OFFSHORE RENEWABLES JOINT INDUSTRY PROGRAMME (ORJIP) FOR OFFSHORE WIND

AppSaS – Apportioning seabirds seen-at-sea

WP1 - Review

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working to accelerate offshore consenting

Contents

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.

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Who we are

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1. Introduction

Within the environmental impact assessment process for offshore wind farms (OWFs) and marine birds, legislation requires an understanding of the potential *connectivity* between designated protected populations (Special Protection Areas, SPAs) and OWFs, and the magnitude of potential impacts from specific effects, such as collision risk. At-sea survey data (e.g. boat or aerial surveys) forms the basis for assessing baseline spatial abundance and distribution of seabirds within a wind farm footprint and the surrounding area. Tagging birds from breeding colonies provides a complimentary method for estimating spatial abundance of birds of known provenance. To assess the impacts of offshore renewables upon SPAs for all types of data, it is necessary to estimate the percentage of birds that may originate from each SPA, termed *apportioning*. That way, the potential numbers of birds impacted by specific effects can be ascribed to SPAs through potential connective pathways. However, there are many methods of deriving such apportioning (Table 1), and they vary by the type of data used at the outset and vary in complexity and assumptions used. These methods may also vary in application potential for specific bird species, and have also been the subject of specific workshops for targeted groups of species, such as gulls (e.g. Quinn 2019).

In general, apportioning relies on being able to estimate (a) the size of each breeding colony and (b) the spatial distribution (e.g. utilisation distribution; UD) of the birds from each colony, because the proportion of birds originating from each colony will be dependent on the product of the colony size and the estimated spatial distribution of birds from that colony. Apportioning methods differ largely based on the sources of data and statistical methods used to estimate colony-specific spatial distributions.

There are broadly five different approaches that are currently available:

a. Scottish Natural Heritage (SNH, now NatureScot) Apportioning Tool
b. Marine Scotland Science (MSS) Apportioning Tool
c. New methods using Global Positioning System (GPS) tracking data in a radial time-distance function approach
d. Biological Defined Meaningful Population Scales (BDMPS)
e. New methods for the non-breeding season based on light-level Geolocation (GLS) data

These are outlined below in Table 1. The SNH apportioning tool is split into two separate evaluations since a further update of the model has been developed, so the total number of methods considered is six (see Table 1). Here, we carry out a full appraisal of each method, assess the advantages and disadvantages of each and assess data requirements and availability.

Table 1. Summary of the main methods of apportioning.

Tool	Season	Methodology
Scottish Natural Heritage Apportioning Tool (SNH 2014)	Breeding	The proportion of birds that originate from each colony, at a particular at-sea location, is proportional to size of the colony (total number of breeding pairs) multiplied by the inverse of the squared distance between the point and the colony, based upon the great circle distance between the point and colony.
Scottish Natural Heritage Apportioning Tool (SNH 2018)	Breeding	The proportion of birds that originate from each colony, at a particular at-sea location, is proportional to size of the colony (total number of breeding pairs) multiplied by the inverse of the squared distance between the point and the colony, based upon the shortest distance by sea, reflecting the fact that most seabird species avoid flying over land.
Marine Scotland Science Apportioning Tool (Butler et al. 2020)	Breeding and non-breeding	GPS tracking data allow us to avoid assuming that bird densities decay in proportion to inverse distance squared, and to estimate this relationship empirically, and also allows other spatial characteristics of bird behaviour (e.g. habitat association) to be estimated and accounted for. The MSS Apportioning Tool uses the maps produced by Wakefield et al. (2017) from multi-colony GPS tracking data to estimate apportioning percentages for every cell on a relatively fine spatial grid that covers the entire UK Exclusive Economic Zone (EEZ).
Sage 2022	Breeding	Uses a time-distance approach in radial bands away from the colony that in turn can be used to quantify the number of birds that may use an OWF and that can then be ascribed back to breeding colonies; application on gulls has allowed assessment for offshore/onshore contexts. Generalisable at the species level and has application for theoretical evaluation of impacts of wind farms apportioned to colonies, building on the SNH method.
Biologically Defined Meaningful Population Scales (Furness 2015)	Non-breeding	Combines knowledge about the distribution of birds outside the breeding season gained from a range of data sources such as ringing recovery data, and to a lesser extent GPS tracking to apportion birds to SPA populations based on the relative sizes of the populations wintering in UK waters and, the size of the population within each SPA.
New GLS methods	Non-breeding	Light-level GLS data offer the opportunity to characterise area use and occupancy of species for adults and immatures during the non-breeding season part of the annual cycle, and using kernel density and overlap approaches, allowing further apportioning to potential colonies of origin.

