

OFFSHORE RENEWABLES JOINT INDUSTRY
PROGRAMME (ORJIP) FOR OFFSHORE WIND



Apportioning seabirds seen-at-sea (AppSaS): Apportioning in the non- breeding season tool (ANBS)

User Guide to the ANBS tool

February 2024



ORJIP Offshore Wind

The Offshore Renewables Joint Industry Programme (ORJIP) for Offshore Wind is a collaborative initiative that aims to:

- Fund research to improve our understanding of the effects of offshore wind on the marine environment
- Reduce the risk of not getting, or delaying consent for, offshore wind developments
- Reduce the risk of getting consent with conditions that reduce viability of the project.

The programme pools resources from the private sector and public sector bodies to fund projects that provide empirical data to support consenting authorities in evaluating the environmental risk of offshore wind. Projects are prioritised and informed by the ORJIP Advisory Network which includes key stakeholders, including statutory nature conservation bodies, academics, non-governmental organisations and others.

The current stage is a collaboration between The Carbon Trust, EDF Energy Renewables Limited, Ocean Winds UK Limited, Equinor ASA, Ørsted Power (UK) Limited, RWE Offshore Wind GmbH, Shell Global Solutions International B.V., SSE Renewables Services (UK) Limited, TotalEnergies OneTech, Crown Estate Scotland, Scottish Government (acting through the Offshore Wind Directorate and the Marine Directorate), and The Crown Estate Commissioners.

For further information regarding the ORJIP Offshore Wind programme, please refer to the [Carbon Trust website](#), or contact Ivan Savitsky (ivan.savitsky@carbontrust.com) and Žilvinas Valantiejus (zilvinas.valantiejus@carbontrust.com).

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- NatureScot

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1.2 Who we are

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3 Summary

The Apportioning in the Non-Breeding Season (ANBS) tool is designed to apportion breeding adult common guillemot (*Uria aalge*) and razorbill (*Alca torda*) in the non-breeding season within the UK Exclusive Economic Zone. The approach uses geolocator tag information collected from both species over three field seasons between 2017 and 2020 from up to 12 colonies. Utilisation distributions were derived from the geolocators and simulations were generated based on locational uncertainty, producing 100 simulations for each species, colony, and month. The tool propagates locational uncertainty through the analysis to give mean estimates of apportioning along with estimates of uncertainty. The tool uses populations defined in BDMPS, including UK SPAs, UK non-SPAs, and non-UK non-SPAs (Furness, 2015). The tool can be used in *map mode*, in which colonies of interest are selected and mean estimates of apportioning are mapped along with 95% CIs. Alternatively, *footprint mode* allows users to upload an offshore renewable energy footprint and mean estimates of apportioning with 95% CIs are calculated based on the spatial extent of the footprint. User-defined inputs allow flexibility in how the ANBS tool is run including the ability to choose the species, months, and season, although default values are provided to aid users in their choices. Populations from the BDMPS are provided along with the number of breeding pairs of adults, which can be changed by users. A hierarchical approach to calculating apportioning is used, based on whether colonies are data rich (using utilisation distributions) or data poor (where utilisation distributions are unavailable). A user-defined distance threshold (with a default value of 270 km) determines how colonies with geolocator data are linked to all other UK SPA colonies. Colonies within the distance threshold are assigned a weighted proportion of the utilisation distributions from colonies with geolocator data, whereas colonies outside of the distance threshold use apportioning from BDMPS.

When in footprint mode, usage is aggregated over the footprint by colony and simulation. Mean, lower, and upper 95% CIs are calculated for each colony and scaled to population level using the number of breeding pairs of adults multiplied by 2. For colonies relying on BDMPS, usage is calculated as the proportion of time adult birds spend in the specified BDMPS region multiplied by the footprint area divided by the BDMPS region area. To scale to population level, each colony is multiplied by the number of pairs of adult breeding birds and multiplied again by 2 to get to the total mean number of adult birds. Standard deviation is estimated by multiplying the standard deviation across all UK SPA colonies by the user-specified BDMPS uncertainty scalar. An uncertainty probability distribution is constructed from colony usage and the BDMPS standard deviation. Lower and upper 95% CIs are calculated from the probability distribution and scaled to population level by multiplying by the number of pairs of adult breeding birds and multiplied again by 2 to get to the total mean number of adult birds.

An output report is produced when running the tool, which presents a summary, user inputs, results in the form of tables and maps, caveats and limitations, and appendices showing system information.

4 How to use the ANBS tool

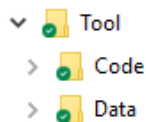
4.1 Set-up

The open-source software R v4.2.2 (<https://cran.r-project.org>) is required to be installed on the device you are running the ANBS tool. R can be downloaded to run on Windows, Linux, and Mac operating systems. However, the ANBS tool has only been tested to run on Windows.

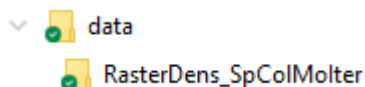
The ANBS tool runs in R and outputs a report into a pdf. To do this, Pandoc software is used. Pandoc is downloaded automatically with the open-source software RStudio (at least v 2022.07.1 Build 554) (<https://posit.co/download/rstudio-desktop/>), and so it is recommended that this software is also installed. Pandoc can be downloaded separately (<https://pandoc.org/installing.html>) without RStudio but the ANBS tool has not been fully tested to incorporate this set-up.

