (36)	2011 (46)	-0.13	0.04	0.92	
	2010 (8)	2009 (36)	-0.31	0.1	0.9	
	2010 (8)	2009, 2011 (82)	-0.235	0.0837	0.8987	
	2010 (8)	2011 (46)	0.18	0.06	0.91	
	2011 (46)	2009 (36)	-0.13	0.04	0.93	
	2011 (46)	2009, 2010 (44)	-0.1509	0.0502	0.9391	
	2011 (46)	2010 (8)	-0.12	0.04	0.92	
Larne Lough	2009 (9)	2010 (10)	-0.02	0.01	1	0.98
	2009 (9)	2011 (11)	-0.05	0.02	1	
	2010 (10)	2009 (9)	-0.13	0.04	0.97	
	2010 (10)	2011 (11)	-0.1	0.04	0.97	
	2011 (11)	2009 (9)	-0.34	0.05	0.98	
	2011 (11)	2010 (10)	-0.14	0.05	0.98	
	2009 (9)	2010, 2011 (21)	-0.034	0.0087	0.9968	
	2010 (10)	2009, 2011 (20)	-0.093	0.0329	0.9687	
	2011 (11)	2009, 2010 (19)	-0.2251	0.0574	0.9798	

Table 54. Cross-validation results based on the AUC score for Phase 2 models for (a) Arctic, (b) common and (c) Sandwich terns. For common and Sandwich terns, results are shown for when the salinity in spring covariate was excluded as this allowed inclusion of North Norfolk (salinity in spring data were not available for this area). For each species the final model chosen (based on three different cross-validation scores, see Methods) is shown in bold. In addition, a model containing only distance to colony and (if different), the model which maximised the AUC score are shown for comparison. For the cross-validation results for all the other models tested, and for all three scores, see Potts *et al* 2013c.

(a) Arctic terns	**AUC score for each test colony**			
Model	Coquet Island	Farne Islands	Outer Ards	Average AUC
Distance to colony	0.790	0.753	0.700	0.747
Distance to colony, bathymetry	**0.789**	**0.755**	**0.713**	**0.752**

(b) Common terns	**AUC score for each test colony (excluding salinity)**						
Model	North Norfolk	Coquet Island	Cemlyn	Larne Lough	Imperial Dock Lock	Glas Eileanan	Average AUC
Distance to colony	0.923	0.801	0.916	0.819	0.655	0.746	0.810
Distance to colony, bathymetry, distance to shore	**0.931**	**0.813**	**0.913**	**0.788**	**0.665**	**0.761**	**0.812**

(c) Sandwich terns	**AUC score for each test colony (excluding salinity)**							
Model	North Norfolk	Coquet Island	Larne Lough	Sands of Forvie	Farne Islands	Cemlyn	Cockle	Average AUC
Distance to colony	0.877	0.850	0.963	0.898	0.889	0.866	0.842	0.884
Distance to colony, bathymetry	0.878	0.899	0.979	0.962	0.956	0.907	0.856	0.920
Distance to colony, bathymetry, distance to shore	**0.821**	**0.911**	**0.979**	**0.973**	**0.970**	**0.907**	**0.850**	**0.916**

5 Discussion

This project has collected and collated a substantial amount of data on the distributions of terns at sea and to our knowledge represents the largest available resource of tracking data for breeding terns; tracking of individual terns of known provenance has rarely been undertaken and never before on the scale of this study. The visual tracking method allowed this to be achieved at a time when bird-borne devices, such as GPS tags, were still unsuitable for deploying on terns. A major benefit of visual tracking compared to remote tracking is the certainty and accuracy with which the spatial location of foraging events can be recorded thus eliminating the need to infer these from characteristics of the track such as speed or sinuosity. The data collected/collated consisted of up to three years of survey around eleven colony SPAs. Datasets from ten of these colony SPAs were suitable for analysis (the Isle of May dataset had to be discarded as the data were considered potentially unrepresentative) and a total of almost 1300 tracks were available to the project across the four species. Geographical coverage across the UK was maximised within the constraints of the time, logistics and resources available. This ensured that data were obtained across a large range of covariate values, and that inter-colony variation could be captured as much as possible for the generic models.

A thorough model development exercise explored and addressed the key analytical issues presented by our tracking data and found that weighted binomial GLMs were the most suitable means of creating predictive foraging distribution models. Their application allowed the development of site-specific models for 16 species/SPAs as well as generic models for each species that were used to extrapolate geographically for 30 species/SPAs. Thus the project delivered predictions of relative distributions of the larger tern species around the full complement of 32 colony SPAs in the UK which were found to be recently and regularly occupied (46 species/SPA models in total).

All of our models predicted highest usage around the colony, with usage generally declining with distance from the colony, which accords well with what we might expect for central place foragers. For Arctic and common terns, the pattern of usage generally radiated out from the colony in all directions out to sea. For Sandwich terns, usage was in most cases confined to a relatively narrow coastal area either side of the colony. Foraging grounds were rarely discrete from the colony (Imperial Dock Lock was the sole exception), indicating that areas used for commuting between the colony and the foraging grounds are likely to have been captured despite commuting data being excluded from the analyses. In all cases, there was negligible use of areas distant from the colony; in general around over three-quarters of the maximum potential foraging range was predicted to be virtually unused; for example, 95% of usage was contained within 5% (Sandwich) – 18% (Arctic) of the total available area within the maximum foraging range around Coquet Island. Consequently, the majority of usage was confined to an area less than that encompassed by the mean maximum foraging ranges (as recorded in this study as well as those in Thaxter *et al* (2012)). So although a simple approach such as applying a mean maximum foraging range radius around the colony, would correctly identify areas being used (and be a simpler method to explain), it would also include large areas of relatively low importance and be rather precautionary. Our habitat modelling approach, although complex, provides more realistic estimates of the relative importance of the areas within the maximum and mean maximum foraging ranges.

Distributions predicted by the Phase 1 models generally matched the underlying data well, but also occasionally identified areas of use which were not captured by our tracking data. This is one of the key advantages of using a habitat modelling approach as it allows extrapolation into areas which were not sampled, but which are predicted to be used based on the suitability of the environment. Interpolation based only on raw data would risk overlooking the potential importance of some areas if they had not happened to be used at the time of tracking by the individuals that were sampled. However, birds might be absent in areas that are predicted to be important because of the effects of an environmental variable that is not available for use in the model, or for behavioural reasons. Behavioural reasons might include benefiting from social feeding elsewhere, or avoiding competition, either with a neighbouring colony or within the same colony. Indeed, analysis of our 2011 tracking data from Coquet Island indicated that roseate terns may minimise inter-specific competition with the morphologically similar Arctic and common terns by partitioning foraging areas, as well as diet (Robertson *et al* 2014). Such behavioural influences on choice of foraging area are likely to be complex and variable, both temporally and spatially, and incorporating these factors within our models was beyond the scope of our project.

In the absence of independent datasets for assessing model predictive ability, the re-sampling technique of cross-validation has become a popular tool for validation of predictive models (e.g. Elith *et al* 2006; Schwemmer *et al* 2009) and was used extensively in this project. We used an AIC approach, supplemented with bootstrapping and considerations of biological plausibility (Phase 1), and cross-validation (Phase 2) to provide a robust basis for model selection. All of the final models were relatively simple, with most containing only two or three covariates and all except one (Sandwich terns at Ythan Estuary, Sands of Forvie and Meikle Loch SPA) containing distance to colony; however for that area distance to colony is highly correlated with one of the covariates in the final model. There was high consistency in the covariates selected in the final models across SPAs both within and between species, with distance to colony, bathymetry and salinity in spring being selected in a third of Phase 1 models for all species. These covariates have previously been shown to influence tern distributions (Garthe 1997; Schwemmer *et al* 2009). Cross-validation exercises confirmed that our models performed well in predicting the distributions of individuals from validation datasets within a colony (Phase 1), as well as performing well when extrapolating to new colonies (Phase 2).

A habitat modelling approach allowed us to apply generic models which benefit from pooling data across multiple colonies, gaining strength from increased sample sizes which are able to identify broad, consistent preference relationships across multiple colonies. However, if there are differences in habitat preference between the sampled and unsampled colonies there is a risk that generic models might not accurately capture important areas at the unsampled colonies. One notable gap in data coverage was the Northern Isles which is where the vast majority of the UK Arctic tern population breed, and there is a risk that there might be regional differences in habitat preferences between birds breeding in the Northern Isles compared to those breeding at the sampled colonies further south. To minimise this risk, we focussed on identifying general, consistent habitat preference relationships across the sampled colonies and based model selection for the generic models on the ability of models to predict to unsampled colonies; the cross-validation results lend confidence to our decision to combine data across sites. We also compared the underlying environmental covariate data between sampled and unsampled colonies (based on box-plots and Principal Component Analysis) to confirm that there overlaps in the range of habitat (as quantified by our covariates) available.

During visual tracking, around 64% of terns tracked were lost before they completed their foraging trip and this might be expected to cause an underestimation of the maximum foraging range. In this context, it is useful to compare our foraging ranges with those in the published literature, although it is important to note that these may not have been collected using comparable methods and may suffer from their own biases. We found that our mean maximum foraging ranges were in fact greater than the most recent published estimates (Thaxter *et al* 2012) for Arctic, common and roseate terns. Our mean maximum foraging range recorded for Sandwich terns was around two-thirds of that recorded in Thaxter *et al* 2012. The value in Thaxter *et al* 2012 was based on only two datasets, both of which were used within our project (available through a data-sharing agreement with ECON Ecological Consultancy Ltd). Given that the mean maximum foraging ranges we recorded for the other species were slightly greater than those recorded in Thaxter *et al* (2012), we feel that the lower mean maximum foraging range that we recorded for Sandwich terns is likely to reflect the fact that it better incorporates the true variation between colonies rather than being a significant underestimate (e.g. due to the survey method).

An important consideration in our study was that the data underlying our models were as representative as possible of the breeding populations of the colonies. We found that birds appeared to generally ignore the presence of the vessel and conclude the foraging behaviour of the sampled birds was unlikely to have been adversely affected by our survey method. We selected individuals at random as they departed from the colony and ensured we captured birds departing the colony from all directions out to sea. A separately commissioned analysis as part of the project based on a subset of our data found that our tracking data for Arctic, roseate and Sandwich terns from Coquet Island SPA and for common terns from Imperial Dock Lock SPA captured an estimated 71 - 74% of the core areas of use of those colonies (Harwood & Perrow 2014). The datasets, on which this analysis was based, sampled 8-14% of the total colony population for Arctic, common and Sandwich terns; and 61% for roseate terns. Although the Harwood and Perrow (2014) assessment is only applicable to the conditions pertaining to the time the samples were collected, it provides reassurance that, even when a relatively small proportion of the colony population is sampled, our data are likely to represent the core areas used by the colony population as a whole.

