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Identification of important marine areas in the UK for red-throated divers (*Gavia stellata*) during the breeding season

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Summary

As part of work to identify possible marine sites for consideration as Special Protection Areas (SPAs) the Joint Nature Conservation Committee (JNCC) and Scottish Natural Heritage (SNH) aim to identify important marine areas for red-throated divers (*Gavia stellata*) during the breeding season.

We present a habitat modelling approach that uses detailed data on diver distribution and ranging behaviour to predict and identify important marine areas for the species across the UK breeding range.

Data were collected over five years (2003-2007) around important and representative red-throated diver breeding territories in Shetland, Orkney, and the Outer Hebrides. The methods of data collection included at-sea surveys of divers, visual tracking of breeding birds to determine their foraging locations, and radio-tracking of foraging birds.

The modelling approach comprised three main stages:

1. A Generalised Additive Model (GAM) was used to describe the marine habitat of the species and to predict the presence/absence of birds at sea based on a range of environmental parameters including bathymetry, tidal bed stress, wave base, probability of fronts, seabed sediments, and coastal physiography. The model explained 33% of the variation in diver presence.

2. Areas predicted by the GAM as important habitat for divers were constrained to include only those areas within the typical maximum foraging range from any known breeding site. The foraging range was 10km based on the maximum flight range and the maximum foraging area derived from visual and radio-tracking. Breeding sites were identified based on a 2006 national survey of breeding divers.

3. For those areas predicted by the constrained GAM as important habitat for divers within foraging range of known breeding sites, the number of pairs breeding within foraging range was calculated based on the 2006 national survey data. This allowed areas to be identified that are potentially used by nationally and internationally important numbers of birds.

The areas predicted by the flight range constrained model compare well with independent data on foraging locations obtained from visual and radio-tracking, suggesting a high level of confidence in the model predictions. The unconstrained habitat model also compares well with the wintering distribution of red-throated divers.

The 2006 national diver survey data allowed identification of those areas predicted by the flight range constrained model that potentially were used by high numbers of breeding birds, especially within the Northern Isles, where the breeding survey coverage was complete, but less so in other areas, where only a stratified sample of areas was surveyed.

Maximum curvature was applied to the model outputs to delineate discrete sites from the wide offshore distribution of the species, and a ranking exercise is presented that may be used to assist the choice of the most suitable sites from these possibilities.

Contents

1 Introduction

1.1 Birds Directive and SPAs

The Joint Nature Conservation Committee (JNCC) currently is progressing work to identify Special Protection Areas (SPAs) in the marine environment (Johnston *et al* 2002), to fulfil the requirements of the EU Birds Directive (1979, codified version 2009) on the conservation of wild birds (commonly known as the Birds Directive). The Birds Directive requires Member States to identify and classify the most suitable territories in number and size as special protection areas (SPAs) for the conservation of those bird species that are listed as rare or vulnerable species in Annex 1 of the Directive, and for regularly occurring migratory species.

The Birds Directive states that conservation measures should be taken both in 'the geographical sea and land area', but most SPAs in the United Kingdom (UK) currently do not include marine areas beyond the mean low water mark (or mean low water springs in Scotland). Work to identify the most important marine bird sites which may be further considered for SPAs beyond the low water mark is currently being undertaken by the Joint Nature Conservation Committee (JNCC) in collaboration with the four UK statutory nature conservation bodies (SNCBs): Scottish Natural Heritage (SNH), the Natural Resources Wales (NRW), Natural England (NE) and the Department of the Environment, Northern Ireland (DOENI). As far as possible the UK SPA selection guidelines applied in the identification of terrestrial SPAs (Stroud *et al* 2001) are also applied in the marine environment.

As part of this work JNCC and SNH aim to identify those marine areas used for foraging by red-throated divers (*Gavia stellata*) during the breeding season for possible further consideration.

1.2 UK Diver population and SPA suite

Based on the national survey of breeding divers conducted in 2006 (Dillon *et al* 2009), an estimated 1,255 pairs of red-throated divers breed in the UK, with around a further 1,636 non-breeding adults present during the breeding season. The entire UK breeding population occurs in Scotland, with approximately 33% in Shetland, 8% in Orkney, 26% in the Outer Hebrides, 17% in the Inner Hebrides, and 17% elsewhere in Scotland (Dillon *et al* 2009). The approximate breeding distribution of red-throated divers in the UK is shown in Figure 1.

These results suggest a significant increase (34%) in the number of breeding pairs overall since the previous national survey in 1994, which estimated a breeding population of 935 pairs (Gibbons *et al* 1997). However, the increase was greatest (83%) outwith the Northern Isles (Shetland and Orkney); where the population has remained roughly stable (decrease of 3-4%).

The 1994 survey (Gibbons *et al* 1997) indicated that there had been a moderate decline (38%) in Shetland from 700 to 430 pairs since a previous Shetland-only survey in 1983 (Gomersall *et al* 1984).

The red-throated diver is listed on the amber list of Birds of Conservation Concern (Gregory *et al* 2002), due to a moderate decline in the UK breeding population (25-49% based on Gibbons *et al* (1997)) and its "unfavourable conservation status" in Europe. The UK population may now be stabilising or increasing (Dillon *et al* 2009), but the species remains one of conservation concern; it is listed on Schedule 1 of the Wildlife and Countryside Act 1981 as a species protected by special penalties at all times, and is listed on Annex I of the Birds Directive as a rare or vulnerable species (EEC, 1979). As an Annex I species, the UK is required to identify and classify the most suitable territories in number and size, on land and at sea as SPAs for the conservation of the species.

Red-throated divers breed mainly on small, upland, freshwater lochs, where their one or two chicks remain until fledging. A suite of terrestrial SPAs has been established for red-throated divers and comprises 10 protected areas covering breeding territories on mainland Scotland, the Inner and Outer Hebrides and the Northern Isles (Stroud *et al* 2001) (Table 1 and Figure 2).

When established, these terrestrial SPAs together contained approximately 42% of the GB breeding population. Based on the results of the 2006 national survey (Dillon *et al* in press.), the number of breeding pairs contained within the SPA suite may have decreased to around 27% of the GB breeding population.

Table 1. The current suite of 10 breeding territory SPAs for red-throated divers in the UK, with changes in protected numbers and % of national population between that presented in Stroud *et al* (2001) (surveys conducted 1992-1996) and Dillon *et al* (2009) (survey conducted 2006).

SPA site name	Est. br. N. Stroud *et al* 2001	% of UK br. pop. Stroud *et al* 2001 (935)	Est. br. N. Dillon *et al* 2009	% of UK br. pop. Dillon *et al* 2009 (1255)	Change in numbers within SPA	Change in % total pop. within SPA
Caithness and Sutherland Peatlands (Highland)	89	9.5	46	3.7	-43	-5.8
Foula (Shetland Islands)	11	1.2	8	0.6	-3	-0.6
Hermaness, Saxa Vord and Valla Field (Shetland Islands)	28	3.0	22	1.8	-6	-1.2
Hoy (Orkney Islands)	56	6.0	46	3.7	-10	-2.3
Lewis Peatlands (Western Isles)	60	6.4	80	6.4	+20	0
Mointeach Scadabhaigh (Western Isles)	48	5.1	17	1.4	-31	-3.7
Orkney Mainland Moors (Orkney Islands)	15	1.6	24	1.9	+9	+0.3
Otterswick and Graveland (Shetland Islands)	27	2.9	23	1.8	-4	-1.1
Ronas Hill – North Roe and Tingon (Shetland Islands)	50	5.4	50	4.0	0	-1.4
Rum (Highland)	11	1.2	13	1.0	+2	-0.2
Totals	395	42.2	329	26.2	-66	-16

1.3 Diver behaviour and vulnerability during the breeding season

Little detailed data exist on the foraging behaviour of red-throated divers during the breeding season. However, it is known that unlike other species of diver that forage for their young in their freshwater breeding lake (or in nearby lakes), breeding red-throated divers forage almost entirely in inshore marine areas close to their freshwater breeding territories (Reimchen and Douglas, 1984; Gibbons *et al* 1997; Okill and Wanless, 1990). The diet of red-throated diver chicks generally comprises small marine fish, Ammodytidae, Clupeidae, small Gadidae. Of a total of 151 fish recorded being passed to chicks during this study, 33% were recorded as sandeels (*Ammodytes* species), 7% were clupeids, 51% were gadoids, and 9% were recorded as unknown species.

During the chick-rearing period (July and August), breeding birds make particularly intensive use of the inshore marine areas close to their breeding territories, with a breeding pair making as many as 10-18 foraging trips every 24 hours (depending on chick age; Reimchen and Douglas, 1984, JNCC unpublished data). At this time, disturbance or exclusion from important marine areas might potentially have significant effects on chick provisioning and breeding success. Chick rearing is the time that parents are most reliant on specific areas, because they are restricted in the time (and therefore distance) they can travel from nest. Thus, areas used during chick rearing are a priority for site-based conservation.

Red-throated divers are known to be sensitive to disturbance from boats, often flying away from or avoiding vessels (Garthe and Hüppop, 2004; pers. obs. this study). This may increase the time required for successful foraging, possibly decreasing chick provisioning and ultimately breeding success. In addition, an increase in the time spent away from the nest may increase the likelihood of unattended eggs or chicks being depredated. Divers are also vulnerable to actual or effective habitat loss as a result of development in marine areas; offshore wind farms are known to displace about 96% of wintering red-throated divers from their “footprint” through disturbance during construction (e.g. Petersen, 2005) and birds may avoid flying through wind farm areas post construction (Halley and Hopshaug, 2007).

Post-fledging (during August), the chicks typically are initially brought to the same inshore marine areas previously used for foraging by the parents (Okill and Wanless, 1990; BD pers. obs.), where they continue to be fed by their parents, before leaving the breeding areas (Okill, 2002). At this stage, both breeding adults and their fledged young spend a large proportion of their time on the sea, again rendering them potentially more vulnerable to impacts in the marine environment.

The best information on causes of mortality comes from ringing recoveries, most of which are from birds ringed in the Northern Isles. More than half of ringed birds with a known cause of death were caught in fishing nets, with various types of net being responsible, including those used at fish farms, set nets for various fish species, and discarded nets. A further 21% of recoveries were attributed to marine pollution, mainly oil. While many of these recoveries may have occurred during the non-breeding season, they highlight in particular the vulnerability of the species to entanglement with fishing gear (Okill, 2002). In addition, future increases in the numbers of renewable energy devices such as wind turbines or wave or tidal devices may present potential collision risks to breeding birds during foraging trips (Furness *et al* 2012, Garthe and Hüppop, 2004).

1.4 Rationale for marine SPAs during the breeding season

Given the potential for red-throated divers nesting within existing breeding territory SPAs to be affected by a number of potential impacts while foraging away from their nest sites, impacts that may result in increased foraging effort, reduced breeding success, or even adult mortality, it might be appropriate to identify marine SPAs for the species, quite apart from the legal obligation to do so. It is not intended to identify specific marine areas for each terrestrial SPA, but coherence should be achieved by focussing on the marine areas around dense breeding territory areas, many of which are contained within terrestrial SPAs for the species.

1.5 Generic modelling approach versus site-by-site surveys

Identification of those marine areas close to the main breeding areas that are used by red-throated divers during the breeding season requires data on the distribution of the species during the breeding season and/or data on how red-throated divers use these areas. Such data could be collected around each breeding territory SPA or other areas of high breeding density on a site-by-site basis, with the data collected around each site informing the selection of the most important inshore areas. As a minimum, such a site-by-site approach would require survey data (e.g. boat-based survey) on the local distribution of red-throated divers to be collected around each of the 10 current breeding territory SPAs, preferably with data from several years for each site. Depending upon the method or methods used, collection of the necessary data for this approach was considered to be too time consuming and prohibitively expensive.

A site-by-site approach where the importance of discrete inshore areas might be assessed by comparing the numbers of divers recorded in the site against population thresholds was also considered inappropriate due to the turnover of breeding birds within these areas; the number of birds making use of an inshore area throughout the breeding season is likely to be far greater than the numbers recorded there at any given time.

We considered it most effective to collect data at/around a small sample of breeding territory areas with the aim of identifying important inshore areas for red-throated divers using a habitat modelling approach. This would allow prediction and identification of important inshore areas around important breeding areas, including the ten breeding territory SPAs.

1.6 Predictive species distribution modelling

Generalised additive models (GAMs) (Hastie and Tibshirani, 1990; Hastie and Tibshirani, 1995) are the non parametric equivalent of generalised linear models (GLMs) (McCullagh and Nelder, 1989); in contrast to GLMs, GAMs are data-driven rather than model-driven in that the shape of the response curves are determined from the data, instead of fitting *a priori* parametric models.

1.7 Boundary delineation

Consideration must be given as to how the most important areas may be identified or prioritised based the model outputs. A boundary delineation method used to identify the most important areas for divers at sea would ideally:

- be robust and minimise subjective judgments;
- identify a site that contains a cohesive aggregation of the highest densities of birds;

- be proportionate with respect to area and number of birds captured;
- be relatively easy to understand and explain;
- be applicable to all sites and species; and
- as far as possible, be consistent with previous work in this area.

1.8 Project aim and objectives

The aim of this project was to identify and delineate potentially important marine areas in the UK for red-throated divers during the breeding season.

The objectives of this project were to:

1. Collect detailed data on the distribution of red-throated divers at sea around a number of selected breeding territories during the breeding season.
2. Collect detailed data on the foraging behaviour and choice of foraging area of known breeding birds during the chick rearing period.
3. Collate data on a range of environmental factors likely to be important elements of the species' foraging habitat.
4. Quantify the relationship between observed distributions and environmental factors using a GAM to allow mapping of suitable marine habitat for red-throated divers.
5. Integrate the predictive model of suitable marine habitat with data on the foraging behaviour and range of known breeding birds during the chick rearing period to help identify important areas.
6. Delineate boundaries around important areas.
7. Develop a ranking system to aid in identification of the most important of these marine areas for further consideration.

2 Methods

2.1 Selection of survey areas

The breeding distribution of red-throated divers in the UK is limited to Scotland and is largely restricted to the north and west of the country, with major strongholds in Shetland, Orkney, and the Outer Hebrides (Gibbons *et al* 1993, Dillon *et al* 2009).

Four main survey areas were chosen at which to undertake detailed data collection. These were selected to focus on the most important breeding areas, represent the geographical spread of breeding areas, and be practical in terms of field work logistics. The selected study areas were Unst, Yell and Fetlar (northern Shetland); Shetland Mainland; Isle of Hoy (Orkney); and North Uist (Outer Hebrides) (Figure 3). These study areas cover the range of breeding red-throated divers across Scotland, and include the high density regions of Shetland and Orkney. Surveys did not cover the mainland breeding area of Caithness and Sutherland due to resource constraints. The spread-out nature of nests make finding aggregations at sea low likelihood and therefore this area was seen as low priority.

2.2 Data collection methods

Within these four survey areas, three methods were used to collect data. Boat-based visual surveys of divers in inshore waters were conducted to collect data on diver distribution in relation to oceanographic and habitat variables. Visual- and radio-tracking studies of breeding birds during foraging trips were conducted to collect data on the species' foraging range, locations, and behaviour.

2.2.1 Survey of breeding pairs

Each season, prior to collecting at-sea distribution and foraging behaviour data, a census of breeding divers within the survey areas was undertaken to identify potential study pairs for visual- and radio-tracking. These censuses were based on existing data on the location of breeding lochs, their history of occupancy, and their history of breeding success. Unpublished historical occupancy and breeding success data for Shetland and Orkney were obtained from D.Okill and E.J.Williams respectively, while the results of the 2006 UK diver census (Dillon *et al* 2009) were used to inform our survey of the North Uist study area.

In order to obtain accurate data on the locations of diver pairs likely to be rearing chicks, our censuses were conducted during the first two weeks of July when most red-throated diver eggs had hatched, or were likely to hatch soon (Okill 2007). All pairs recorded as apparently incubating eggs, brooding chicks, or with chicks visible on the breeding loch were regularly revisited to maintain up-to-date information on their status.

2.2.2 Boat surveys

Boat-based visual surveys were conducted in the inshore waters around Shetland Mainland, Unst, Yell and Fetlar (2003 and 2006), Hoy (2005) and North Uist (2007) (Table 2). All surveys were conducted during the chick rearing period (July-August).

Study areas were defined which included the seas around the breeding/nest site aggregations in each of the three study areas (Figure 3). The aim of the surveys was to attempt to record all divers present in these study areas at the time of the survey. The typical dive duration of red-throated divers is <90 seconds (Cramp and Simmons, 1977), so in order to maximise the probability of detecting birds between dives the speed of the boat was maintained at approximately 14km h-1 (7 – 8 knots).

The typical range of depths for foraging dives by red-throated divers is cited as between 2 and 9m (Cramp and Simmons, 1977), although birds may dive deeper and may not necessarily dive to the seabed. We planned our survey routes to cover waters up to 50m deep. Two types of survey route were used, each designed to maximise coverage of areas expected to be used by divers given what is known about their foraging behaviour and preferences within the time available (it can aid model power to define preferences if there is a higher resolution of data collected from the most likely foraging areas, BioSS pers comm.). During surveys conducted in 2003, 2005, and 2007 the survey route ran approximately 500m from and roughly parallel to the shoreline. During the 2006 surveys the survey route ran in a regular pre-determined zigzag pattern along the coastline varying between 50m and 4km offshore. The zig-zag pattern was designed to allow a greater range of environments to be surveyed, but due to resource constraints this method could not be undertaken every year. The pattern of environmental preferences detected was not different between the zig-zag survey design and the parallel to coast survey design. A broad range of environments is captured even with the parallel to coast survey method.

During the surveys, two observers (one port, one starboard) used binoculars and the naked eye to detect divers before they moved in reaction to the boat. The maximum distance from the boat that observers could reliably detect divers on the water was estimated to be approximately 750m. Survey routes covered a range of environmental conditions including depths ranging from 0 to 100m. All red-throated divers on the water, or flying were recorded. Observers recorded: time of sighting (to nearest five seconds), estimated range and bearing to the bird, whether on the sea or flying, and whether foraging or carrying a fish.

The position of the boat was recorded using a Geographical Positioning System (GPS). The survey tracks recorded by GPS are mapped in Figures 4-6.

Table 2. Details of boat-based surveys conducted between 2003 and 2007.

Year	Area	Number of Days	Total transect km	Transect method	Vessel
2003	Yell, Unst, and Fetlar	2	461	Parallel to coast	MV Dunter II
2005	Hoy and Scapa Flow	3	358	Parallel to coast	MV Girl Kilda
2006	Most of Shetland coast	5	578	Zigzag	MV Dunter III
2007	East and north of North Uist	1	53	Parallel to coast	Seatrek Delta RHIB
Totals		11	1450		

2.2.3 Flight-line observations

Visual tracking of breeding birds during foraging trips was conducted on Unst and Fetlar (2003), Hoy (2005), and North Uist (2007). All visual tracking was carried out during the July and August when study pairs were rearing chicks.

At each survey site, a sample of breeding pairs with chicks was selected from the initial survey of potential breeding birds (Table 3). As far as possible, the sample breeding pairs were selected to be representative of the geographical spread of nest sites within each survey area.

A network of up to six observers was variably positioned to allow observation of selected nest sites and possible foraging areas within published range of nest. Observers used Citizens Band (CB) radios and mobile phones to exchange information on flying birds and attempted (as a network) to follow individual birds by eye flying between a breeding loch and at sea foraging areas. Observations therefore consisted of birds leaving their breeding lochs and heading for a foraging area, birds leaving a foraging area carrying a fish and returning to the breeding loch, and locations at which birds were actively foraging. Birds were assumed to be making a foraging trip if they were observed diving and/or returning to the breeding loch with prey.

Where possible, observers recorded the origin and destination of each flight (breeding loch, or foraging area) as an Ordnance Survey Great Britain 1936 (OSGB1936) grid reference, plus the departure and arrival times. In many cases the start or end point of a birds flight was not observed, in which case the unknown location was inferred from the observed direction of the flight (measured using a compass) superimposed on a map of the area. Observers also recorded details of any fish caught or carried and the fate of any captured fish (i.e. fed to chick, or eaten by adult).

Some birds were recorded foraging at sea, but could not be linked to a nest site. These birds were assumed to be breeding if they were observed carrying food when leaving a foraging area. The locations and behaviour of these foraging birds were also recorded.

For sensitivity/confidentiality reasons, maps of nest sites used for this work are not provided.

Table 3. Numbers of breeding pairs for which visual flight-line observations were attempted in each survey area.

Year	Area	Number of Breeding Pairs Tracked
2003	Unst, and Fetlar (Shetland)	15
2005	Hoy (Orkney)	21
2007	North Uist (Outer Hebrides)	14
Totals		50

2.2.4 Radio-tracking

Radio-tracking of breeding birds during foraging trips was carried out on Mainland Shetland (2004 and 2006) and North Uist (2007). All radio-tracking was conducted during the chick rearing period (July-August). At each survey site, a sample of breeding pairs with chicks was selected from the initial census of potential breeding birds. As far as possible, the sample breeding pairs were selected to be representative of the geographical spread of nest sites within the survey area. However, the main considerations in selecting sample breeding pairs were that they had at least one chick of 10 days or older (minimum ringing age) and that these were breeding on lochans of a suitable size for capture using a net of 21m in length.

Capture and tagging

Capture of one adult and all chicks (up to two) was attempted from each sample breeding pair, using the method described in Okill (1981) and modifications thereof. A large (21×2.5m) single-shelf mist net, 7.5cm wader net, attached by guy-cord at each end to a 1.8m pole. The net was stretched horizontally over the loch, lowered into the water and held submerged.

By positioning fieldworkers around the loch, chicks and adults were forced to the down-wind end of the loch from where it was difficult to take off. Birds would then either swim over the top of the net, at which point the net was quickly lifted to entangle the bird, or swim under the net, becoming entangled, or attempt to take-off from the loch, at which point the extended net was ‘flicked up’ to capture the bird during take-off. Capture was undertaken by a qualified ringer under SNH license. Once a bird was captured, the net was carried to the bank and the bird carefully extracted.

Captured chicks and adults were ringed using the method described in Okill (1981) and the following biometric measurements were taken: wing length, bill length, tarsus length, and total weight. Using these measurements, it was possible to determine the sex of most breeding adult red-throated divers, males being larger than females (Okill *et al* 1989).

A total of 19 tags was deployed on 18 breeding adult birds during the chick rearing period (one bird was tagged in 2004 and subsequently in 2006).

Radio-transmitter tags (Biotrack Ltd.) weighed approximately 4.4g; between 0.25% and 0.29% of the average adult body weight. Tags measured approximately 18mm × 16mm × 7mm, with a 230mm flexible whip-antenna extending from one end and a 140mm secondary flexible antenna extending from the other. The Effective Radiated Power (ERP) of the transmitters was approximately -18 dBm, transmitting at 173 MHz. The estimated battery life was approximately 30 days. Components were set in a waterproof acrylic casing in which a 40×40mm square of surgical gauze was embedded to increase surface area for attachment to the bird (Figure 7).

The range of the signal emitted by the tags was tested prior to deployment. These tests suggested that with line-of-sight, we could expect to detect tags up to 20km from their location. The expected range during deployment was likely to have been less than this, but still well in excess of the anticipated requirements of this study. Prior to each attachment, the radio-transmitter signal was tested using a Lintec rigid 5 element Yagi antenna connected to a Biotrack Sika receiver.

Tags were attached to the dorsal side of a bird's tail feathers using Evo-Stick contact adhesive applied to embedded gauze square of the tag and the central four main tail feathers. Tags were positioned far enough back to be clear of the uropygial gland, but far enough forward to give water clearance when the bird was swimming (Figure 8).

Time spent at the breeding loch was kept to a minimum. Attachment of tags (including curing of adhesive) took approximately 5-10 minutes depending on weather conditions. Total processing time from capture to release was approximately 15–20 minutes, including 5 minutes to measure, weigh and ring chicks.

Tracking tagged birds

Radio-tagged birds were monitored from various tracking locations using Lintec rigid 5 element Yagi antennas connected to Biotrack Sika receivers. Signals were monitored from between two and five tracking locations simultaneously, with the aim of triangulating the source of the signal. The direction of the strongest signal was determined and the direction was measured using a compass. Where possible, observers at all tracking stations recorded the direction of signals at synchronised 5 minute intervals, but observers also recorded regular signal directions when birds were moving. Where possible, signals were used to track tagged birds down to an approximate location or direction and the bird was located visually.

Signals were also used to determine the behaviour of tagged birds in their foraging areas. By observing a bird and monitoring its signal at the same time it was possible to determine the types of signal (quality and duration) produced during different behaviours; e.g. diving, preening, and sitting on the surface or swimming. Birds were assumed to be making a foraging trip if they were observed to engage in diving behaviour and/or to return to the nest with prey, or if their signal corresponded to the type observed during foraging behaviour.

2.3 Analysis

Data manipulation was carried out within Microsoft Access. Spatial data processing was carried out within ArcGIS 9.2 (© 1999-2006 ESRI Inc.), Hawth's Analysis Tools (Beyer, 2004), and xtools (DeLaune, 2000). All data within ArcGIS 9.2 were projected in British National Grid (OSGB 1936 Transverse Mercator).

Where visual fixes on tagged birds could not be obtained, their locations were estimated by triangulation of the signal bearings recorded from two or more locations within the same 5 minute periods. Estimation of bird locations by means of triangulation was made using LOAS 4.0 Beta (© 1998-2005 Ecological Software Solutions). Generalised Additive Models were implemented within S-PLUS 2000 (© 1985-1999 MathSoft Inc.)

2.3.1 Analysis of foraging flight data

For visually tracked foraging flights where there was a high degree of certainty of the link between nest site and foraging site, flight distances, distance from coast and distance from nest were calculated in ArcGIS. For radio-tracked foraging trips flight distances were calculated in ArcGIS as the straight line distance between the flight origin and the geometric centre of the area used for foraging.

Multiple flights between a nest site and the same location at sea were removed to avoid pseudo replication. Flight distances were used to assess the maximum foraging range for breeding red-throated divers.

2.3.2 Analysis of foraging area data

For each radio-tracked bird, the at-sea foraging area for each foraging trip, i.e. the maximum area of sea used during each single foraging trip, was calculated as the area of a Minimum Convex Polygon (MCP) drawn around all estimated and visually confirmed locations recorded for that foraging trip.

2.3.3 Analysis of boat survey data; modelling

Study area

An area was defined for applying the model outputs that included all waters within the UK breeding range for red-throated divers as described by Gibbons *et al* (1993).

To create sample points to be used for modelling and predictions, the study area was subdivided into a 1km grid. 1km^2 was selected as best representing the scale over which birds in this study foraged; mean MCP foraging area size = 0.69km^2 (n=13; 95% Confidence Limits = 0.25 – 1.12km^2). This resolution was also greater than the estimated error in plotted locations for birds recorded during the surveys.

Environmental covariate data

Environmental data were collated from various sources, collected at different times and spatial scales to the bird data; full details of these data are given in Table 7.1 in Appendix 1. The digital elevation model (DEM) of seabed depth was produced by SeaZone Solutions Limited at a 250m resolution (grid cell size). Seabed slope and aspect were calculated from the DEM using the Aspect and Slope functions in ArcGIS Spatial Analyst. Data on maximum wave base, tidal bed stress, sea surface temperature, salinity, stratification (surface to seabed temperature difference), and probability of fronts were provided for the UKSeaMap project (Connor *et al* 2006) by the Proudman Oceanographic Laboratory (POL). Distance to coast was calculated from the Ordnance Survey (OS) high-water mark using the Straight Line Distance function in ArcGIS Spatial Analyst, from the centre of each grid square. Surficial[1] seabed substratum data were prepared as described by Cooper *et al* (2005) and provided for the UKSeaMap project (Connor *et al* 2006) by the British Geological Survey (BGS). Coastal physiographic features were taken from the UKSeaMap project (Connor *et al* 2006).