2. Details of the approaches

Scottish Natural Heritage Apportioning Tool (SNH 2014, 2018)

Background

This rule-based tool was developed by SNH (now NatureScot) based on the principle that breeding season area usage of seabirds is limited by central place foraging constraints of individuals, and therefore can be determined by use of foraging ranges of seabird species (Thaxter et al. 2012). In turn, the relative proportional number of individuals and their connectivity to SPAs can be estimated using a theoretical approach based on three key pieces of information: the size of colonies, the area within foraging range that is sea, and distance, either Euclidean (SNH 2014, presented below) or shortest sea route upon later revision of implicit assumptions of travel constraints of seabirds over land (SNH 2018). The proportion of birds at location *i* that arise from colony *j* will be proportional to (SNH 2014):

$$\text{(Size of colony } j\text{)} * \text{(1 - proportion of the area within the foraging range of colony } j \text{ that is sea)} / \text{(Distance from location } i \text{ to colony } j\text{)}^2$$

[Equation 1]

The tool therefore uses three weighting factors: the size of the colony, the distance of the colony from a development, and the sea area. Colonies with greater populations will contribute more individual hypothetical birds to the assumed distribution in the area and thus the birds recorded within a survey of an OWF site will proportionally assign more individuals back to larger populations. Distance measurement is taken from the centre of an OWF to the centre of colonies, but it is acknowledged that complexities may arise in boundary issues; further, the inverse-squared distance weighting factor relates to expected declines over proportional area increase, with a further revised assumption included in SNH (2018) with improved realism whereby distance is calculated as the nearest straight-line over-sea distance.

Strengths and weaknesses

As noted by Butler et al. (2020), the SNH apportioning tools have no minimum data requirements, making them attractive for the study of large numbers of colonies across all breeding seabird species, and are very straightforward to apply, thus also representing cost-savings. The use of the method across all species is an advantage as more detailed methods such as the MSS approach may require tracking data that may not be feasible for some species. However, they suffer from a lack of biological realism, making strong assumptions; i.e. the lack of use of empirical data therefore assumes all populations have the same distance-decay function over space, and further do not account for effects of competition between neighbouring colonies and environmental heterogeneity that may influence space use within foraging range of species, i.e. homogenous species distributions are assumed. Many of these aspects are acknowledged in the approach documentation, hence the advice has therefore been for this approach to be used until a more complex, evidence-based model is developed (SNH 2018).

In the absence of GPS tracking data, however, it is still possible to extend the SNH Apportioning Tool so that it estimates the rate of decay of bird density with distance empirically for each species, using published foraging ranges, rather than fixing densities to always decay in proportion to inverse distance squared. This is a worthwhile task because further studies have found that the effect of distance to colony is crucial in determining the spatial distribution of seabirds during the breeding season (e.g. Wakefield et al., 2017), and systematic biases in quantifying the relationship between bird density and distance to colony will therefore lead to substantial errors in the calculation of apportioning percentages. More recent estimates of foraging ranges are also now available (Woodward et al., 2019), and these can be used to estimate the rate of decay with distance for each species and extend the SNH Apportioning Tool to use these estimated decay rates, as opposed to a flat 1/distance^2 fixed rate. The SNH Apportioning Tool further assumes that foraging ranges are the same for all colonies, but estimates of inter-colony variations in foraging ranges are also now available (Woodward et al. 2019), making it also possible to extend the tool to quantify the uncertainty in apportioning percentage that results from inter-colony variability in foraging range, using a simple simulation-based approach (MS SEANSE project; Searle et al. 2020).

Data requirements and availability

As mentioned, the method does not require extensive detailed data, and can be parametrised just with information on species foraging range and the size of individual colonies. The former foraging range information is available from reviews for many UK species using Thaxter et al. (2012) or more recent updates from Woodward et al. (2019). Colony size information for seabirds is available from the JNCC Seabird Monitoring Programme (SMP). As is common with all methods, it is important to make sure the eventual colony dataset upon which the apportioning is made is current and robust. To assess true distance decay functions within this approach, colony-specific tracking data can be used, constituting a further data requirement if such precision of the decay function is required.