Tern distributions might be expected to vary between years, for example if the distribution of their prey changes. Therefore we were careful to obtain multiple years of data from a selection of our study sites. Of the 16 site-specific models, nine (56%) are based on three years of data, one (6%) is based on two years, and six (38%) are based on one year. Analysis (based on including year as an interaction term in the GLM models) showed there was little evidence to suggest any differences between years in environmental preferences, with only weak evidence of the relationship with distance to shore varying between years for Sandwich terns around Coquet Island SPA and no evidence of other relationships varying between years. However, there is a possibility that a lack of statistical power in the data (due to large variation/small sample sizes) prevented detection of significant differences between years. In other words, variation between years may be small relative to variation between colonies or between individuals. In addition, it is important to note that the dynamic covariate data were gathered over a different time period than our tern distribution data, so we were not assessing real-time relationships. Cross-validation showed that our models performed well in predicting validation data from other years, in all cases bar one, suggesting that overall our models were able to capture relationships that were consistent between the years of survey.

Our surveys were timed and targeted to focus on breeding birds, largely during the chick-rearing period. The collection of a relatively small proportion of data was timed to coincide with the incubation period but we were unable to confirm the true breeding status of most of the birds tracked, so data collected during the incubation period may have included birds which were rearing chicks, and birds tracked during the chick-rearing period may have been incubating. Therefore we combined data across the incubation and chick-rearing period for analysis. Foraging ranges might be expected to be greater during incubation as birds are less constrained to return to their colony so frequently (because they do not have to regularly feed chicks several times a day). Indeed the foraging ranges of roseate terns have been found to be greater during courtship and incubation than during the chick-rearing period (Newton & Crowe 2000). Shorter foraging tracks for Sandwich terns at North Norfolk during chick-rearing might be linked to seasonal inshore movements of prey as well as the imposed constraints of chick provisioning (Eglington & Perrow 2014). Thus, incubating birds may be exposed to different or additional levels of pressures during incubation. Inclusion of incubating birds might lead to elevated estimates of usage in areas more distant from the colony than they would have been had we used only chick-rearing data, but we expect that any difference would be marginal due to the relatively small proportion of our sampled birds likely to have been incubating. So the models are unlikely to fully capture areas of importance during incubation. Foraging ranges might also vary within different stages of the incubation and chick rearing period. A separate analysis of the Coquet Island 2011 tracking data for common, Arctic and roseate terns, using home range analysis found that Arctic and common tern core foraging areas moved closer to the colony and were smaller during late chick-rearing compared to early chick-rearing, corresponding with an increased provisioning rate of Arctic Terns observed at the colony (Robertson *et al* 2014).

Any survey method can provide information only about distributions during the conditions experienced at the time of survey. The visual tracking method is constrained by weather conditions and becomes difficult to undertake in sea states greater than three and/or during rainfall. Therefore the data may not capture areas that are important during poor weather if these differ from those used during favourable survey conditions. Tern foraging success has been shown to vary between different weather conditions, with success generally lower in windier and/or wetter conditions (see Eglington & Perrow (2014) and references therein). Such conditions may make prey less available to terns but it is not clear whether or how it might affect their spatial use of the marine environment; Steinen *et al* (2000) speculated that Sandwich terns may switch to foraging in more sheltered areas during windy weather.

The analytical approach we used in our study applied logistic regression modelling to our foraging location data by comparing it with a generated control dataset which represented available but unused locations (a use-availability design, Keating & Cherry 2004). This type of approach has recently been applied to seabird tracking data (Langston *et al* 2013; Wakefield *et al* 2011). But there is now an increasing variety of alternative species distribution modelling techniques designed to deal with presence-only data (see Elith *et al* 2006). ‘Maximum Entropy’ in particular is becoming increasingly popular in this respect (Elith *et al* 2006, 2011; Phillips *et al* 2006). Although there have been comparisons of different modelling methods (mainly for terrestrial species e.g. Brotons *et al* 2004; Elith *et al* 2006, but see Oppel *et al* 2012 for a seabird example) conclusions are mixed and it has been argued that the literature on species distribution modelling is not yet mature enough to provide clear guidance for selecting relevant methods (Elith & Graham 2009). Indeed, given different model methods have their own strengths and weaknesses, and may provide different predictions based on the same input data, some studies combine different modelling techniques within an ensemble or model-averaging approach (e.g. Oppel *et al* 2012; Marmion *et al* 2009; McGowan *et al* 2013, Lavers *et al* 2014).

The development of techniques for analysing presence-only data is rapidly expanding and becoming more sophisticated (e.g. Aarts *et al* 2012, 2013). It is apparent that spatial point process modelling methods are likely to become more common place particularly as solutions to provide increased computing efficiency evolve (e.g. Johnson *et al* 2013). In the meantime, our model development exercise used one of the more common and well accepted regression approaches to analyse and predict distributional patterns from presence-only data (MacDonald *et al* 2013) as it provided a solid basis to develop pragmatic and practical solutions to the various complexities and issues presented by our data.

Until relatively recently, spatial statistics were rarely used to analyse seabird distributions at sea and link them with oceanographic variables (Tremblay *et al* 2009). Traditional analysis of tracking data has tended to be restricted to simple descriptions of distributions (e.g. Le Corre *et al* 2012), often based on interpolation or smoothing of the data such as home range analysis (e.g. DeLord *et al* 2014). Habitat modelling allows a better understanding of the distribution patterns and habitat associations, and allows predictions both spatially and temporally (into the future), all of which are invaluable for effective conservation planning. Coupled with major advancements in the quantity and resolution of both seabird distribution and environmental data (Tremblay *et al* 2009), this has resulted in habitat modelling being increasingly used as a basis to inform the locations of marine protected areas for seabirds (e.g. Amorim *et al* 2009; Lascelles *et al* 2012; Lavers *et al* 2014; Louzao *et al* 2006, 2009, 2011). The importance of habitat modelling as a powerful tool to predict patterns of species occurrence is particularly recognised within the context of identifying marine Important Bird Areas (IBAs) (e.g. Arcos *et al* 2009; Fric *et al* 2012; Ramirez *et al* 2008; Birdlife 2011 and Oppel *et al* 2012). Our project developed a novel application of an established approach (though only recently applied within a seabird context) and represents one of the few multi-colony habitat modelling studies carried out at a national level for multiple species. Moreover, to our knowledge this is the first example where habitat modelling of tracking data has been applied to make geographically extrapolated predictions for unsampled areas. We have shown that, though logistically challenging, such an approach is feasible and invaluable for informing conservation of terns in the marine environment, including the identification of marine SPAs, marine planning and environmental impact assessments. Moreover, it can contribute to our overall understanding of factors affecting seabirds at sea at different spatial scales. The outputs from this work form a useful and valuable resource given the increasing political, environmental and legal imperatives to identify protected areas at sea for the conservation of seabirds.

6 References

AARTS, G., MacKENZIE, M., McCONNELL, B., FEDAK, M. & MATTHIOPOULOS, J. 2008. Estimating space-use and habitat preference from wildlife telemetry data. *Ecography*, **31**, 140-160.

AARTS, G., FIEBERG, J. & MATTHIOPOULOS, J. 2012. Comparative interpretation of count, presence–absence and point methods for species distribution models. *Methods in Ecology and Evolution*, **3**, 177–187.

AARTS, G., FIEBERG, J., BRASSEUR, S. & MATTHIOPOULOS, J. 2013. Quantifying the effect of habitat availability on species distributions. *Journal of Animal Ecology*, DOI:10.1111/1365-2656.12061.

AMORIM, P., FIGUEIREDO, M., MACHETE, M., MORATO, T., MARTINS, A., & SERRA˜O SANTOS, R. 2009. Spatial variability of seabird distribution associated with environmental factors: a case study of marine Important Bird Areas in the Azores. *ICES Journal of Marine Science*, **66,** 29–40.

ARCOS, J. M., BÉCARES, J., RODRÍGUEZ, B. & RUIZ, Y.A. 2009 *Áreas Importantes para la Conservación de las Aves marinas en España*. LIFE04NAT/ES/000049-Sociedad Española de Ornitología (SEO/BirdLife). Madrid

AUSTIN, M. 2007. Species distribution models and ecological theory: A critical assessment and some possible new approaches. *Ecological Modelling,* **200**, 1-19.

BEALE, C.M., LENNON, J.J., YEARSLEY, J.M., BREWER, M.J. & ELSTON, D.A. 2010. Regression analysis of spatial data. *Ecology Letters*, **13**, 246-264.

BECKER, P.H., FRANK D. & SUDMANN, S.R. 1993. Temporal and spatial pattern of common tern (Sterna hirundo) foraging in the Wadden Sea. *Oecologia,* **93**, 389-393.

BIRDLIFE. 2011. *Habitat modelling using satellite tracking data: a workshop to advance this process. Results from a workshop held 21-23 September 2011 at University of Coimbra, Portugal*. BirdLife International report. Cambridge, UK. Available from: http://www.birdlife.org/datazone/userfiles/file/Marine/CoimbraHabitatModellingReport.pdf

BREWER, M.J., POTTS, J. M., DUFF, E. I. & ELSTON, D. A. 2012a. *To carry out tern modelling under the Framework Agreement C10-0206-0387*. Contract Report to JNCC, March 2012.

BREWER, M.J., POTTS, J. M., DUFF, E. I. & ELSTON, D. A. 2012b. *Prediction of new colonies – seabird tracking data (under Agreement C10-0206-0387)*. Contract Report to JNCC, November 2012.

BREWER, M.J., POTTS, J. M., DUFF, E. I. & ELSTON, D. A. 2012c. *Additional Work Coquet Colony – Seabird Tracking Data (under Agreement C10-0206-0387).* Contract Report to JNCC, December 2012.

BRINDLEY, E. 1998. *Little terns in 1997*. Unpublished report of the Royal Society for the Protection of Birds, Sandy.

BROTONS, L., THUILLER, W., ARAUJO, M. B. & HIRZEL, A. H. 2004. Presence-absence versus presence-only modelling methods for predicting bird habitat suitability. *Ecography*, **27**, 437-448.

BROWN, R. A. & MCAVOY, W. 1985. Nesting terns in Strangford Lough, 1969-84 – a review. *Irish Birds,* **3**, 33-47.

BURNHAM, K.P. & ANDERSON, D.R. 2002. *Model selection and multimodel inference: a practical information-theoretic approach*. Second Edition. Springer-Verlag, New York.

CRAMP, S. (ed.) 1985. *The Birds of the Western Palearctic, Vol. 4*. Oxford University Press.

DELORD, K., BARBRAUD, C., BOST, C-A., DECEUNINCK, B., LEFEBVRE, T.,LUTZ, R., MICOL, T., PHILLIPS, R. A., TRATHAN P. N. & WEIMERSKIRCH, H. 2014. Areas of importance for seabirds tracked from French southern territories, and recommendations for conservation. *Marine Policy* **48,** 1–13.

DUNN, E. K. & MEAD, C.J. 1982. Relationship between sardine fisheries and recovery rates of ringed terns in West Africa. *Seabird,* **6**, 98-104.

EGEVANG, C., STENHOUSE, I. J., PHILLIPS, R. A., PETERSEN, A., FOX, J. W. & SILK, J. R. D. 2010. Tracking of Arctic terns *Sterna paradisaea* reveals longest animal migration. *Proceedings of the National Academy of Sciences of the United States of America* **107**: 2078-2081.