The model was established using bird data (presence or absence from boat surveys), and various environmental data sets including continuous variables: seabed depth (m), seabed slope (º incline), seabed aspect (direction that seabed slope faces, º from true north), maximum wave base (maximum depth at which wave passage causes significant water motion, m), tidal bed stress (force exerted by the tide at the seabed, N m^{-2}), sea surface temperature (ºC), salinity (‰), stratification (ΔºC surface to seabed), probability of fronts (probability P that a front will form at given location during summer), and distance to coast (km); and categorical variables: seabed sediments, coastal physiography (Figures 8.1 to 8.12 in Appendix 2).

Model parameterisation

Given issues of bird turnover, which would be exacerbated with the lack of repeat surveys, no attempt was made to model densities. Instead focus was on parameterising a presence-absence model.

Each $1km^2$ cell that was surveyed was assigned a value of either 1 (presence, diver(s) observed) or 0 (absence, no diver observed). This is the response, or dependent, variable. No correction was made for undetected birds because we would not know where undetected birds should be placed spatially. As long as any 'un-detection' of birds is not spatially biased, then the absence of a detection correction should not influence our resulting spatial predictions. It should be noted that no measure of survey effort was included in the model. Only cells through which the some observation effort occurred, were included in the analysis. This means that cells through which the transect passed, or in which observers could have observed within the 750m range of transect strip, were included in the analysis.

A single model was created which used all observations from all three study areas from all years. This avoided the effects of region or year specific effects, given that we only had one year of survey data from each region. Only the surveyed cells were used in parameterising the model. This includes cells through which the transect did not pass but which could be detected by observers: For example if a transect passed within 100m of a grid cell. The model was built using a binomial distribution and logit link for presence-absence data. A smoothing function (either loess or spline) was applied separately to each continuous environmental variable. The response of diver presence to each predictor was modelled and the responses (additive terms) were then added to make an additive model.

$$\boldsymbol{Y = f_1(X_1) + f_2(X_2) + \ldots\ldots + f_n(X_n)}$$

Where ***Y*** is the probability of occurrence, ***f*** is a smoothing function, and ***X*** is an environmental predictor variable.

The number of predictors used, the choice of smoothing function and the fit of each model were determined using the model deviance, which represents the difference between predictions and observations for the model building data.

[1]Surficial refers to processes or entities pertaining to or occurring on or near the earth's surface.

First, backwards selection of the environmental (predictor) variables was used to rank variables in order of importance: A global model including all variables was calculated. From this model, several reduced models were calculated by withdrawing one variable at a time. Deviances for all models were calculated and predictor variables were ranked in order of importance (Koubbi *et al* 2006).

Second, additive models were then calculated using forward selection: The final model was calculated by selecting the highest ranked variable and then consecutively adding the next highest ranked variable, and then the next, until the model that explained the most deviance with the fewest variables was reached. The significance of decreasing deviance between consecutive models was tested using an F test (Loots *et al* 2007; Quinn and Keough, 2002) and the model with the minimal significant deviance was retained as the final model.

Model predictions

All cells (surveyed and un-surveyed) were assigned values for each of the environmental parameters (the predictor variables). The centre coordinates of each cell, along with all bird and environmental data were exported into an S-PLUS data table.

The final model, established as above, can be used to extrapolate (predict) to unsurveyed areas within the wider study. Specifically, the model can predict the probability of occurrence of divers in any unsampled area where environmental variables are known .

The final model was applied to all 1km^2 cells in the study area in order to predict the probability of red-throated divers being present in each cell, based on the recorded values of the environmental predictor variables at those cells.

Converting predicted probability of occurrence into presence or absence

For surveyed grid cells, predicted values for probability of occurrence (values between 0 and 1) were reclassified as either presence (1) or absence (0) based on a range of probability of occurrence thresholds ranging from 0.05 to 0.95 in 0.05 intervals. Predicted values for each sample point, at each threshold were compared (cross validated) to the original recorded (survey) presence/absence data and scored accordingly as: correctly predicted presence, correctly predicted absence, incorrectly predicted presence, or incorrectly predicted absence.

The results of these comparisons at each threshold were used to calculate a Kappa statistic (Cohen, 1960), an index that compares the level of agreement against that which might be expected by chance. The Kappa statistic can be thought of as a measure of the chance-corrected proportional agreement between observed and predicted values, ranging from +1 (perfect agreement) via 0 (no agreement above that expected by chance) to -1 (complete disagreement):

Kappa = (Observed agreement – Chance agreement) / (1 – Chance agreement)

The probability threshold that resulted in the maximum Kappa statistic value was selected and applied to the probability of occurrence predictions to give a prediction of presence/absence for all 1km^2 grid cells within the study area.

Constraining the model

To render the model predictions relevant to breeding red-throated divers the model predictions were further constrained by maximum foraging flight range from breeding territories, plus the typical foraging area used at sea, as calculated from the flight-line and radio-tracking data.

Thus the constrained model output shows where divers are predicted to present (from the GAM model) within the foraging range of breeding territories, throughout Scotland.

Using the raw survey data (nest locations and breeding status) from the 2006 national survey, plus additional breeding sites recorded during this study, we counted the number of pairs breeding within range of each cell from the constrained model output surface.

Validation of model predictions

The best way to validate a model is by assessing its ability to accurately predict an independent data set. Although shore-based visual and radio-tracking data represent such an independent data set, they are not appropriate because they substantially under-record longer foraging trips, as well as being of restricted spatial coverage within the wider study area. Another way of assessing model predictive ability is based on resampling of the original data set (e.g. Wintle *et al* 2005, Schwemmer *et al* 2009). This involves running the model a number of times with a different sub-sample of the data left out each time. This sub-sample is then used to test the predictive performance of the model. A number of statistics have been used for assessing this predictive performance, with the most widely used being based on receiver operating characteristic curves (Elith 2002, Phillips *et al* 2006).

The receiver operating characteristic (ROC) curve shows the ratio of true positive predictions (cells that are predicted by the model to contain the species and which are shown to do so by the independent or withheld data set) to false positive predictions. This assessment is repeated over different thresholds for presence (the prediction above which the species is deemed to be present). The larger the area under this curve (AUC), the more accurately the model predicts the withheld presence locations. The AUC provides a single measure of model performance independent of any particular choice of threshold. AUC has an intuitive interpretation; the probability that a random positive instance and a random negative instance are correctly classified by the model. An AUC of 0.5 represents a model which correctly classifies presence and absence instances no better than random.

A four-folds cross validation, where the model was run four times, with each run performing the analysis on one subset of the data (called the *training set*), and validating the analysis on the remaining subset (called the *validation set* or *testing set*) performed using AUC. The four folds represented the four distinct study areas, ie subset geographically (which is also temporally). So each survey area was used as a testing set once. This means that the assessment indicates how well the model might perform in predicting to a new, unsampled, area. The AUC calculations were carried out in R version 2.9.0 (R Development Core Team) using package gam version 1.0 (Hastie 2008).

An assessment of the rate of true and false positive predictions, and true and false negative predictions, using the threshold value for ‘presence’ produced from the kappa statistic, was made for all cells which had been surveyed, ie all cells which were used to build the model. This allows an assessment of which type of error the model is more likely to make.

2.4 Boundary delineation - maximum curvature

Initially, three boundary delineation methods were considered. Appendix 4 provides details of two of these methods and assessment of their suitability for delineation of important marine areas for breeding red-throated divers. Maximum curvature (Mel'nikov 1995) is identified in Appendix 4 as being the most appropriate method that is applicable across all sites, and so it was applied to the model outputs presented herein.

Maximum curvature has been used as a boundary delineation method for identifying marine SPAs for inshore waterbirds (O'Brien *et al* 2012); all cells that contained birds in a gridded study area were ranked with respect to bird density. The cumulative number of birds captured by successive numbers of cells and the cumulative number of cells were plotted against each other. Identifying the point of maximum curvature of the resulting graph defines in an objective, formulaic way the point at which adding further cells to an area begins to capture relatively fewer birds within that area. This law of diminishing returns, as it were, may define the threshold density around which a site boundary can be drawn. O'Brien *et al* (2012) identified a marine SPA for wintering red-throated divers in the Outer Thames Estuary using this method. The resulting SPA now protects 78% of the red-throated divers originally estimated to be within the survey area, captured within a boundary that includes only 39% of the study area.

In this inshore example the cumulative number of birds protected by adding the next highest density cell to the site was calculated as each cell was added down to the lowest density cell. At that point the cumulative number of birds captured equaled the total number of birds in the study area. These cumulative values are used by the maximum curvature formula to find the point at which the slope of the relationship between cumulative number of birds and cumulative area changes the most. In the case of breeding red throated divers, however, an alternative metric (to density) was required.

We considered two metrics: the number of nests known to be within foraging range of each cell, and the modelled habitat suitability scores.

The 2006 national survey of red-throated divers (Dillon *et al* 2009) aimed to achieve a complete count of breeding sites in the Northern Isles and two SPAs in the Hebrides (Rum and Mointeach Scadabhaigh), but only a stratified sample of 5-km grid squares in the remainder of the known breeding range. Strata used for selecting sample grid squares were based on overlap with terrestrial SPAs; only 27.8% of cells overlapping SPAs, and 9.3% of cells not overlapping SPAs, were sampled. Data from the 2008-2011 BTO breeding birds atlas were used to supplement the known nest site distribution in the Western Isles. This data-set was also incomplete so the total number of nests within foraging range remains unknown, and is an underestimate for the Western Isles.

The approach taken here is therefore twofold. Where there are complete data on nest site distributions, this is taken into account when delineating boundaries. The nest data are therefore used here in combination with the model predictions of habitat quality in order to delineate boundaries in the Northern Isles and for Rum. This metric to which maximum curvature was applied here was nestsXgam, which is the GAM weighted number of nests within foraging range of a cell. The GAM prediction is a habitat suitability score ranges from 0 to 1, with 0 representing very unsuitable habitat for red-throated divers and 1 representing very suitable habitat for red-throated divers. If we assume that a cell with a GAM prediction of 1 would be used by all nests within foraging range, we can think of this metric as usage; the predicted number of pairs of red-throated divers which would forage in that cell

For all other areas, predicted habitat suitability scores (from 0 to 1) are used to aid boundary delineation.

Maximum curvature was applied to regions; Orkney, Shetland, and the Western Isles. The density of nests varies across these regions, and splitting the data into these regions ensures a geographic spread of important areas identified, and so ecological considerations such as range are not lost. In addition, maximum curvature is sensitive to the size of the area of search, so it is important that this is restricted to the area where the species might be expected to be observed. All maximum curvature analysis was restricted to the cells that have already been selected as containing suitable marine habitat for breeding red-throated divers: they are above the threshold for presence (as determined by kappa) and are within foraging range of at least one known nest site.

The potentially most important marine areas used by breeding red-throated divers were delineated by drawing boundaries around the cells identified by maximum curvature. In each area, the simplest boundary was drawn, along lines of 15 seconds of latitude and longitude (longitude and latitude are used for this stage to align with management as most developers and users of the marine environment will work in WGS1984 rather than OSGB1936). Along the coastline, the boundary was clipped to the high-water polygon

2.5 Expert opinion

In order to increase confidence in the suitability of the areas identified for the Outer Hebrides, given the relative lack of nest census data, expert opinion was sought from ornithologists who know the areas and species well. This approach was applied to all areas considered in this report except for the Isle of Rum, where the analysis was not completed in time to be included in the peer review exercise. In the first stage of what was a two stage approach, ornithologists working in the areas of interest were contacted and sent blank maps, and asked to indicate where, in their opinion, were the ‘most important’ marine areas for foraging red-throated divers during the breeding season. These areas were then overlaid with the boundaries selected using maximum curvature to determine the number of experts who indicated that this area is important. This provided a measure of confidence that the area within this boundary represents an important foraging area.

In the second stage of the peer opinion exercise, the same experts were contacted and provided with maps that showed the boundaries resulting from the nestsXgam threshold chosen by maximum curvature (or the GAM probability threshold for the Western Isles). The local experts were asked to rank each of the areas shown on the map as either ‘very important’, ‘important’ or ‘not important’.

2.6 Regular occurrence

The UK SPA Selection Guidelines advise that possible SPAs are used *regularly* by qualifying species (Stroud *et al* 2001). One of the determinants of regularity of use of the areas identified here was assessed indirectly by using data from two of the three national breeding bird atlas data-sets. Evidence of breeding in tetrads (2x2 m cells) within the foraging range of each boundary is available from two atlas periods - 1988-91 and 2008-11. Data from an earlier atlas period, 1968-1972, were collected only at a coarser 10x10km grid square resolution, and were therefore not used here.

The atlas data can tell us whether or not cells within foraging range of known recent nest sites were within range of breeding territories during the 1988-1991 period. This was used as indirect evidence of regularity in the absence of a finer measure for regularity. The most recent atlas data (2008–2011) has already been used to supplement the known current nest site distribution in the Western Isles.

2.7 Prioritisation of areas identified as important

Maximum curvature produces boundaries that incorporate extensive areas. The data we collected on red throated diver at sea distributions do not allow population sizes to be estimated or regularity of occurrence within boundaries to be determined. As proxies, and to further aid selection of the most suitable areas for possible SPA classification, the important areas within each region of interest were ranked with respect to each of the following attributes:

- average habitat suitability prediction within the boundary;
- potential number of breeding pairs using the area;
- number of breeding territory SPAs within foraging range of the boundary;
- regularity of use; and
- confidence in areas from local experts (peer opinion).

The highest ranking area was given a rank of 1, and the next highest 2, etc. The ranks were then summed across criteria for each region, allowing identification of the highest ranking area(s) (ie those with the lowest summed rank) within each region.

Average habitat suitability was calculated for each area from the original GAM model output. The potential number of breeding pairs of red-throated divers using each area was estimated for the Northern Isles and the isle of Rum, where nest site distribution is known. Outwith these locations, the potential number of pairs is not known Instead ,the number of *known* nests within foraging range using all data sources available (national breeding atlas data 2008-2011, Dillon *et al* 2009, and additional census carried out as part of the work presented here) was used. This should be treated with caution because they might underestimate the number of actual nests within foraging range of some of the important marine areas. The number of breeding territory SPAs within foraging range of the areas identified was assessed by overlaying the boundaries with a map of existing (terrestrial) SPAs. Regularity of use and peer review confidence were assessed as described above.

3 Results

3.1 Results of data collection

3.1.1 Boat surveys

During 11 days of survey over four breeding seasons (2003, 2005, 2006, and 2007) a total of 1450 km of transect was surveyed and a total of 557 red-throated divers was recorded, giving an overall encounter rate of 0.38 birds km^{-1}(Table 4). Surveys covered areas of varying diver density, and encounter rate varied considerably between areas with only 0.16 birds km^{-1} recorded around Yell, Unst and Fetlar in 2003 and 1 bird km^{-1} recorded around the east and north coasts of North Uist in 2007.

Table 4. Numbers of birds recorded during boat-based surveys conducted between 2003 and 2007.

Year	Area	Number of Birds	Total Transect Length (km)	Encounter Rate birds km^{-1}	Number of Days	Transect Method
2003	Yell, Unst, and Fetlar	72	461	0.16	2	Set Distance
2005	Hoy and Scapa Flow	106	358	0.30	3	Set Distance
2006	Most of Shetland coast	422	578	0.73	5	Zigzag
2007	East and north of North Uist	53	53	1.0	1	Set Distance
Totals		557	1450	0.38 (overall)	11	

Using the boat position data (from the GPS) and the range and bearing data, all recorded bird observations were plotted in ArcGIS. Based on the likely error in GPS position (<10m) and rounding errors in the distance and bearing data, it is estimated that all recorded birds were plotted within $100m^2$ of their true location.

A frequency distribution plot of the distances from the boat at which birds were recorded (Figure 9) suggests that some birds may have actively avoided the survey boat, and that observers failed to detect some birds beyond 400-500m. For this reason the numbers recorded probably under represent the total numbers of birds present at the time of the surveys by an unknown degree. As only diver presence or absence data within $1km^2$ grid cells were used in the modelling, it was not necessary to correct for undetected birds.

3.1.2 Flight-line observations

A total of 369 flights from 50 nests was recorded over three breeding seasons (2003, 2005, and 2007). Of these flights, 155 were recorded with sufficient certainty to link a foraging site with a nest site. Of these, 101 were repeat flights between a given nest and given foraging site (i.e. a repeat occurrence of a flight already recorded). Removing repeat flights left 54 unique links between nest sites and foraging sites (Table 5).

Table 5.Visual flight-lines recorded between nests and foraging sites between 2003 and 2007.

Year	Area	Number of Nests	Number of Flights	Number	Number Unique
2003	Unst, and Fetlar	15	75	36	18
2005	Hoy	21	202	85	21
2007	North Uist	14	92	34	15
Totals		50	369	155	54

In addition to foraging flight ranges, the flight observation work also succeeded in recording 182 specific foraging locations for known breeding birds (Table 6).

Table 6.Visual records of birds foraging at sea.

Year	Area	Number of Foraging Observations of breeding birds	Total Number of breeding birds
2003	Unst, and Fetlar	31	36
2005	Hoy	85	85
2007	North Uist	51	61
Totals		167	182

3.1.3 Radio-tracking

Based on days when tags were recorded or observed, tag deployments lasted between 1 and 43 days before tags were removed or stopped functioning. Some tags may have lasted longer than this, but were not recorded beyond this (Table 7).

Estimated (triangulated) and/or visual locations were obtained for 11 of the 18 birds tagged. Twenty-one unique foraging trips were at least partially recorded using a combination of radio-tracking and visual location of tagged birds. Only a single foraging trip was recorded from most tagged birds, but as many as six trips were recorded for one bird. Using the strength and quality of the signals received it was possible to distinguish the behaviour of tagged birds into those flying, swimming/loafing, diving, and at the nest loch.

3.2 Foraging flight ranges

From visual flight observation data, the mean straight line distance (foraging flight ranges) between nest and foraging site for all unique links (between nest locations and foraging sites) over all study areas was 2.9km (SD = 2.1, range = 0.4 – 11.7, n=54). However, the frequency distribution of straight line distances was skewed towards shorter distances and included some much longer flights (Figure 12).

From radio-tracking data, the mean straight line distance (foraging flight ranges) between nest and foraging site (mean location at sea) for all unique foraging trips over all study areas was 4.5km (SD = 1.9, range = 1.2 – 8.9, n=21). The frequency distribution of straight line distances was approximately normal, but skewed slightly towards shorter distances (Figure 11).

The maximum foraging flight range, observed from either visual or radio tracking flight lines is 12km. When data were separated for different study regions this distance was consistent for each region - Shetland, Orkney, and North Uist. The visual flight data has low precision associated, especially in terms of foraging distances for foraging which occurred further from coast. The radio tracking is felt to more accurately capture distance from coast, and hence the foraging distances recorded during radio tracking (9km) was used in latter analysis stages.

Table 7. Numbers of location fixes (telemetry and visual), foraging trips, and days in operation achieved for each tagged bird during the radio-tracking studies in 2004, 2006, and 2007.

Year	Area	Tag	Number Fixes	Number Foraging Trips	Minimum Days in Operation
2004	Mainland Shetland	SA2	9	1	26
2004	Mainland Shetland	SA6	8	2	10
2004	Mainland Shetland	SA7	7	1	11
2004	Mainland Shetland	SA9	7	2	43
2006	Mainland Shetland	SB2	34	3	7
2006	Mainland Shetland	SB5	9	1	1
2006	Mainland Shetland	SB6	318	6	15
2006	Mainland Shetland	SB10	9	2	4
2007	North Uist	U1	10	1	10
2007	North Uist	U4	15	1	7
2007	North Uist	U8	12	1	7
Totals		11	438	21	141

3.3 Foraging area ranges

Recognised A plot of foraging area (the area of sea used during each single foraging trip calculated as Minimum Convex Polygons, MCPs, Mohr 1947) against the number of locations recorded for each single foraging trip suggests that MCP areas were highly dependent upon the number of fixes available. This appeared to be particularly true for MCPs constructed from fewer than 10 locations. MCPs constructed from fewer than 10 locations were therefore excluded from calculations of mean foraging range size, which was 0.79km^2 (SD = 0.74; range = 0.02 – 2.56; n = 11).

3.4 Final model

Using a forward selection of ranked predictors, the final model with the minimal significant deviance was:

P = s(Depth)+s(Dist)+s(Tidal)+s(Wave)+s(Front)+Seds:Coast

Where ***P*** is the global response (probability of occurrence), **s** is a spline smoothing function, ***Depth*** is seabed depth (m), ***Dist*** is distance to coast (km), ***Tidal*** is tidal bed stress (N m^{-2}) (this is a measure of the energy on the seabed attributed to tidal movement of water), ***Wave*** is maximum wave base (m), ***Front*** is probability of thermal fronts (P), and ***Seds:Coast*** is an interaction term combining seabed sediment classes and coastal physiography classes. Using an F test, the relationship between diver presence and each of the selected predictor variables was statistically significant ($p<0.01$). Individual response curves for each of the selected predictor variables are shown in Appendix 3 Figures 9.1 to 9.7. Model predictions (probability of occurrence) are mapped, along with observations from boat surveys, in Figures 12 to 16.

This model explained 33% of the variation in red-throated diver presence/absence for surveyed grid cells. The predictor variables seabed slope (º incline), seabed aspect (º from true north), sea surface temperature (ºC), salinity (%), and stratification (ΔºC surface to seabed) were ranked lowest in importance (highest residual deviances) and were not selected for inclusion within the model.

3.5 Model predictions

The model was used to predict probability of occurrence values for all grid cells in the study area. Predicted probability of occurrence was then reclassified as presence or absence based on a probability threshold of 0.25, selected using Kappa statistic tests (Cohen, 1960) at different probability thresholds. Probability values <0.25 were classified as absence and values ≥ 0.25 were classified as presence. This 0.25 probability threshold gave a Kappa score of 0.44, indicating moderate agreement between observed and predicted values (Landis and Koch, 1977). Presence-absence maps are shown Figures 17 to 21.

3.6 Model validation and evaluation

The average (from cross-validation runs) Area Under the ROC value (AUC), measuring the rate of correctly predicted presences and of incorrectly predicted presences, for a range of probability of occurrence thresholds, is 0.724. This value represents the probability that a randomly chosen presence observation is predicted by the model to have a higher probability of occurrence than a randomly chosen absence observation.

From Table 8 we see that, if we look at the grid cells which had survey effort, there are more cells which had no observation of divers than which had observations, and more predictions of absence than of presence. The rate of true negative prediction is higher than the rate of false negative prediction, and the rate of true positive prediction is higher than the rate of false positive predictions.

Table 8. Number of true and false presence and absence predictions for the surveyed cells. Numbers in brackets are the proportion of total surveyed cells.

	Predicted presence (1) or absence (0)			
Actual presence (1) or absence (0)		1	0	TOTAL
	1	193 (0.21) (true positives)	91 (0.10) (false negative)	284 (0.31)
	0	152 (0.17) (false positive)	475 (0.52) (true negative)	627 (0.69)
	TOTAL	345 (0.38)	566 (0.62)	

3.7 Constraining the model

The model predicted a high probability of diver presence in some areas far from breeding territories where no divers would be expected (based on maximum foraging flight distances for breeding individuals) during the breeding season. These were areas which, although ostensibly suitable according to the model, where perhaps unmodelled attributes of the habitat were unsuitable or, more prosaically, simply outside the breeding range of the species. During the breeding season, the distribution of breeding divers at sea is constrained by the location of the breeding territories, the maximum foraging flight range, and the size of the typical foraging area.

Model predictions were similarly constrained. The maximum typical flight range as determined from visual and radio- tracking studies was 9km, and the approximate size of a typical foraging area was 1km^2. These two added together represent a distance from the nest beyond which we do not expect breeding red-throated divers to travel for foraging purposes. Thus model predictions beyond 10km from a breeding territory were discarded from further study. Those breeding sites recorded during the 2006 national survey (Dillon *et al* in press.), plus additional breeding sites recorded during this study, plus grid cells which had recorded breeding red-throated divers during the 2008–2011 survey period for the BTO breeding bird atlas series were used to represent breeding territories in this selection.

The constrained selection of 1km^2 grid cells with predicted diver presence (ie gam predictions above 0.25) represented those cells that were predicted to be used by foraging red-throated divers during the breeding season, particularly breeding birds during the chick rearing period. These areas which are predicted as ‘used by breeding divers’ are mapped, along with diver observations from the boat transect surveys, in Figures 22 to 26.

3.8 Numbers of breeding pairs within foraging range of important areas

The number of red-throated diver pairs breeding within the foraging range (10 km radius) of each GAM prediction grid cell; that is, the number of pairs that potentially make use of that area for foraging, was calculated).

Large areas around the main concentrations of breeding territories are potentially used by 12 or more breeding pairs (1% of the British breeding population; Dillon *et al* 2009), while some areas around the more northerly islands of Shetland are potentially used by 71 or more breeding pairs (1% of the biogeographic population; Hagemeijer and Blair, 1997).

If we assume the model output relates directly to probability of presence of red-throated divers (the number is likely to be more accurately interpreted as a relative probability rather than absolute, because the absolute values will depend on turnover rate of feeding divers and survey effort amongst other factors) then we can say that the predicted probability of presence multiplied by the number of nests within range of a grid cell is a representation of likely usage of that cell. This would mean that a grid cell in range of, say ten nests, and with a predicted probability of usage of 1 would actually be used by all ten pairs of divers within range of that cell. This nests within range multiplied by relative predicted probability of usage value is called nestsXgam and is a relative measure of usage for each grid cell within foraging range of any known nest sites.

3.9 Maximum curvature

3.9.1 Northern Isles and Rum

Maximum curvature was applied to nestsXgam to identify the threshold above which cells should be selected for inclusion within possible marine SPA boundaries for breeding red throated divers. The curve of cumulative nestsXgam value against cumulative area for Shetland is shown in Figure 27.

Figure 28 shows that the point of maximum curvature corresponds to a cumulative nestsXgam of 13,217. The value of nestsXgam at this point was 23.4 Cells with a nestsXgam value of 23.4 or higher, ie those above the threshold identified by maximum curvature for Shetland, are shown in Figure 29.

The same method applied to the Orkney islands shows that the point of maximum curvature corresponds to a cumulative nestsXgam of 1,435.5. The nestsXgam at this point was 3.9. Plots are displayed in Appendix 4. These cells selected by maximum curvature are shown in Figure 30.

The same method applied to the isle of Rum gives a point of maximum curvature at a nestsXgam value of 1.40.

No boundary delineation was attempted for Mainland Scotland because only two isolated cells were deemed as ‘presence’ by the model predictions in the waters around Caithness and Sutherland the main nesting area on mainland Scotland).

3.9.2 Northern mainland Scotland and the Outer Hebrides

Nest site distribution data are incomplete for the Caithness and Sutherland Peatlands, with known nests being widely dispersed. In addition, habitat suitability predictions here are mostly very low, with only a few, dispersed cells predicted to be suitable. Consequently, given the relatively few available data and the analyses thereof, we judged that it would not be appropriate to determine boundaries of potentially important marine areas for red-throated divers adjacent to the Caithness and Sutherland Peatlands SPA.