Marine Scotland Science Apportioning Tool (Butler et al. 2020)

Background

The MSS Apportioning Tool provides an alternative to the SNH Apportioning Tool. This method (see Butler et al. 2020), introduces an R interface to a habitat-association modelling approach using species tracking data based on the method of Wakefield et al. (2017), thus, the MSS Apportioning Tool uses an empirical modelling approach based on these habitat use models. The Wakefield statistical method uses a weighted Poisson generalised linear mixed effects model (GLMM), considered to be cutting-edge – see Butler et al. (2020) for further appraisal of the method itself. At present the model is available for four species of seabird (European shag *Phalacrocorax aristotelis*, black-legged kittiwake *Rissa tridactyla*, common guillemot *Uria aalge*, razorbill, *Alca torda*), and as such these statistical environmental associations have already been determined, and thus the Poisson GLMM can be used to calculate apportioned percentages of birds for each colony and spatial location. The MSS Apportioning Tool therefore carries the same assumptions as the Wakefield method, that the colony-specific utilisation distribution (proportion of birds from colony *j* in area *i*) is a mathematical function of accessibility (e.g. distance to colony), neighbouring competition, and further environmental variables that may drive concentrations in distributions. As noted by Butler et al. (2020), the proportion of birds in area *i* that originate from colony *j* can be represented as:

(Proportion of birds from colony j within area i) * size of colony j

[Equation 2]

re-normalised to sum to 1 across all colonies.

The method also encompasses 'sub-methods' here termed variants that make novel improvements on the original **Wakefield** approach, i.e. here defined as the same as the original paper using the same data, but with the MSS apportioning extension applied; the **UCC** variant extends this further, by including more recent population data**,** as Wakefield et al. (2017) relied on Seabird 2000. For this 'UCC' model variant, Butler et al. (2020) use either more recent data or imputed counts (where more recent data are not available), and although for the four species considered there have been some notable population changes, agreement between the original Wakefield model and UCC models was high. A further variant considered **non-breeding as well as breeding birds (BNB)** by including spatial survey data to estimate distribution (Waggitt et al. 2020). The BNB variant performed relatively well, for example showing fairly good agreement with the Wakefield method through application of the models to independent datasets, but notable differences emerged; these were particularly driven through the different relationships over age classes between spatial distribution and distance to the colony, i.e. immature birds may or may not be similarly distributed to adults over distance, which was also species-specific with varying results among different species. Further issues with the BNB model variant arise due to the lack of comparability in the different data sources of GPS and at-sea data used as well as temporal mismatch in data sources. To rule out potential error, however, it was concluded as meriting further investigation pending more work (Butler et al. 2020).

Strengths and weaknesses

An advantage of the MSS approach is that it accounts for species- and colony-specific habitat use, informed by the environmental availability of each colony. This makes the eventual assignment of number of individual animals back to colonies more realistic by incorporating mechanistic linkages to explain habitat use based on environmental (prey-proxy) drivers and interactions. The method brings in important determinants of at-sea usage above that of simply population size, including the distance to conspecific populations within and between species, accounting for density-dependent sympatric and parapatric competition effects. Further, the method can incorporate the distribution of non-breeders during the breeding season if using the BNB variant of the model, combining different data sources, but that also includes further processing of at-sea datasets and is dependent on their availability. Of note is that the MSS tool (Butler et al. 2020) was concerned with calculating, for a given location, the percentage of birds present that come from sites for each species, and thus estimated the 'relative' numbers of birds potentially originating from each site.

However, a disadvantage is that the tool, and the maps that underpin it, is currently only available for the four species as outlined above. The MSS tool may need to be applied to these same species but incorporating more recent tracking data, which may alter the habitat relationships observed and the outcome of the apportioning. Alternatively, new species may need to be considered that may require different covariate information that underpins the habitat association or different model structure. Newer (i.e. updated) covariate information may also need to replace existing data within the original model. Any further use of the tool for more recent data or different species would involve re-building of the Wakefield model and statistical relationships for further use in the MSS tool. However, building the modelling framework 'from scratch' represents potentially very high time-effort overheads in data acquisition (which may be in the region of terabytes of data processing from new remote sensing datasets), model set-up, and importantly computational run-time costs. As acknowledged by Butler et al. (2020), the existing tool already has extensive resolution and a large amount of information to run the R interface. Wakefield et al. (2017) also acknowledge computer run-time to have been an issue in the development of the models underpinning the MSS tool, and state a number of experimental phases that were carried out in a stage-wise manner before settling on the final methodology; whether such steps would be needed for completely fresh data, or even a variation of the underlying statistical model itself, is at present unknown. Finally, the method, to date, has only been applied to species with relatively short tracking durations within the breeding season, and it is unknown how extensive the modelling may be with longer duration datasets and those that span multiple years for the same individuals, thus likely requiring appraisal of the statistical assumptions underpinning parts of the model. Further use of variants of the MSS model to incorporate distribution of non-breeding individuals during the breeding season would require further sourcing of at-sea data for those species, which may also require extensive collation. The BNB variant of the model also assumes the ratio of breeders to non-breeders is constant across all colonies; the ratio is related to the demography and population structures of the populations, likely to differ between increasing and declining colonies, for example. Further, the method assumes the same explanatory environmental covariates are used for both population components.