EGLINGTON, S. & PERROW, M. R. 2014. *Literature review of tern Sterna sp. foraging ecology*. Report to JNCC, under Contract ref. C13-0204-0686.

ELITH, J. & GRAHAM, C.H. 2009. Do they? How do they? Why do they differ? On finding reasons for differing performances of species distribution models. *Ecography,* **32**, 66–77.

ELITH, J, GRAHAM, C.H., ANDERSON, R.P., DUDÍK, M., FERRIER, S., GUISAN, A., HIJMANS, R.J., HUETTMANN, F., LEATHWICK, J.R., LEHMANN, A., LI, J., LOHMANN, L.G., LOISELLE, B.A., MANION, G., MORITZ, C., NAKAMURA, M., NAKAZAWA, Y., OVERTON, J.M., PETERSON, A.T., PHILLIPS, S.J., RICHARDSON, K., SCACHETTI-PEREIRA, R., SCHAPIRE, R.E., SOBERÓN, J., WILLIAMS, S., WISZ, M.S. & ZIMMERMANN, N.E. 2006. Novel methods improve prediction of species' distributions from occurrence data. *Ecography* **29**, 129-151

ELITH, J., PHILLIPS, S.J., HASTIE, T., DUDIK, M., CHEE, Y.E. & YATES, C.J. 2011. A statistical explanation of MaxEnt for ecologists. *Diversity and Distributions*, **17**, 43–57.

EU 2009. Council Directive 2009/147/EC of 30 November 2009 on the conservation of wild birds. *Official Journal of the European Union*. L 20/7 (26.1.2010). http://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=OJ:L:2010:020:0007:0025:EN:PDF

EVERAERT, J. & STIENEN, E. W, M. 2007. Impact of wind turbines on birds in Zeebrugge (Belgium). *Biodiversity and Conservation*, ***16*** (12), 3345-3359.

FASOLA, M., SANCHEZ, J.M., & ROSELAAR, C.S. 2002. *Sterna albifrons* Little tern. *BWP Update,* **4**, 89-114.

FRIC, J., PORTOLOU, D., MANOLOPOULOS, A. & KASTRITIS, T. 2012. *Important Areas for seabirds in Greece*. LIFE07 NAT/GR/000285 – Hellenic Ornithological Society (HOS / BirdLife Greece), Athens.

FUCHS, E.1977. Predation and anti-predator Predation and Anti-Predator Behaviour in a Mixed Colony of Terns *Sterna* sp. and Black-Headed Gulls *Larus ridibundus* with Special Reference to the Sandwich Tern *Sterna sandvicensis*. *Ornis Scandinavica,* **8**, 17-32

GARTHE, S. 1997. Influence of hydrography, fishing activity, and colony location on summer seabird distribution in the south-eastern North Sea. *ICES Journal of Marine Science,* **54,** 566-577

GASTON 2004. *Seabirds: A Natural History*. Poyser.

GOCHFELD, M., BURGER, J. & NISBET, I.C.T. 1998. Roseate Tern (Sterna dougallii). In: Poole, A. & Gill, F. (eds.) *The birds of North America*. Birds of North America Inc., Philadelphia, PA & American Ornithologists' Union, Washington DC.

HANNON, C., BERROW, S. D. & NEWTON, S.F. 1997. The status and distribution of breeding Sandwich *Sterna sandvicensis*, Roseate *S. dougallii*, Common *S. hirundo*, Arctic *S. paradisaea* and Little Terns *S. albifrons* in Ireland in 1995. *Irish Birds*, **6**, 1-22.

HARWOOD A. J. P. & PERROW, M. R. 2014. *Analysis of JNCC visual tracking data*. Report to JNCC, under Contract ref. C13-0204-0686

HASTIE, T. & TIBSHIRANI, R. 1990. *Generalized Additive Models*. Chapman and Hall.

HUDDLESTON, J. (Ed) 2010. *Understanding the Environmental Impacts of Offshore Windfarms*. COWRIE.

JIMÉNEZ-VALVERDE A. 2012. Insights into the area under the receiver operating characteristic curve (AUC) as a discrimination measure in species distribution modelling. *Global Ecology and Biogeography,* **21**, 498-507.

JNCC 2013. *Seabird Population Trends and Causes of Change: 1986-2012 Report* (http://www.jncc.defra.gov.uk/page-3201). Joint Nature Conservation Committee. Updated July 2013. Accessed December 2013.

JOHNSON, D.S., HOOTEN, M.B. & KUHN, C.E. 2013. Estimating animal resource selection from telemetry data using point process models. *Journal of Animal Ecology*, **82**, 1155–1164.

KEATING, K.A. & CHERRY, S. 2004. Use and interpretation of logistic regression in habitat-selection studies. *The Journal of Wildlife Management*, **68**, 774–789.

KRESS, S.W., WEINSTEIN, E.H. & NISBET, I.C.T.1983. The Status of Tern Populations in Northeastern United States and Adjacent Canada. *Colonial Waterbirds,* **6**, 84-106.

KRESS, S. W. 1997. Using animal behavior for conservation: case studies in seabird restoration from the Maine Coast, USA. *Journal of the Yamashina Institute for Ornithology,* **29**,1–26.

LANGSTON, R. H. W., TEUTEN, E. & BUTLER, A. 2013. *Foraging ranges of Northern gannets* Morus bassanus *in relation to proposed offshore wind farms in the UK: 2010-2012*. RSPB report to DECC ISBN No. 978-1-905601-43-1. https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/270402/OESEA2_North_Sea_Gannet_Tracking_Year3_Report.pdf

LASCELLES, B. G., LANGHAM, G. M., RONCONI, R. A. & REID, J., B. 2012. From hotspots to site protection: Identifying Marine Protected Areas for seabirds around the globe. *Biological Conservation,* **156,** 5-14. http://dx.doi.org/10.1016/j.biocon.2011.12.008

LAVERS, J. L., MILLER, M. G. R., CARTER, M. J. SWANN, G. & CLARKE, R. J. 2014. Predicting the Spatial Distribution of a Seabird Community to Identify Priority Conservation Areas in the Timor Sea. *Conservation Biology*. DOI: 10.1111/cobi.12324

LE CORRE, M., JAEGER, A., PINET, P., KAPPES, M. A., WEIMERSKIRCH, H., CATRY, T., RAMOS, J. A. RUSSELL, J. C., SHAH, N. & JAQUEMET, S. 2012 Tracking seabirds to identify potential Marine Protected Areas in the tropical western Indian Ocean. *Biological Conservation*. doi:10.1016/j.biocon. 2011.11.015

LOBO J.M., JIMÉNEZ-VALVERDE A. & REAL, R. 2008. AUC: a misleading measure of the performance of predictive distribution models. *Global Ecology and Biogeography,* **17**, 145-151.

LOUZAO, M., BECARES, J., RODRIGUEZ, B., HYRENBACH, K.D., RUIZ, A. & ARCOS, J.M., 2009. Combining vessel-based surveys and tracking data to identify key marine areas for seabirds. *Marine Ecology Progress Series*, **391**, 183–197.

LOUZAO, M., HYRENBACH, K. D., ARCOS, J. M., ABELLÓ, P., GIL DE SOLA L. & ORO, D. 2006. Oceanographic habitat of an endangered Mediterranean procellariiform: implications for marine protected areas. *Ecological Applications,* **16**(5),1683-95

LOUZAO, M., PINAUD, D., PÉRON, C., DELORD, K., WIEGAND, T. & WEIMERSKIRCH, H., 2011. Conserving pelagic habitats: seascape modelling of an oceanic top predator. *Journal of Applied Ecology, **48***, 121–132.

MACHETE R. L. 2013. Contrasting probabilistic scoring rules. *Journal of Statistical Planning and Inference,* **143**, 1781-1790.

MARMION, M., PARVIAINEN, M., LUOTO, M., HEIKKINEN, R. K., & THUILLER, W. 2009. Evaluation of consensus methods in predictive species distribution modelling. *Diversity and distributions*,**15**(1), 59-69.

MASON, S.J. & GRAHAM, N.E. 2002. Areas beneath the relative operating characteristics (ROC) and relative operating levels (ROL) curves: Statistical significance and interpretation. *Quarterly Journal of the Royal Meteorological Society,* **128**, 2145–2166.

MATTHIOPOULOS, J. 2003. The use of space by animals as a function of accessibility and preference. *Ecological Modelling,* **159**, 239–268.

MCCULLAGH, P. & NELDER, J.A. 1989. *Generalized Linear Models*, Second Edition. Chapman and Hall.

MCDONALD, L., MANLY, B., HUETTMANN, F. & THOGMARTIN, W. 2013. Location-only and use-availability data: analysis methods converge. *Journal of Animal Ecology,* **82**, 1120–1124

MCGOWAN, J., HINES, E., ELLIOTT, M., HOWAR, J., DRANSFIELD, A., NUR, N., & JAHNCKE, J. 2013. Using Seabird Habitat Modeling to Inform Marine Spatial Planning in Central California's National Marine Sanctuaries. *PLoS ONE,* **8**(8), e71406. DOI:10.1371/journal.pone.0071406

MCSORLEY, C.A., DEAN, B.J., WEBB, A. & REID, J.B. 2003. *Seabird use of waters adjacent to colonies Implications for seaward extensions to existing breeding seabird colony Special Protection Areas*. JNCC Report No. **329**.

MCSORLEY, C.A., WILSON, L.J., DUNN, T.E., GRAY, C., DEAN, B.J., WEBB, A. & REID, J.B**.** 2008. *Manx shearwater evening rafting behaviour around colonies on Skomer, Rum and Bardsey*. JNCC Report No. **406**

MEAD, C. J. 1978. Tern mortality in West Africa as shown by British and Dutch ringing results. *Ibis,* **120**, 110.

MITCHELL, I. P., NEWTON, S. F., RATCLIFFE, N. & DUNN, T.E. 2004. *Seabird Populations of Britain and Ireland*. T. and A. D. Poyser, London. 511 pp.

MONAGHAN, P., UTTLEY, J.D., BURNS, M. D., THAINE, C. & BLACKWOOD, J. 1989. The relationship between food supply, reproductive effort and breeding success in Arctic Terns *Sterna paradisaea*. *Journal of Animal Ecology*, **58**, No. 1, pp. 261-274.

MONAGHAN, P., UTTLEY, J.D. & BURNS, M. D. 1992. Effect of changes in food availability on reproductive effort in Arctic Terns *Sterna paradisaea*. *Ardea,* **80**, 71-81.

MUSGROVE, A. J., AUSTIN, G. E., HEARN, R. D., HOLT, C.A., STROUD, D. A. & WOTTON, S. R. 2011. Overwinter population estimates of British waterbirds. *British Birds,* **104**, 364–397.