The ANBS code can be downloaded from GitHub (<https://github.com/thecarbontrust/ANBS>) as a zip file. Extract this file to a permanent location on a device, i.e. the tool will not be able to run if it is stored on a USB drive. The tool will extract automatically and be stored in a folder called **Code**.

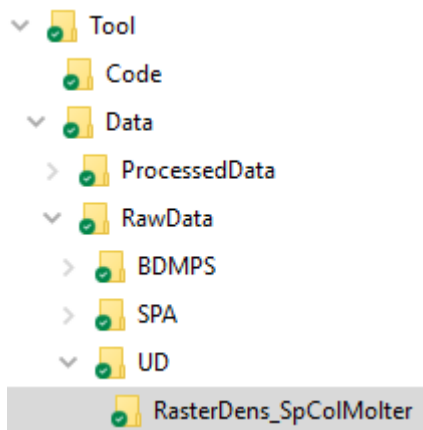
The ANBS tool uses data which must also be downloaded. This can be extracted and comprises of a folder called **Data** with sub-folders called **RawData** and **ProcessedData**. Further sub-folders are present, and the data are explained in detail below. The structure of the data folders must be preserved for the tool to work correctly. To enable the tool to find the data automatically and run correctly, the **Data** folder should be stored at the same level as the **Code** folder.



One set of data required to run the ANBS tool are too large to put on the GitHub repository. Therefore, seabird utilisation distribution (UD) data should be downloaded (<https://ctprodstorageaccountp.blob.core.windows.net/prod-drupal-files/direct-downloads/data.zip>). The **data.zip** folder should be extracted to a **data** folder. Within **data**, another folder called **RasterDens_SpColMolter** contains 16,200 UD .rds files.



To ensure that the ANBS tool works correctly, the **RasterDens_SpColMolter** folder and all its contents should be placed in the location of the ANBS tool, within the folder structure **Tool/Data/RawData/UD**



4.2 Running the tool

The tool is run either from the RStudio or the R console.

Open the file **RunANBSTool.R**

- If you open the file in RStudio, click on the  button in the top-right toolbar.
- If using the R console, the file should run automatically.

Navigate to the file called **10.RunANBSTool.rmd**, which is in the **Code** folder. Click **Open** or double-click the selected file.

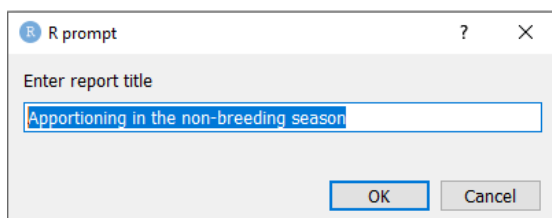
A set of pop-up boxes will appear for the user inputs parameters. The boxes have instructions of how to select the relevant inputs but more detail on the user input parameters is below.

The tool will run in the background and a report will be generated as a pdf file, output to the same folder as the **Code** is saved.

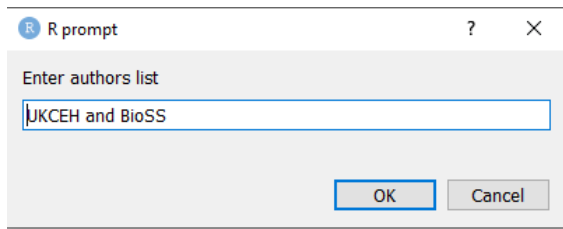
4.3 Input parameters

4.3.1 Title and authors

Two pop-up boxes will appear, the first asking for the user to input a title of the output report. The default is **Apportioning in the non-breeding season**.

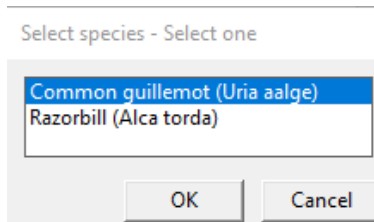


The second box is for the user to enter an author list to appear in the output report. The defaults is **UKCEH and BioSS**.



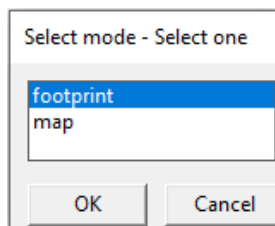
4.3.2 Species

The options are **Common guillemot (*Uria aalge*)** or **Razorbill (*Alca torda*)**. One species may be selected per run of the ANBS tool.



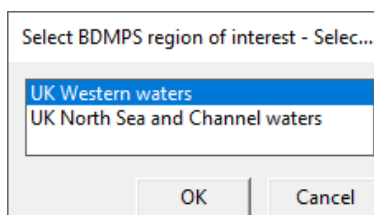
4.3.3 Mode

The tool can be run in two modes: **footprint** or **map**. Footprint mode is the default and the tool calculates apportioning based within the specified footprint. Map mode does not require a footprint and calculates apportioning over the entire spatial extent of the chosen BDMPS region.



4.3.4 BDMPS region

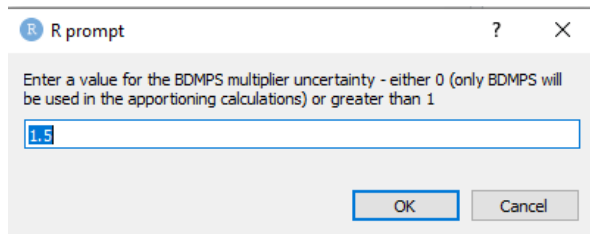
If **map** mode is chosen, the user is requested to select which BDMPS region the apportioning will be calculated over. The default is **UK Western waters**. One region must be selected.