There are also no complete nest site distribution data for the Outer Hebrides, but a slightly different approach to identifying important marine areas was possible here. In the absence of complete nest site distribution data, the distribution of the most important breeding territories, that is breeding SPA locations, provided a focus for application of the modelling approach. So maximum curvature was applied to the habitat suitability predictions for the Outer Hebrides areas of interest. This resulted in a predicted habitat suitability score (from the GAM models) of 0.3254 at the point of maximum curvature (shown in Figures 31 and 32).

Boundaries were drawn around the cells exceeding the thresholds (nestsXgam or predicted habitat suitability scores). These are shown in Figures 33 to 37.

3.10 Expert Opinion

At least three experts from each of the areas of interest were asked to indicate which marine areas they thought were important foraging areas for breeding red-throated divers, on blank maps provided to them. We received no response from Orkney, one from Shetland, one from the Uists, and two from Lewis and Harris. The areas identified by the experts were overlaid with the boundaries selected using maximum curvature to determine the number of experts who agreed the importance of each area predicted to be so by the models (Figures 38 to 42). This served as a measure of confidence of the model-assigned importance of each foraging area.

In addition to the important areas identified by the gam model and maximum curvature, some additional areas in the southern and eastern parts of Shetland, and a few small additional areas along the coast of the northern half of Lewis, were suggested by experts, but none of these met the maximum curvature threshold and so are not shown. Given that we are interested at this stage primarily in finding support for the areas identified by our analysis, it was not deemed appropriate to consider possible additional areas (ie areas not identified by our analysis of the data) at this stage.

The second stage of peer review attracted a similar response rate as the first stage; three responses were received from Shetland, one from Orkney, and none from the Outer Hebrides. The responses were of limited use in allowing a quantitative assessment of confidence in the boundaries as the experts chose not to rank the areas according to importance, and instead provided only a vague indication of where they thought additional important areas might be, and that all of the boundary areas presented were ‘important’. The second stage of the peer review exercise is not presented here.

3.11 Site prioritisation

Figures 39 to 62 show the boundaries colour-coded for each of the criteria listed above (Methods: prioritisation). Figures 63 to 67 show the overall combined ranks.

The ranking exercise applied equal weighting to all criteria in order to be as objective as possible. However, given that the total number of nest sites within foraging range of cells in the Western Isles is not known, the exercise was also carried out applying the criterion *number of nests within range* a weight of only half of that of all other criteria. This resulted in the same boundaries being ranked highest, though the two joint highest ranks in Lewis become split into 1st and 2nd highest ranking. The same occurs in the Uists.

One of the criteria is *number of breeding territory SPAs within foraging range* (Figures 53 to 57). Table 9 looks at this the other way around, and shows how many areas have been delineated within foraging range of each breeding territory SPA. This shows coherence between the terrestrial suite and a possible marine suite of SPAs for this species, if the latter were to be based on these analyses.

Table 9. Red-throated diver breeding territory SPAs, change in numbers between 2001 and 2009, and number of boundaries presented in this report that are within foraging range.

Location	SPA	Breeding numbers. Stroud *et al* 2001	Breeding numbers. Dillon *et al* 2009	Change in numbers within SPA mid 1990's-2006	Number of boundaries within foraging range
Shetland	Otterswick and Graveland	27	23	-4	4
Shetland	Foula	11	8	-3	0
Shetland	Hermaness, Saxa Vord and Valla Field	28	22	-6	3
Shetland	Ronas Hill – North Roe and Tingon	50	50	0	5
Orkney	Hoy	56	46	-10	3
Orkney	Orkney Mainland Moors	15	24	+9	3
Outer Hebrides	Mointeach Scadabhaigh	48	17	-31	6
Outer Hebrides	Lewis Peatlands	60	80	+20	7
Rum	Rum	11	13	+2	4
Mainland	Caithness and Sutherland Peatlands	89	46	-43	0

4 Discussion

We adopted a modelling approach to identifying those marine areas that are potentially important for red-throated divers during the breeding season, particularly breeding birds. We collected data on foraging ranges and on the use of inshore areas by red-throated divers, and used these to build a model of suitable habitat for the species, and to predict which are the important marine areas for all birds associated with breeding territories during the breeding season (i.e. both breeding birds and prospecting non-breeders) in Scotland. The relative importance of these areas with respect to numbers of birds that potentially use them was also assessed. This work aims to inform any further consideration of these important marine areas for the species as possible marine SPAs.

This study has applied and developed new methods for studying the behaviour and distribution of red-throated divers including at-sea survey methods, visual tracking of birds during foraging flights, and radio-tracking. This combination of methods over five breeding seasons in four study areas enabled a generic approach to the identification of important areas, some of which might be suitable for consideration as possible SPAs.

4.1 At-sea distribution

During boat surveys, the largest concentrations of red-throated divers were recorded within shallow and sheltered bays, sea lochs and sounds. No similar surveys have previously been made of red-throated diver distribution at sea during the breeding season, but where the species' foraging habits have been studied (e.g. Reimchen and Douglas, 1948) the species has used similar shallow and sheltered areas. The survey design used in this study aimed to maximise power of the model to define habitat preferences, but this leads to a risk of bias in the pattern of environments sampled. Although preliminary investigations suggested a broad range of environments was sampled during the survey, an ideal survey design would include some sampling of a broader range of possible foraging areas before focusing on the core areas to maximise model power.

The collection of distance and angle data during the surveys allowed the location of birds to be plotted within $100m^2$ of their true location (often much closer). Any error was well within the resolution of the model grid cells ($1km^2$) and allowed bird observations to be linked to local environmental variables with a sufficiently high degree of confidence.

4.2 Foraging flight range

The maximum foraging flight range (the straight-line distance between nest and foraging site) was 9km. This distance was consistent between regions and is unlikely to be a recording artefact as it was well within the maximum range of the tag signal reception (20km). This distance was also consistent for each study area - Shetland, Orkney, and North Uist.

A flight range of 9km is also consistent with the few previous observations of red-throated diver foraging range. Eriksson *et al* (1989) found that birds nesting more than 12km inland in south-west Sweden flew up to a maximum of 8.1km to forage in freshwater lakes, and Eberl and Picman (1993) have shown that chick rearing success in red-throated divers nesting in Arctic Canada was significantly lower for nests further than 9km from the sea.

4.3 Foraging area requirements

The mean recorded foraging area (the area of water used by a foraging bird in a single foraging trip) was small, only $0.79km^2$. However, it is likely that too few data were available from the radio-tracking study to allow a robust assessment of foraging area size. The maximum foraging area of $2.56km^2$ was recorded for the tagged bird for which by far the most data were recorded (318 location fixes during six foraging trips). $2.5km^2$ may be more representative of the typical foraging area required during a single trip; the total area covered by these six trips was $7.3km^2$. This may be more representative of the typical foraging area required for a single bird during the breeding season.

Assuming that the range of recorded foraging areas ($0.02 – 2.56km^2$) was representative of the range over which birds forage during a single trip, $1km^2$ may be considered as a suitable grid cell size for modelling, allowing discrete areas such as individual sea lochs and bays to be identified either as important or unimportant.

4.4 Analysis and modelling

Using a forward selection of ranked predictors, the final model with the minimal significant deviance incorporated seabed depth, distance to coast, tidal bed stress, maximum wave base, probability of fronts, seabed sediment categories, and coastal physiography categories as predictor variables. The survey design sampled a broad range of environmental variables, but it should be noted that predictions were made beyond the range of those sampled for distance to coast, and so there may be lower confidence in predictions beyond the 4.75km from coast sampled. This might have a larger effect on final boundaries for the Western Isles given the heavier reliance on the GAM predictions there (ie the effect is not diluted by scaling to number of nests within foraging range).

The model took no account of survey effort beyond including only cells which had some survey effort. Although survey effort might be less important when we are looking at predictions of presence/absence rather than density, it will still have a bearing on the likelihood of having observed at least one diver, and hence may have an influence on model parameterisation. Effort is linked with detection and no attempt was made to look at detection as a function of distance (perpendicular) to the transect line. Although 'un-detection' is not expected to vary spatially along the transect line, it is highest the further a grid-cell is perpendicularly from the transect line, thus compounding the issue of lack of effort in those grid cells through which a transect did not pass directly.

This model explained 33% of the variation in red-throated diver probability of occurrence for surveyed grid cells. Morrison *et al* (2006) suggest that wildlife-habitat models typically explain around a 30-50% of the variation in species distributions. Peak *et al* (2003) suggested that ecological models may typically explain roughly half of the variation in variables of interest. The performance of this model may therefore be considered to be good given the scale and generic scope of the model, incorporating bird data from surveys across the UK breeding range and environmental data from various sources with differing temporal and spatial scales.

From Table 10 we see that although the model makes more predictions of presence than of absence at the chosen threshold for presence, the surveyed grid cells have a higher proportion of absence observations than the predictions. This could be seen as precautionary from a conservation perspective.

But this describes how well the model explains the data used to build the data, and says nothing about how well the model might predict to other areas/independent observations. The AUC value is a more appropriate measure of how well the model might perform in this sense. The AUC value of 0.724 suggests good model performance in terms of predictive ability, comparing well with AUC of published models (Table 11). An AUC of 0.5 represents a model that predicts no better than a random distribution; more than 0.5 is an improvement on a random distribution.

Table 10. Area under ROC curve (AUC) of published habitat suitability models.

Species	Method	AUC	Validation basis	Reference
Brown-throated sloth (*Bradypus variegatus*)	Maximum Entropy (Maxent)	0.819 – 0.919	Resampling	Phillips *et al* 2006
Seven priority species in New South Wales, Australia	GAM	0.61 – 0.85	Resampling	Wintle *et al* 2005
Mean over up to 226 species	Range of methods used	0.54 - 0.82 (range of mean AUC over all species for different modelling methods)	Independent data	Elith *et al* 2006
Hen harrier (*Circus cyaneus*).	GAM	0.503-0.930	Independent data	Anderson *et al* 2009

Before being constrained by foraging flight distance the model predicted a high probability of occurrence (and therefore presence of divers) in some areas far from breeding territories, out-with foraging range of breeding territories. These were areas where, according to the model, the marine environmental conditions/habitats were suitable for foraging divers. During the breeding season, the distribution of breeding divers at sea is constrained by the location and availability of suitable breeding territories and the maximum foraging flight range of breeding birds.

While the visual validation of the model with foraging location data not used in the model is rather coarse, it allows an assessment to be made as to whether the model predictions include those areas used by known breeding birds (visually- or radio- tracked birds), providing confidence that the model is capable of identifying important areas used by breeding birds for foraging. The method does not allow an assessment of the extent to which the model predicts areas not used by breeding birds because the geographic scope of the visual and radio- tracking is limited to those areas used only by the focal birds.

4.5 Constraining the model by foraging flight range

Given the consistently observed maximum foraging range (9km) for breeding red-throated divers during this study, the distribution of breeding birds in the UK is highly likely to be constrained to within a similar distance from potential foraging areas. In addition to the 9km foraging flight range, the foraging area covered by a foraging bird on the sea may extend the total distance from the nest by at least a further 1km. A total foraging range of 10km from the nest/breeding territory was therefore selected by which to constrain model predictions.

The constrained model predictions given here (Figures 22 to 26) are based on model-selected cells within 10km of all breeding sites recorded during the 2006 national survey (Dillon *et al* 2009) and all additional sites recorded during this study. Given the possible changes in the distribution of birds within the current SPA suite highlighted in Dillon *et al* (2009), the appeal of this approach is that it allows important areas to be identified based on the most up-to-date information on breeding distribution.

4.6 Numbers of breeding pairs within foraging range of important areas

The technique described for counting the number of breeding pairs within typical foraging range of each model prediction cell is a robust and objective method for selecting possible sites under stage 1.1 of the UK SPA guidelines around Shetland and Orkney, where there was complete survey coverage in the 2006 national survey of breeding sites. It should be noted though that the method estimates the number of birds potentially using the area, rather than the number of birds definitely using the area. The latter is difficult to estimate because of the continual turnover of birds within inshore areas.

While the method works well in the Northern Isles, it does indicate that virtually all of the areas identified as important diver habitat are used potentially by at least 1% of the GB population; the bays at the south end of the mainland are the main exception. Shetland is clearly the most important breeding area for the species in the UK, and while there are many nationally important areas, a judgement needs to be made on which are the most suitable for further consideration. Outwith the Northern Isles and the SPAs of North Uist and Rum, survey coverage of breeding locations was not complete; only a stratified sample of 5km squares was surveyed.

Nevertheless, outwith the Northern Isles, the method does identify several areas around each of the breeding territory SPAs as the most important local inshore areas for divers nesting within those SPAs.

4.7 Boundary delineation and site selection

Maximum curvature has identified thresholds of nestXgam values (a proxy for potential usage) or of GAM predicted habitat suitability for use in identifying the most important feeding areas of breeding red-throated divers. Such analyses would be helpful in any future consideration of possible red-throated diver marine SPAs and their boundary delineation for all areas of interest (the Northern Isles, Outer Hebrides, and Rum). Together, these boundaries identify marine areas that are within the species' foraging range of eight out of the 10 breeding territory SPAs as well as other breeding territories that are not SPAs and where nest densities are relatively high.

This exercise has identified four areas around Orkney totalling 237.54km^2, ten around Shetland totalling 246.58km^2, four around Rum totalling 103.72km^2, eight around Lewis and Harris totalling 323.65km^2, and ten areas around North Uist, South Uist and Benbecula (Uist) totalling 71.98km^2.

The two breeding territory SPAs for which no associated marine areas were identified are Foula (Shetland) and Caithness and Sutherland Peatlands (Scottish mainland). Delineating important areas for the latter of these was deemed inappropriate because of the dispersed nature of both the nest sites within this SPA and of the marine grid cells deemed as 'suitable habitat' (there were only two grid cells classed as suitable around Caithness and Sutherland waters). Foula appears to have surrounding marine areas that are of low habitat suitability compared with other areas. The reasons for the low predictions of habitat suitability around Foula are not clear. It could be because:

- the model is not appropriate for making predictions around Foula, a small exposed island whose surrounding marine habitats might be quite different from the rather more sheltered bays and voes elsewhere in Shetland;

- in order to reach good foraging areas birds nesting on Foula travel further than the 10km maximum foraging range recorded. To reach one of the identified boundaries, they would need to travel at least 30km; and/or

- birds nesting on Foula forage in sub-optimal habitat because that is what is available.

The number of nests on Foula is low compared with some other parts of Shetland (there are 12 nest sites on Foula) but as a breeding territory SPA this area has already been identified as important. Given that some of the birds breeding at nest sites within the Caithness and Sutherland Pealtands SPA would have to travel 28 km to reach marine waters, and 30km to reach marine waters that are suitable foraging habitat according to the model, it is likely that birds would indeed fly 30km if necessary. The boundaries presented here might therefore include important marine areas for birds nesting on Foula. Further data collection might help in identifying the important foraging areas for birds breeding on Foula and in Caithness and Sutherland.

The ranking exercise indicates the highest ranking site for each region of interest, both overall, and for particular criterion of interest. The ranks are not sensitive to the weighting applied to the ‘number of nests within foraging range’ criterion (which has considerable uncertainty attached in the Western Isles); this reassures us that this criterion is not determining the overall ranks. Other weighting rules could be considered but this would be quite subjective, and it was for this reason that a formal multi-criteria analysis was not undertaken instead of a simple ranking exercise.

The final stages of selecting which, if any, of the boundaries presented here might be suitable for SPA definition might be based on judgments informed by the analyses presented. However, it is worth noting that, if areas for multi-species assemblages are a priority, there are other conservation planning tools; for example Marxan (used for MPA location in European waters, Smith *et al* 2009) or Zonation (Leathwick *et al* 2008, Moilanen *et al* 2005). Further investigation of the applicability of these might be merited.

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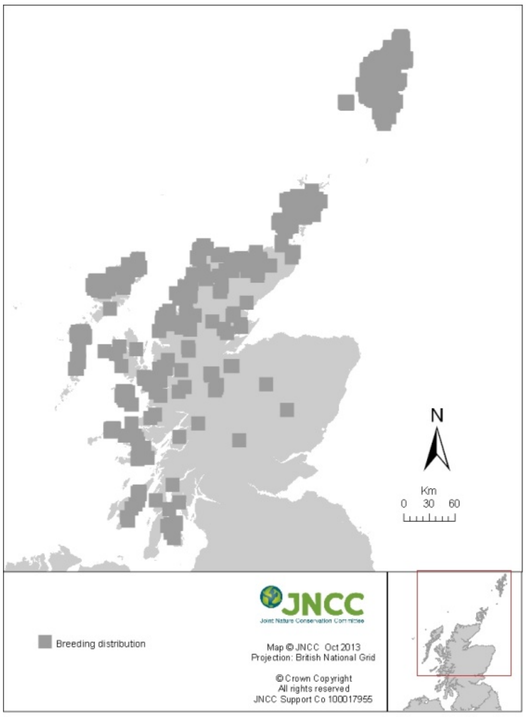


Figure 1. Breeding distribution of red-throated divers in Scotland

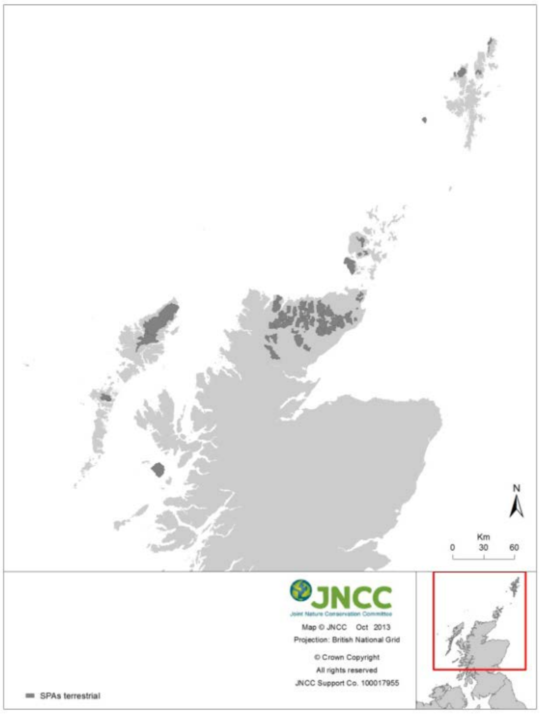


Figure 2. Terrestrial, breeding territory, SPAs for red-throated diver

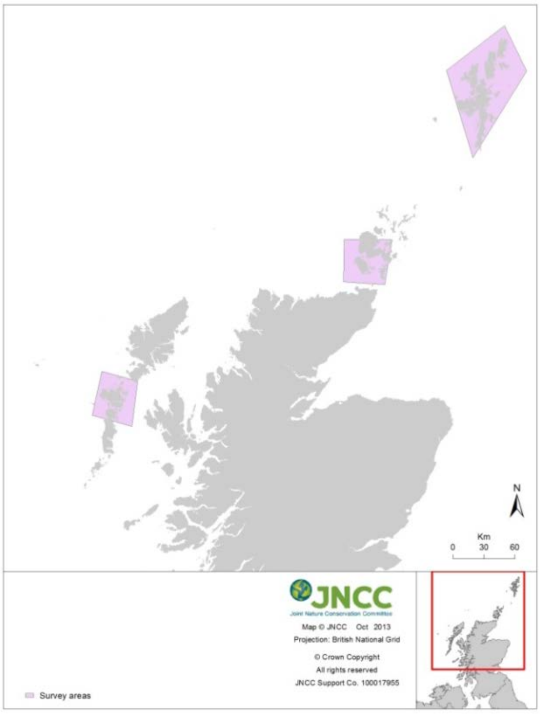


Figure 3. Study areas (survey)

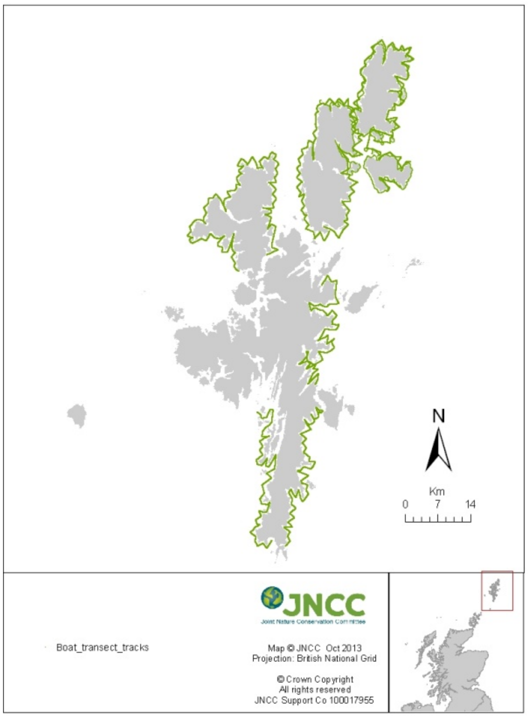


Figure 4. Boat transect route, Shetland

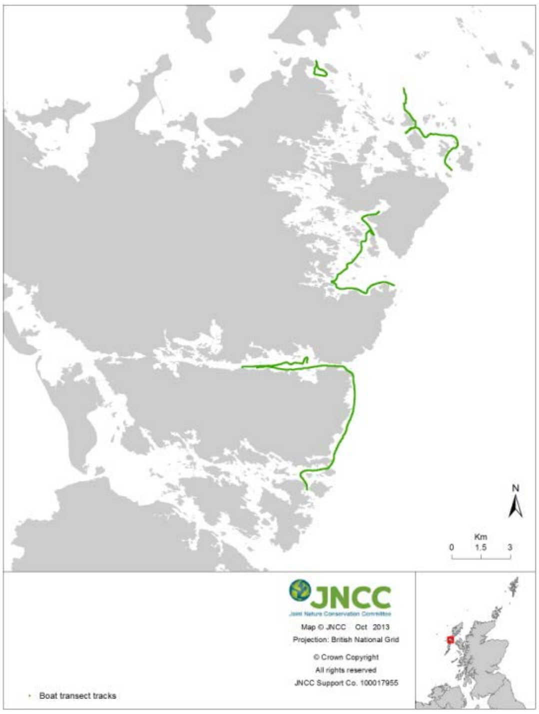


Figure 5. Boat transect route, Uist

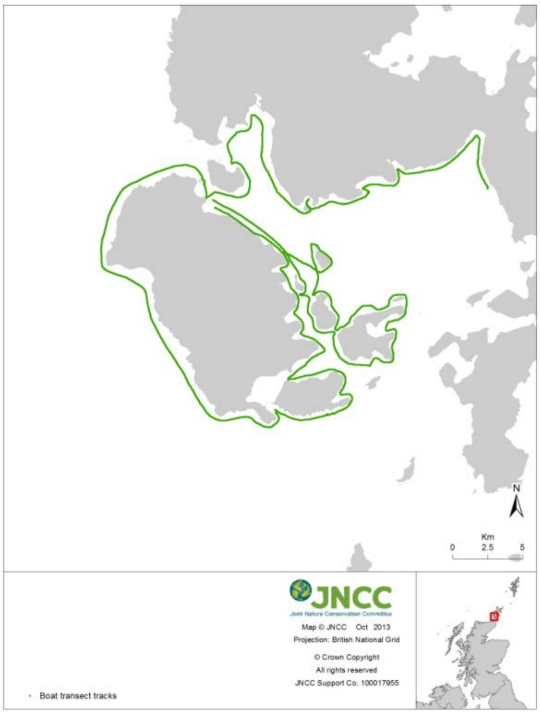


Figure 6. Boat transect route, Orkney

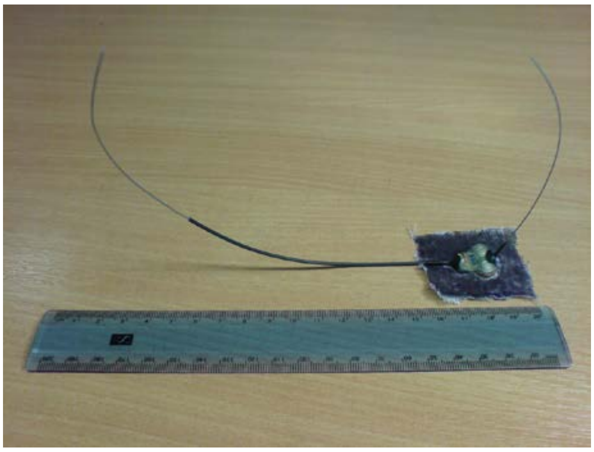


Figure 7. Radio tracking tag with antennae ready to attach to bird, with a ruler to show scale and size.