NEWTON S.F. & CROWE O. 2000. *Roseate Terns - The Natural Connection*. Maritime Ireland / Wales INTERREG Report No. 2

NTIAMOA-BAIDU, Y., PIERSMA, T., WIERSMA, P., POOT, M., BATTLE, P. & GORDON C. 1992. Water depth selection, daily feeding routines and diets of waterbirds in coastal lagoons in Ghana. *Ibis,* **140**, 89–103.

O'BRIEN, S.H., WEBB, A., BREWER, M. J. & REID, J. B. 2012 Use of kernel density estimation and maximum curvature to set Marine Protected Area boundaries: Identifying a Special Protection Area for wintering red-throated divers in the UK. *Biological Conservation,* **156,** 15–21

OPPEL, S., MEIRINHO, A., RAMIREZ, I., GARDNER, B., O'CONNELL, A., MILLER, P.I. & LOUZAO, M., 2012. Comparison of five modelling techniques to predict the spatial distribution and abundance of seabirds. *Biological Conservation,* **156**, 94-104.

ORIANS, G. H. & PEARSON, N. E, 1979. On the theory of central place foraging. p155–177 In: Horn, D. J., Mitchell, R. and Stair, G. R, (Eds) *Analysis of ecological systems*. Ohio State University Press, Columbus, Ohio.

PERROW. M. R., SKEATE, E. R. & GILROY, J. J. 2011. Visual tracking from a rigid-hulled inflatable boat to determine foraging movements of breeding terns. *J. Field Ornithol.* **82**(1):68–79

PHILLIPS, S.J., ANDERSON, R.P. & SCHAPIRE, R.E. 2006. Maximum entropy modelling of species geographic distributions. *Ecological Modelling*, **190**, 231–259.

PICKEREL, G. (ed.) 2002. *Little terns in Britain and Ireland, 2001*. Unpublished report of the Royal Society for the Protection of Birds, Sandy.

POTTS J.M., BREWER M.J., DUFF E.I. & ELSTON D.A. 2012. *Additional Work Coquet Colony - Seabird Tracking Data (Under Agreement C10-0206-0387).* Contract Report to JNCC, December 2012.

POTTS, J. M. BREWER, M.J., DUFF, E. I. & ELSTON, D. A. 2013a. *Additional Work Other Colonies – Seabird Tracking Data (Under Agreement C10-0206-0387).* Contract Report to JNCC, March 2013.

POTTS, J. M. BREWER, M.J. & DUFF, E. I. 2013b. *Refinements of tern Sterna sp. tracking data modelling (Phase 1) (Under Agreement C10-0206-0387)* Contract Report to JNCC, September 2013.

POTTS, J. M. BREWER, M.J. & DUFF, E. I. 2013c. *Refinements of tern Sterna sp. tracking data modelling (Phase 2) (Under Agreement C10-0206-0387*). Contract Report to JNCC, October 2013.

POTTS, J. M.& BREWER, M. J. 2013. *Cross-Validation of tern Sterna sp. tracking data modelling (Phase 1) (Under Agreement C10-0206-0387).* Contract Report to JNCC, December 2013.

POTTS, J. M. & BREWER, M. J. 2014. *Revised model for roseate terns (Under Agreement C10-0206-0387).* Contract Report to JNCC, May 2014.

RAMÍREZ, I., GERALDES, P., MEIRINHO, A., AMORIM, P. & PAIVA, V. 2008. *Áreas Importantes para as Aves Marinhas em Portugal [Marine Important Bird Areas in Portugal]*. Lisboa: Sociedade Portuguesa Para o Estudo das Avas.

RATCLIFFE, N. & MERNE, O. 2002. Roseate tern *Sterna dougalli*. In: Wernham, C. V., Toms, M., Marchant, J., Clark, J., Siriwarden A. G. & Baillie, S. (eds). *The Migration Atlas: Movements of the Birds of Britain and Ireland*. T. & A. D. Poyer, London.

ROBERTSON, G. S., BOLTON, M., GRECIAN, W. J., WILSON, L. J., DAVIES, W. & MONAGHAN, P. 2014. Resource partitioning in three congeneric sympatrically breeding seabirds: Foraging areas and prey utilization. *The Auk*, **131**, 434–446.

RUE H., MARTINO S. & CHOPIN N. 2009. Approximate Bayesian Inference for Latent Gaussian Models Using Integrated Nested Laplace Approximations (with discussion). *Journal of the Royal Statistical Society, Series B*, **71**, 319–392

SCHMUELI, G. 2010. To Explain or to Predict? *Statistical Science*, **25**, No. 3, 289–310. DOI: 10.1214/10-STS330

SCHWEMMER, P., ADLER, S., GUSE, N., MARKONES, N. & GARTHE, S. 2009. Influence of water flow velocity, water depth and colony distance on distribution and foraging patterns of terns in the Wadden Sea. *Fisheries Oceanography,* **18** (3), 161-172

SHEALER, D. 1999. Sandwich tern (*Sterna sandvicensis*). In: Poole, A. & Gill, F. (eds) *The Birds of North America*. Birds of North America Inc., Philadelphia, P.A. & American Ornithologists' Union, Washington DC.

STIENEN, E. W. M., COURTENS, W., EVERAERT, J. & VAN DE WALLE, M. 2008.Sex-biased mortality of common terns in wind farm collisions. *The Condor*, **110** (1), 154-157.

STIENEN, E. W. M., VAN BEERS, P. W. M., BRENNINKMEIJER, A., HABRAKEN, J. M. P. M., RAAIJMAKERS, M. H. J. E. & VAN TIENEN, P. G. M. 2000. Reflections of a specialist: patterns in food provisioning and foraging conditions in Sandwich Terns *Sterna sandvicensis*. *Ardea,* **88**, 33-49.

STIENEN, E. W. M. & BRENNINKMEIJER, A. 2002a.Variation in growth in Sandwich tern chicks *Sterna sandvicensis* and the consequences for pre- and post-fledging mortality.*Ibis*, **144**, 567-76.

STIENEN, E. W. M. & BRENNINKMEIJER, A. 2002b. Foraging decisions of Sandwich Terns in the presence of kleptoparasiting gulls. *Auk,* **119**, 473-486.

STROUD, D. A., CHAMBERS, D., COOK, S., BUXTON, N., FRASER, B., CLEMENT, P., LEWIS, I., MCLEAN, I., BAKER, H. & WHITEHEAD, S. 2001. *The UK SPA network: its scope and content. Volumes 1-3.* JNCC, Peterborough.

SUDDABY, D. & RATCLIFFE, N. 1997. The effects of fluctuating food availability on breeding Arctic Terns (*Sterna paradisaea*). *Auk,* **114**, 524-30.

SWETS, J. A. 1988. Measuring the accuracy of diagnostic systems. *Science* **240**:1285–1293.

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.

THOMAS, G. J. 1972. Review of gull damage and management methods at nature reserves. *Biological Conservation,* **4**, 117-27.

THOMAS, G. J. 1982. Breeding terns in Britain and Ireland, 1975-1979*. Seabird,* **6**, 59-69.

TREMBLAY, Y., BERTRAND, S., HENRY, R. W., KAPPES, M. A., COSTA, D. P. & SHAFFER, S. A. 2009. Analytical approaches to investigating seabird–environment interactions: a review. *Marine Ecology Progress Series*, ***391***, 153-163.

UTTLEY, J., MONAGHAN, P. & WHITE, S. 1989. Differential effects of reduced sandeel availability on two sympatrically breeding species of tern. *Ornis Scandinavica,* **20,** 273-7.

VISSER, J. M. & PETERSON, G. M. 1994. Breeding populations and colony site dynamics of seabirds nesting in Louisiana. *Colonial Waterbirds,* **17,** 146-52.

WAKEFIELD, E. D., PHILLIPS, R. A., TRATHAN, P. N., ARATA, J., GALES, R., HUIN, H., ROBERTSON, G., WAUGH, S. M., WEIMERSKIRCH, H. & MATTHIOPOULOS, J. 2011. Habitat preference, accessibility, and competition limit the global distribution of breeding Black-browed Albatrosses. *Ecological Monographs,* **81** (1), 141-167.

WENDELN, H. & BECKER, P. H. 1999. Parental care of replacement clutches in common terns (*Sterna hirundo*). *Behavioural Ecology and Sociobiology,* **47,** 382-92.

WOOD, S. N. 2006. *Generalized Additive Models: An Introduction with R*. Chapman and Hall/CRC.

YORIO, P. & QUINTANA, F. 1997. Predation by Kelp Gulls *Larus dominicanus* at a mixed-species colony of Royal Terns *Sterna maxima* and Cayenne Terns *Sterna eurygnatha* in Patagonia. *Ibis,* **139,** 536-41.

7 Appendix 1 Candidate covariates and their rankings

This appendix describes the candidate covariates used in the modelling. All of the covariates for the tern modelling were chosen based on whether they might represent potential biological mechanisms which might influence tern distributions (as well as what was available to us with coverage at a UK level). In almost all cases, the proposed mechanisms were indirect (e.g. potentially acting on primary productivity or prey availability). Some covariates may be more useful to predict tern distributions than others. This could be due to a number of reasons relating to the degree to which the proposed biological mechanism is realistic, and the quality of our covariate data. We therefore undertook a ranking exercise to indicate which covariates are most biologically plausible and this was used to inform the model selection process to ensure that the final models were as biologically plausible as possible (see Section 2.2.3 and Appendix 2). The table below ranks the covariates based on their relative merits, i.e. the robustness of the proposed biological mechanism, while taking account of how good the data may be for making predictions (e.g. whether the data are static, measured directly, their resolution and coverage).

Procedure used to determine ranks
Firstly, for each covariate, different characteristics were categorised as ‘high’, ‘med’ or ‘low’. Note that these categories are only relative within this covariate dataset. They do not imply for example, that a covariate is the best or worst available. Secondly, covariates were given an overall rank based on the rankings of the characteristics.

1. Covariate characteristics

(i) Potential biological mechanism:
Without direct experimental evidence, we can only infer what the biological mechanisms might be using informed judgement. This category was ranked according to whether there was a clear mechanism in principle, and the degree of evidence which supports this (i.e. whether the covariate, or a similar measure of it, has been previously shown in the scientific literature to have a relationship with the distributions of terns and / or their principle prey species (e.g. sandeels)).

High = potential mechanism acting on the terns, supported by literature;
Med = potential mechanism acting on prey abundance and/or availability, supported by literature;
Low = potential theoretical mechanism acting on prey abundance and/or availability, but no support from literature

(ii) Predictability of covariate:
Our tern models aim to predict areas which are consistently important for terns (rather than temporarily important e.g. due to ephemeral oceanographic conditions). Thus covariates which best represent long-term conditions are most useful.

High = static covariate;
Med = dynamic covariate, but data averaged over time, including at least one of the tern survey years;
Low = dynamic covariate, data very restricted in time or based on years outwith tern survey period.

(iii) Data measurement:
How the data are derived will affect how representative it is of what it is aiming to represent.

High = direct measurement;
Med = indirect measurement, or modelled;

Low = derived from indirect measurement or derived from another model (i.e. additional data treatment involved)

(iv) Resolution:

For model input, each tern/control observation is matched with covariate values which are nearest to the observation location. Our model outputs are at a 500m^2 resolution.