A further current drawback of the MSS tool and the Wakefield method is the tracking data underpinning the modelling relate to area used for all behaviours, which also includes travelling (commuting) to and from a central place (breeding colony) and resting as well as the likely key behaviour of interest ‘foraging’ that may be most closely associated with habitat/covariates modelled. As such the models may not properly capture the functional drivers of the spatial distribution. This could easily be rectified by re-running the models but only using the foraging locations, as assessed through additional sensors such as time-depth recorders, or movement modelling approaches such as Hidden Markov Models.

The MSS approach outlines two sources of uncertainty from (a) the overall percentage apportioning values (i.e. % birds from a given colony in space in relation to the total number expected for all colonies), associated with the number of breeding birds (colony sizes), and the estimated UDs, and (b) given the percentages, the uncertainty associated with a given sample of birds of particular size that feeds into the calculations. The latter was addressed by simulation and re-estimation of percentages for varying sample sizes of birds to give a 95% confidence interval. However, the former (a) above, could not fully be accounted for; as stated by Butler et al. (2000), colony size uncertainty was absent from Seabird 2000 Seabird Census, and although the error in UDs for colonies could be extracted, pseudoreplication was an issue within the Wakefield underlying approach preventing reliable use of those model errors. Thus, only ‘partial’ estimates of uncertainty are available for the MSS method due to the methodology, which is still an improvement on the SNH and BDMPS methods where uncertainty could not be represented.

Data requirements and availability

A full appraisal of the variables and their availability for further use of the ‘UCC’ variant of the MSS model are provided in WP2 of this project. However, the model requires tracking data and further information on foraging range of species that are further combined with covariates with the habitat modelling framework. As also noted above, the BNB variant of the model can include non-breeding individuals during the breeding season by sourcing data from at-sea survey data collection platforms such as boat or aerial surveys.

Tracking data are now available for a variety of species of seabirds in the UK. However, related to the above uncertainty, a further concern with the MSS approach is that application of the method may be driven by the overall sample of empirical tracking data across colonies within the species' range that may be available. Extrapolating predictions based on only a few sites may therefore be problematic. Related to this is the geographic distribution of colonies, which could be biased to a part of the species range – for example, groups of animals could behave differently or use different habitats, which is further linked to resource availability and could introduce model transfer errors. These are wider points therefore associated with appropriate coverage and characterisation of the species and capturing natural behavioural variation within the population. In the case of large gulls, such as lesser black-backed gulls (*Larus fuscus*) for example, the behaviour and use of offshore areas may vary by different breeding 'strata', i.e. groups of breeding environments that vary by geography (i.e. urban, natural coastal, inland and island sites), which would therefore require consideration of sample size coverage of those environments.

Time-distance function (Sage 2022)

Background

A further very recent method has been developed by Sage (2022). This approach is based on a time-distance function (TDF) where the total time spent (*t*) within given distances for a colony is estimated as a proportion of the entire colony time budget across the season, over distance segments (*r*) up to the maximum foraging range radius (r_{max}) – see Equation 3 below; note also that the t_i sum over all radii equates to the total seasonal colony time budget. The method has so far only been applied to lesser black-backed gulls. This method is also solely focused on tracking data and seeks to better quantify the decay in distance utilisation based on spatio-temporal units rather than pure spatially-static ones, as a realistic time-distance-decay function. The TDF then has merit in further application in applied scenarios for OWFs – see below. The TDF of each colony (TDFc) was first estimated by summing up all GPS time intervals of all individuals of a colony for incremental radial distances of 1 km from the colony centre, to calculate the proportion of time spent within each radial distance, P_r

$$P_r = \sum_{i=0}^{r} t_{i} \div \sum_{i=0}^{r_{max}} t_i \quad [\text{Eq.} 3]$$

[Equation 3]

Colony-specific TFs were further combined as a species-wide TDF by normalisation (dividing each distance by the maximum distance of the colony) and taking a median proportion of time for each distance interval, in turn multiplied back by the normalised distance to rescale the TDF (Sage 2022). Non-linear models were then used to describe the shape of the TDF statistically.

The TDF method can potentially be used for apportioning across multiple colonies. Using hypothetical scenarios Sage (2022) used the TDF to estimate the proportion of time spent (at distance) in the "Development Area" of hypothetical proposed OWFs. The first step in this process was to estimate the proportion of time in the Development Area $PD_{c.}$ for a given colony *c*. This is estimated by first calculating the proportion of time birds spend at the required distance from the colony as estimated from the TDF using cumulative time proportion between two distance measurement increments. This temporal proportion is then divided by the area of the band (assuming a circular distribution) to give a relative density in the area. This value can then be multiplied by the area of the wind farm to give PD_c. The estimates of PD_c can be used to calculate colony site-specific weights in apportioning depending on the colony size, i.e. weight = PD_c * colony size (N_c). Across multiple colonies, the site weights can then be further normalised to give proportional weights. This calculation can be made for land or sea masks of the distribution for relative available land or sea area. Explicit comparison is also made by Sage (2022) to the SNH apportioning methods (SNH 2018) over varying hypothetical OWF distances from colonies. The approach above could be used with a species-wide TDF as estimated across observed colonies that could be transferred potentially to where tracking data has not been collected. Note, however, these methods are not yet published and are a new approach that has not yet been widely tested.