Figure 8. Attachment of radio tag to bird

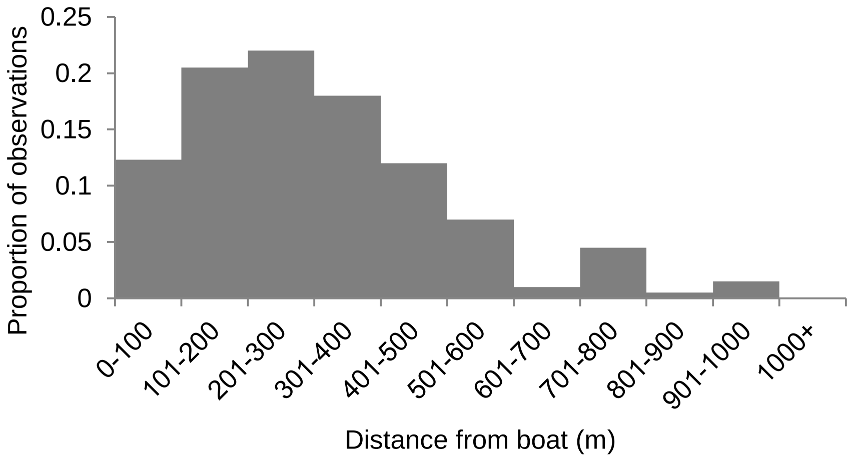


Figure 9. Histogram of distance from boat at which birds were observed

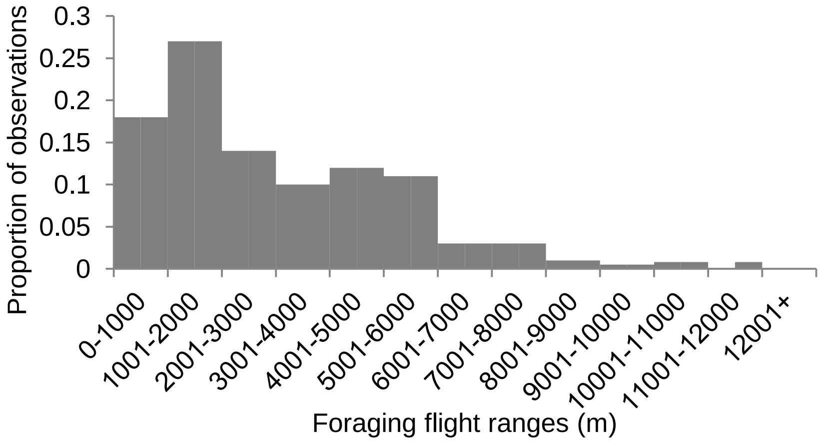


Figure 10. Histogram of straight line foraging flight ranges obtained from visual foraging flight observations

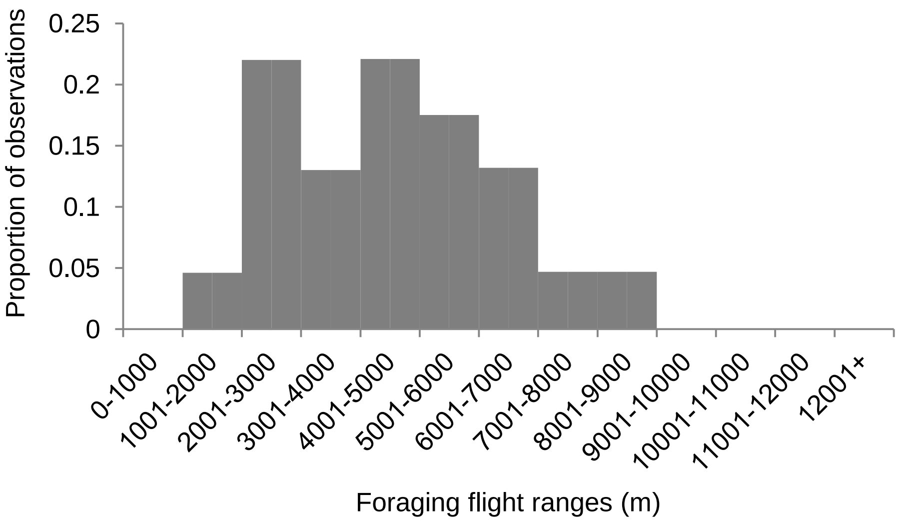


Figure 11. Histogram of straight line foraging flight ranges obtained from radio tracking

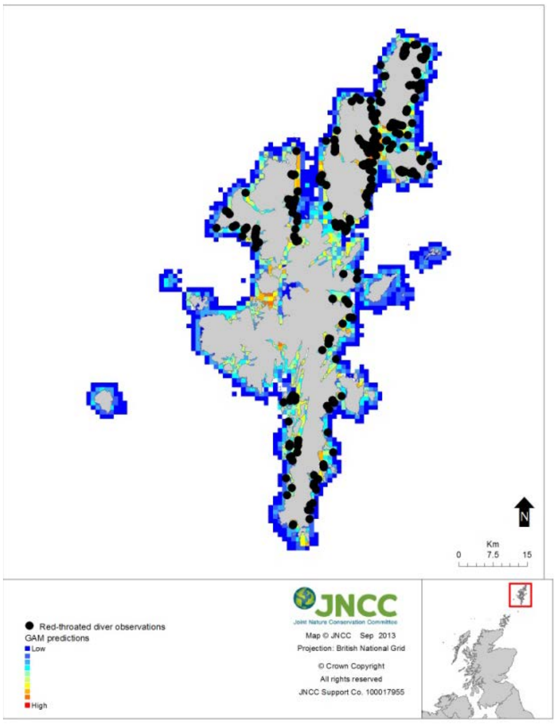


Figure 12. Model predictions, with observations, Shetland

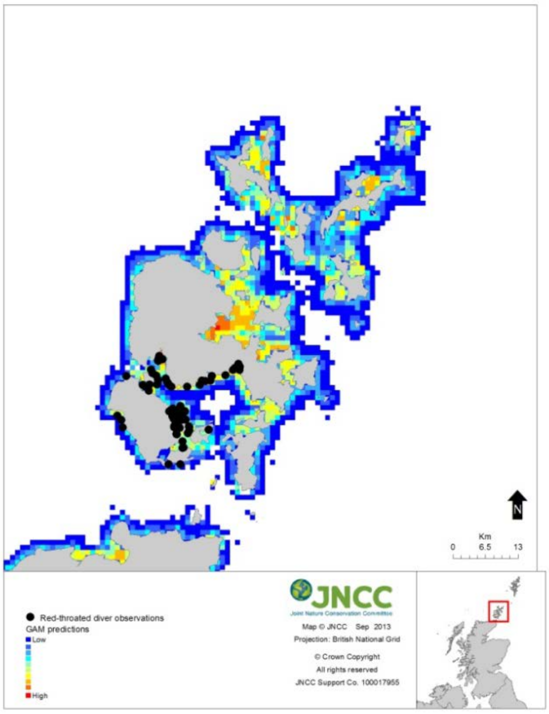


Figure 13. Model predictions, with observations, Orkney

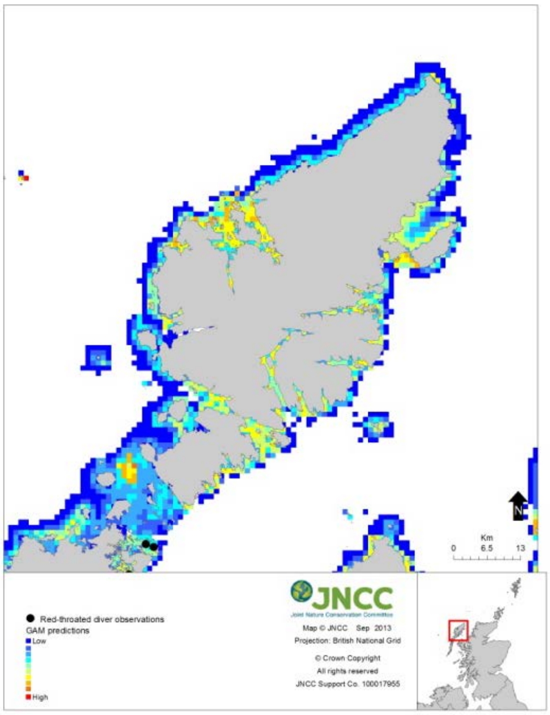


Figure 14. Model predictions, with observations, Lewis

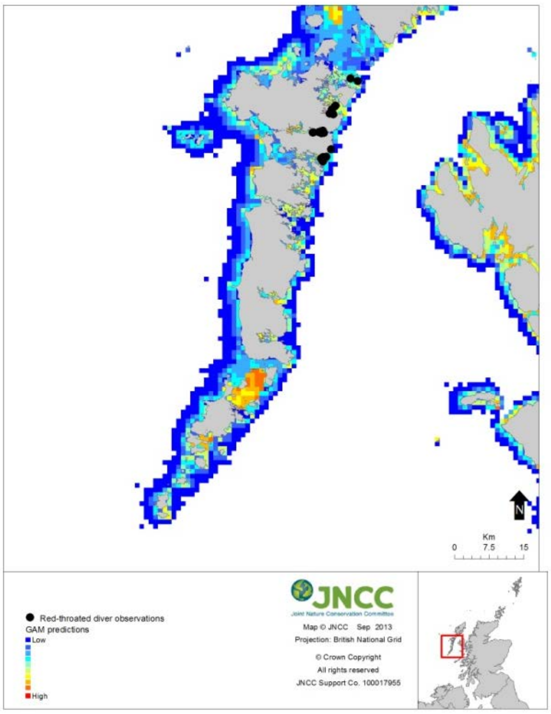


Figure 15. Model predictions, with observations, Uist

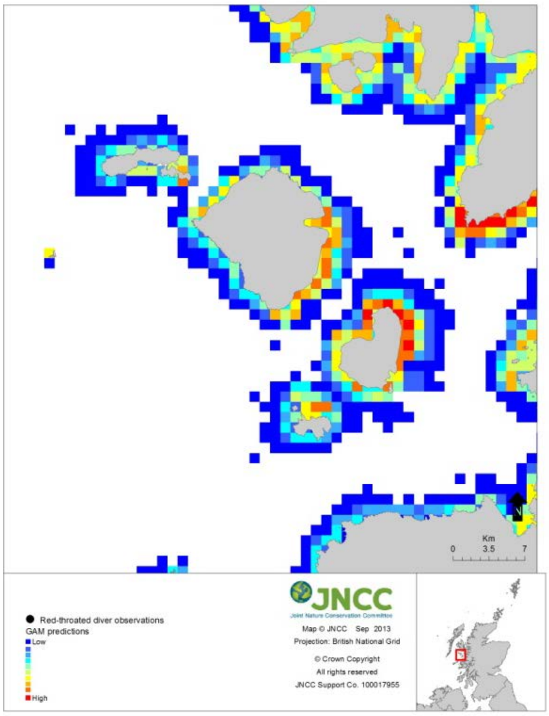


Figure 16. Model predictions, with observations, Rum

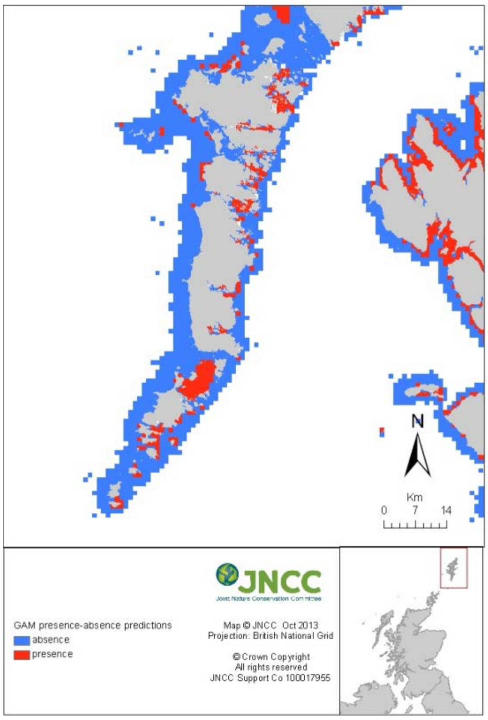


Figure 17. Presence absence predictions, Uist

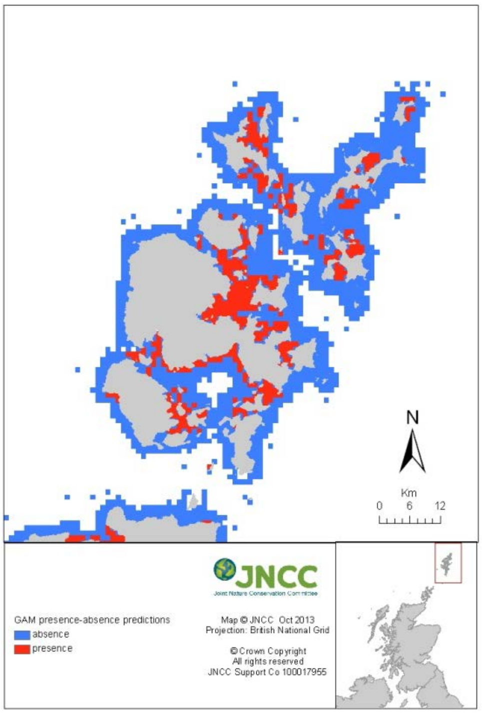


Figure 18. Presence absence predictions, Orkney

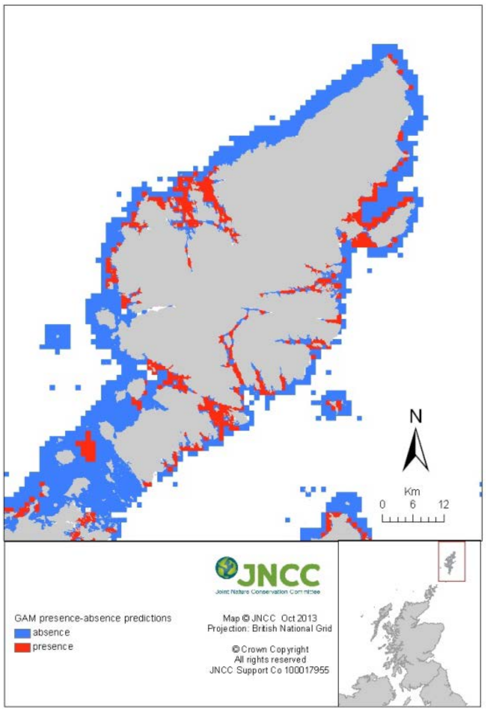


Figure 19. Presence absence predictions, Lewis

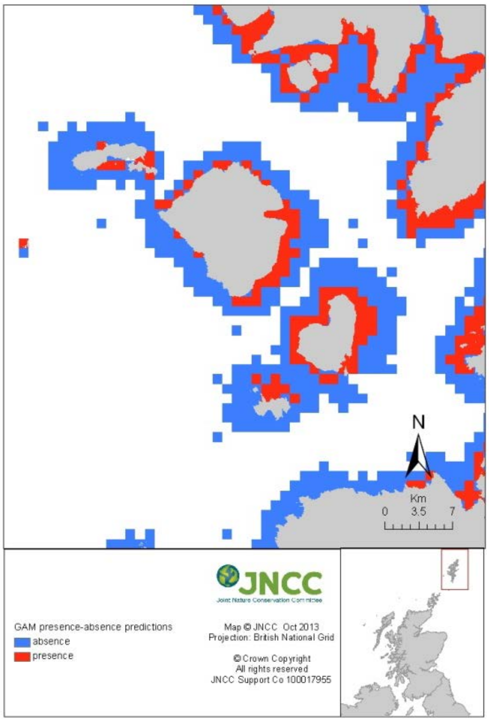


Figure 20. Presence absence predictions, Rum

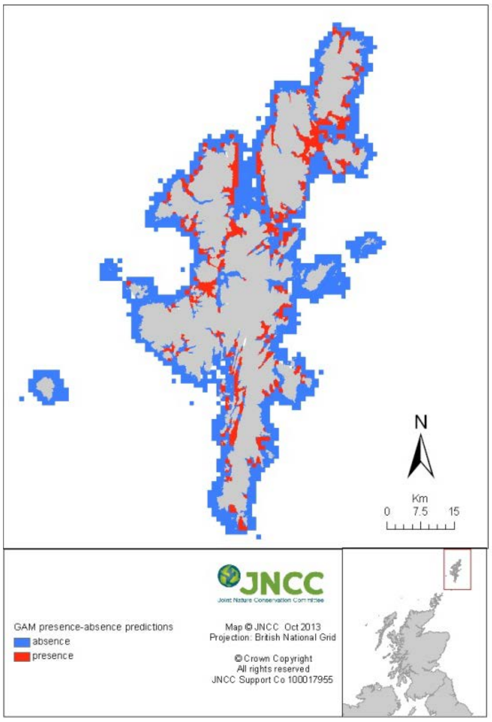


Figure 21. Presence absence predictions, Shetland

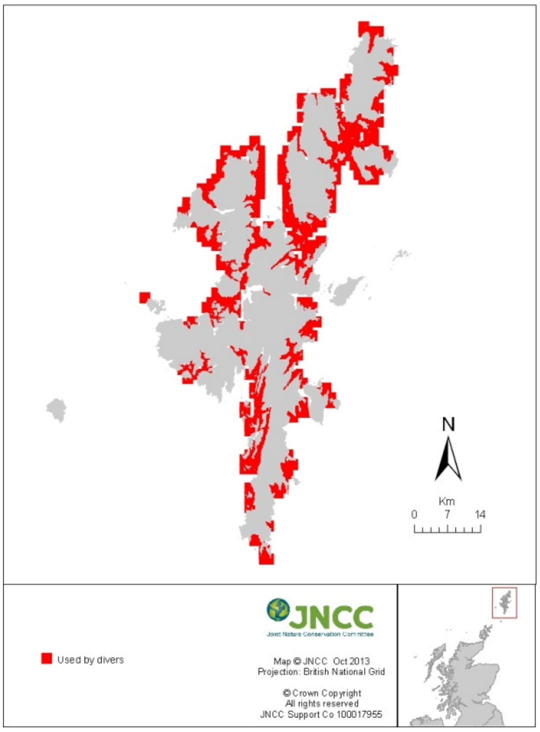


Figure 22. Cells predicted as used by foraging breeding red-throated divers, Shetland

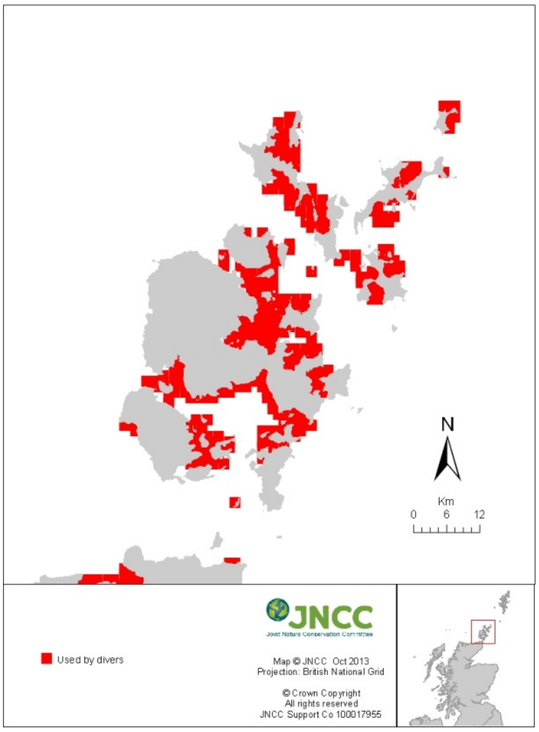


Figure 23. Cells predicted as used by foraging breeding red-throated divers, Orkney

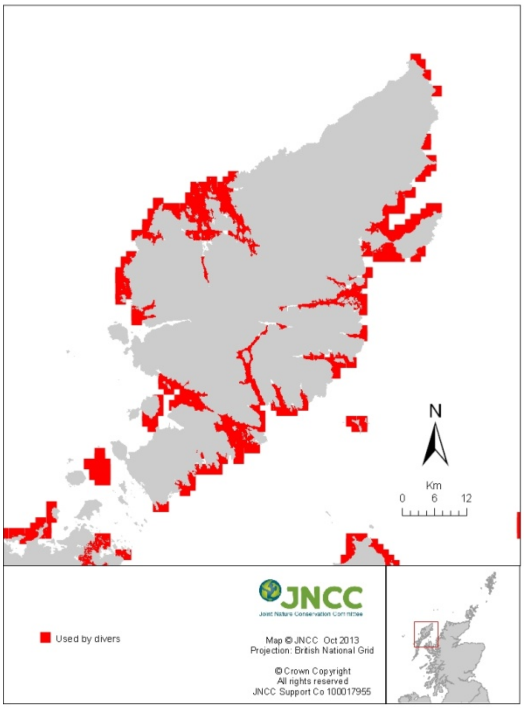


Figure 24. Cells predicted as used by foraging breeding red-throated divers, Lewis and Harris

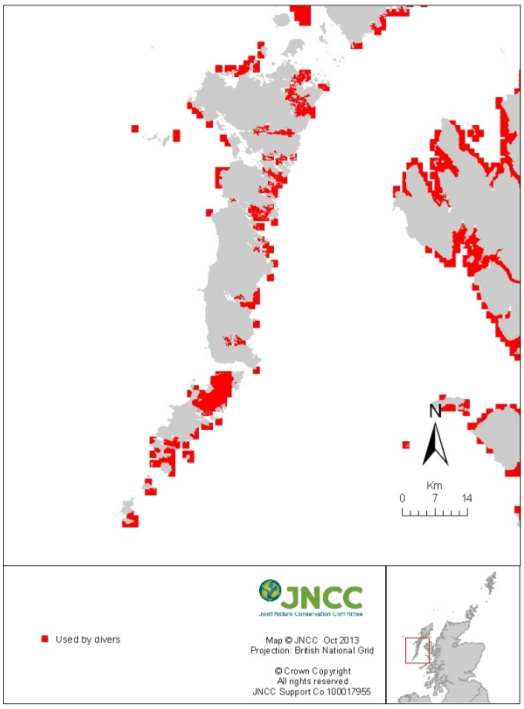


Figure 25. Cells predicted as used by foraging breeding red-throated divers, Uist

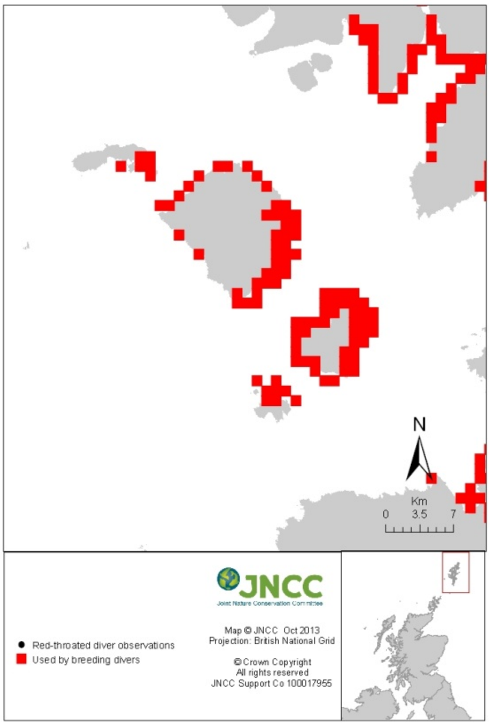


Figure 26. Cells predicted as used by foraging breeding red-throated divers, Rum

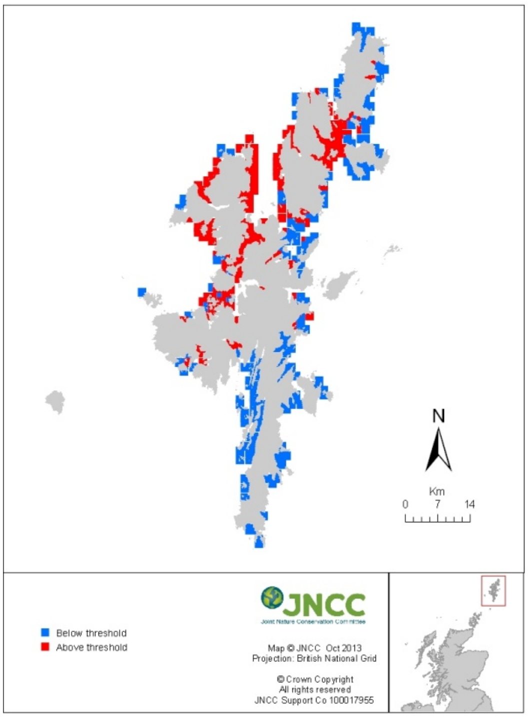


Figure 29. Cells exceeding maximum curvature threshold, Shetland

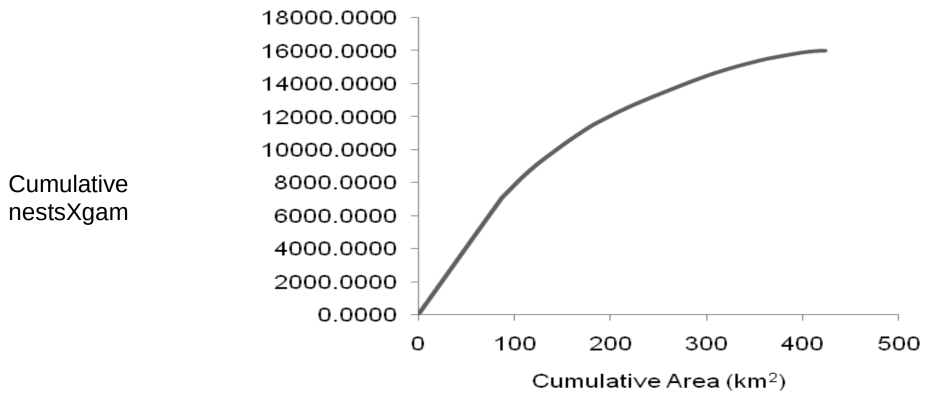


Figure 27. Cumulative nestsXgam against cumulative area, Shetland

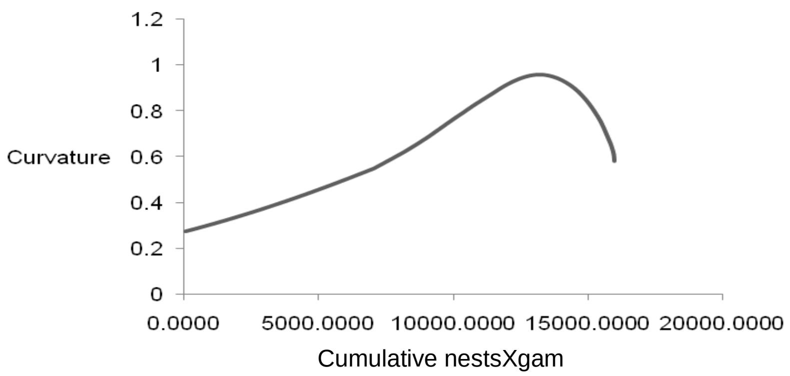


Figure 28. Curvature against cumulative nestsXgam, Shetland

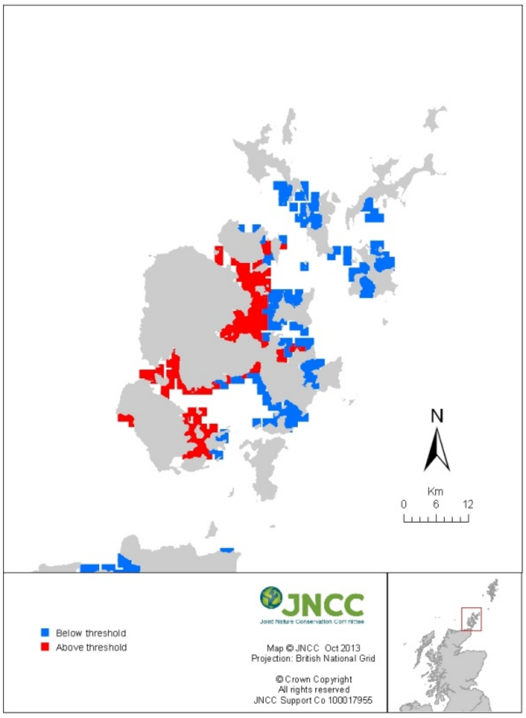


Figure 30. Cells exceeding maximum curvature threshold, Orkney

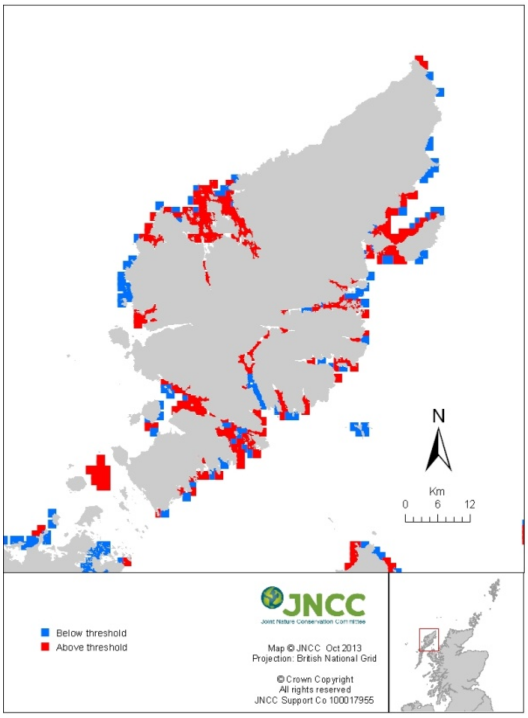


Figure 31. Cells exceeding maximum curvature threshold, Lewis and Harris

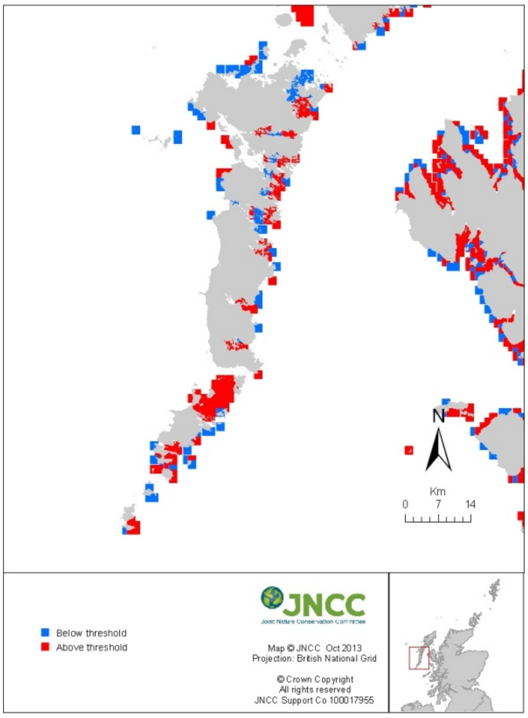


Figure 32. Cells exceeding maximum curvature threshold, Uists

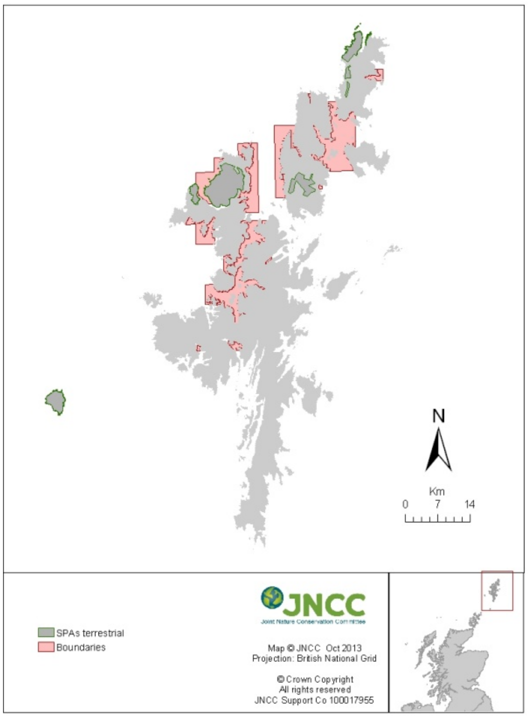


Figure 33. Boundaries drawn around cells exceeding maximum curvature threshold for nestXgam, Shetland. Terrestrial breeding territory SPAs for the species also shown