High = <500m;
Med = 0.5-1km;
Low = >1km.

(v) Coverage:

We cannot use any tern observations which do not have underlying covariate values and we cannot predict to those locations without covariate values (if that covariate has been chosen in the model).

High = complete coverage within and across sites;
Med = incomplete coverage within a site (data missing close to shore);
Low = complete coverage within sites but data missing for some other sites.

2. Overall Covariate Ranks:

Covariates were given an overall rank using the individual rankings of their constituent characteristics, as follows. The main aim of the ranking exercise is to help ensure the robustness of our final models by indicating which covariates (and ultimately which models) are most biologically plausible, therefore ‘potential biological mechanism’ is given highest priority. We recognise that even if there is a sound biological basis for a covariate, if it has not been measured accurately, then its relationship with our tern data may not be apparent. Therefore the characteristic of how the data are derived is given second priority. The extent of coverage for each covariate is given lowest priority. This is because it will be considered as part of the modelling process, both within a site (covariates with insufficient coverage will not be used within site-specific models in Phase 1) and across sites (covariates which lack coverage across different sites will not be used within Phase 2). It is still useful to retain it however, in case it is useful to distinguish between equally ranked covariates. Of the two remaining characteristics (predictability and resolution), ‘predictability of covariate’ is given third priority as one of our key aims for the modelling is to predict consistently important areas. In addition, we have already restricted the covariates to only those which are around 1km^2 resolution, so we have already aimed to minimise resolution issues.

Thus, covariates were given an overall rank (see Table A1.1) using the individual rankings of their characteristics, in this order of priority:

1) Biological plausibility (High>Med>Low):
2) Data measurement (High>Med>Low)
3) Predictability of covariate (High>Med>Low):
4) Resolution (High>Med>Low)
5) Coverage (High>Med>Low)

Table A1.1. Details of the candidate covariates used in the modelling in order of biological plausibility rank, based on potential biological mechanism, and various aspects of data quality.

Rank	Covariate	Potential biological mechanism	Data measurement	Predictability of variable	Resolution	Coverage
1	Distance to colony	High: Clear mechanism acting on central place foraging energetic constraints on terns (Gaston 2004) – distance to colony directly related to this; Distance to colony almost always shown to be important across seabird literature, including terns (e.g. Schwemmer *et al* 2009).	High: Directly measured (straight-line distance) by JNCC within GIS.	High: Static variable	High: Resolution of a few metres	High: Complete coverage
2	Depth	Med: Biological production is higher in shallow water Sandeels prefer shallow waters, given favoured sediment requirements (Wright *et al* 2000) Terns forage more often in shallow waters (Birdlife foraging factsheets and references therein)	High: Directly measured, by triangulation with linear interpolation. From Defra's Digital Elevation Model.	High: Static variable	High: Resolution of 30-180m^2	High: Complete coverage
2	Distance to shore	Med: No clear biological mechanism, but likely to act as a proxy for several of our covariates (and possibly others) acting on prey abundance/availability (e.g. depth) because of colinearity. Distance to shore often shown to be important across seabird literature	High: Directly measured by JNCC within GIS.	High: Static variable	High: Accurate to a few metres	High: Complete coverage
3	Temp stratification (difference in temp between surface and seabed)	Med: Stratification and tides affects primary production Some evidence of sandeels preferring more stratified waters (van der Kooij *et al* 2008)	Med: Modelled simulation; sourced from Proudman Oceanographic Laboratory	Med: Dynamic variable, but based on 10 year simulation, 2006-2010, so includes two of the survey years	Low: Resolution of 0.01^2 decimal degrees GCS WGS 1984 (*c.* 500-700m or 1.1km?)	High: Complete coverage

Rank	**Covariate**	**Potential biological mechanism**	**Data measurement**	**Predictability of variable**	**Resolution**	**Coverage**
4	Chlorophyll concentration April, May, June:	Med: Primary productivity acts as a proxy for prey abundance; But potential for spatio-temporal mis-match between trophic levels; April or May values may make more sense as they allow for temporal lag Mixed results in seabird studies with some showing relationships while others not– may depend on how Chl data are presented (Suryan *et al* 2012; Scott *et al* 2010)	Med: Based on satellite imagery; sourced from Plymouth Marine Laboratory	Med: Dynamic variable; Only one year of data, but this matches one of our survey years (2009)	Low: Images taken at 1.2km^2	Med: Complete coverage across sites, but accuracy low close to coast within sites
4	SST April, May, June	Med: Copepod and sandeel abundance and distribution influenced by temperature But potential for spatio-temporal mis-match between trophic levels; April or May values may make more sense as they allow for temporal lag	Med: Based on satellite imagery of SST, sourced from Plymouth Marine Laboratory	Med: Dynamic variable; averaged across 2006-2010, so includes two of the survey years	Low: Images taken at 1.2km^2	Med: Complete coverage across sites, but accuracy low close to coast within sites
5	Sea Surface Salinity -Spring -summer	Med (although conflicting evidence): Sandeel abundance greater with higher surface salinity (van der Kooij *et al* 2008) Terns favour low salinity in the north Sea (Garthe 1997)	Med: generated from 10 year simulation model of POLCOMS; sourced from Proudman Oceanography Laboratory	Low: Dynamic variable, but based on 10 year simulation (years unknown, assume doesn't include survey years)	Low: Resolution of 0.01^2 decimal degrees GCS WGS 1984 (*c.* 500-700m or 1.1km?)	Low: Missing in East Anglia
6	Sand (seabed sediment)	Med: Acts as a proxy for sandeel habitat. Sandeel abundance related to sediment grain size and sediment types (Holland *et al* 2005).	Low: % of different sediment types (from samples), simplified into BGS DigSBS250 Folk categories, supplemented by additional data and further reduced to binary variable for model.	High: Static variable, based on seabed samples	Low: Categorical variable (5 types); very coarse resolution Vector dataset GCS WGS 1984	High: Complete coverage

Rank	**Covariate**	**Potential biological mechanism**	**Data measurement**	**Predictability of variable**	**Resolution**	**Coverage**
7	Shear-stress currents (peak seabed current kinetic energy)	Med: Stronger currents could increase prey abundance and availability at the surface. Tidal currents influence suspended particles in water and therefore turbidity (water clarity). Turbid waters provide more food for small fish and reduce detection of predators. Terns in North Sea prefer turbid waters (Garthe 1997) Forster's tern prefers turbid waters (REF) Relationship between tern foraging locations and tidal cycle (Schwemmer *et al* 2009) Temporal and spatial pattern of foraging in common terns shown to be caused by the tide-related fluctuations of food availability (Becker *et al* 1993)	Low: Inverse distance weighted interpolation of UK SeaMap 2010 data, derived from National Oceanography Centre current model ('POLCOMS' model); 'ss_current' is also an indirect measure of current speed.	Low: Dynamic variable, modelled for 2000-2004, so does not include our survey years	High Resolution: 0.003^2 decimal degrees GCS WGS 1984 (*c.* 300m)	High: Complete coverage
8	Probability of front -Spring - Summer Probability of a frequent thermal front.	Med: Prey, and therefore seabirds might accumulate at oceanographic fronts (where there is a strong spatial gradient in thermodynamic characteristics) (Schneider 1990)	Low: Based on satellite observations of SST, converted to ratio of strong thermal fronts to observations; sourced from Plymouth Marine Laboratory	Low: Dynamic, and averaged over 1998-2008, so does not include our survey years.	Low: Resolution: Approx 1.2km^2 Perhaps likely to operate at larger spatial scales than what we are looking at.	High: Complete coverage
9	Seabed slope (º incline between adjacent grid cells)	Low: Seabed slope may interact with energy layers to influence how water column is mixed, and the extent to which items are carried to the surface	Med: Derived from Defra digital elevation model data by JNCC using Spatial Analyst tool in ArcGIS.	High: Static variable	High: Resolution to *c.*30m^2	High: Complete coverage
9	Aspect -Eastness -Northness	Low: Seabed aspect may interact with energy layers to influence how water column is mixed, and the extent to which items are carried to the surface	Med: Derived from Defra digital elevation model data, then converted by JNCC into 'eastness' and 'northness'	High: Static variable	High: Resolution to *c.*30m^2	High: Complete coverage

Rank	**Covariate**	**Potential biological mechanism**	**Data measurement**	**Predictability of variable**	**Resolution**	**Coverage**
10	Shear Stress wave (Peak seabed wave kinetic energy, Nm^2)	Low: Stronger wave energy could increase prey abundance and availability at the surface, and influence suspended particles in water and therefore turbidity (water clarity). No evidence from the literature of relationships with wave energy.	Low: Inverse distance weighted interpolation of UK SeaMap 2010 data, derived from National Oceanography Centre ProWAM wave model (12.5km resolution) and DHI Spectral Wave model (100-300m resolution)	Low: Dynamic variable, modelled for 2000-2004, so does not include our survey years	Low: Resolution: 300m-12.5km	High: Complete coverage

References specific to Appendix 1

BECKER, P.H., FRANK D. & SUDMANN, S.R. 1993. Temporal and spatial pattern of common tern (*Sterna hirundo*) foraging in the Wadden Sea. *Oecologia* 93: 389-393.

BIRDLIFE INTERNATIONAL. Seabird foraging factsheets. Available from http://seabird.wikispaces.com

GARTHE, S. 1997. Influence of hydrography, fishing activity, and colony location on summer seabird distribution in the south-eastern North Sea. *ICES Journal of Marine Science* 54, 566-577

GASTON 2004. Seabirds: A Natural History. Poyser.

HOLLAND, G.J., GREENSTREET, S.P.R., GIBB, I.M., FRASER, H.M. & ROBERTSON, M.R. 2005. Identifying sandeel *Ammodytes marinus* sediment habitat preferences in the marine environment. *Marine Ecology Progress Series* 303, 269-282

SCHNEIDER, D. 1990. Seabirds and fronts: a brief overview. *Polar Research* 8:17–21

SCHWEMMER, P., ADLER, S., GUSE, N., MARKONES, N. & GARTHE, S. 2009. Influence of water flow velocity, water depth and colony distance on distribution and foraging patterns of terns in the Wadden Sea. *Fisheries Oceanography* 18 (3), 161-172

SCOTT, B. E., SHARPLES, J. ROSS, O. N., WANG, B. J., PIERCE, G. J. & CAMPHUYSEN, C. J. 2010. Sub-surface hotspots in shallow seas: fine-scale limited locations of top predator foraging habitat indicated by tidal mixing and sub-surface chlorophyll. *Marine Ecology Progress Series* Vol. 408: 207–226

SURYAN, R. M., SANTORA, J. A. & SYDEMAN, W. J. 2012. New approach for using remotely sensed chlorophyll *a* to identify seabird hotspots. *Marine Ecology Progress Series* Vol. 451: 213–225

VAN DER KOOIJ, J., SCOTT, B.E. & MACKINSON, S 2008. The effects of environmental factors on daytime sandeel distribution and abundance on the Dogger Bank. *Journal of Sea Research* 60 (3), 201-209

WRIGHT, P.J, JENSEN, H. & TUCK, I. 2000. The influence of sediment type on the distribution of the lesser sandeel, *Ammodytes marinus*. *Journal of Sea Research* 44: 243-256

8 Appendix 2 Results of model selection for Phase 1 colonies

Please refer to Section 2.2.3 for more detail on model selection methods, and Section 8 (Appendix 1) for details on covariate ranks. For some species at some colonies it was not possible to use all the covariates due to large amounts of missing data, especially close to the coast (see colony/species specific sections for more details).