Strengths and weaknesses

The method is empirically driven but can also be applied/transferred to colonies lacking data using the generalised species-wide TDF, which is a strength of the approach. Further, complexities can be investigated in movements over time, e.g. for seasonal effects moving beyond just the spatial component of prior methods. Additionally, the method explicitly deals with onshore and offshore components, which is important for species that may span both environments – this is achieved by considering parts of the time budget per colony spent in each environment. The Wakefield et al. (2017) MSS tool method only considered species using marine environments. This may be suitable for other species solely using marine environments but could require further model development to account for more generalist species that use a wider range of different environments. The TDF method is also simpler than that of Wakefield et al. (2017) and has less setup overheads and model runtime computational costs, and is further advanced than the SNH apportioning approach by using elements of time to estimate the TDF rather than an inverse distance weighted approach. That said, the method still makes assumptions that the species-wide TDF is appropriately characterised and biologically meaningful, dependent on the data feeding in (as noted above under the MSS approach).

In terms of uncertainty, the TDF method also uses a best-fit non-linear regression line fitted to the TDF proportion of time~distance relationship to better draw out the trends, which will also carry a small amount of model error. Theoretically, the species-wide TDF across all colonies will also carry aggregation error, for example a median and upper and lower confidence limits of the TDF curve, which could then be propagated further for example if being applied more widely in apportioning, e.g. for colonies with no data. However, as noted elsewhere, the TDF method is in the early stages of potential application, and therefore if the method is refined, the limitations may change.

However, the TDF does have similar disadvantages to previous SNH apportioning methods in that it assumes a radial approach for the time-distance function, thus assuming homogeneity in radial distributions, i.e. without further considering environmental covariate correlations with hotspots of use. The TDF approach can be applied where no tracking data exists, but the use of the upper radius would likely require use of species-level foraging ranges – this requires further testing and exploration. In addition, the method may lack realism, for instance by not accounting for conspecific sympatric and parapatric competition as in the MSS Wakefield method. The method thus needs observed tracking data to reliably parameterise the initial TDF for the species. As the TDF method is a new approach, the processing and calculation time to reach eventual apportioning estimations is unknown at present. However, with a coded workflow, the process will be substantially less than the Wakefield MSS approach, being, for the most part, a data manipulation exercise (rather than statistical computation) with simple GIS tasks (i.e. offshore delineation), binning of data over distance and summed time calculations. With a sizeable tracking dataset, the TDF approach would need increasing data manipulation, but one that is not insurmountable.

Data requirements and availability

As above, the data required for this approach are tracking datasets to initially build the TDF but may require further information on species foraging ranges in estimation of a species-wide TDF. The method also requires information on population estimates of species for sites/colonies where apportioning is to be made; however, this is the case for all other methods reviewed here. The method also suffers the same constraints as the Wakefield method in characterising the species and sample size of number of colonies with tracking data at the outset. However, the method otherwise has minimal overall complexity.

Biologically Defined Meaningful Population Scales (Furness 2015)

Background

Currently, the BDMPS methodology (Furness 2015) is the default method for apportioning numbers of seabird species to colonies in the non-breeding season. This approach arose from work within the UK renewable energy industry and identified a need to understand and define non-breeding season seabird populations for apportioning work. Areas within the biogeographic range in UK territorial waters are unlikely to be homogenous in spatial distribution and so may contain quite different numbers of birds whose provenance may differ. This was the main motivation behind the development of the BDMPS method, and facilitated the definition of geographic scope of these populations for different species, for more meaningful use in apportioning of birds within the Special Protection Area (SPA) network. This work, therefore, informed the Habitats Regulations Assessment (HRA) process within Environmental Impact Assessments. Such BDMPS areas may be anywhere from the biogeographic range of a species downward (Furness 2015) and at lower scales relates to the biogeographic population with connectivity to UK waters, i.e. UK breeding individuals plus overseas immigration/emigration during the non-breeding season. The report by Furness (2015) defined three main aspects for further use in EIAs for several UK seabird species: (a) the biogeographic population with connectivity to UK waters, (b) numbers of birds (adults and immatures) within seasonal periods, and (c) the numbers of birds per season in BDMPS for each species, with contribution from UK and overseas further defined.