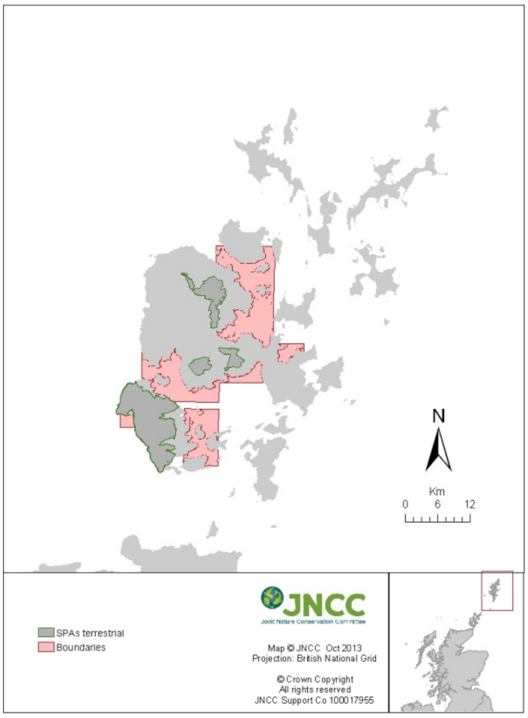


Figure 34. Boundaries drawn around cells exceeding maximum curvature threshold for nestXgam, Orkney. Terrestrial breeding territory SPAs for the species also shown

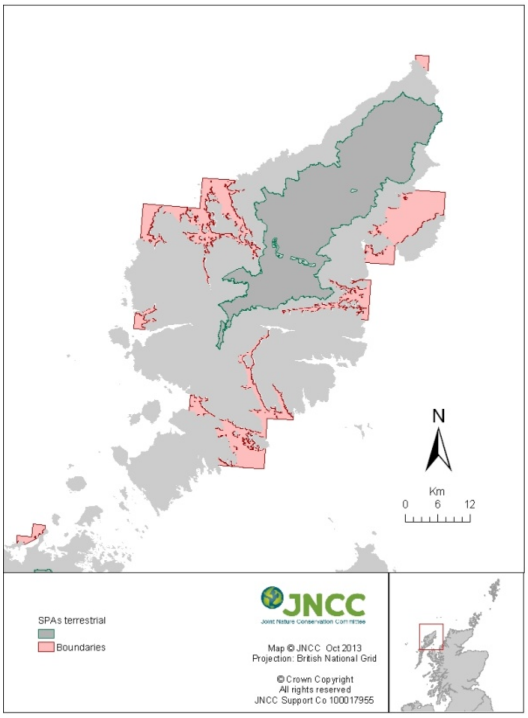


Figure 35. Boundaries drawn around cells exceeding maximum curvature threshold for gam predictions, Lewis and Harris. Terrestrial breeding territory SPAs for the species also shown.

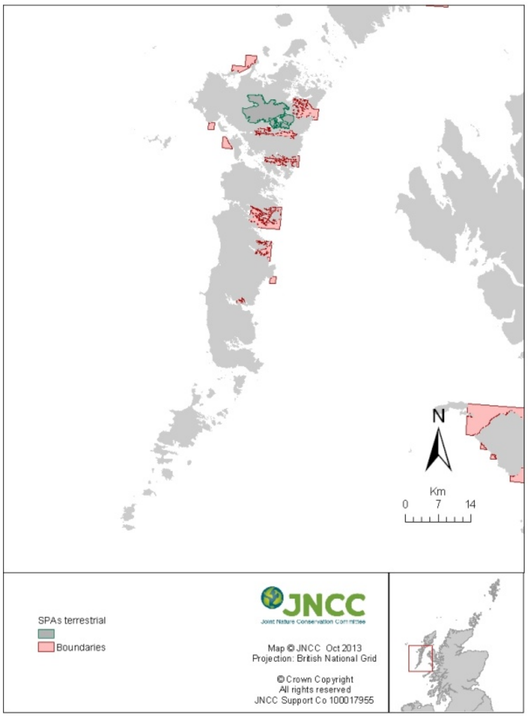


Figure 36. Boundaries drawn around cells exceeding maximum curvature threshold for gam predictions, Uists. Terrestrial breeding territory SPAs for the species also shown.

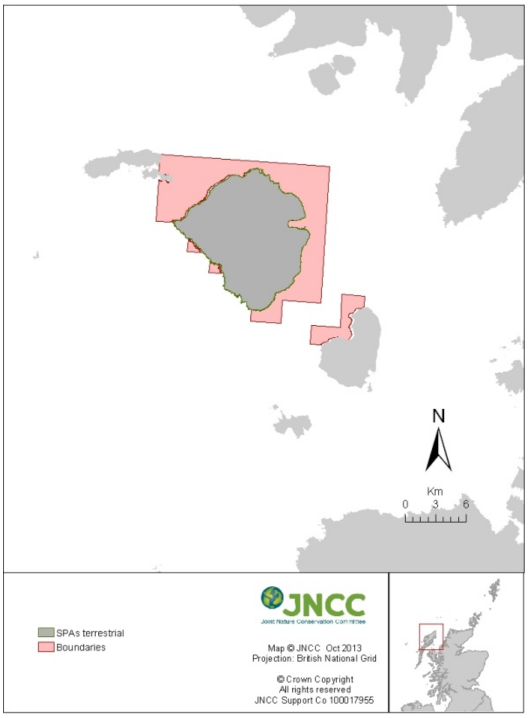


Figure 37. Boundaries drawn around cells exceeding maximum curvature threshold for gam predictions, Rum. Terrestrial breeding territory SPAs for the species also shown.

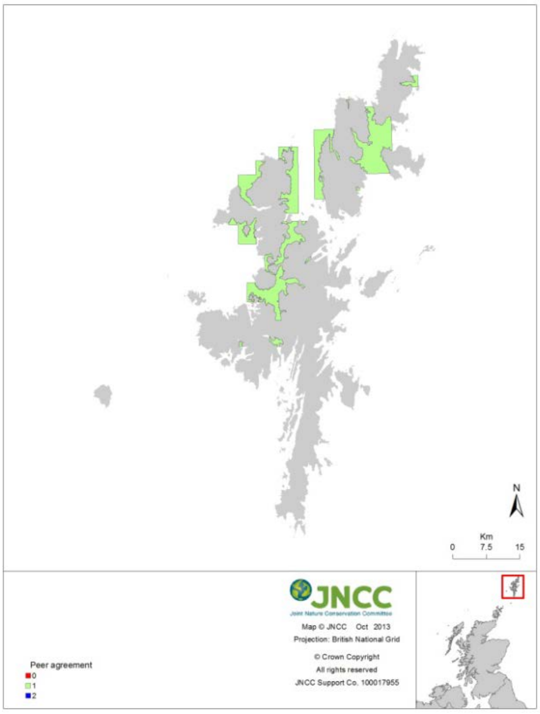


Figure 38. Number of experts, or peers, who indicated important areas which overlap with each of the delineated areas, Shetland

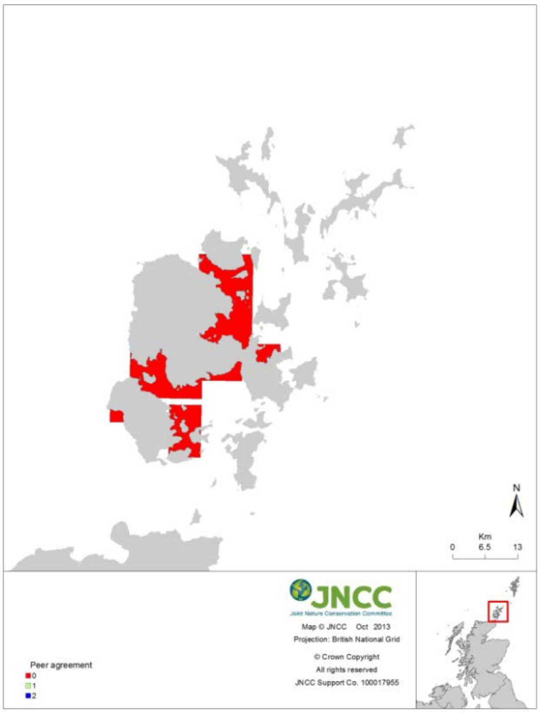


Figure 39. Number of experts, or peers, who indicated important areas which overlap with each of the delineated areas, Orkney

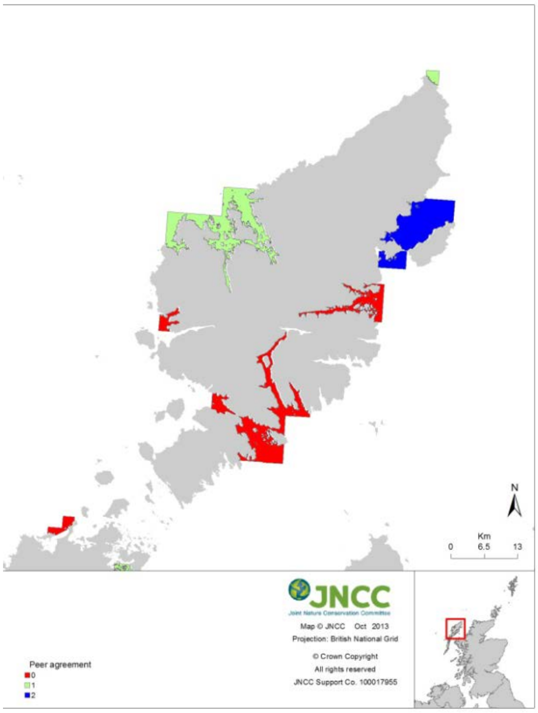


Figure 40. Number of experts, or peers, who indicated important areas which overlap with each of the delineated areas, Lewis and Harris

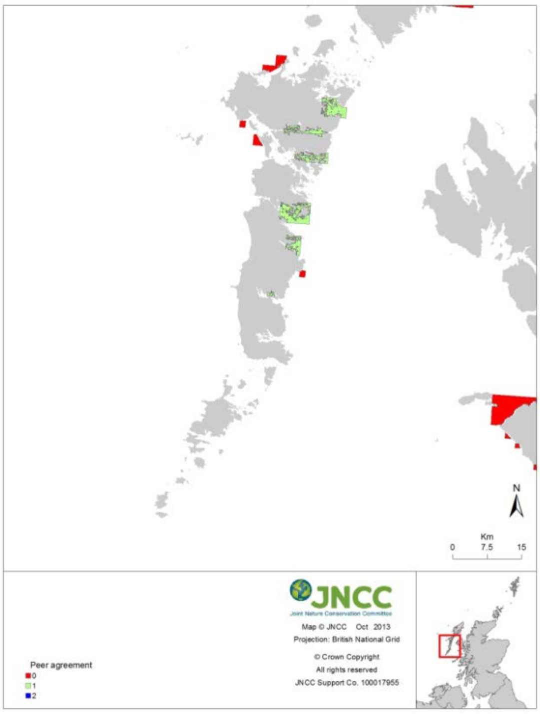


Figure 41. Number of experts, or peers, who indicated important areas which overlap with each of the delineated areas, Uists

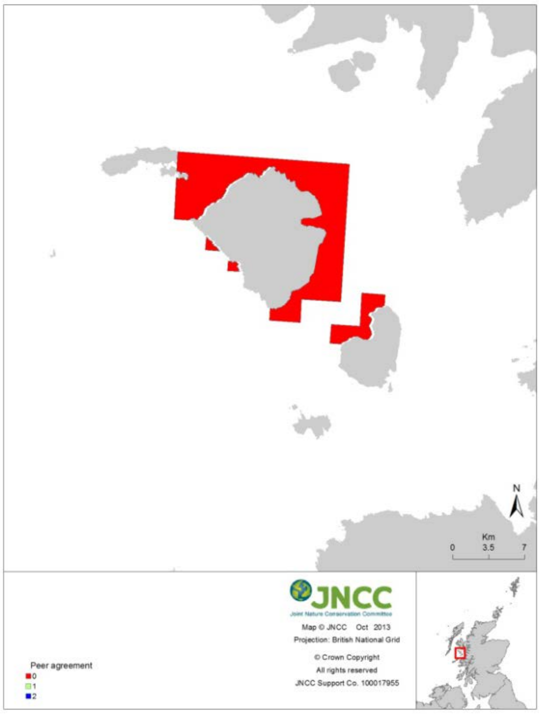


Figure 42. Number of experts, or peers, who indicated important areas which overlap with each of the delineated areas, Rum

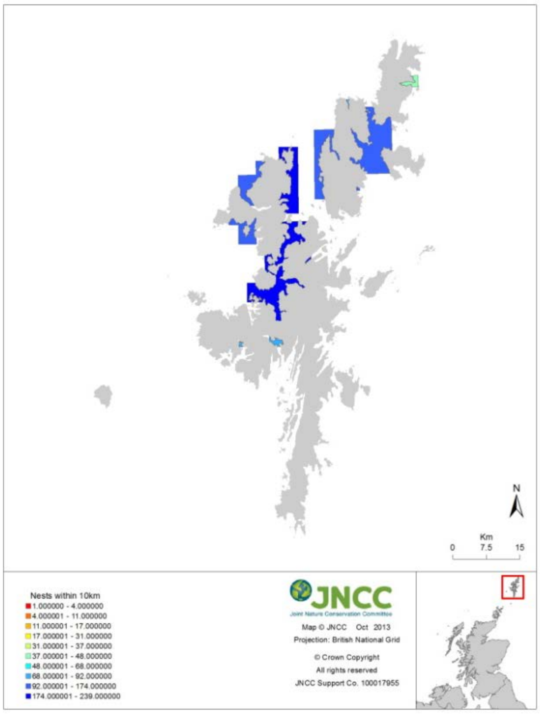


Figure 43. Nests within 10km of each delineated area, Shetland

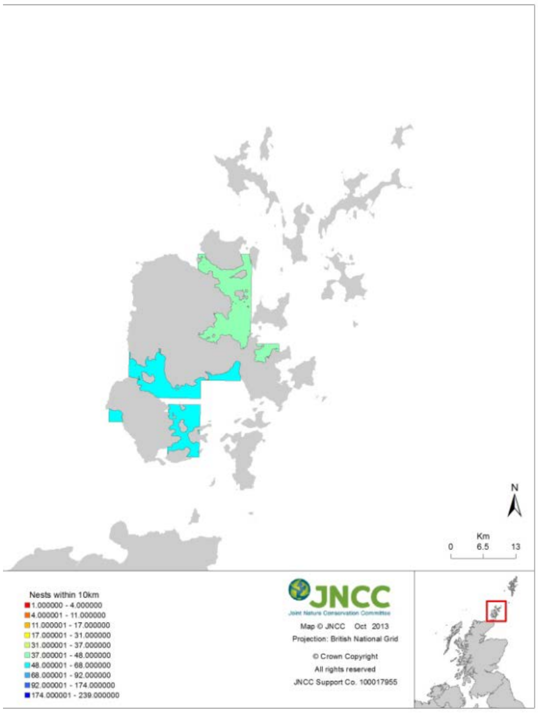


Figure 44. Nests within 10km of each delineated area, Orkney

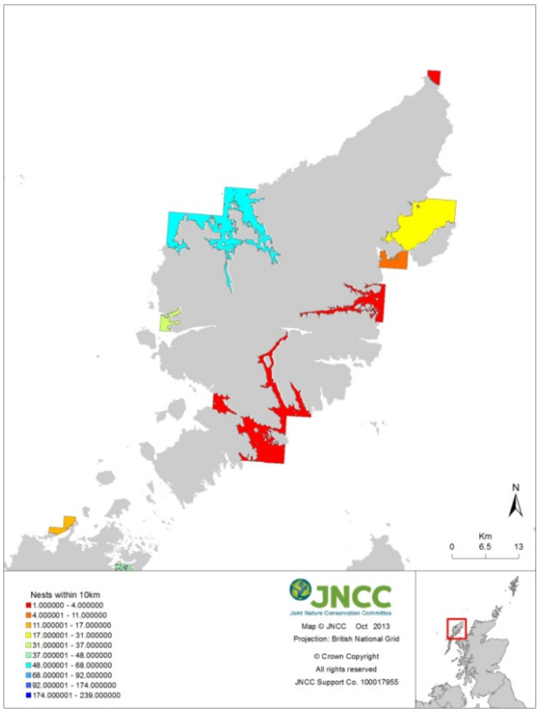


Figure 45. Nests within 10km of each delineated area, Lewis and Harris

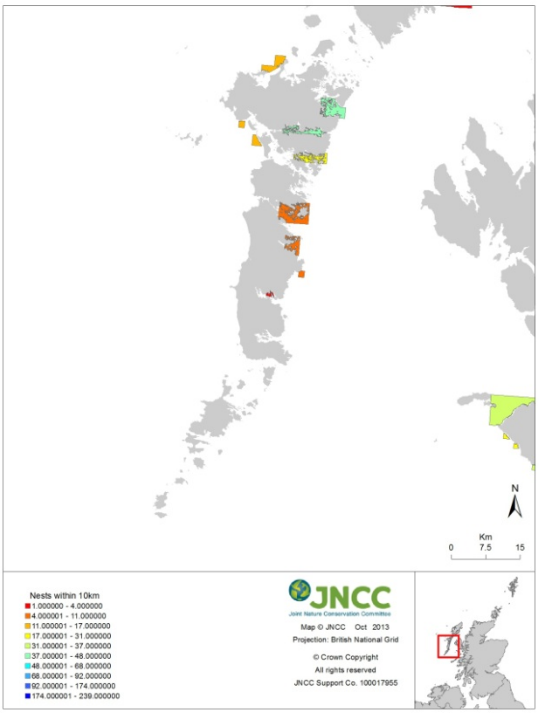


Figure 46. Nests within 10km of each delineated area, Uists

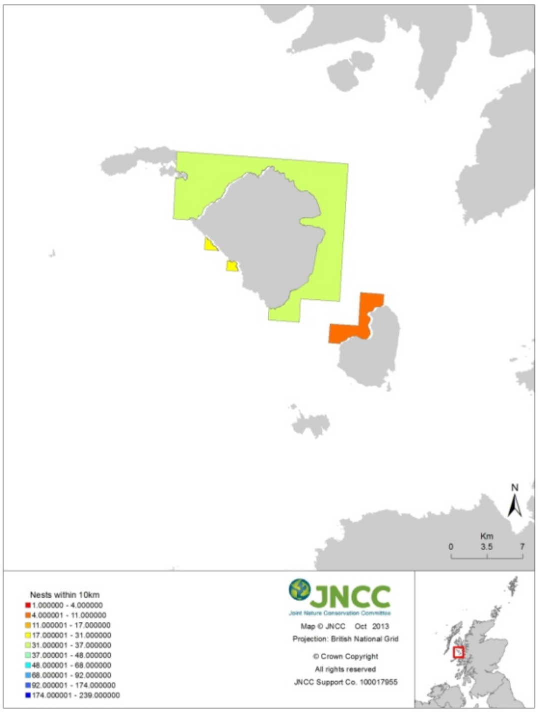


Figure 47. Nests within 10km of each delineated area, Rum

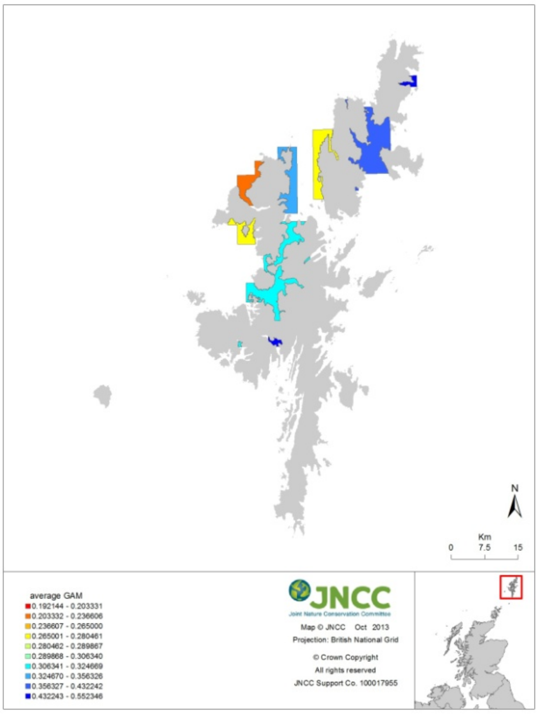


Figure 48. Average GAM prediction within each delineated area, Shetland

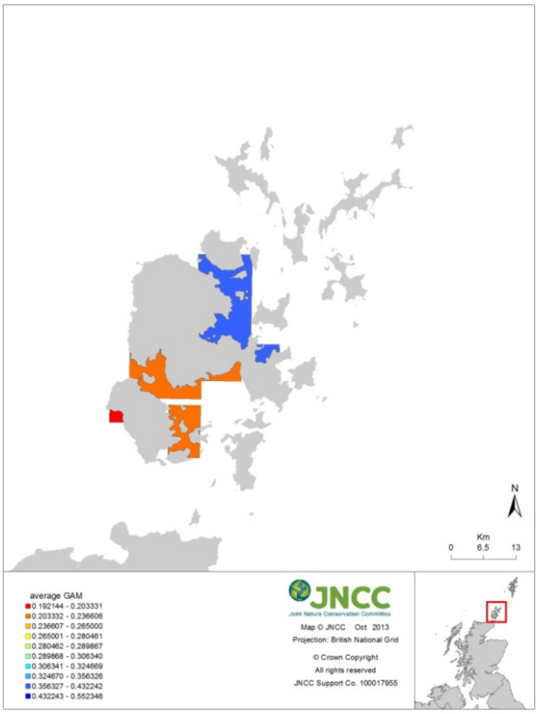


Figure 49. Average GAM prediction within each delineated area, Orkney

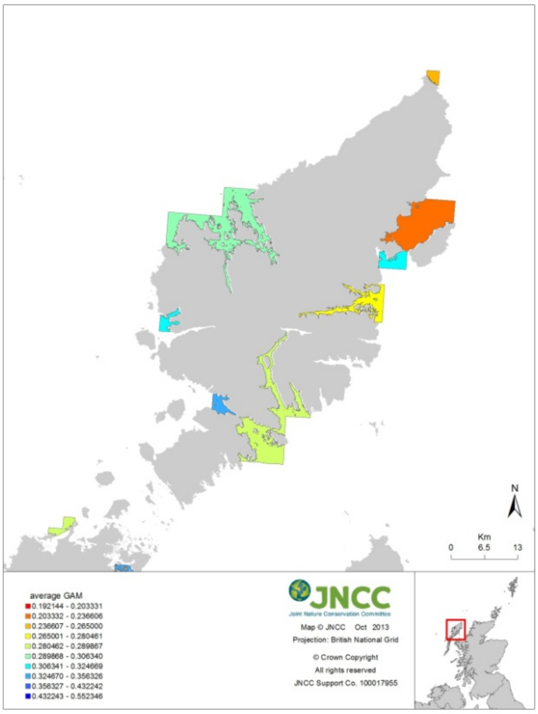


Figure 50. Average GAM prediction within each delineated area, Lewis and Harris

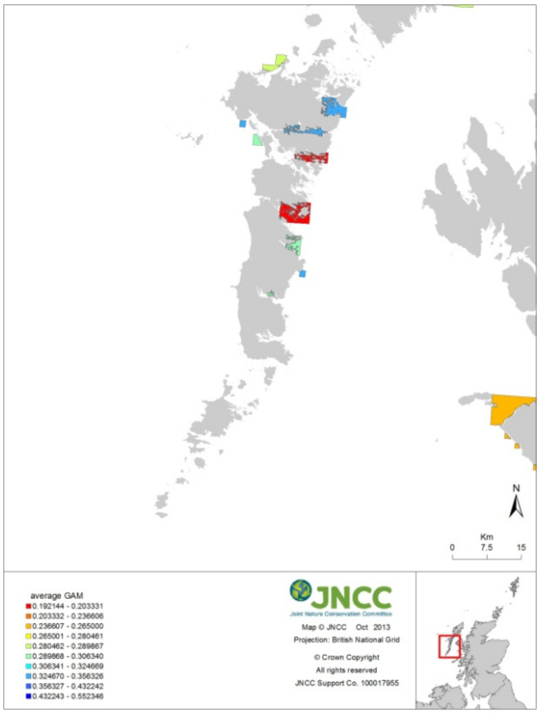


Figure 51. Average GAM prediction within each delineated area, Uists

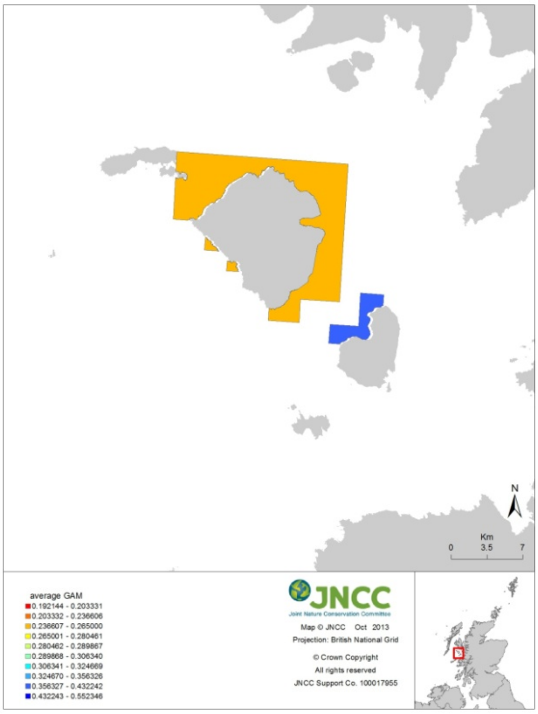


Figure 52. Average GAM prediction within each delineated area, Rum

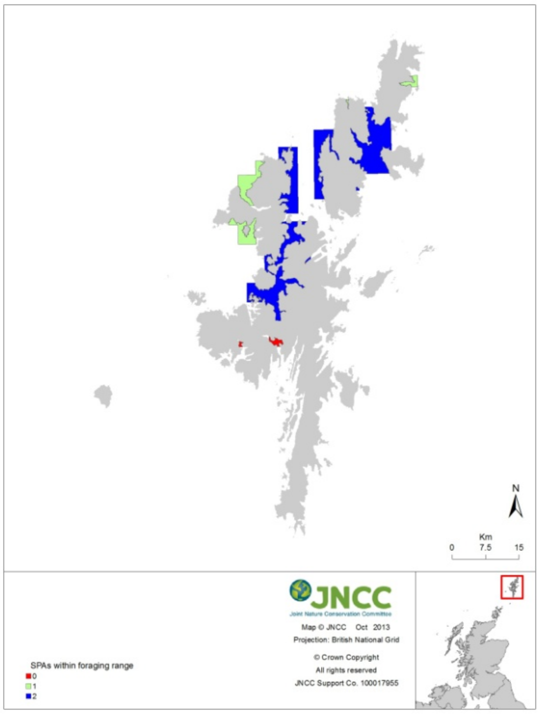


Figure 53. Number of terrestrial breeding territory SPAs within foraging range of each delineated area, Shetland