4.3.5 BDMPS uncertainty scalar

Uncertainty is estimated for both geolocator and BDMPS colonies. BDMPS colonies do not have uncertainty associated with them, so uncertainty for these colonies is derived by calculating the standard deviation across colonies and simulations utilisation distributions and multiplying by a scalar. The default for the scalar is 1.5 to ensure that colonies using BDMPS (which are data poor) do not result in having values of uncertainty equivalent or lower

than colonies that use geolocator information (which are data rich). Users can change this value to any number greater than 1. Setting the value to 0 will result in only BDMPS colonies being used in the current tool run (i.e. no geolocator colonies will be included). If the BDMPS uncertainty scalar is set to 0, the apportioning results will not have uncertainty associated with them, and the results will be similar to the BDMPS (Furness, 2015).



R prompt

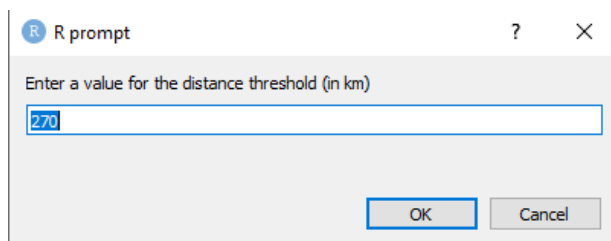
Enter a value for the BDMPS multiplier uncertainty - either 0 (only BDMPS will be used in the apportioning calculations) or greater than 1

1.5

OK Cancel

4.3.6 Distance threshold

The distance threshold defines the maximum distance (by sea) used to associate colonies with geolocator tag tracks with SPA colonies that do not have any tracking information associated with them. The default distance is 270km ([see WP3 report for details](#)), and any value greater than 0 can be inputted. If only BDMPS colonies are used (defined through setting the BDMPS uncertainty scalar to 0), the ANBS tool will automatically use a distance threshold of 0 and the distance threshold pop-up box will not appear to the user.



R prompt

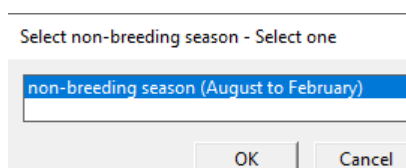
Enter a value for the distance threshold (in km)

270

OK Cancel

4.3.7 Season

Users can select which non-breeding season to use, which are aligned with the BDMPS seasons. For common guillemot, there is only one non-breeding season defined, **non-breeding season (August to February)** and so this is the only option presented in the pop-up box.

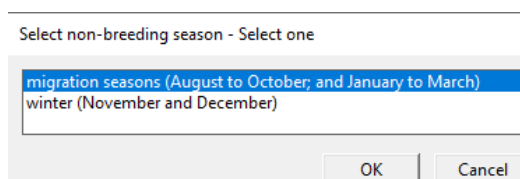


Select non-breeding season - Select one

non-breeding season (August to February)

OK Cancel

For razorbill, two seasons are defined, **migration seasons (August to October; and January to March)** and **winter (November and December)**. The user can select one of these.



Select non-breeding season - Select one

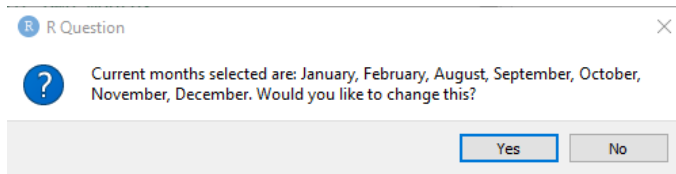
migration seasons (August to October; and January to March)

winter (November and December)

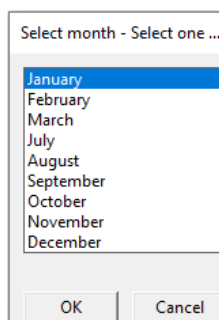
OK Cancel

4.3.8 Months

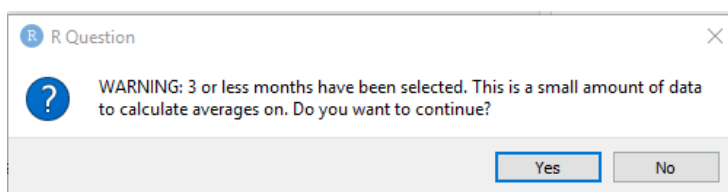
The months used to calculate apportioning from the geolocator utilisation distributions can be specified. Months available are July-March inclusive (data from April-June were not available as geolocator tags were attached between mid-June and early July). By default, the ANBS tool matches the **months** with the selected **season** (e.g. when **non-breeding season (August to February)** has been chosen, default months August-February are selected).



However, users may change the default months and select one or more months that are available. Multiple months can be chosen using CTRL + mouse left-click.



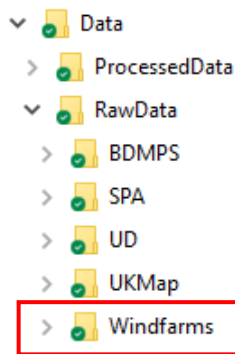
If less than three months are chosen, a warning message appears because estimating the mean and confidence intervals for colonies using small sample sizes can give unexpected results.



If only BDMPS colonies are being used in the tool run (i.e. BDMPS uncertainty is 0), the boxes to select **months** will not appear to the user, as these are only required when geolocator information is being used.