Seabirds may experience four main effects from offshore wind farms: collision, displacement, barrier effects and indirect effects on prey, and the BDMPS method has been used for apportioning within EIAs, particularly for collision and displacement effects. Here, density is first estimated within wind farm footprints from at-sea survey data. For displacement, simple matrices of displacement rate and mortality rate per species have typically been used to highlight likely rates (i.e. based on expert judgement) to inform the numbers of birds impacted. These values can then be used in conjunction with the BDMPS for that species and seasonal definitions, summing winter and summer components, to apportion those impacts within the SPA network. For the effect of collision, a collision risk model (CRM), such as the Band (2012) model and subsequent versions and extensions (Masden & Cook 2016) is initially used for estimating potential numbers impacted by the development; this stage also requires various data inputs that are beyond the scope here but see Masden & Cook (2016); thereafter apportioning follows a similar workflow as above, to apportion to SPAs. This is achieved by dividing the SPA population by the relevant seasonal BDMPS per species, to obtain the proportion of the BDMPS population expected to originate from the SPA.

Strengths and weaknesses

The BDMPS method is simple and relatively straightforward to apply, using a spreadsheet to transfer pieces of information within a stage-wise approach. The method brings together existing information and knowledge to make better-informed judgements, and was an important step forward in being able to attempt apportioning for the non-breeding period. However, the method naturally carries several limitations, with decisions often based on limited data with some further strong biological assumptions made.

Expert judgement is used within the BDMPS initial estimations, from the initial regions used to originally estimate the BDMPS in Furness (2015), through to the assumptions made with respect to specific effects as part of EIA. For the BDMPS regions, the numbers of birds in different areas are not well known, and the movement patterns of immatures are highly uncertain, which is a constraint on estimating proportions of UK birds from overseas, requiring assumptions based on best available data (Furness 2015). Expert biological judgement is therefore made when initially identifying the species-specific BDMPS, which further, may also not remain static over time. The BDMPS areas can be very large in size, and there is an implicit assumption, that each not only has a constant population per species but that the areas of sea within each BDMPS have the same apportioning proportions.

For assessment of effects and eventual apportioning, decisions are made for mortality rates for displacement and avoidance rates for collision risk, often taken as a single species value for components of populations that could have much greater complexity temporally or spatially for a given species. Further assumptions for specific effects in relation to offshore wind farms are also made for example in collision risk assessment assuming spatial homogeneity in collision risk, for example for passage movements. For displacement, the approach makes simplistic assumptions of population demography. Summer and winter seasonal components (for adults and immatures) are assumed separate and are considered additively in the final estimations of numbers; this calculation could double count mortality given that in summer changes in body mass are not independent of winter mortality. Effects on productivity are ignored, i.e. the loss of animals estimated for each population is a single static estimate without further consideration of effects on reproductive output.

Within each of these steps there is no quantification of uncertainty.

Data requirements and availability

In the initial identification of BDMPS, the flux movements of birds from the UK to and from overseas involve consideration of a range of data types, such as seawatching data, ringing data, geolocation information (where available), and other markers of origin such as biometric variation, genetic phenotypic variation, stable isotopes and pollutants (Furness 2015). These data are broadly available across most species; however, as noted above, these data carry approximation and generalisation meaning the initial BDMPS characterisation has numerous assumptions and unquantified levels of error. Numbers of birds in UK waters come from at-sea survey information such as ESAS, biogeographic estimates from Stroud et al. (2001), and more recent updated values. Similarly, the data for estimating density comes from at-sea surveys such as aerial and boat-based platforms carried out within the wind farm footprint.

Demography data (survival rate, age of first breeding, productivity) can be included within this method for the species assessed, for example, to assess apportioning through to different demographic components of the population, i.e. to ascertain numbers of immature birds per breeding population. As noted above, the timing of breeding and migration are also required for seasonal delineations per species, also sourced through a review of the literature (Furness 2015).

Future work could include updating the population sizes used, most logically to be undertaken on completion of the new Seabirds Count full UK census. Priority for future work would also include updating with the latest information on demographic rates (survival rates, age of first breeding, productivity), in order to most accurately assess the numbers of immature birds. Adjustment is also made for seasonal phases that may differ from the original recommendation (Furness 2015). Hence future work could incorporate the latest data and insights into timing of breeding and migration from populations breeding inside and outside the UK to inform those periods.