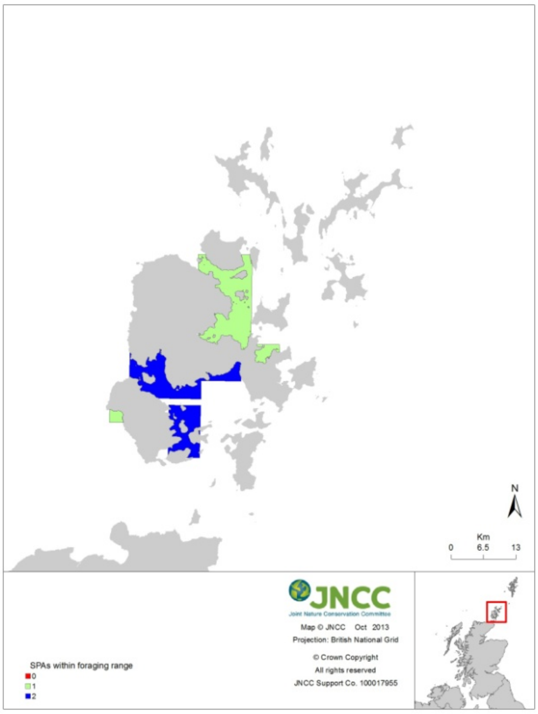


Figure 54. Number of terrestrial breeding territory SPAs within foraging range of each delineated area, Orkney

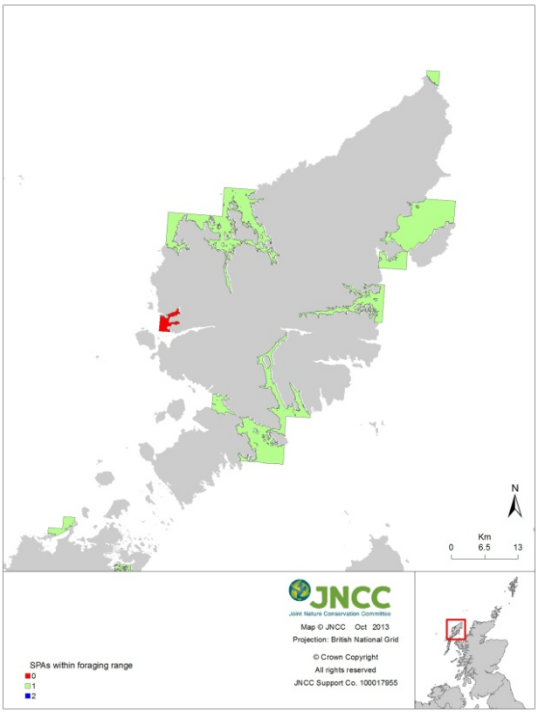


Figure 55. Number of terrestrial breeding territory SPAs within foraging range of each delineated area, Lewis and Harris

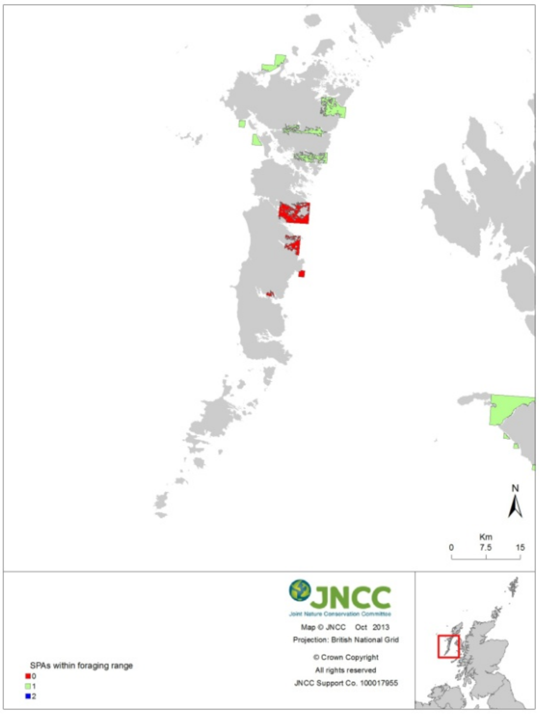


Figure 56. Number of terrestrial breeding territory SPAs within foraging range of each delineated area, Uists

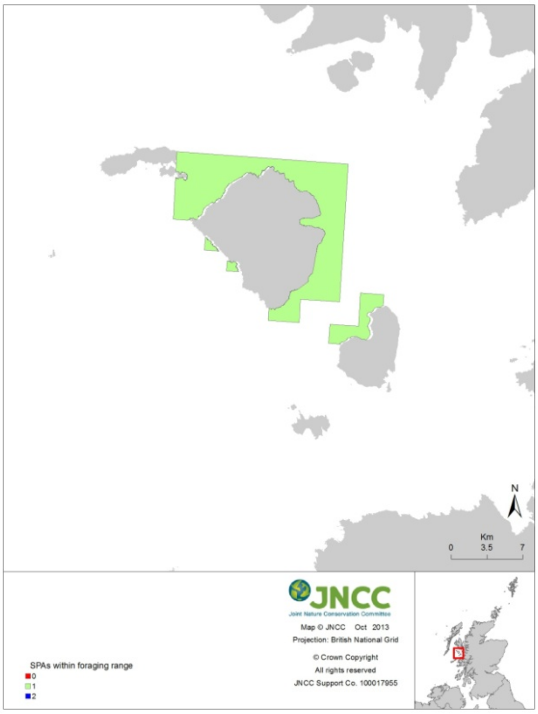


Figure 57. Number of terrestrial breeding territory SPAs within foraging range of each delineated area, Rum

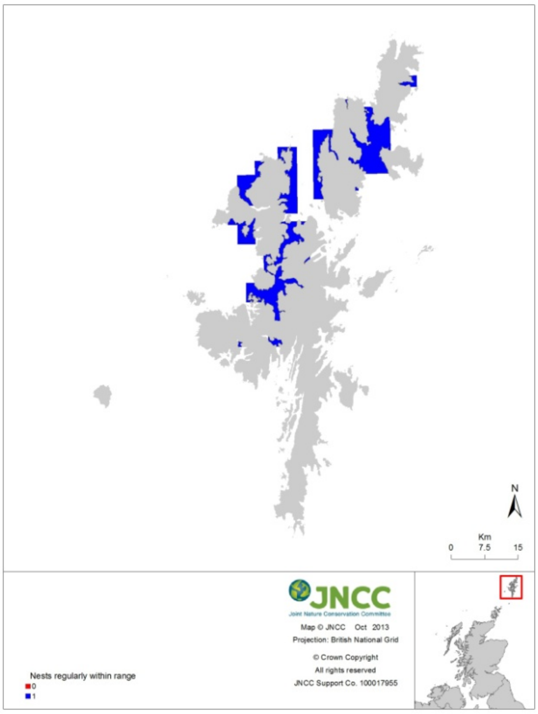


Figure 58. Whether nests were observed or not, within range of each delineated area, during BTO breeding bird surveys, 1988-1991, Shetland

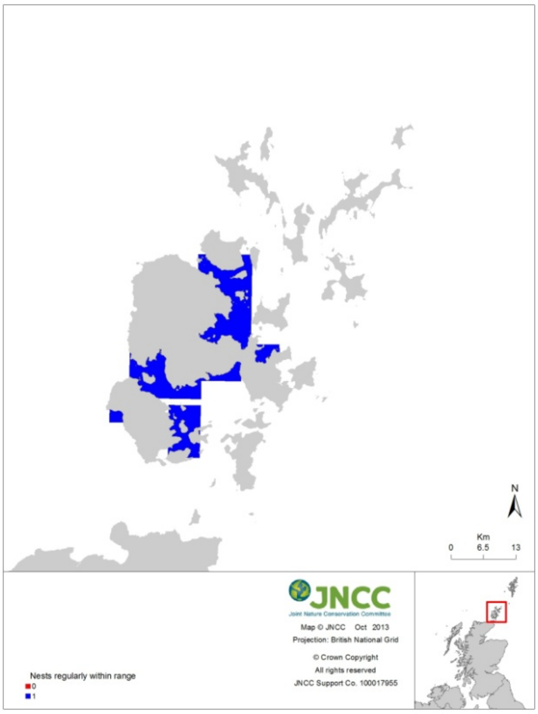


Figure 59. Whether nests were observed or not, within range of each delineated area, during BTO breeding bird surveys, 1988-1991, Orkney

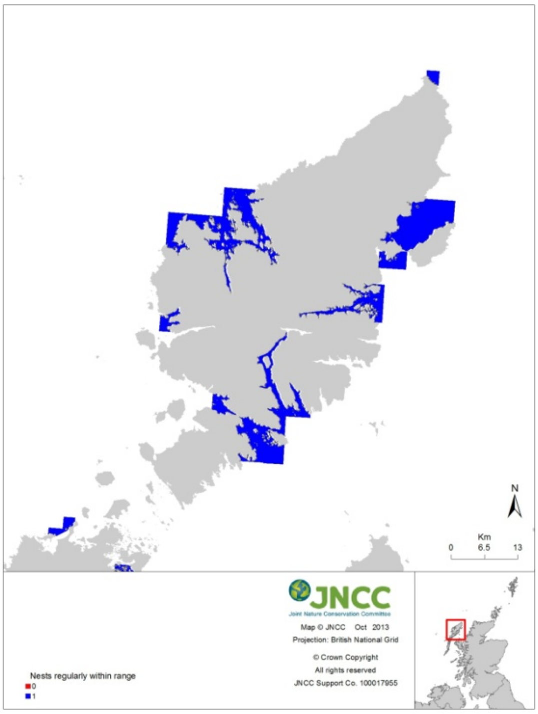


Figure 60. Whether nests were observed or not, within range of each delineated area, during BTO breeding bird surveys, 1988-1991, Lewis and Harris

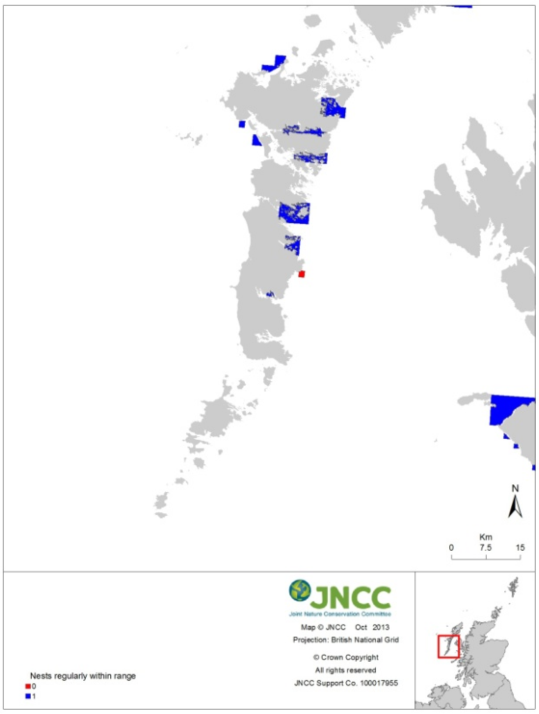


Figure 61. Whether nests were observed or not, within range of each delineated area, during BTO breeding bird surveys, 1988-1991, Uists

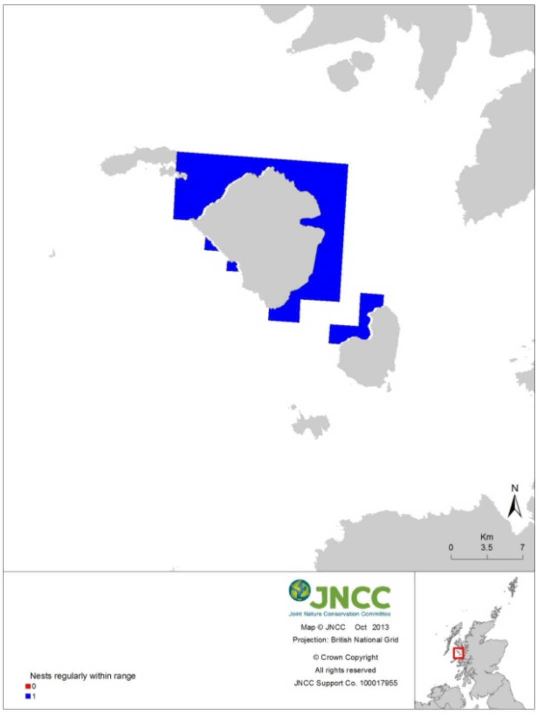


Figure 62. Whether nests were observed or not, within range of each delineated area, during BTO breeding bird surveys, 1988-1991, Rum

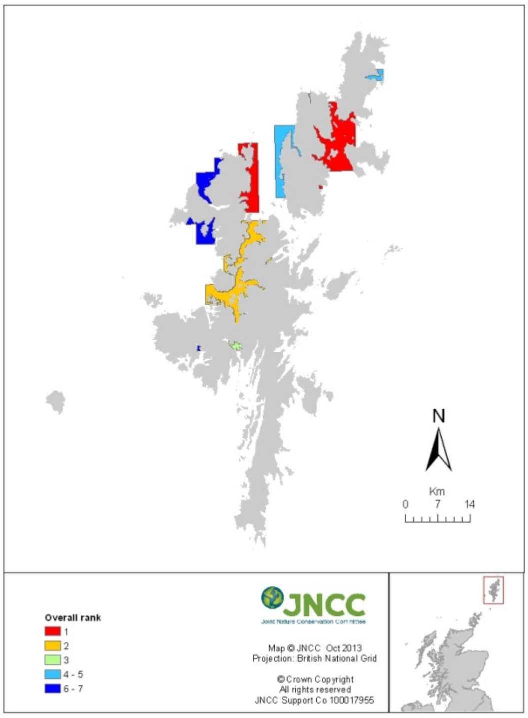


Figure 63. Overall, combined rank, Shetland

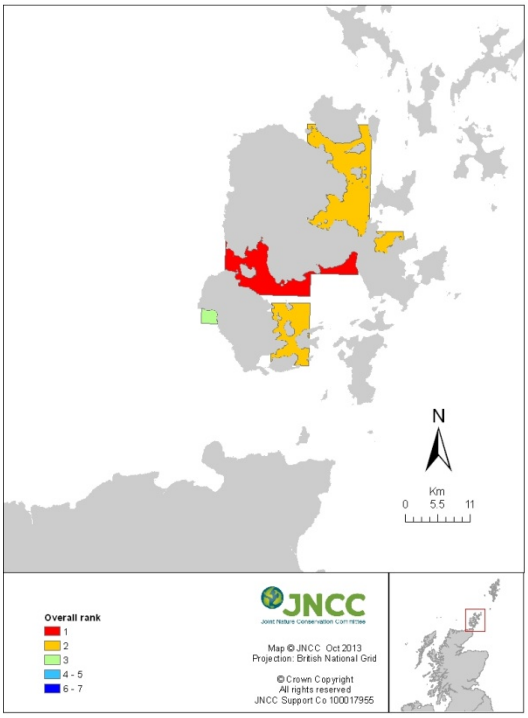


Figure 64. Overall, combined rank, Orkney

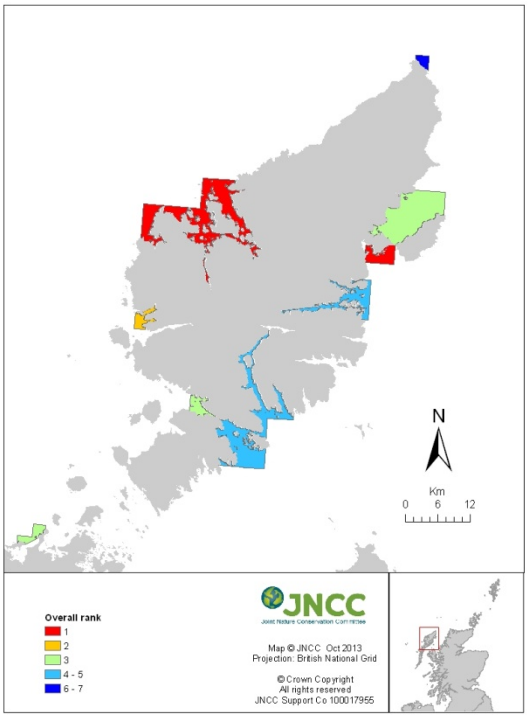


Figure 65. Overall, combined rank, Lewis and Harris

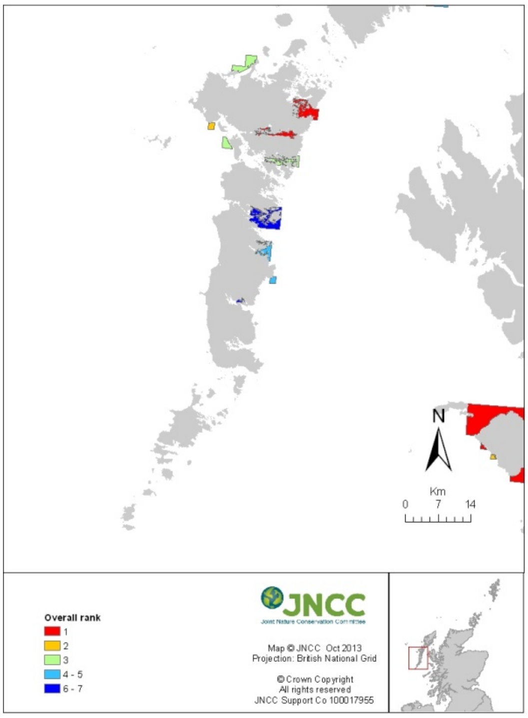


Figure 66. Overall, combined rank, Uists

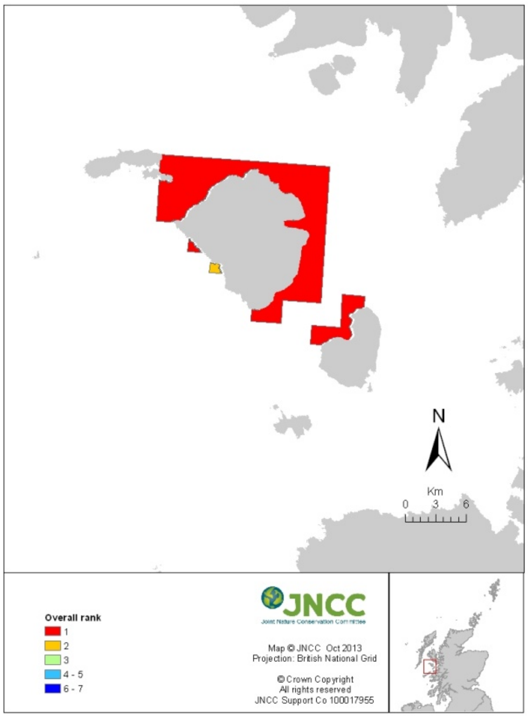


Figure 67. Overall, combined rank, Rum

7 Appendix 1: Environmental data sources used in the GAM

Table 7.1. Details of environmental data sources used as predictor variables in the GAM.

Parameter	**Data set**	**Source**	**Date collected**	**Processing**	**Original scale and projection**	**Data type**
Seabed depth	Seabed depth (m below lowest astronomical tide)	SeaZone Solutions Ltd.	NA	Triangulation with linear interpolation	approx. 250m^2 grid cells GCS WGS 1984	"Continuous" depth values
Seabed slope	Seabed slope (º incline between adjacent grid cells)	Derived from SeaZone Solutions Ltd.	NA	Slope function in ArcGIS Spatial Analyst	1km^2 grid cells OSGB 1936 Transverse Mercator	Slope calculated values
Seabed aspect	Seabed aspect (º based on slope between adjacent grid cells)	Derived from SeaZone Solutions Ltd.	NA	Aspect function in ArcGIS Spatial Analyst	1km^2 grid cells OSGB 1936 Transverse Mercator	Aspect calculated values
Maximum wave base	Maximum wave length in summer (m)	Proudman Oceanographic Laboratory	10 year period	Inverse distance weighted interpolation	0.01^2 decimal degrees GCS WGS 1984	"Continuous" wave length values derived from proWAM 12km wave model (interpolated)
Maximum tidal bed stress	Maximum tidal force in summer (Newtons/m^2)	Proudman Oceanographic Laboratory	2000-2004	Inverse distance weighted interpolation	0.01^2 decimal degrees GCS WGS 1984	"Continuous" tidal force values derived from POLCOMS model (interpolated)

Parameter	**Data set**	**Source**	**Date collected**	**Processing**	**Original scale and projection**	**Data type**
Sea surface temperature	Mean surface temperature in summer (ºC)	NASA/NOAA	1985-1999	NA	0.01^2 decimal degrees GCS WGS 1984	“Continuous” average temperatures values
Salinity	Sea surface salinity in summer (‰)	Proudman Oceanographic Laboratory	10 year simulation	Inverse distance weighted interpolation	0.01^2 decimal degrees GCS WGS 1984	“Continuous” salinity values derived from simulation of POLCOMS
Stratification	Surface to seabed temperature difference in summer (ºC)	Proudman Oceanographic Laboratory	10 year simulation	Inverse distance weighted interpolation	0.01^2 decimal degrees GCS WGS 1984	“Continuous” temp diff. values derived from simulation of POLCOMS
Probability of fronts	Probability of fronts in summer (P)	Proudman Oceanographic Laboratory	10 year simulation	Inverse distance weighted interpolation	0.01^2 decimal degrees GCS WGS 1984	P values (0-1) derived from simulation of POLCOMS
Seabed substratum	Seabed sediment/substrata	British Geological Survey (DigSBS250)	NA	Simplification of DigSBS250 Folk categories supplemented by additional data	Vector dataset GCS WGS 1984	Substrata categories: mud and sandy mud, sand and muddy sand, mixed sediments, coarse sediments, rock

Parameter	Data set	Source	Date collected	Processing	Original scale and projection	Data type
Coastal physiography	Coastal physiographic types	JNCC MNCR/UKSeaMap	NA	Reconsideration of JNCC MNCR classification	Vector dataset GCS WGS 1984	Coastal type categories: estuary, embayment, sound, bay, sealoch, open coast