Here we present all of the short-listed models that we considered according to our model selection criteria. Note that the number of models considered varies between sites/species and in some cases our model selection criteria meant that only the model with the lowest AIC was considered.

8.1 Model selection for Farne Islands models

8.1.1 Arctic terns

The minimum AIC model (distance to colony, salinity in spring and probability of a summer front) did not include the covariates of chlorophyll concentration or sea surface temperature. As these have a lot of missing data compared to other covariates we re-ran the stepwise search for minimum AIC with these covariates removed as candidates to ensure a more reliable AIC statistic.

Table A2.1 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.2 shows the recalculated minimum AIC model using the full tracking dataset, along with other models considered.

The minimum AIC model (using the recalculated AIC statistics) now contained distance to colony and probability of a spring front. Removing probability of a spring front (because it has a biological plausibility rank of >5 and was selected <50% of the time in the bootstrap samples (Table A2.1)) increased the AIC by >2 (Table A2.2).

In comparison, the previous minimum AIC model containing distance to colony, salinity in spring and probability of a summer front had an AIC of 186.58 which was an increase of <2 from the recalculated min AIC model (Table A2.2). When probability of a summer front was removed (because it was selected <50% of the time (Table A2.1) and has a biological plausibility rank of >5), then the AIC was 185.67, while when salinity in spring was removed (because it was selected <50% of the time (Table A2.1)), the AIC was 186.55. As salinity in spring has a lower rank (more biologically plausible) than either probability of a spring front or summer front, and was selected more frequently, the final model chosen therefore contained distance to colony and salinity in spring.

Table A2.1. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for Arctic terns at the Farne Islands, using all candidate covariates except chlorophyll concentration and sea surface temperature variables.

Variable	Count
dist_col	73
dist_shore	42
sal_spring	41
sand	37
strat_temp	30
sal_summ	28
bathy_1sec	27
spring_front	27
ss_current	22
ss_wave	22
summ_front	11
eastness_1s	8
slope_1s_deg	8
northness_1s	6

Table A2.2. Shortlisted models and AIC statistics for Arctic terns at the Farne Islands. A model containing only distance to colony is shown for comparison. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col	187.9
dist_col, sal_spring, summ_front	186.58
dist_col, summ_front	186.55
dist_col, sal_spring	**185.67**
dist_col, spring_front	185.62

8.2 Model selection for Coquet Island models

8.2.1 Arctic terns

Table A2.3 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.4 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The model obtained by the stepwise search for a minimum AIC model included distance to colony, chlorophyll concentration in June, bathymetry, sea surface temperature in May and shear stress current, and had an AIC value of 416.47. Only one of the covariates (shear stress current) has a biological plausibility rank of >5, and the results of the bootstrapping exercise show that all but one of these covariates were selected >50%, with sea surface temperature in May only having been selected 38% of the time (Table A2.3). When either sea surface temperature in May or shear stress current were removed from the model, the change in AIC value was <2 but was greater than the change when both were removed together (Table A2.4). Thus, the final model contained distance to colony, chlorophyll concentration in June and bathymetry.

Table A2.3. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for Arctic terns at the Coquet colony, using all candidate covariates.

Variable	Count
dist_col	99
chl_june	62
ss_current	55
bathy_1sec	52
sal_spring	50
sst_april	46
chl_may	42
dist_shore	41
sal_summ	40
sst_may	38
strat_temp	29
sst_june	28
spring_front	27
ss_wave	27
sand	23
chl_apr	20
summ_front	11
slope_1s_deg	10
northness_1s	8
eastness_1s	4

Table A2.2 Shortlisted models and AIC statistics for Arctic terns at Coquet Island. A model containing only distance to colony is shown for comparison. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col	418.38
dist_col, chl_june, bathy_1sec, sst_may	417.84
dist_col, chl_june, bathy_1sec, ss_current	416.91
dist_col, chl_june, bathy_1sec	**416.63**
dist_col, chl_june, bathy_1sec, sst_may, ss_current	416.47

8.2.2 Common terns

Table A2.5 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.6 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The model obtained by the stepwise search for a minimum AIC model included distance to colony, chlorophyll concentration in June, bathymetry, sea surface temperature in April and sea surface temperature in June, and had an AIC value of 317.9. All of these have a biological plausibility rank of ≤5, and all except sea surface temperature in June were selected >50% of the time in the bootstrap samples (Table A2.5). When sea surface temperature in June was removed, the difference in AIC was <2 (Table A2.6). Thus, the final model contained distance to colony, chlorophyll concentration in June, bathymetry and sea surface temperature in April.

Table A2.5. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for common terns at Coquet Island, using all candidate covariates.

Variable	Count
dist_col	90
chl_june	71
sst_april	61
bathy_1sec	58
summ_front	37
chl_may	36
sal_spring	36
sand	34
dist_shore	33
sst_june	31
ss_wave	29
strat_temp	27
ss_current	24
sst_may	20
sal_summ	19
chl_apr	17
slope_1s_deg	14
spring_front	11
eastness_1s	2
northness_1s	2

Table A2.6. Shortlisted models and AIC statistics for common terns at Coquet Island. A model containing only distance to colony is shown for comparison. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col	326.84
dist_col, chl_june, bathy_1sec, sst_april	**318.48**
dist_col, chl_june, bathy_1sec, sst_april, sst_june	317.9

8.2.3 Roseate terns

For roseate terns at Coquet Island, sand, sea surface temperature and chlorophyll concentration were removed as candidate covariates at the outset due to the high amount of missing data. Table A2.7 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.8 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The AIC model obtained by the stepwise search for a minimum AIC model included distance to colony, temperature stratification, shear stress current and eastness. Although both eastness and shear stress current were selected >50% of the time in the bootstrap samples (Table A2.7), they both have a biological plausibility ranking >5. Removal of either eastness or shear stress current, or both together, increased the AIC by <2. When temperature stratification was then removed (because it was selected in <50% of the time in the bootstrap samples) from the most parsimonious of these alternative modes, the AIC increased by >2. The final model chosen was therefore one involving distance to colony and temperature stratification. .

Table A2.7. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for roseate terns at Coquet Island, using available candidate covariates.

Variable	Count
dist_col	85
ss_current	83
dist_shore	66
eastness_1s	61
sal_spring	59
sal_summ	51
spring_front	47
summ_front	46
strat_temp	45
bathy_1sec	19
slope_1s_deg	16
ss_wave	16
northness_1s	13

Table A2.8. Shortlisted models and AIC statistics for roseate terns at Coquet Island. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col, strat_temp, eastness, ss_current	169.80
dist_col, strat_temp, ss_current	171.57
dist_col, strat_temp, eastness	170.77
dist_col, strat_temp	**171.35**
dist_col	212.09

8.2.4 Sandwich terns

The model obtained by the stepwise search for a minimum AIC model (distance to shore, distance to colony, chlorophyll concentration in April and chlorophyll concentration in June) did not include any sea surface temperature variables. As these have a lot of missing data compared to other covariates we re-ran the stepwise search for minimum AIC with sea surface temperature covariates removed as candidates. This was to ensure the analysis involved a more complete grid coverage, and hence, a more reliable AIC statistic, because grid cells which covariates fail to make predictions to due to incomplete datasets are automatically removed from the analysis.

Table A2.9 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.10 shows the recalculated minimum AIC model using the full tracking dataset, along with other models considered.

The minimum AIC model (using the recalculated AIC statistics) now involved distance to colony, distance to shore and chlorophyll concentration in May, all of which have biological plausibility ranks of ≤5. The results of the bootstrapping exercise shows that both chlorophyll concentration in May and distance to shore were selected <50% of the time (Table A2.8). When chlorophyll concentration in May was excluded, the difference in AIC was <2 but when distance to shore was excluded the difference was >2 (Table A2.10). Removing both these covariates increased the AIC by >2 (Table A2.10). Therefore the model containing distance to colony and distance to shore was chosen as the final model.

For comparison the original minimum AIC model when sea surface temperature was included is also shown, together with the AIC statistics when chlorophyll concentration in May and in June were removed from this model (because they were selected <50% of the time) (Table A2.10).

Table A2.9. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for Sandwich terns at Coquet Island using all candidate covariates except the sea surface temperature variables.

Variable	Count
ss_wave	65
bathy_1sec	62
dist_col	62
chl_may	48
strat_temp	44
chl_june	39
ss_current	39
dist_shore	36
sal_summ	22
sand	19
summ_front	19
sal_spring	18
chl_apr	16
slope_1s_deg	16
eastness_1s	13
spring_front	12
northness_1s	10

Table A2.10. Shortlisted models and AIC statistics for Sandwich terns at Coquet Island. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col	319.30
dist_col, chl_may	304.47
dist_col, dist_shore, chl_apr	282.38
dist_col, dist_shore, chl_apr, chl_june	282.31
dist_col, dist_shore	**280.44**
dist_col, dist_shore, chl_june	280.36
dist_col, dist_shore, chl_may	280.26

8.3 Model selection for North Norfolk models

8.3.1 Common terns

For common terns at Blakeney Point, sand, sea surface temperature and chlorophyll concentration for April were removed as candidate covariates at the outset due to the high amount of missing data. Salinity data was not available for this area.

Table A2.11 shows the frequency with which the remaining covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.12 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The minimum AIC model included distance to colony and shear stress wave, and had an AIC value of 52.19. Shear stress wave has a biological plausibility rank of >5 and was selected <50% of the time in the bootstrap sample (Table A2.11). However, the removal shear stress wave resulted in an increased AIC value of >2 and, thus, distance to colony and shear stress wave were chosen as the final model.

Table A2.11. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for common terns at Blakeney Point colony, using available candidate covariates.

Variable	Count
bathy_1sec	68
dist_shore	57
strat_temp	57
dist_col	55
chl_june	38
ss_wave	36
ss_current	31
chl_may	28
spring_front	21
slope_1s_deg	18
summ_front	15
eastness_1s	12
northness_1s	12

Table A2.12. Shortlisted models and AIC statistics for common terns at Blakeney Point. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col	58.26
dist_col, ss_wave	**52.19**

8.3.2 Sandwich terns

For Sandwich terns at Scolt Head and Blakeney Point, sand, sea surface temperature and chlorophyll concentration for April were removed as candidate covariates at the outset due to the high amount of missing data. There was no salinity data available for this area.