4.3.9 Footprint or colonies of interest

If **footprint** mode is selected, the user is requested to upload a .shp file of the footprint. The file cannot be stored on a portable drive, and it is recommended (although not essential) that it is stored within the file structure of the **Data** from the tool, e.g. adding a folder called **Windfarms** and storing the .shp file within this folder. A pop-up box allows the user to navigate to the chosen footprint file and upload it. The footprint file must contain a single polygon denoting the ORE footprint, which must be within the outline of the BDMPS regions (i.e. the UK EEZ).



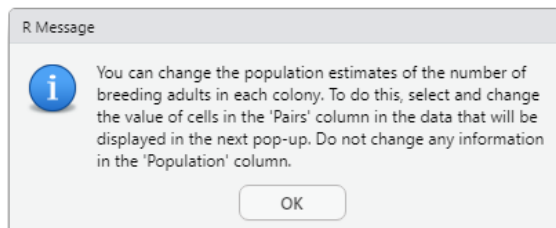
If **map** mode is selected, a pop-up box allows the user to select colonies of interest. Any selected colonies that are associated with geolocator utilisation distributions (i.e. not BDMPS colonies) will be mapped in the output report. And BDMPS colonies that are selected are not mapped in the output report as their distribution is uniform across the BDMPS region. Multiple colonies can be selected using CTRL + mouse left-click. The list of colonies shown is aligned with the BDMPS populations (Furness, 2015), and is dependent on user selections for **season** and **BDMPS region**.



4.3.10 Population sizes

Each colony has a default population estimate, which is defined as the number of breeding adult pairs. Colonies and default population sizes are derived from Furness (2015). The

number of breeding pairs of adults of any colony can be changed to any non-negative integer (whole number) if required. A pop-up box explains how to do this.



A data editor table appears and any value in the **Pairs** column can be edited. The **Population** column should not be edited, as this will cause the ANBS tool to error.

Data Editor		
File Edit Help		
	Population	Pairs
1	Ailsa Craig SPA	5247
2	Buchan Ness to Collieston Coast SPA	12928
3	Calf of Eday SPA	6300
4	Canna and Sanday SPA	3913
5	Cape Wrath SPA	27359
6	Copinsay SPA	5607
7	East Caithness Cliffs SPA	106500
8	Fair Isle SPA	13066
9	Farne Islands SPA	33532
10	Faroe Islands	1e+05
11	Flamborough and Filey Coast pSPA	39641
12	Flannan Isles SPA	9807
13	Forth Islands SPA	14674
14	Foula SPA	16615
15	Fowlsheugh SPA	30100
16	Germany and Denmark	5000
17	Handa SPA	37993
18	Hermaness; Saxavord and Valla Field SPA	4620
19	Hoy SPA	6300

4.4 Outputs

The output report (default name **Apportioning in the non-breeding season.pdf**) is outputted into the **Code** folder. The report changes dynamically depending on user inputs.

4.4.1 Summary

The summary gives an overview of the key parameters and outputs from the ANBS tool, including species, season, footprint (if selected), and BDMPS region. High-level estimates of mean apportioning, population, and birds per km² within either the footprint (*footprint mode*) or BDMPS region (*map mode*), and the corresponding lower and upper 95% CIs for each metric (if geolocator colonies are used). The number of BDMPS and geolocator-based colonies are presented.

If geolocator colonies are included, a table summarises the geolocator colonies, SPA codes, and sample sizes of tags used in the analysis.

4.4.2 **User inputs**

Two tables are presented. The first shows most of the input parameters, whilst the second shows the colonies and estimates pairs of breeding adults used in the ANBS tool run.

4.4.3 **Results**

4.4.3.1 **Apportioning**

This section shows two tables: the first shows all colonies used in the apportioning calculations with the number of adults from each population, the number of adults per km² from each population, and the proportion of adult birds from each colony that contribute to the total in the chosen area. If geolocator colonies are included in the analysis, lower and upper 95% CIs are presented for each metric. The metrics are shown for either the total footprint (in **footprint** mode) or over the selected BDMPS region (in **map** mode). The second table shows the cumulative totals for number of adults (at a population-level), adults per km² and the proportion of adult bird from each colony that contribute to the total in the chosen area. If geolocator colonies are included, lower and upper 95% CIs for each metric are included. The column is sorted in descending order so that the colony that contributes the highest proportion of usage is ranked first in the table.

4.4.3.2 **RAG status**

A Red-Amber-Green (RAG) status map shows all colonies that contribute to the ANBS tool run (Figure 1). Tracked SPA colonies are defined as colonies where geolocator birds were tagged and are denoted by dark green circles. Tracked non-SPA colonies (light green circles) are also used to calculate apportioning by contributing some of their usage to untracked SPA colonies. However, tracked non-SPA colonies (which also include SPAs that were not included in the BDMPS tables for the species, for example because the species of interest was not a qualifying interest in SPA designation) themselves are not directly considered within the apportioning calculations because BDMPS already accounts for these colonies within the aggregations of non-SPA colonies so including them within the calculations would lead to double counting). Untracked SPA colonies that are within the user-specified distance threshold of at least one tracked colony are denoted by amber circles. BDMPS colonies, which are outside the distance threshold, and therefore could not be associated with any tracked colony are denoted by red circles. It should be noted that the apportioning of non-UK populations (Norway, Germany and Denmark, and Faroe Islands) and aggregated UK non-SPA populations (UK North Sea, UK West coast) will always be determined through BDMPS regardless of how large the distance threshold is set. These populations are high-level aggregations covering large spatial areas, and so cannot in any meaningful way be linked to a single colony location (which is a prerequisite for associating them with tracked colonies).