New tools for the non-breeding season based on GLS data

Background

Geolocation-immersion (GLS) tags are now widely deployed across several UK seabird species (e.g. Linnebjerg et al. 2013, Harris et al. 2015). These devices are light-level data loggers and are lightweight and long-lasting. Since position is estimated using ambient light intensities, elapsed time, and saltwater immersion, GLS locations have relatively large uncertainties of 100-200 km (Merkel et al. 2016). However, they offer important insights into the movement and distribution of seabirds during the non-breeding season that cannot be obtained using any other method (e.g. year-round deployments of GPS loggers is not currently an option for many seabirds). These data offer the opportunity to develop a data-driven approach for apportioning in the non-breeding season. However, there are currently no examples where such an approach has been carried out. Consequently, the following appraisal of this method is based on any further anticipated data manipulation and potential strengths and weaknesses.

If colony-specific utilisation distributions (UDs) can be estimated from GLS data then, as with GPS data in the breeding season, these colony-specific UDs can, together with counts of colony size, be used to apportion birds to colonies within the non-breeding season. Modelling of spatial distributions from GLS data has similarities with the modelling of GPS data, but there are some important differences in the data collected:

- GLS data are much lower frequency than GPS data – typically 1-2 records per day, which means detailed modelling of spatial movement is not possible.
- Levels of observation error in GLS data are much higher than for GPS data, and are sufficiently large that models which ignore observation error are unlikely to be defensible.
- The levels of observation error in GLS data are likely to be heterogeneous, and it seems that as they vary according to known factors (e.g. time of year) this variability can be modelled.

These differences mean that the methods used to build models to apportion in the non-breeding season will likely differ from those used in the breeding season. However, using advanced kernel-density estimation methods, the above data issues could be accounted for and thus produce utilisation distributions in a similar way as used for the breeding season. The GLS tracks could be split into different phases such as moulting and wintering seasons and utilisation distributions obtained. Several steps, however, may be required, for example, initial data visualisation, the aforementioned kernel density estimation, and further overlap assessment and novel apportioning using predicted shared space estimated among populations.

Data visualisation in space and time can allow the tracks from colonies to be mapped and uncertainty to be explored. A valuable approach could be the use of space-time cubes (Demšar et al. 2015), which visualise spatio-temporal data. This approach can gain insights into pathways to their non-breeding sites including whether all birds from a colony use the same transition corridors or whether their tracks vary markedly by individual.

Utilisation kernels are a broad church of methods that range in complexity from time-static approaches, through to more complex distribution models. For satellite-based data, advancements have been to characterise location uncertainty into ecological process models such as resource selection functions (e.g. Thurfjell et al. 2014) and movement approaches (e.g. McLintock & Michelot 2018). Recently, for GLS data, azimuthal telemetry models (ATM) have been proposed that include location uncertainty (Gerbel et al. 2018) and could be used to produce a set of utilisation distributions as part of the apportioning workflow.

Area overlap metrics, such as Bhattacharyya's affinity, between sets of distributions could then be generated i.e. among colonies, species, and per year (if such data allow). Estimation of potential population usage could then be generated in a similar way to breeding season data. These overlaps could then allow apportioning to be made (scaled up to population size using colony counts) by looking at the shared space use of a combined set of colonies, with a measure of uncertainty. New regions to aggregate colonies could further be defined for colonies of a given species without tagging data, and apportioning carried out according to the region they are placed in.

As a final step in this potential workflow, species will vary with how consistent their distribution is by colony and over time. A qualitative Red-Amber-Green visual system could therefore be useful to label how confident apportioning metrics are for each species/area.

Strengths and weaknesses

This approach has not been used and so cannot be fully scrutinised. The steps involved do require a degree of modelling and computational overheads, thus being more complex than for example a simple spreadsheet-based approach of the BDMPS. However, the use of empirical information to define non-breeding home ranges would be a significant advancement over the expert-judgement approach used within the BDMPs (see section 2.4 above). Further, the incorporation of error, if feasible within the modelling workflow, would make this method one of the few to explicitly deal with uncertainty.

Although new regions could be defined for colonies without tracking data, it is perhaps less clear how well this will work in practice, i.e. in a more predictive sense without further habitat association modelling. The GLS approach as with all methods directly using tracking data, assumes the data collected adequately characterise the species non-breeding distributions, which may carry significant error if colonies around the UK are not widely represented. Further issues of annual and within-seasonal variation complexity may also become apparent, and the use of utilisation distributions directly incorporating error is perhaps more in its infancy for azimuthal location data, although advancements have been made recently. Overall, this method would be worth exploring for further datasets if they become available over a suitable number of colonies for a given species.

Data requirements and availability

As above the GLS data are the main input into this approach, and SPA population size information is to be used within the apportioning. This makes the approach attractive in relying less on further data that carry extra assumptions.

3. Discussion

This review builds on previous assessments and comparisons of methods such as Butler et al. (2020). Here we consider six main methods for apportioning impacts of renewables back to breeding populations. These include a very recent method of Sage (2022) but that at the time of writing has not yet been published, and potential further use of GLS data for non-breeding season data. The various advantages and disadvantages of the approaches are summarised in Table 2 below.