Table A2.13 shows the frequency with which the remaining covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.14 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The minimum AIC model obtain by the stepwise selection included distance to colony, distance to shore, chlorophyll concentration in May, shear stress wave, bathymetry and northness, and had an AIC value of 371.82. Of these, distance to colony, distance to shore and bathymetry have biological plausibility ranks of ≤5 and were selected >50% of the time in the bootstrap samples (Table A2.13). To find the most robust model the three remaining covariates (chlorophyll concentration in May, shear stress wave and northness) were removed in varying combinations.

Removal of northness and chlorophyll in May either individually or together resulted in models with an AIC score of ≤2 from the minimum AIC model (Table A2.14). The most parsimonious of these (i.e. removal of both covariates) was chosen as the final model and involved distance to colony, distance to shore, bathymetry and shear stress wave.

Table A2.13. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for Sandwich terns at Scolt Head and Blakeney Point colony, using available candidate covariates.

Variable	Count
dist_col	100
dist_shore	93
ss_wave	71
bathy_1sec	56
chl_june	56
ss_current	23
chl_may	16
summ_front	15
slope_1s_deg	11
northness_1s	10
spring_front	9
strat_temp	9
eastness_1s	5

Table A2.14. Short-listed models and AIC statistics for Sandwich terns at Scolt Head and Blakeney Point. A model containing only distance to colony is shown for comparison. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col	402.89
dist_col, dist_shore, bathy_1sec	389.38
dist_col, dist_shore, chl_may, bathy_1sec	388.22
dist_col, dist_shore,bathy_1sec, northness	385.95
dist_col, dist_shore, chl_may, bathy_1sec, northness	385.18
dist_col, dist_shore,ss_wave, bathy_1sec	**373.44**
dist_col, dist_shore,ss_wave, bathy_1sec, northness	372.87
dist_col, dist_shore, chl_may, ss_wave, bathy_1sec	372.11
dist_col, dist_shore, chl_may, ss_wave, bathy_1sec, northness	371.82

8.4 Model selection for Ynys Feurig, Cemlyn Bay and The Skerries models

8.4.1 Common terns

Table A2.15 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset. The minimum AIC model (distance to colony and salinity in spring) found by the stepwise search did not include either sea surface temperature or chlorophyll concentration variables, both of which have extensive missing data. Model selection was therefore re-run with these variables removed (to obtain more accurate estimates of AIC).

The recalculated minimum AIC model contained distance to colony, salinity in spring and the probability of a spring front, and had an AIC value of 66.622. Removal of the probability of a spring front variable (because it has a biological plausibility rank of >5 and was selected <50% in the bootstrap samples) increased the AIC value by <2 (Table A2.16). Therefore we chose this as the final model. Thus, regardless of whether sea surface temperature and chlorophyll concentration covariates were included as candidate covariates, the final model was distance to colony and salinity in spring.

Table A2.15 Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Cemlyn colony, using all candidate covariates.

Variable	Count
dist_col	100
sal_spring	84
spring_front	31
bathy_1sec	27
chl_may	27
sst_may	23
summ_front	22
strat_temp	18
sal_summ	15
chl_apr	14
dist_shore	14
northness_1s	14
chl_june	12
ss_wave	12
eastness_1s	11
sst_april	11
ss_current	10
sst_june	3

Table A2.16 Shortlisted models and AIC statistics for common terns at the Cemlyn colony excluding chlorophyll and SST variables; the proposed final model is indicated in **bold**. A model containing only distance to colony is shown for comparison.

Terms	AIC
dist_col	79.044
dist_col, sal_spring	**67.157**
dist_col, sal_spring, spring_front	66.622

8.4.2 Sandwich terns

For Sandwich terns at Cemlyn Bay, probability of a spring front, probability of a summer front, sea surface temperature and chlorophyll concentration were removed as candidate covariates at the outset due to the high amount of missing data.

Table A2.17 shows the frequency with which the remaining covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.18 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The minimum AIC model found by the stepwise search included distance to colony, distance to shore and salinity in spring, and had an AIC value of 297.53. All three variables have a biological plausibility rank of ≤5 and were selected more than 50% of the time in the bootstrap samples (Table A2.17). Therefore, the minimum AIC model was used as the final model.

Table A2.17. Frequency with which covariates were selected for 100 bootstrap samples for Sandwich terns at the Cemlyn colony, using available candidate covariates.

Variable	Count
dist_col	100
dist_shore	91
sal_spring	82
ss_wave	49
bathy_1sec	35
ss_current	35
sal_summ	30
eastness_1s	28
slope_1s_deg	25
northness_1s	18
strat_temp	16
sand	8

Table A2.18. Shortlisted model and AIC statistic for Sandwich terns at the Cemlyn colony; the proposed final model is indicated in **bold**. A model containing only distance to colony is shown for comparison.

Terms	AIC
dist_col	414.09
dist_col, dist_shore, sal_spring	**297.53**

8.5 Larne Lough

8.5.1 Common terns

For common terns at Larne Lough, sand was removed at the outset due to large amounts of missing data.

Table A2.19 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset. The minimum AIC model obtained by the stepwise search (distance to colony, distance to shore and bathymetry) did not include sea surface temperature or chlorophyll concentration variables, both of which have extensive missing data. We therefore re-ran model selection with these variables removed to obtain a more accurate estimate of AIC. The resulting minimum AIC model using the full tracking dataset, along with other models considered, is shown in Table A2.20.

The recalculated minimum AIC model found by the stepwise search contained distance to colony, distance to shore, bathymetry, seabed slope and shear stress wave, and had an AIC value of 90.104. Both shear stress wave and seabed slope have a biological plausibility rank of >5, and seabed slope was selected <50% of the time in the bootstrap samples (Table A2.19). Removing shear stress wave increased the AIC value by <2 but removing seabed slope increased it by >2 (Table A2.20). The removal of both (which would result in the original minimum AIC model) also increased the AIC value by >2 (Table A2.20). The final model chosen therefore included distance to colony, distance to shore, bathymetry and seabed slope.

Table A2.19. Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Larne Lough colony, using available candidate covariates.

Variable	Count
dist_col	99
bathy_1sec	96
ss_wave	68
dist_shore	67
sal_summ	34
chl_apr	31
sal_spring	28
spring_front	22
sst_june	22
strat_temp	19
northness_1s	15
slope_1s_deg	15
sst_may	14
chl_june	13
eastness_1s	13
ss_current	9
chl_may	7
sst_april	5
summ_front	2

Table A2.20. Shortlisted models and AIC statistics for common terns at the Larne Lough colony with chlorophyll and SST variables excluded; the proposed final model is indicated in **bold**. A model containing only distance to colony is shown for comparison.

Terms	AIC
dist_col	117.55
dist_col,dist_shore,bathy_1sec	93.743
dist_col,dist_shore,bathy_1sec,ss_wave	92.53
dist_col,dist_shore,bathy_1sec,slope	**90.369**
dist_col,dist_shore,bathy_1sec,slope,ss_wave	90.104

8.6 Outer Ards

8.6.1 Arctic terns

Table A2.23 shows the frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset. The minimum AIC model (distance to colony and chlorophyll concentration in June) found by the stepwise search did not include any sea surface temperature variables. As there are a lot of missing data for these variables compared to other covariates, we re-ran model selection with sea surface temperature removed as candidate covariates. The resulting minimum AIC model, along with other considered models, is shown in Table A2.24.

The minimum AIC model obtained by the stepwise search now contained distance to colony and shear stress current, and had an AIC value of 114.53. Shear stress current has a biological plausibility rank of >5 and was selected <50% of the time (Table A2.23). The removal of shear stress current increased the AIC value by >2 (Table A2.24).

For comparison, the original minimum AIC model when sea surface temperature was included is also shown, together with the AIC statistics when chlorophyll concentration in June was removed from this model (because it was selected <50% of the time (Table A2.23)). The resulting AIC value was reduced by <2 but was still much greater than that of the model containing distance to colony and shear stress current only (Table A2.24). Thus, the final model included distance to colony and shear stress current.

Table A2.23. Frequency with which covariates were selected for 100 bootstrap samples for Arctic terns at the Outer Ards colony, using all candidate covariates.

Variable	Count
dist_col	74
dist_shore	58
chl_apr	57
chl_june	46
sal_spring	44
chl_may	28
sal_summ	27
ss_wave	24
strat_temp	24
sst_april	21
bathy_1sec	19
sand	17
sst_june	17
summ_front	15
sst_may	11
eastness_1s	8
ss_current	6
pring_front	5
northness_1s	1
slope_1s_deg	1

Table A2.24. Shortlisted models and AIC statistics for Arctic terns at the Outer Ards colony when SST variables are excluded; the proposed final model is indicated in **bold**.

Terms	AIC
dist_col, chl_june	123.39
dist_col	121.41
dist_col, ss_current	**114.53**

8.7 Ythan Estuary, Sand of Forvie and Meikle Loch

8.7.1 Sandwich terns

Sand, sea surface temperature and chlorophyll concentration were removed as candidate covariates at the outset due to the high amount of missing data.

Table A2.25 shows the frequency with which remaining covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.26 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The minimum AIC model obtained from the stepwise search involved temperature stratification, shear stress current and bathymetry, and had an AIC of 89.376. Dropping shear stress current (because it has a biological plausibility rank of >5) increased the AIC by <2 (Table A2.26). Removing bathymetry (because it was selected <50% of the time in the bootstrap sample (Table A2.25)) and removing both bathymetry and shear stress current together resulted in an increase of the AIC value by >2 (Table A2.26). Therefore the final model chosen contained bathymetry and temperature stratification.

Table A2.25. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for common terns at the Sand of Forvie colony, using available candidate covariates.

Variable	Count
ss_current	67
ss_wave	54
strat_temp	53
dist_col	46
slope_1s_deg	44
sal_spring	43
bathy_1sec	37
dist_shore	27
spring_front	22
sal_summ	18
northness_1s	12
eastness_1s	3

Table A2.26. Shortlisted models and AIC statistics for Sandwich terns at the Forvie colony; the proposed final model is indicated in **bold**. A model containing only distance to colony is shown for comparison.

Terms	AIC
dist_col	201.07
strat_temp	169.78
ss_current,strat_temp	162.58
bathy_1sec, strat_temp	**90.462**
bathy_1sec,ss_current,strat_temp	89.376

8.8 Model selection for Imperial Dock Lock models

8.8.1 Common terns

For common terns at Imperial Dock Lock, sea surface temperature and chlorophyll concentration were removed as candidate covariates at the outset due to the high amount of missing data.

Table A2.27 shows the frequency with which the remaining available covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset while Table A2.28 shows the minimum AIC model using the full tracking dataset, along with other models considered.

The minimum AIC model obtained by the stepwise search included distance to colony, seabed slope, salinity in spring, distance to shore, bathymetry and probability of a spring front, and had an AIC value of 653.98. All of these were selected >50% of the time in the bootstrap samples (Table A2.27), but probability of a spring front and seabed slope have a biological plausibility rank of >5. When probability of a spring front was removed, the difference in AIC was <2, while removal of seabed slope increased the AIC value by >2 (Table A2.28). Removal of both these covariates together increased the AIC value by >2 (Table A2.28). Thus the final model contained distance to colony, seabed slope, salinity in spring, distance to shore and bathymetry.