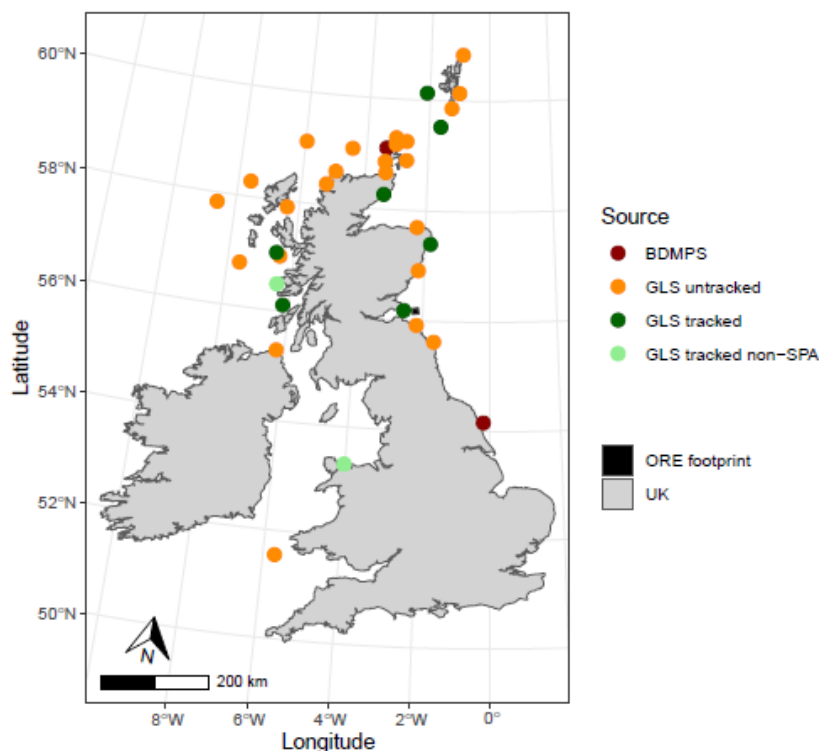


Figure 1. Example of RAG status map showing colonies used in the ANBS tool run. Red = BDMPS, Amber = GLS untracked, Green = GLS tracked, Light Green = GLS tracked non-SPA

4.4.3.3 Apportioning maps

If geolocator colonies are included in the model run, a set of maps will be included in this section. In **footprint** mode, the two tracked or untracked SPA colonies that contribute highest to apportioning in the footprint are shown as maps of mean number of adult birds per 10km² along with lower and upper 95% CIs. In **map** mode, user-specified colonies of interest will be shown as maps of mean number of adult birds per 10km² along with lower and upper 95% CIs. If only BDMPS colonies are included in the model run, this section will not appear in the output report.

4.4.4 Caveats and limitations

Caveats, limitations, and assumptions of the data and ANBS tool are reported.

4.4.5 Appendices

Information on the device operating system, version of R and packages used in the ANBS tool run are listed in Appendix 1.

5 Data

All data required to run the ANBS tool are provided, except for the user-specified offshore renewable footprint. The integrity of the **Data** file structure should be preserved to ensure the tool runs correctly.

The datasets on BDMPS population sizes (4.1.1), BDMPS spatial distribution (4.1.2), SPA list (4.2.1) and SPA coordinates (4.2.2) correspond to the versions within the MSS Cumulative Effects Framework (CEF) Data Store on 7 April 2021 but several of these datasets were required to be amended for the ANBS tool. In these instances, the folder where the data is located has an updated name, e.g. jul2023. The datasets on seabird distributions from geolocator data (4.3) and BDMPS regions (4.1.3) are not currently part of the CEF.

5.1 BDMPS

5.1.1 Population sizes

These data show the estimated number of breeding adults by species for each UK SPA colony, aggregate of UK non-SPA colonies, or aggregate of overseas colonies. The data were derived from Furness (2015), appendices (Tables 1-69) and formatted for accessibility.

Folder	202_BDMPSpopsizes
Version	vers_bdmppopulationsizes
Data	bdmppopulationsizes.csv
Fields	fields_bdmppopulationsizes.csv
Metadata	metadata_bdmppopulationsizes.rmd

5.1.2 Spatial distribution

These data provide estimates of the proportion of adults and immature birds by UK SPA colony, aggregate of UK non-SPA colonies, or aggregate of overseas colonies, BDMPS region, season, and species. The data were derived from Furness (2015), appendices (Tables 1-69) and formatted for accessibility.

Folder	704_BDMPSspatdist
Version	vers_bdmppspatialdistribution
Data	bdmppspatialdistribution.csv
Fields	fields_bdmppspatialdistribution.csv
Metadata	metadata_bdmppspatialdistribution.rmd

5.1.3 Regions

These data show the two BDMPS regions (UK North Sea waters and Channel and UK Western waters) as polygons in a .shp file with projection ESRI:102017.