8 Appendix 2: Maps of environmental covariates for Scottish waters

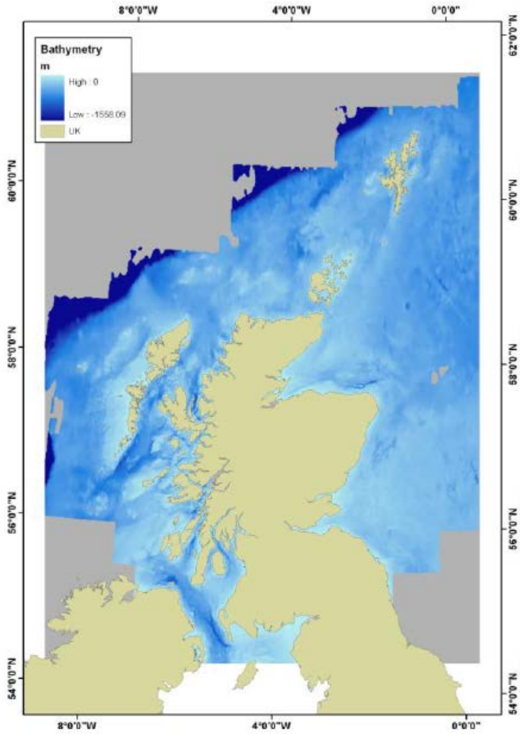


Figure 8.1Bathymetry

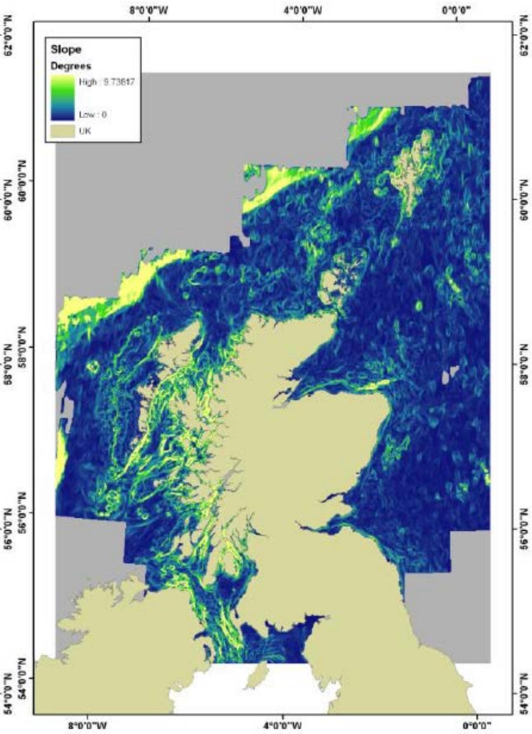


Figure 8.2 Seabed slope

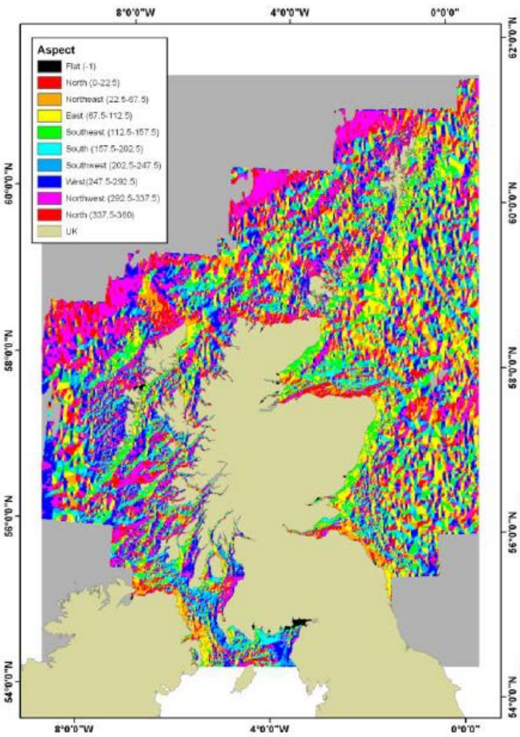


Figure 8.3 Seabed aspect

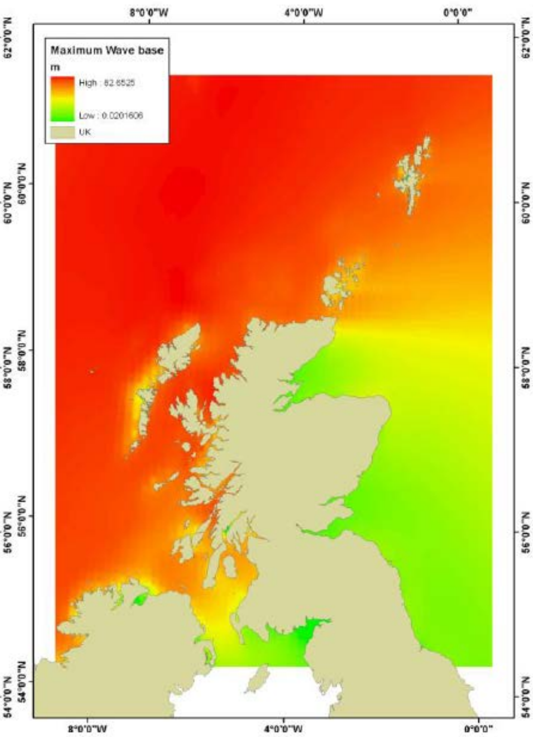


Figure 8.4 Maximum wave base

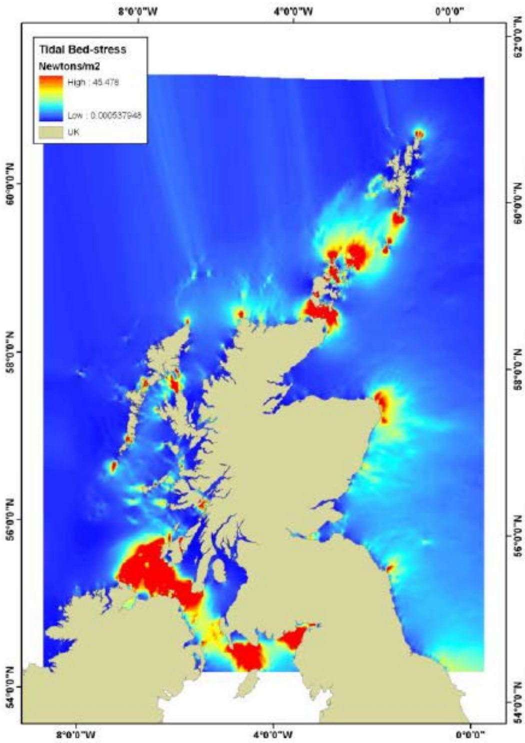


Figure 8.5 Tidal bed-stress

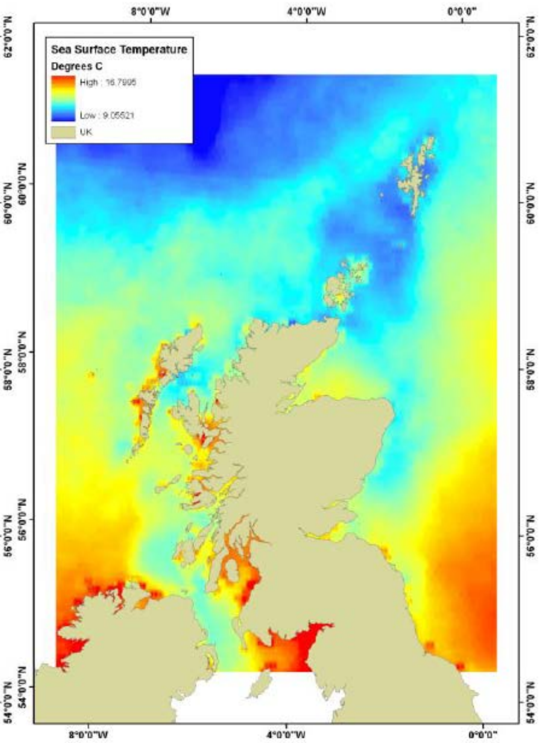


Figure 8.6 Sea surface temperature

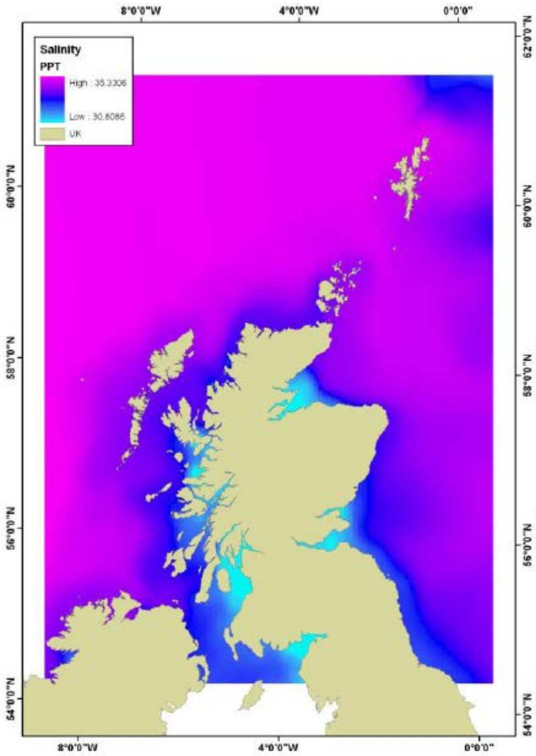


Figure 8.7 Salinity

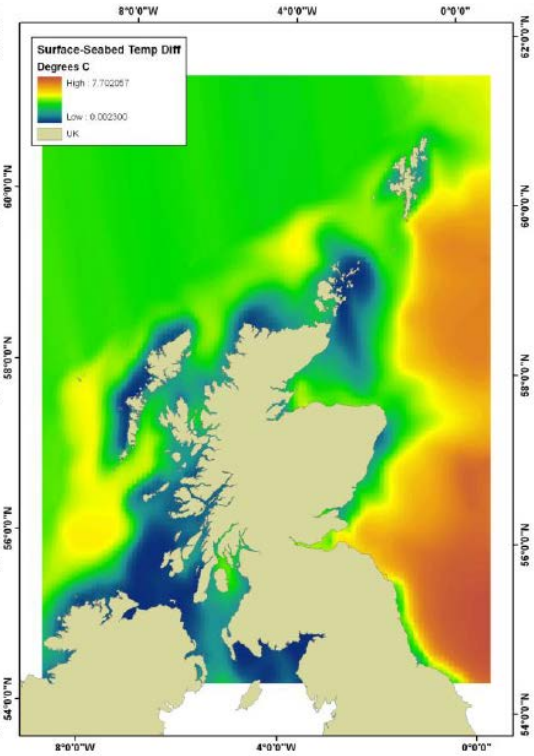


Figure 8.8 Surface-seabed temperature difference

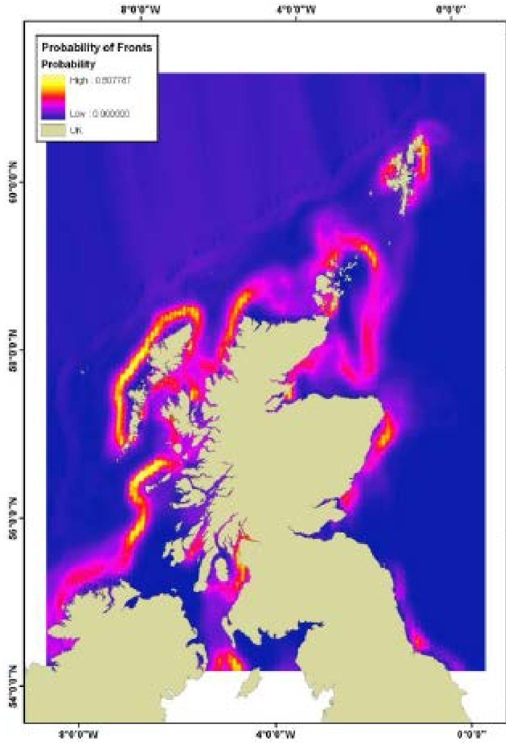


Figure 8.9 Probability of thermal fronts

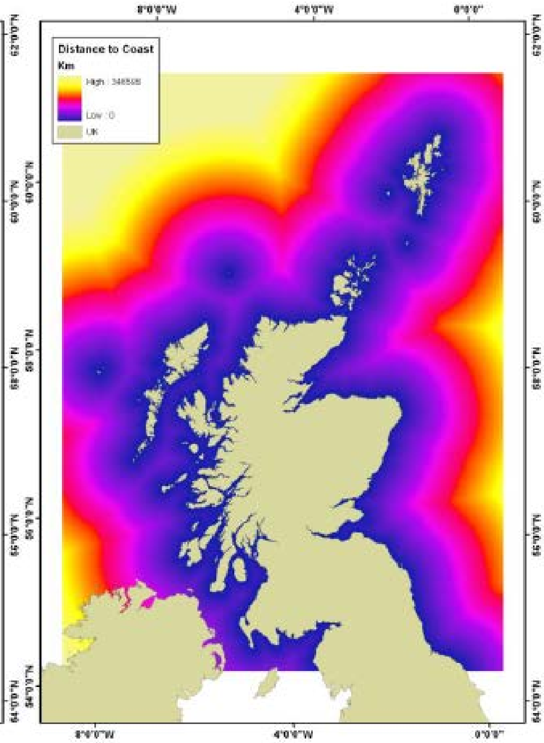


Figure 8.10 Distance to coast

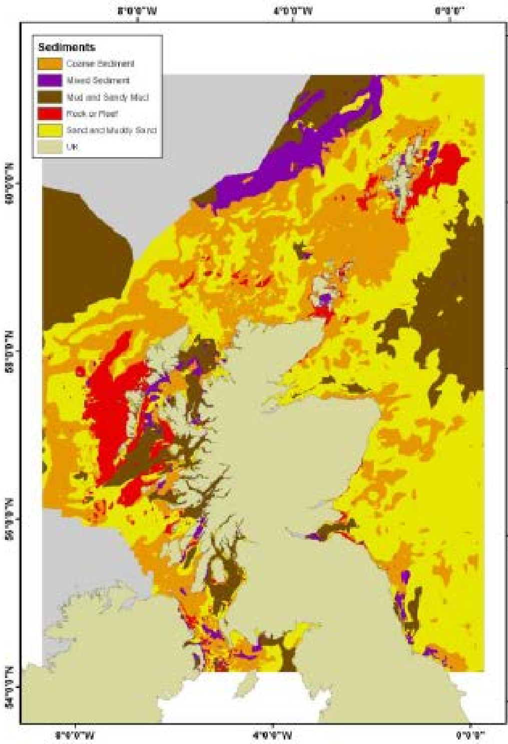


Figure 8.11 Sediment type

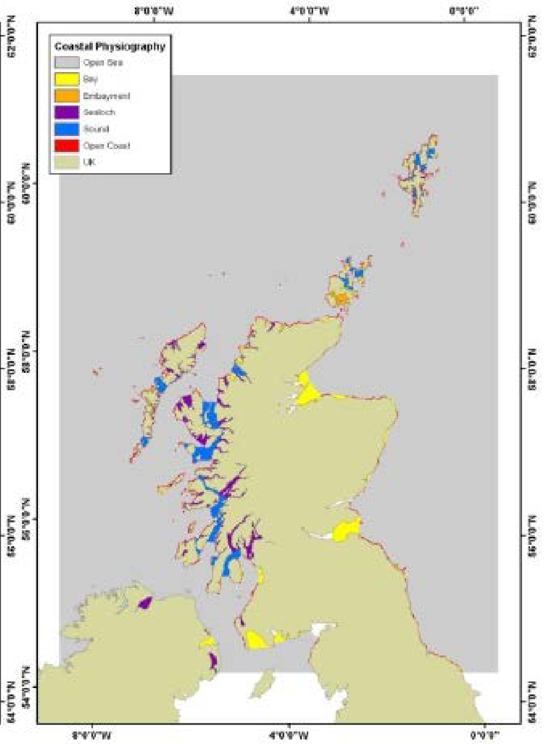
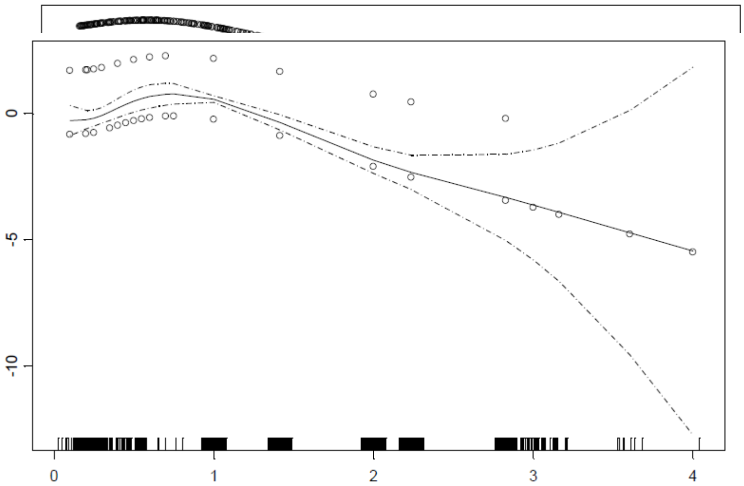


Figure 8.12 Coastal physiography

9 Appendix 3: Environmental covariate response curves from final GAM model

S(bathymetry)
S(distance to coast)

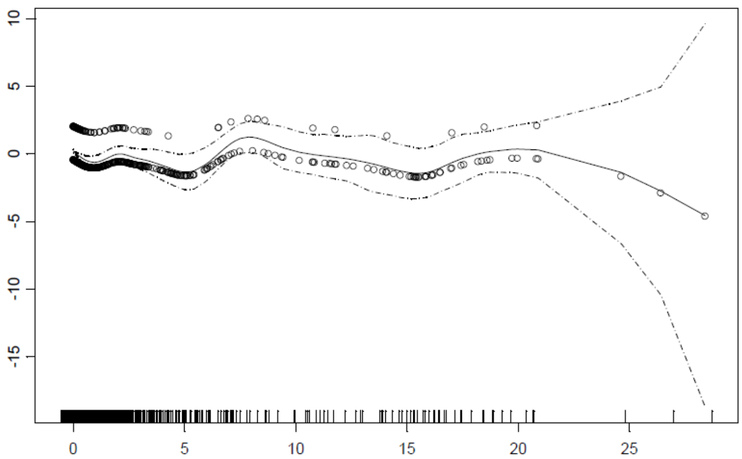


Distance to coast (km)

Figure 9.1 GAM response curve for bathymetry. The solid line is the predicted value of the dependent variable (habitat suitability) as a function of bathymetry. The dashed line shows 2 times the SE of the estimate, and the open dots show the residuals. The vertical lines along the bottom of the plot are the 'rugs', showing the bathymetry values of the observation data.

Figure 9.2 GAM response curve for distance to coast.

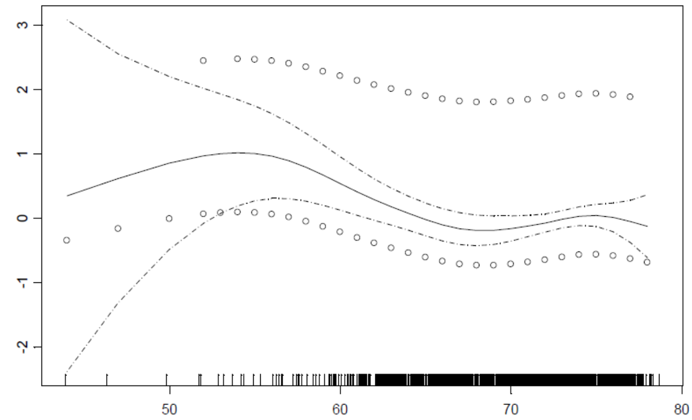
S(tidal bed stress)



Tidal bed stress (N m^{-2})

Figure 9.3 GAM response curve for tidal bed stress.

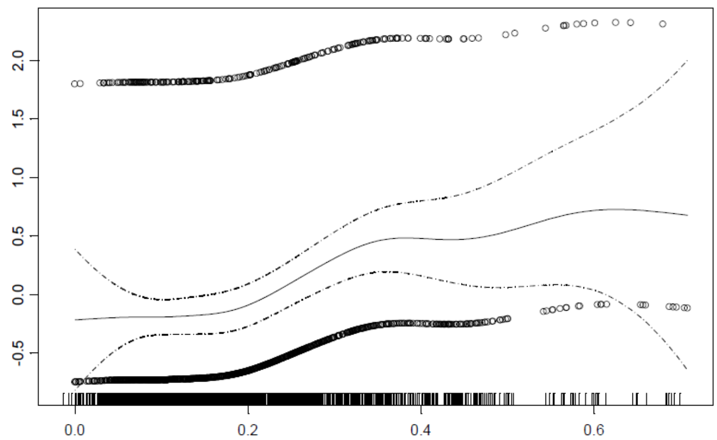
S(maximum wave base)



Maximum wave base (m)

Figure 9.4 GAM response curve for maximum wave base.

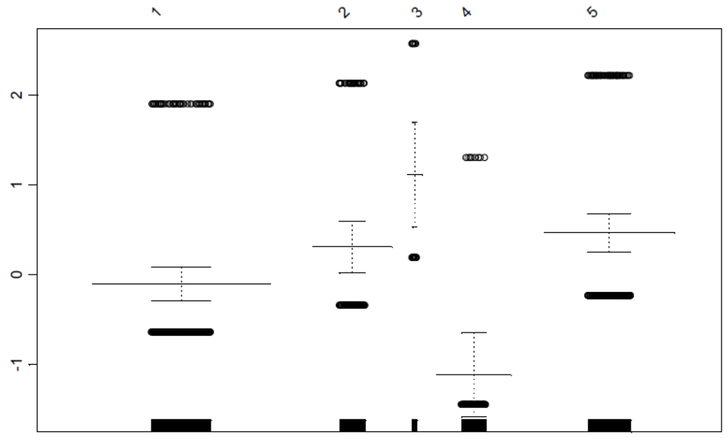
S(probability of front)



Probability of front

Figure 9.5 GAM response curve for probability of a thermal front.

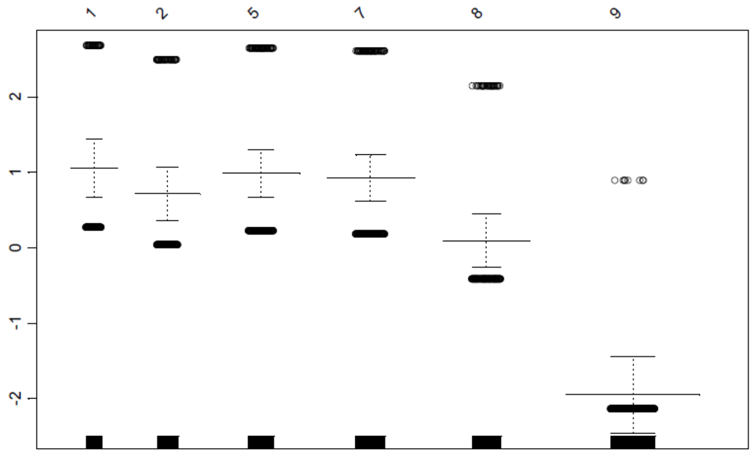
S(sediment type)



Sediment type

Figure 9.6 GAM response for sediment type. 1 coarse sediment, 2 mixed sediment, 3 sandy mud, 4 rock or reef, 5 muddy sand.

S(coastal physiography)



Coastal physiography

Figure 9.7 GAM response for coastal physiography. 1 bay, 2 embayment, 5 sealoch, 7 sound, 8 open coast, 9 open sea.

10 Appendix 4: Possible options for selection of areas as potential marine SPAs.

10.1 Background

Figures 17-26 show that there are extensive areas of coastal waters around Shetland, Orkney and the Outer Hebrides which have been identified as suitable diver habitat by the GAM model and which are within foraging range of breeding red-throated divers.

Consideration must be given as to how the most important sites may be identified or prioritised based on the grid cells identified as important by the model. A boundary delineation method should ideally:

- Be robust and minimise subjective judgements
- Identify a boundary which contains a cohesive, aggregated highest densities of birds
- Use a trade-off between number of birds and size of area
- Be relatively easy to understand and explain
- Be applicable to all sites and species.
- Not conflict with work already done

This Appendix discusses three broad boundary delineation options for identifying possible red throated diver marine SPAs based on the GAM model outputs.

For all three areas (Shetland, Orkney and Outer Hebrides), the GAM probability output is available. In addition to this, nest location data is available for the Orkneys and Shetlands but NOT for the Hebrides. This census data on breeding locations can be incorporated into the different options in two ways: either alone, i.e basing our measure of importance on the number of nests which are observed to be within foraging range of the cell (or polygon), or by combining it with the raw GAM probability output to provide the number of nests within foraging range weighted by the GAM prediction. We recommend the latter as it takes account of both habitat suitability and accessibility. Where census data are not available, we are necessarily restricted to using the raw GAM output for basing our decisions on.

All of these options are applied only to cells which have already been selected as being suitable habitat for red throated divers based on the GAM model predictions: they are above the threshold for presence (0.25, as objectively found using the Kappa statistic). For Shetland and Orkney (which have recent census data), they also have at least one nest within foraging range of the cell. Thus, for Shetland and Orkney, even if the final solution is based on GAM predictions only, we know that no areas will be highlighted which are not actually within foraging range of any red throated divers, and if the solution is based purely on nest numbers, we know that no areas will be highlighted which are not suitable breeding red throated diver foraging habitat.

Table 10.1 summarises the options along with their risks and benefits. The second and third options have been applied to Shetland and Orkney, and a variation of the maximum curvature approach is applied to the western isles. These results are preliminary and the methods used to produce such maps require further investigation and consideration.

The third option is based on 'polygons'. Polygons were created by joining all those cells which share an edge (but excluding cells which only touch at corners).

Table 10.1. Summary of three options for identifying the most important sites for consideration for protection.

Summary	Risks	Benefits
1. Target-based approach Finds the minimum area required to protect a target proportion of the population. The single best cell (in terms of the number of nests within range) is chosen, followed by the next cell with the highest number of ADDITIONAL nests within range, ie those not already afforded protection by being within range of the first cell. This is continued until the target proportion of the local population is captured. For this option, we suggest an appropriate target is 42% i.e. the proportion of the GB population protected within the suite of terrestrial SPAs. Could be applied to cells OR polygons (as in those created for option 3 below).	This is a novel approach to decision making for marine SPA designation and may have implications on our approaches for other marine SPA work. This approach requires us to measure the number of ADDITIONAL 'new' nests within range of a cell rather than the total number of nests within range. This will lead to cells with a small number of nests within range being chosen over cells with a large number of nests within range. This will also mean that the approach will tend to choose scattered cells in favour or clusters of adjacent cells, due to the method requiring capture of 'additional' nests which are not already captured. Therefore, it is more likely to produce a scattered surface. This option can only be used where census data are available (i.e. Shetland and Orkney)	If the target based approach is deemed appropriate this gives a clear objective.
2. Maximum curvature This method starts with the best cell according to the chosen value metric, adds the next highest value cell, then the next, etc. Cumulative area is plotted against cumulative value to determine the cut-off, or point of maximum curvature. This point represents the point at which the slope of the relationship between the chosen measure of value and cumulative area changes the most.	There are possible interpretation issues of applying maximum curvature to this kind of data. Essentially the 'cumulative' number of nests does not equal the actual number of nests in the area because we are not measuring the marginal (or additional) nests but simply the number of nests within range of one cell plus the number within range of the next cell even if these are the SAME nests (see Figure 102 for demonstration of this). Similar issues if applying max. curve. to the GAM prediction.	This method has been used for inshore boundary delineation and so would provide consistency of approaches. This method has been published in peer reviewed scientific journal (O'Brien *et al* 2012). The method can be used for all three areas, as it can be applied to the GAM prediction alone, and does not require breeding location census data. However, it can be further improved if census data are available by incorporating this as a measure of accessibility.
3. **Polygon area regression** This method looks for polygons which have, for their size, a high value by plotting a linear model of value (nests within foraging range, weighted by GAM prediction) against polygon size and identifying polygons which are above the line of best fit. Larger polygons are expected to have more nests within 10km, and so the line of best fit is expected to have a positive slope.	There may be cells within the chosen polygon which are of themselves not as high value as some cells which are not within a polygon (creating polygons depends only if cells are adjacent, and does not account for cell values). This method will always identify approximately half of the polygons by nature of the way a line of best fit is estimated.	Chooses polygons rather than individual cells, so may be likely to result in more coherent and distinct 'areas' rather than scattered cells. However many polygons will be single cells so there may remain an element of scatter in the results.

Two options, maximum curvature and the polygon regression-based approach, are here further investigated. The target-based approach was not trialled at this stage because there are many more risks than benefits (Table 10.1) and (despite its apparent simplicity) it will be the most difficult method to apply to the data in terms of data manipulation and analysis.

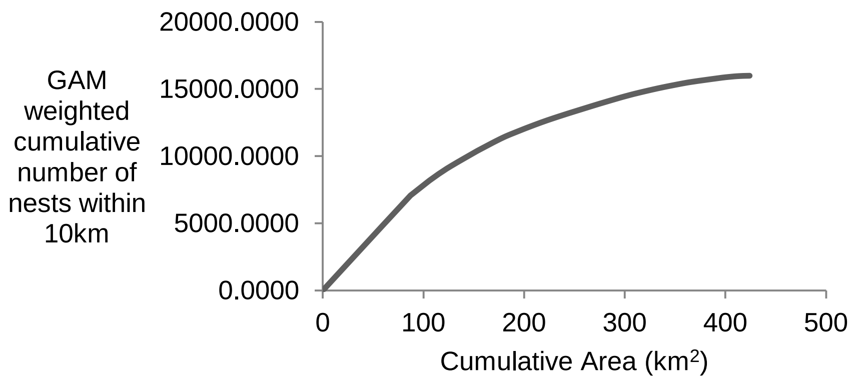
10.2 Methods and results

10.2.1 Maximum curvature

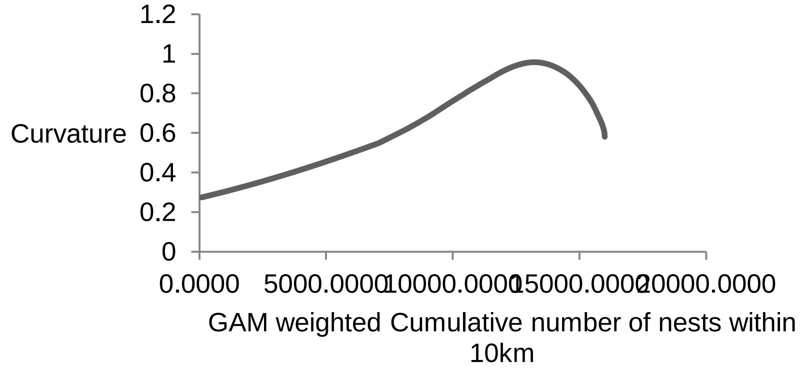
Maximum curvature borrows a boundary delineation method used previously within the marine SPA work for inshore waterbirds (O'Brien *et al* 2012). This is normally applied to numbers of birds within a cell, and the cumulative number of birds protected by adding the next highest density cell to the selection is calculated for each cell, in order of density, down to the lowest density cell, by which point the cumulative number of birds should be equal to total number for the study area as a whole. These cumulative values are used by the maximum curvature formula to find the point at which the slope of the relationship between cumulative number of birds and cumulative area changes the most. In the present, breeding red throated diver, case however, the cumulative 'nestsXgam' has a different meaning. This is because the nests which are within foraging range of one cell might be shared with other cells, so the SAME nests are counted in multiple cells. Thus the final cumulative number of nests is likely to be a number which is orders of magnitude greater than the actual total number of nests within the study area. The cumulative number used by maximum curvature can be interpreted as: potential total useage of all cells. If we were to recalibrate the numbers using each cell by the total number of nests within the study area, then the value could be interpreted as a snapshot of predicted average useage of each cell, and the cumulative number of nests would not exceed the actual number within the study area (this calibration would not affect the actual outcome of maximum curvature).