Table A2.27. Frequency with which covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset for common terns at Imperial Dock Lock SPA, using available candidate covariates.

Variable	Count
dist_col	100
dist_shore	95
bathy_1sec	90
spring_front	81
slope_1s_deg	80
sal_spring	63
sal_summ	42
summ_front	34
ss_current	31
sand	30
northness_1s	11
ss_wave	10
eastness_1s	8
strat_temp	4

Table A2.28. Shortlisted models and AIC statistics for common terns at Imperial Dock Lock SPA. A model containing only distance to colony is shown for comparison. The proposed final model is indicated in **bold**.

Terms	AIC
dist_col	685.82
dist_col,dist_shore,sal_spring,bathy_1sec	658.61
dist_col, slope_1s_deg, sal_spring, dist_shore, bathy_1sec	**655.46**
dist_col, sal_spring, dist_shore, bathy_1sec, spring_front	656.46
dist_col, slope_1s_deg, sal_spring, dist_shore, bathy_1sec, spring_front	653.98

8.9 Model selection for Glas Eileanan models

8.9.1 Common terns

For common terns at Glas Eileanan, it was decided to remove sand, sea surface temperature and chlorophyll concentration covariates at the outset due to the high amount of missing data.

Table A2.29 shows the frequency with which remaining covariates were selected in the minimum AIC models from 100 bootstrap samples of the tracking dataset, while Table A2.30 shows the minimum AIC model using the full tracking dataset, along with other models considered

The minimum AIC model obtained from the stepwise selection contained distance to colony, distance to shore, eastness and seabed slope, and had an AIC value of 282.88. All these covariates were selected in >50% of the bootstrap samples (Table A2.29), but eastness and seabed slope both have a biological plausibility rank of >5. When eastness was removed, the difference in AIC was <2 (Table A2.30). When seabed slope was removed, the difference in AIC was >2 (Table A2.30). Equally, the removal of both eastness and seabed slope together also increased the AIC by >2 (Table A2.30). Therefore, the final model selected contained distance to colony, distance to shore and seabed slope.

Table A2.29 Frequency with which covariates were selected for 100 bootstrap samples for common terns at Glas Eileanan, using available candidate covariates.

Variable	Count
dist_col	100
slope_1s_deg	83
eastness_1s	70
dist_shore	68
strat_temp	23
ss_wave	21
sal_summ	19
bathy_1sec	17
sal_spring	14
ss_current	14
northness_1s	12
summ_front	12

Table A2.30. Shortlisted models and AIC statistics for common terns at Glas Eileanan; the proposed final model is indicated in **bold**. A model containing only distance to colony is shown for comparison.

Terms	AIC
dist_col	290.24
dist_col, dist_shore	289.52
dist_col, dist_shore, eastness	287.85
dist_col, dist_shore, slope	**283.94**
dist_col, dist_shore, eastness, slope	282.88

9 Appendix 3 Equations for the final GLM models

Colony SPA	Species	Model equation
Coquet Island	Arctic	Usage = -3.74 - 0.22(dist_col) + 1.53(chl_june) - 0.04(bathy_1sec) + Ɛ*i*
Farne Islands	Arctic	Usage = 5218 - 0.27(dist_col) - 148.82(sal_spring) + Ɛ*i*
Outer Ards	Arctic	Usage = -1.59 - 0.11(dist_col) + 0.93(ss_current) + Ɛ*i*
Generic	Arctic	Usage = -0.96 - 0.22(dist_col) - 0.01(bathy_1sec) + Ɛi
Coquet Island	Common	Usage = -16.11 - 0.24(dist_col) + 2.97(chl_june) - 0.05(bathy_1sec) + 1.42(sst_april) + Ɛ*i*
Larne Lough	Common	Usage = 0.22 -0.45(dist_col) + 0.54(dist_shore) + 0.03(bathy_1sec) + 0.64(slope_1s_deg) + Ɛi
Glas Eileanan	Common	Usage = -2.15 - 0.16(dist_col) + 0.45(dist_shore) + 0.37(slope_1s_deg) + Ɛi
Imperial Dock Lock	Common	Usage = -724.88 - 0.21(dist_col) + 0.03(bathy_1sec) - 0.29(dist_shore) + 20.66(sal_spring) + 0.19(slope_1s_deg) + Ɛi
North Norfolk	Common	Usage = -5.71 - 0.48(dist_col) + 1.61(ss_wave) + Ɛi
Cemlyn Bay	Common	Usage = -3888.32 - 0.81(dist_col) + 113.26(sal_spring) + Ɛi
Generic	Common	Usage = -0.74 - 0.19(dist_col) - 0.001(bathy_1sec) - 0.10(dist_shore) + Ɛi
Coquet Island	Roseate	Usage = -79.24 - 0.21(dist_col) + 1.81(chl_june) + 8.13(sst_may) + Ɛi
Coquet Island	Sandwich	Usage = 0.37 - 0.08(dist_col) - 0.51(dist_shore) + Ɛi
Farne Islands	Sandwich	Usage = -2.071e+04 - 4.124e-01(dist_col) - 1.958e+00(dist_shore) + 5.904e+02(sal_spring) + Ɛi
Larne Lough	Sandwich	Usage = -4677.47 - 0.43(dist_col) - 3.35(dist_shore) + 133.89(sal_spring) + Ɛi
Ythan Estuary, Sands of Forvie and Meikle Loch	Sandwich	Usage = 4.06 - 2.38(strat_temp) + 0.26(bathy_1sec) + Ɛi
North Norfolk	Sandwich	Usage = -4.19 - 0.17(dist_col) + 0.09(dist_shore) + 0.06(bathy_1sec) + 1.16(ss_wave) + Ɛi
Cemlyn Bay	Sandwich	Usage = -1.717e+03 - 2.770e-01(dist_col) - 3.661e-01(dist_shore) + 5.001e+01(sal_spring) + Ɛi
Generic	Sandwich	Usage = 0.28 - 0.09(dist_col) + 0.03(bathy_1sec) - 0.20(dist_shore) + Ɛi

10 List of Annexes

Annex 1

Contract report of work carried out to develop and apply modelling techniques to visual-tracking data to produce site-specific (Phase 1) models for 13 species/colony SPAs. The mapped outputs are from the GAM models.

BREWER, M.J, POTTS, J. M., DUFF, E. I. & ELSTON, D. A. 2012a. *To carry out tern modelling under the Framework Agreement C10-0206-0387*. Contract Report to JNCC, March 2012.

A separate Results Appendix provides the text and graphical output from the analysis of the main report.

Annex 2

Contract report of work carried out to extend the modelling techniques developed in Brewer *et al* 2012a for application in a geographic extrapolation (Phase 2) context for 14 species/colony SPAs for which little or no visual tracking data were available. Analysis was restricted to GLMs.

BREWER, M.J., POTTS, J. M., DUFF, E. I. & ELSTON, D. A. 2012b. *Prediction of new colonies – seabird tracking data (under Agreement C10-0206-0387)*. Contract Report to JNCC, November 2012.

A separate Results Appendix provides the text output for the principal component analysis of Section 5.1 of the main report.

Annex 3

Contract report to re-run GAM models developed in Brewer *et al* 2012a for the four larger tern species at Coquet Island SPA after removing outliers and transforming environmental covariates where necessary.

BREWER, M.J., POTTS, J. M., DUFF, E. I. & ELSTON, D. A. 2012c. *Additional Work Coquet Colony – Seabird Tracking Data (under Agreement C10-0206-0387)*. Contract Report to JNCC, December 2012.

Annex 4

Contract report to re-run GAM models developed in Brewer *et al* 2012a for the four larger tern species at all other Phase 1 colonies (except Coquet Island, covered in Brewer *et al* 2012c) after removing outliers and transforming environmental covariates where necessary.

POTTS, J. M., BREWER, M. J., DUFF, E. I. & ELSTON, D. A. 2013a. *Additional Work Other Colonies – Seabird tracking data (under Agreement C10-0206-0387).* Contract Report to JNCC, March 2013.

Annex 5

Contract report of work re-running GLM models for Phase 1, incorporating more robust approach to model selection and generating confidence intervals for the predictions. These are the final Phase 1 models used.

POTTS, J. M., BREWER, M. J., & DUFF, E. I. 2013b. Refinements of tern Sterna sp. tracking data modelling (Phase 1) (under *Agreement C10-0206-0387)*. Contract Report to JNCC, September 2013.

Annex 6

Contract report of work re-running GLM Phase 2 models based on a revised shortlist of candidate covariates resulting from the Potts *et al* 2013b (Annex 5) work. Included clearer audit of model selection based on three different scores of cross-validation. These are the final Phase 2 models used.

POTTS, J. M., BREWER, M. J., & DUFF, E. I. 2013c. Refinements of tern Sterna sp. tracking data modelling (Phase 2) (under *Agreement C10-0206-0387)*. Contract Report to JNCC, October 2013, Revised December 2013.

Annex 7

Contract report of cross-validation work carried out on Phase 1 models.

POTTS, J. M., BREWER, M. J. 2014. *Cross-Validation of tern Sterna sp. tracking data modelling (Phase 1) (Under Agreement C10-0206-0387).* Contract Report to JNCC, December 2013. Revised January 2014

Annex 8

Contract report of a literature review of tern foraging ecology.

EGLINGTON S. & PERROW, M. R. 2014. Literature review of tern *Sterna sp.* foraging ecology. Report to JNCC, under Contract ref. C13-0204-0686

Annex 9

Contract report analysing a subset of the JNCC visual tracking data to determine sufficiency of sample sizes for estimating foraging ranges of the colony population.

HARWOOD A. J. P. & PERROW, M. R 2014. Analysis of JNCC visual tracking data. Report to JNCC, under Contract ref. C13-0204-0686

Annex 10

Contract report revising the roseate tern model for Coquet Island, excluding covariates with extensive missing values.

POTTS, J. M.& BREWER, M. J. 2014. Revised model for roseate terns *(Under Agreement C10-0206-0387).* Contract Report to JNCC, May 2014

11 Version Control

Version / Date	**Drafted by**	**Issued to / comments from**	**QA**	**JNCC sign-off/date**
V1: 04 December 2013 Filename: JNCC Tern Report Dec 2013. Doc	LJ Wilson	A Kuepfer; I Win; J Black	Incorporated minor comments	
V2: 09 December 2013 Filename: JNCC Tern Report Dec 2013._V2. doc	LJ Wilson and A Kuepfer	J Reid	Incorporated minor comments	
V3: 16 December 2013 Filename: JNCC Tern Report Dec 2013._V3. doc	LJ Wilson	L Way	Incorporated minor comments	18/12/2013
V4: 20 December 2013 Filename: JNCC Tern Report Dec 2013._V4. doc	LJ Wilson	SNCBs	Incorporated minor comments from SNCBs; corrected Table 53	
V5: 3 March 2014. Filename: JNCC Tern Report_V5. doc	LJ Wilson	Independent review	Addressed reviewer comments	31/07/2014
V6: 31 July 2014 Filename: JNCC Tern Report_V6.doc	LJ Wilson	Publicly available pre-publication draft		