5.2 SPA

5.2.1 SPA list

List of Special Protection Areas (SPAs) included in the Cumulative Effects Framework (CEF). The data were created by BioSS by using an R script to extract SPA sites names and codes Nature 2000 site details then matched by name against SPAs in the JNCC SPA species designations and in the Seabird Monitoring Programme (SMP) and BDMPS data. This automated process provided a draft version of this file, indicating which SPAs were to be included in the CEF and how, but the final version was then created by JNCC by manually

modifying this file to adjust situations where the automated rules did not yield the best decision.

Folder	201_SPAList
Version	vers_spalist
Data	spalist.csv
Fields	fields_spalist.csv
Metadata	metadata_spalist.rmd

5.2.2 SPA coordinates

The CEF uses a list of seabird colonies or SPAs including coordinates representing their locations. Within the CEF, the SPA coordinates are given by a single point and all distances and flights are measured from this point. Where possible, the point location is taken from the SPA Site Details dataset (derived from Natura 2000) but some have been amended for this dataset. Calculating distance by sea between colonies, which links geolocator tracked colonies to other colonies based on a distance threshold, requires colonies grid cells to be at-sea. Therefore, where colonies are exclusively on land, the location has been moved to the nearest sea location.

Folder	207_SPACoords
Version	vers_spacoordinates
Data	spacoordinates.csv
Fields	fields_spacoordinates.csv
Metadata	metadata_spacoordinates.rmd

5.3 Seabird Utilisation Distributions (UD)

Full details of common guillemot and razorbill utilisation distributions can be found in the [AppSaS WP3 report](#). In summary:

Geolocator tags (Biotrack model MK3006 and Migrate Technology Intigeo models C65, F100 and C65-Super, under licence from the British Trust for Ornithology) were deployed on 695 common guillemots and 339 razorbills during three breeding seasons (June-July 2017, 2018 and 2019) at 12 breeding colonies around the north of the UK (Buckingham et al. 2022). The geolocators measured light levels, saltwater immersion and sea-surface temperature, from which daily locations were estimated. Adults were recaptured during each breeding season, resulting in a deployment duration of one to four years. The data were pooled data from three non-breeding seasons: 2017-18, 2018-19 and 2019-20.

Using the R package *probGLS*, two locations per day were derived from the geolocators. Integrating variables of light, saltwater immersion and temperature data to determine the most likely track reduces geolocation error (Phillips et al. 2004; Halpin et al. 2021) and allowed estimates of locations during the equinoxes and surrounding periods, unlike methods that solely rely on light data. Multiple iterations were run to estimate the locational error associated with each track of the geolocator data (Dunn et al. 2020; Buckingham et al. 2022).

The utilisation distribution (UD) for birds from each tracked colony during each month of the non-breeding season (July – March) was calculated using kernel density estimation from R package *adehabitatHR* (Calenge 2006). Bivariate normal kernels were used with ad-hoc

smoothing and a grid cell size of 100km². Any density (5%) that was on land as a result of the kernel smoothing was removed. Buckingham et al (2022) conducted a bootstrapping procedure to calculate 50% kernel density contours for each dataset to determine whether sample sizes were sufficient to capture colony- and year-specific distributions for 2017-18 and 2018-19. The results informed the selection of colonies for kernel density estimation, which excluded Farnes guillemots, Foula razorbills and Colonsay razorbills.

Locational uncertainty was accounted for by applying kernel smoothing separately to the simulated tracks within each of the 100 iterations of *probGLS*. This resulted in 100 simulated kernel density estimates for each tracked colony for each month of the non-breeding season.

Utilisation distributions of 100 simulated iterations were produced by species, colony, and month and were stored as .rds files.

5.4 UK Map

Global Self-consistent, Hierarchical, High-resolution Geography Database (GSHHG) shoreline data version 2.3.7 from NOAA were used to represent land, available from <https://www.ngdc.noaa.gov/mgg/shorelines/> (Wessel & Smith, 1996). The data were reprojected to of North Pole Lambert Azimuthal Equal Area, datum World Geodetic Series 1984 (ESRI:102017).

5.5 Distance to colony

When calculating distances by sea between colonies, a surface on which to base movement between cells is defined. Termed a cost grid, the surface allows movement between cells at-sea but penalises movement onto land, effectively creating a barrier. In this way, distances between colonies can be calculated at-sea.

6 Methodology

The ANBS tool uses a projection of North Pole Lambert Azimuthal Equal Area, datum World Geodetic Series 1984 (ESRI:102017). This projection was chosen because the spatial extent of the geolocator utilisation distributions was comparatively large compared to the UK and equal area projections retain the relative size of areas in the map. The ANBS tool was written using R version 4.2.2 (2022-10-31 ucrt), Pandoc version 2.18, and RStudio 2022.07.1+554 "Spotted Wakerobin" Release (7872775e, 2022-07-22) for Windows.

The tool has a simple interface comprising of a series of pop-up boxes where users can choose one or more components from a selection, or inputs values. The R library *svDialogs* (Grosjean, 2022) was used to create the pop-up boxes and create warning and error messages when incorrect or invalid values are input.

All data are automatically loaded into an R workspace using bespoke functions and projections and transformed to ESRI:102017 where required. Based on user inputs defining species and months of interest, relevant utilisation distributions from geolocator colonies were loaded (termed *tracked* colonies). Using the R library *raster* (Hijmans, 2023), the mean was taken across months and the resulting raster was standardised to 1 for each geolocator colony. The spatial extent and resolution (10 km x 10 km) of the raster and the 100 simulations were preserved. A cost distance layer based on directional travel in 16 directions was created using the R library *gdistance* (Van Etten, 2017). The layer provided a surface at a spatial resolution of 0.62 km x 0.92 km, which allowed travel at-sea but penalised travel on land. In this way, at-sea distances between tracked colonies and UK SPA colonies (termed *untracked* colonies) were calculated.