Maximum curvature was applied to the cell by cell nestsXgam values to identify a threshold of nestsXgam above which cells should be selected for consideration for inclusion within marine SPAs for foraging breeding red throated divers. The curve of cumulative GAM weighted number of nests against cumulative area for Shetland is shown in Figure 10.1 (a). The plot of curvature, Figure 10.1 (b) shows that the point of maximum curvature corresponds to a cumulative GAM weighted number of nests of 13,217. The GAM weighted number of nests within 10km per cell at this point was 23.4. These cells selected by maximum curvature for Shetland are shown in Figure 10.2.

The same method applied to Orkney (plotted in Figure 10.2) shows that the point of maximum curvature corresponds to a cumulative GAM weighted number of nests of 1435.5. The GAM weighted number of nests within 10km per cell at this point was 3.9. These cells selected by maximum curvature are shown in Figure 10.3.

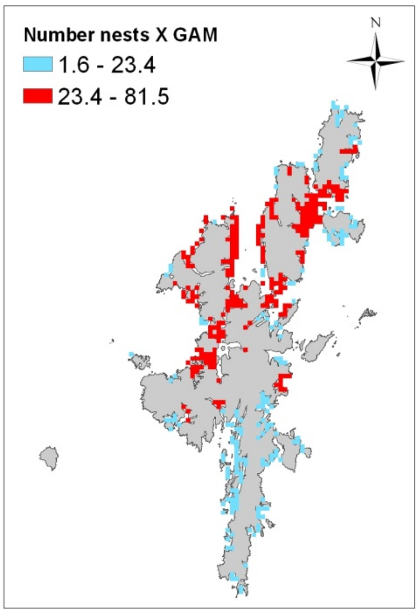


a)

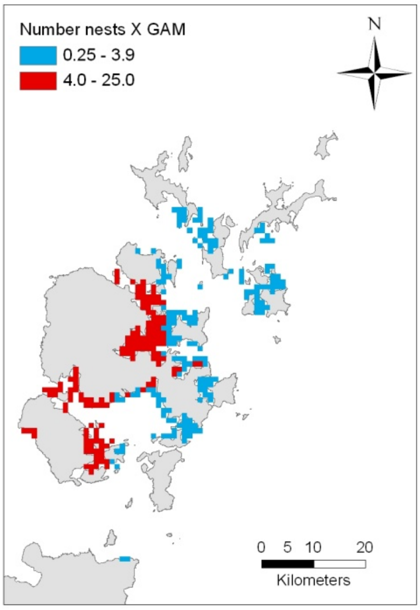


b)

Figure 10.1. Maximum curvature for GAM weighted nest distributions for Shetland. Note that the cumulative number of nests is not an ACTUAL number of nests, as many nests will be counted multiple times as each is in within foraging range of multiple nests. a) shows the cumulative value plotted against cumulative area, b shows the curvature plotted against cumulative value.

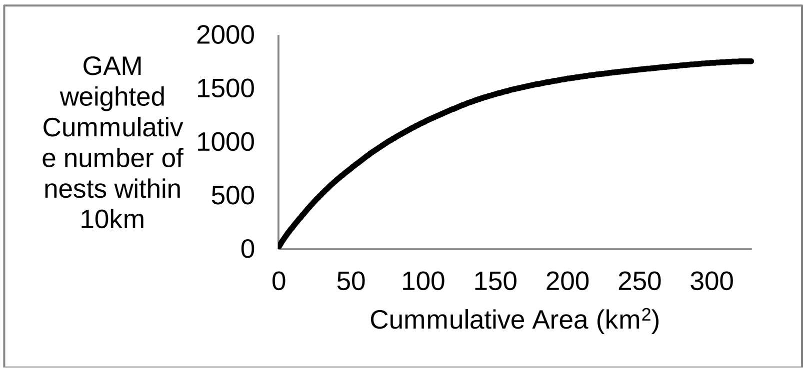


a) Shetland

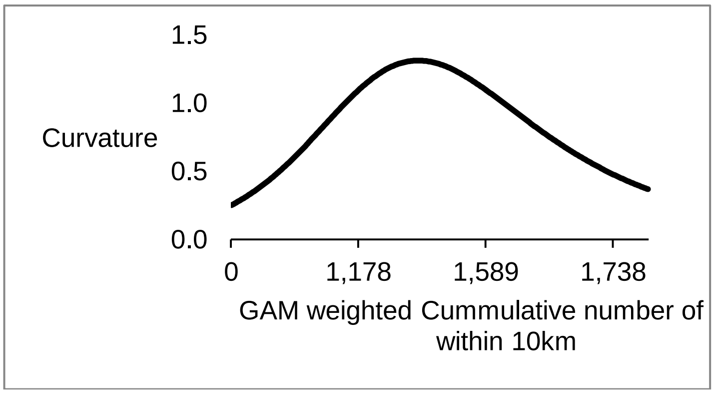


b) Orkney

Figure 10.2. Cells above the nestsXgam threshold selected by maximum curvature in red, with all cells not meeting the selected threshold shown in blue.



a)

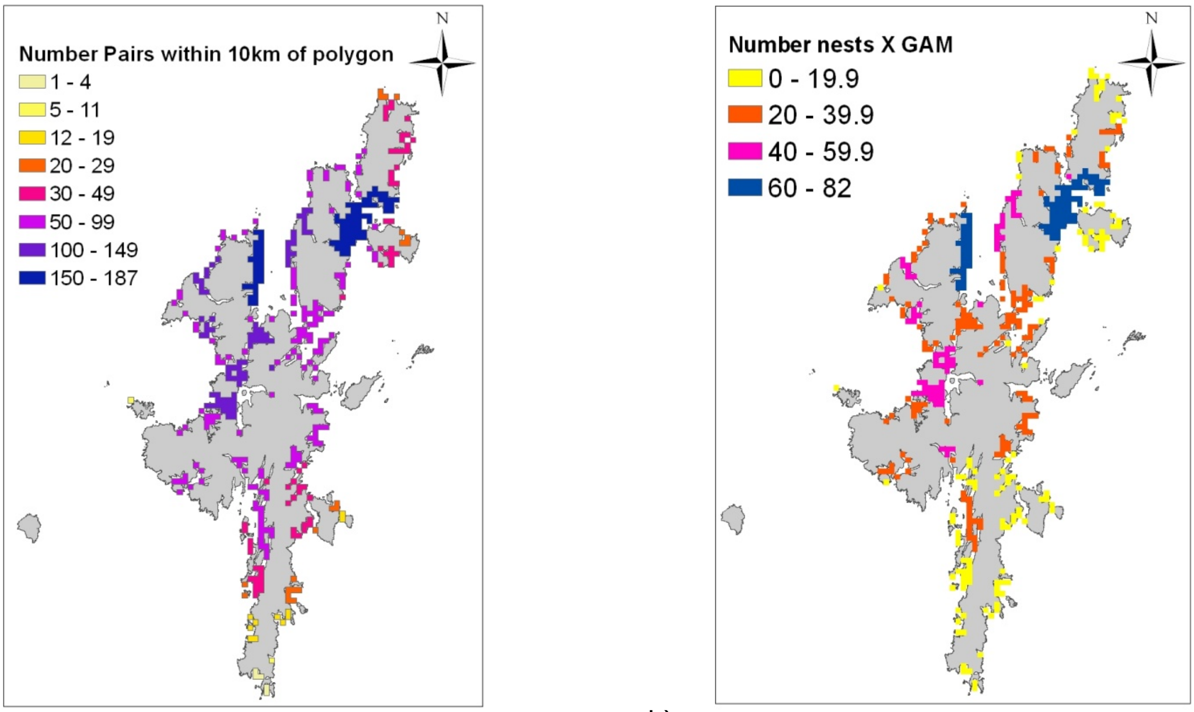


b)

Figure 10.3. Maximum curvature for GAM weighted nest distributions for Orkney. Note that the cumulative number of nests is not an ACTUAL number of nests, as many nests will be counted multiple times as each is within foraging range of multiple nests. a) shows the cumulative value plotted against cumulative area, b shows the curvature plotted against cumulative value.

10.2.2 Polygon regression

The polygon based method described in Table 10.1 identifies which of the polygons shown in Figure 10.4 have, for their size, a high value. The polygons created for Shetland are shown in Figure 10.4 colour coded according to the number of nests within 10km of the whole polygon (a) and according to the number of nests within 10km of the whole polygon weighted (multiplied by) the average GAM prediction for cells within the polygon (nestsXgampoly) (b).



a) b)

Figure 10.4. Polygons created by joining adjacent cells. Colour coded according to a) the number of nests within foraging range (10km) of the polygon as a whole, and b) this number of nests weighted by the average GAM value within the polygon.

A linear model of nestsXgampoly against polygon size was run, and the residuals were checked for meeting the assumptions of a linear model. Where these were violated, the best transformation to allow these assumptions to be met was found, and the slope of this relationship was taken as the line of best fit. For Shetland: There are two outliers in terms of polygon size (59 and 28 cells) which might bias the relationship found. In the absence of any reason to doubt that these polygons are representative for their size, it seems prudent to leave them in. The regression was however ran with and without these outliers, and the results are very similar in terms of the slope of the regression and the polygons deemed good value for their size. The results presented are for the regression with all polygons included.

The regression line for Shetland is shown in Figure 10.5. The predicted, or expected, nestsXgampoly for each polygon, based on the relationship with polygon size discovered in the linear regression, was calculated, and those polygons whose ACTUAL nestsXgampoly value was higher than its expected value were highlighted. These polygons are shown in Figure 10.6.

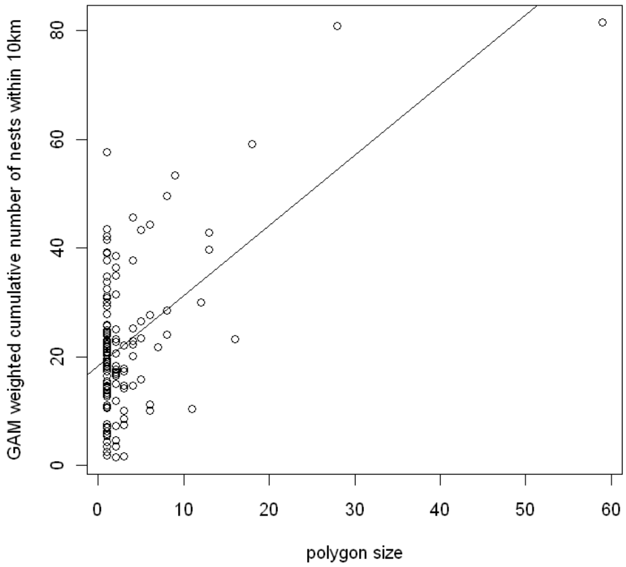


Figure 10.5. Linear regression line for the average GAM weighted cumulative number of nests against polygon size.

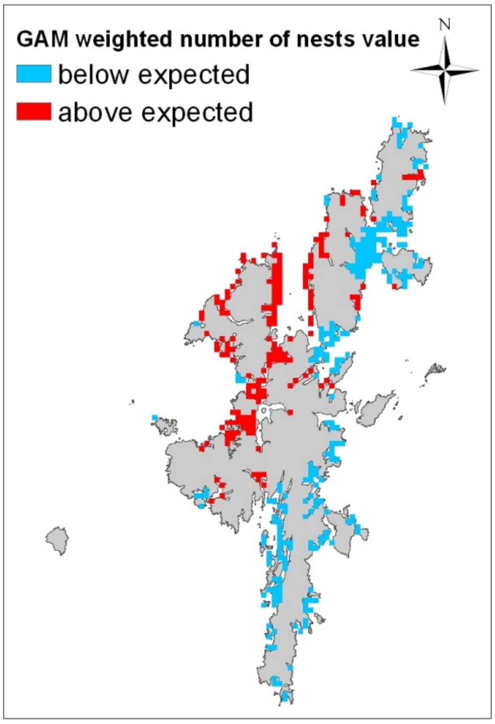


Figure 10.6. Polygons value based on the linear regression of average GAM weighed number of nests against polygon size for Shetland. Polygons with a value above expected, and therefore representing good value for their size, are shown in red, those below are shown in blue.

The method was also applied to Orkney. Here there is one outlier in terms of polygon size (95 cells) which might bias the relationship found. In the absence of any reason to doubt that this polygon is representative for its size, it seems prudent to leave it in. The regression was however ran with and without this outlier, and the results are very similar in terms of the slope of the regression and the polygons deemed good value for their size. The results presented are for the regression with all polygons included.

The regression line is shown in Figure 10.7. The predicted, or expected, log(nestsXgampoly) for each polygon, based on the relationship with polygon size discovered in the linear regression, was calculated, and then converted back to a nestsXgam value for the polygon. Those polygons whose ACTUAL nestsXgampoly value was higher than its expected value were highlighted. These polygons are shown in Figure 10.8.

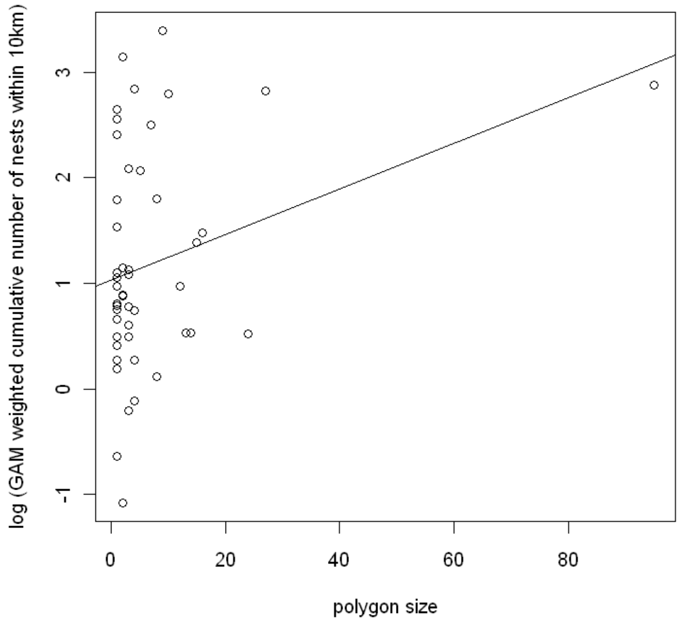


Figure 10.7. Linear regression line for the average GAM weighted cumulative number of nests against polygon size for Orkney.

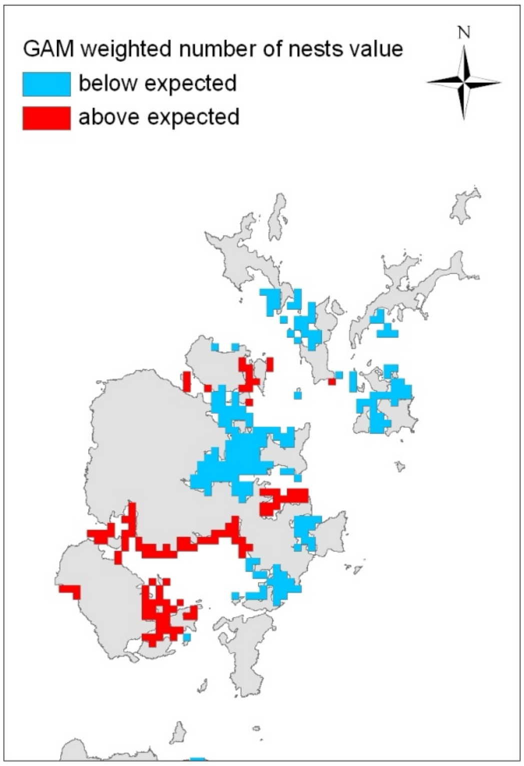
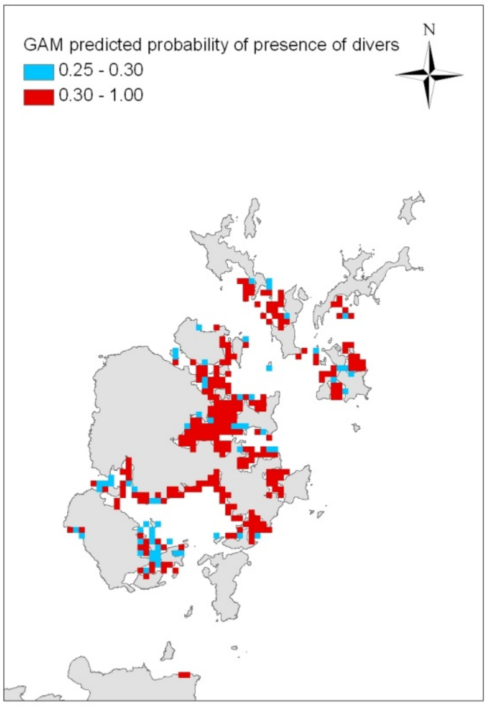


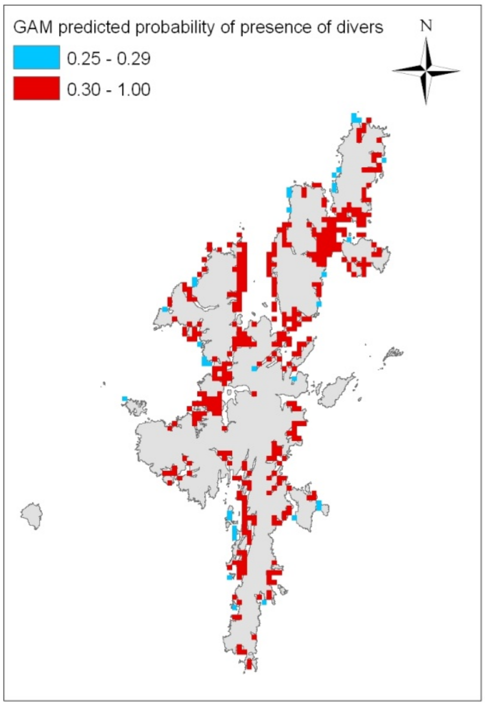
Figure 10.8. Polygons value based on the linear regression of average GAM weighed number of nests against polygon size for Orkney. Polygons with a value above expected, and therefore representing good value for their size, are shown in red, those below are shown in blue.

10.2.3 Maximum Curvature of GAM predictions

Given the lack of nest distribution data on the western isles, and therefore the necessity to rely on GAM prediction data alone in deciding which are the most important cells, maximum curvature was applied to the cell by cell GAM values around Orkney and Shetland for comparison with the results of applying maximum curvature to the GAM weighted nests data. For Orkney, the threshold chosen by maximum curvature is 0.30, and for Shetland the threshold is 0.29. The areas that are chosen by using the GAM prediction for maximum curvature are shown in Figure 10.9 below. These are much larger than the areas chosen when looking at GAM weighted nest data.



a)



b)

Figure 10.9. Cells above the GAM predicted value threshold selected by maximum curvature in red, with all cells not meeting the selected threshold shown in blue, for Orkney (a) and Shetland (b).

Although the results may not be comparable to those we would get if we had complete nest census data, due to lack of an alternative, maximum curvature was applied to the GAM output for the western isles. This results in a GAM prediction of 0.3254 at the point of maximum curvature (Figure 10.10).

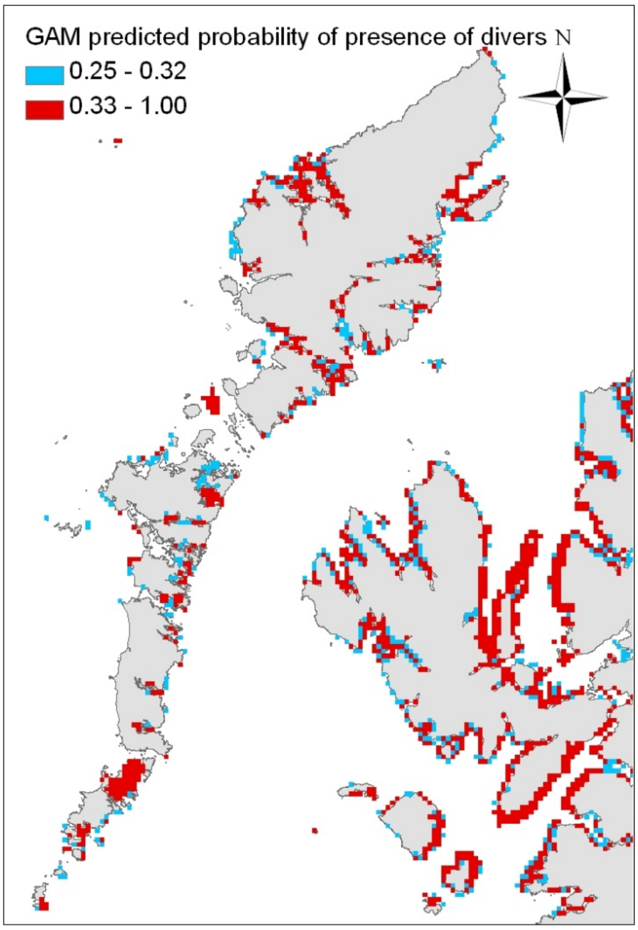


Figure 10.10. Cells above the GAM predicted value threshold selected by maximum curvature in red, with all cells not meeting the selected threshold shown in blue, for the western isles.

Although there is no complete nest census for the western isles, and we can therefore not use the potential density (number of nests within foraging range) to help us prioritise areas, we can restrict our selected cells to those within known range of at least one nest. The Dillon *et al* (2009) survey was designed to achieve a complete census in the Northern Isles and two Special Protection Areas (SPAs) in the Hebrides: Rum and Mointeach Scadabhaigh, and a stratified sample of 5-km grid squares in the rest of the known breeding range. Strata were based on overlap with terrestrial SPAs, and only 27.8% of cells overlapping SPAs, and 9.3% of cells not overlapping SPAs, were sampled. Thus, although restricting our surface to those cells within known range of at least one red throated diver nest avoids us protecting areas which are not potentially used by any breeding red throated divers, we cannot say that all areas NOT within our suite are not important areas potentially used by breeding red throated divers. To minimise this risk, additional nest distribution data from other sources such as the soon to be released BTO breeding bird atlas ought to be sought. Restricting the maximum curvature selected cells to those within range of the nest site data from Dillon *et al* (2009) and the JNCC surveys (ie those presented in the main Dean *et al* red throated diver report) produces the map shown in Figure 10.11.

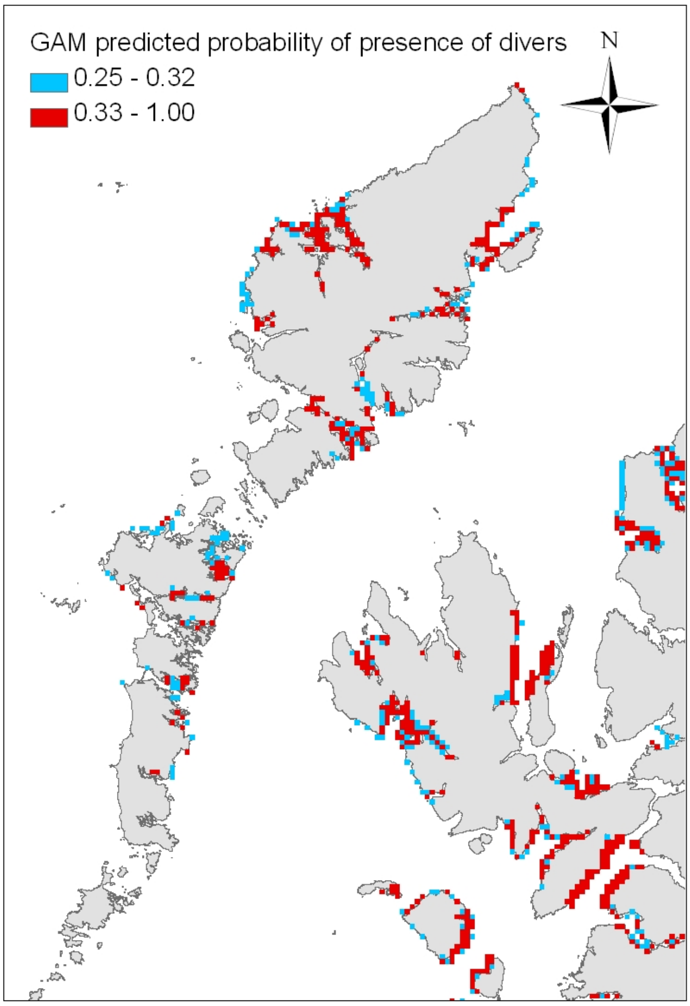


Figure 10.11. Cells above the GAM predicted value threshold selected by maximum curvature in red, with all cells not meeting the selected threshold shown in blue, for the western isles, with only those cells which are within foraging range of a known nest site shown.

10.3 Discussion

The options in Table 10.1 represent those that were deemed potentially appropriate for the data we have, and which might be expected to produce a selection of cells or areas which are deemed the most important for foraging breeding red throated divers. Which of these methods is deemed the most appropriate depends in part on the value metric that we choose (number of nests within foraging range, GAM predictions, are a combination of these). The combination of these metrics has been identified as the most appropriate because it incorporates both suitability and accessibility to observed nest sites. Where the nest distribution data is not available, GAM predictions must be used instead. Of those methods in Table 10.1, only the second, maximum curvature is suitable for applying to GAM predictions alone.

Referring to the list of requirements of a boundary delineation in the introduction: Both methods presented here minimise subjective judgements, they both use a trade-off between number of nests protected and size of area, they are both relatively easy to explain. Only the maximum curvature method can be applicable across all sites (if we apply it to the GAM predictions), and neither of these methods can be assessed for how well they contain the highest densities of birds.

Both of the methods trialled have produced a selection of areas or cells that could be considered as the most important for consideration for classification. There is considerable overlap of selected cells/areas in the north western part of the Shetland isles and the southern Shetland waters between the maximum curvature of GAM weighted nests data and the polygon regression, but one noticeable discrepancy in the north eastern side; the large polygon in the waters around eastern Yell and southern Unst, as well as a couple of smaller areas further down the eastern waters. The maximum curvature method chooses a cut off in value, and ALL cells above this value are included in the selection of cells for consideration. The polygon method on the other hand highlights areas which are, for their size, of high value, and so the threshold value for inclusion varies with polygon size. So for example we see that although individual cells within the large polygon to the east of Yell are of high individual value, the polygon as a whole is not of high value for its size.

Similarly, on Orkney, we see differences in results between these two approaches, with a large polygon on the central northern mainland being rejected by the polygon regression method, but many cells within this being selected by maximum curvature. Also some smaller polygons around Rousey show differences between the two methods.

Maximum curvature of the GAM predictions tends to lead to most cells being above the value at the point of maximum curvature, and hence being selected as important. This is an issue for the western isles because we do not have nest data to base our selection on. However, we do have some, selected, survey data, and it may be that we can assume this has been targeted towards the most important or likely nesting areas for red throated divers on these islands. If that is the case, then we can restrict our maximum curvature analysis to those cells which are within foraging range of at least one known nest. This avoids the risk of selecting cells for protection which cannot be actually used by any red throated divers.

10.4 References

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