Apportioning relies on knowledge of the spatial distribution of birds at each colony. A hierarchical approach was developed to attribute utilisation distributions from the tracked colonies for as many UK SPA untracked colonies as is reasonable, based on a distance threshold. The distance threshold has a default value of 270 km, based on rationale set out in the WP3 report of this project. However, users have the option of changing this threshold to any non-negative integer. If distance threshold is set to 0, geolocator information is not used in the tool run and the resulting apportioning should be consistent with BDMPS values. For each untracked colony (j), the distance to each tracked colony (d_{ij}) is subtracted from the distance threshold (d). Any tracked colony above the distance threshold is not considered (and its distance is set to NA). For tracked colonies (i) that are within the distance threshold, a weighting (w_{ij}) is applied to determine the contribution that each tracked colony makes to the untracked colony's utilisation distribution.

$$w_{ij} = (d - d_{ij}) / \sum_{i=1} (d - d_{ij}) \text{ where } \sum w_{ij} = 1$$

Based on the assumption that colonies that are nearer are more similar, the weighting allows tracked colonies that are closer to an untracked colony to have a higher weighting than tracked colonies that are further away. If no tracked colonies are within the distance threshold of an untracked colony, BDMPS is used to calculate apportioning for the untracked colony (termed *BDMPS* colony). All tracked colonies associated with an untracked colony were used to build 100 realisations of utilisation distributions for the untracked colony. Selection probabilities were constructed using $P = w_{ij}/100$ and a multinomial distribution selected 100 utilisation distributions from all possible colony/simulation combinations, based on the

selection probabilities. Tracked colonies that did not appear in the BDMPS because the selected species was not a qualifying SPA feature (and therefore they were UK non-SPA colonies with respect to the selected species), were excluded from the analysis at this point (although some or all their spatial usage contributed to the utilisation distributions of untracked colonies).

If footprint mode is selected, the footprint is overlaid with the BDMPS regions to determine which BDMPS region the footprint is located in. If the footprint is in more than one BDMPS region, the user can select which BDMPS region to assign the footprint to. If any of the footprint is outside of the UK EEZ, the ANBS tool will produce an error and the user will be required to upload a footprint that is within the UK EEZ in the next tool run. If map mode is selected, the user selects a BDMPS region and the tool run is calculated over this region. The area of the footprint/region is calculated in km². Usage for all UK SPA colonies (i.e. tracked and untracked) is extracted within the footprint/region. Usage is reweighted to account for cells partially within the footprint polygon. The usage is aggregated within the footprint/region by colony and simulation.

For each BDMPS colony (m), usage (μ_m) was calculated as the proportion of time that adult birds from the colony spend in the specified BDMPS region multiplied by the footprint area divided by the BDMPS region area. Although the scaling from the BDMPS region to the footprint is not required for apportioning in a context where only BDMPS is being used (because the same scaling applies to all populations for which BDMPS is being used), this scaling is essential to convert BDMPS into units that are comparable to the geolocator-based maps, and therefore an essential part of the hierarchical approach.

To estimate uncertainty for BDMPS colonies (i.e. non-UK non-SPAs, UK non-SPAs, and UK SPAs outside the distance threshold to any tracked colony), standard deviation (σ_{BDMPS}) across all usage within the footprint for UK SPA colonies was taken on a logit scale and then multiplied by the user-specified BDMPS uncertainty scalar. Calculating the standard deviation over all UK SPAs colonies aims to capture within- and between- colony variation. Finally, simulations ($n=100$) were generated from a normal distribution $N(\mu_m, \sigma_{BDMPS})$ and the inverse logit was taken to result in an uncertainty probability distribution on the original scale.

The usage for the geolocator and BDMPS colonies are combined. To scale to population level within the footprint/region, the mean usage is multiplied by the number of pairs of adult breeding birds and multiplied again by 2 to get to the total number of adult birds. The number of birds per km² is calculated by dividing by the footprint area. To estimate apportioning, each simulation of the number of adult breeding birds is divided by the sum of all usage in each simulation within the footprint/region (scaling to one). The mean and lower and upper 95% confidence intervals are then calculated for each metric for colony.

If geolocator (tracked and untracked) colonies are not included in the tool run, the process is as above but lower and upper 95% confidence intervals are not calculated. Confidence intervals can only be calculated when tracked and untracked colonies are included because estimating uncertainty for BDMPS colonies is dependent on calculating the uncertainty associated with tracked and untracked colonies and then multiplying the uncertainty to scale it for BDMPS colonies.

7 Constraints

- Apportioning for one species (common guillemot or razorbill) can be calculated in each run of the ANBS tool. To obtain estimates of apportioning for both species, two runs of the tool are required.
- An ORE footprint which is a single polygon .shp file can be loaded in each run of the tool. If multiple ORE footprints are required, multiple runs of the tool must be carried out.
- Given that geolocator tags were placed on adult breeding birds, the ANBS tool does not include immatures in the apportioning calculations as information about their distributions are not available.
- ORE footprints must be located entirely within the UK Exclusive Economic Zone (EEZ). If the spatial extent of the footprint spans more than one BDMPS region, the user can select which region to use in the tool run.
- The list of populations to be apportioned is fixed to be as in BDMPS (Furness, 2015), although the sizes of these populations may be modified by users.
- The BDMPS region boundaries are treated as fixed, and the outer boundaries are assumed to be given by the boundary of the UK EEZ.

8 Glossary of terms

Term	Description
BDMPS	Biologically Defined Minimum Population Scales
Footprint	Polygon(s) representing an area of an ORE development
Footprint mode	Footprint mode of is the default and the tool calculates apportioning based within the specified footprint.
Map mode	Map mode does not require a footprint and calculates apportioning over the entire spatial extent of the chosen BDMPS region.
ORE	Offshore Renewable Energy
SPA	Special Protection Area
UK EEZ	UK Exclusive Economic Zone

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10 Appendix

10.1 Case Studies

Five case studies (Table 1) have been defined to provide examples of the report that is produced when the ANBS tool is run. The case studies were chosen to represent a wide range of input parameters but are not a set of exhaustive possibilities that cover all scenarios. Five case studies were chosen so that users could refer to them quickly and concisely in this User Guide. In summary, the case studies are:

Case study	Species	Mode	Usage	Distance threshold	Season	Months	BDMPS region
1	Common guillemot	Footprint – East Scotland	GLS & BDMPS	270 km	non-breeding season (Aug-Feb)	Aug-Feb	UK North Sea and Channel waters
2	Razorbill	Footprint – East England	GLS & BDMPS	150 km	migration seasons (Aug-Oct; Jan-Mar)	Aug-Oct; Jan-Mar	UK North Sea and Channel waters
3	Common guillemot	Footprint – West England	BDMPS-only	0 km	non-breeding season (Aug-Feb)		Western waters

4	Razorbill	Map	GLS & BDMPS	270 km	winter (Nov-Dec)	Nov-Dec	Western waters
5	Razorbill	Map	BDMPS-only	0 km	migration seasons (Aug-Oct; Jan-Mar)		UK North Sea and Channel waters

Table 1. Parameters of the five case studies used to illustrate running the ANBS tool.

10.2 Footprints

For the case studies, simulated footprints of offshore wind farms were used, based on the ORJIP Bird Sensitivity Mapping Phase II project (Figure 2Figure 1). These are designed to be realistic based on area and location around the UK coastline but do not relate to any specific offshore wind farm development at any stage of the planning, consenting, or development process. For the case studies, three footprints were chosen to represent a range of locations around the UK: Firth of Forth in east Scotland, north-east of The Wash in east England, and at the edge of Liverpool Bay in west England.

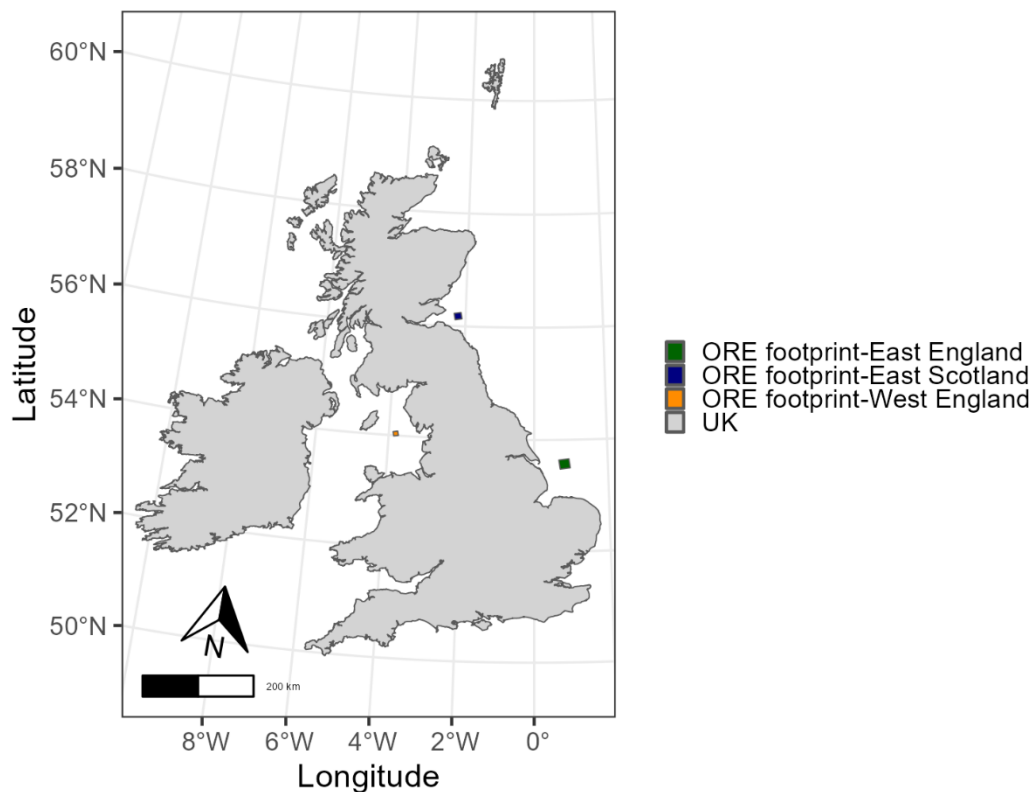


Figure 2. The three simulated ORE footprints used in the case studies, which are based on the some of the footprints used for the ORJIP Bird Sensitivity Mapping Phase II project.

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