All methods reviewed here ingest population estimate data. Population size and proximity to conspecifics were among the most important predictors found by Wakefield et al. (2017), making it important to source reliable estimates of population size, and handle these data appropriately. Population data will be particularly important for some species where survey coverage may vary depending on the breeding habitat, for species such as large gulls for example where characterisation of urban habitats is of potential concern and has been subject to recent further estimation since the last seabird census (Burnell et al. 2020a, b). Interpolation methods of Butler et al. (2020) can be used, i.e. the UCC variant of the model, should more recent estimates be unavailable from some sites beyond the Seabird 2000 survey.

Breeding season

All methods focused on the breeding season further require an estimation of foraging range, including both the MSS tool of Butler et al. (2020) and the TDF method of Sage (2022). The breeding season methods have some further general commonality in assuming an area- or distance-time approach for quantifying a number of animals that may utilise a given space that can then be shared among colonies believed to be in the vicinity of likely provenance. These are matters of establishing likely ‘connectivity’ between potential development areas and populations, such as SPAs. This is a straightforward task where tracking data exist. This still means, however, that when making predictions, all methods assume certain connectivity to other sites or colonies within the foraging range, or for the MSS tool, within the range identified in predictive modelled surfaces. Verification of connectivity from further direct tracking data for specific sites is always a useful endeavour and could be used to further validate the underlying model assumptions, enabling greater certainty that apportioning methods have been assigned sensibly.

Among other shared aspects, the methods have a common disadvantage in being unable to fully account for uncertainty in final propagated apportioning. The MSS tool goes part way to addressing this by including consideration of varying sample size and how that affects uncertainty in the percentage apportioning values but as stated by Butler et al. (2020), colony size uncertainty and the error in the UDs from the Wakefield method could not be accounted for (see section 2.2.2). Potentially the Sage (2022) method may be able to incorporate uncertainty in the TDF based on the species-level modelled curves more explicitly. However, this method is at the stage of demonstration only having not been directly applied.

However, the methods have a number of differences and particular key advantages and disadvantages. The original SNH methods are among the most simplistic to apply during the breeding season and would be useful in any apportioning study to trial alongside more advanced methods, to test and understand the underlying distance-based decay assumptions involved. The SNH methods, however, suffer a lack of biological realism and unquantified uncertainty, sacrificed in favour of simplicity. Indeed more advanced methods could potentially feed those relationships back into the SNH tools.

The MSS apportioning tool of Butler et al. (2020) is by far the most advanced of all the methods, encompassing biological realism, and is based on the original Wakefield statistical framework, with further extension through R scripts to apportioning; extensions of the tool are provided using more recent population data, and further still inclusion of non-breeding space use from at-sea datasets alongside breeding-season tracking datasets that give high value, widening flexibility in scope. However, these advantages come at a price. The MSS tool has high computational overheads and potential complexity when applied to new species that could also need alteration to the underlying model and sourcing of new covariate information. Nonetheless, the value of this approach is worthwhile applying across other species.

Non-breeding season

For the non-breeding season, the BDMPS method is at present the most widely used tool for the non-breeding season. This method is straightforward – arguably more simple than the SNH apportioning tools – and, should the existing BDMPS regions and seasonal definitions be used as in Furness (2015), only needs population data, as well as the metric to be apportioned. Further complexity is introduced in the EIA process for the specific effects being apportioned, such as displacement and collision risk that carry further assumption and data requirements. The BDMPS, however, is highly prone to many assumptions that are also acknowledged in Furness (2015), including the data feeding into initial constructs of the BDMPS, but further, the areas themselves still represent homogenous units, that may still be biologically unrealistic.

Further new methods may be possible using GLS data to better characterise area use of species during the non-breeding period, which would bypass the use of BDMPS. The potential of these are explored here but they are as yet untested and limited to where feasible for certain populations where such data exist. Potentially the MSS tool variant BNB of the model could be useful alongside BDMPS in future studies for the breeding season, i.e. for examining population components including breeders and non-breeders as a potential comparison.

4. Final conclusions and recommendations

This review has highlighted the strengths and weaknesses of the methods reviewed. The methods all have merit and it was not possible to recommend one single way of carrying out apportioning, as much will depend on the nature of the species and data available. The MSS tool, however, emerged as one such method worthy of wider investigation, being based on the most biological realism of all methods. At the time of writing no new species or time periods have been modelled following on from the Wakefield method, but potentially more species could be investigated that have data available to fit the MSS tool framework, such as northern gannet *Morus bassanus*, Manx shearwater *Puffinus puffinus*, and species of gull, such as lesser black-backed gull. Combined with the UCC method of Butler et al. (2020) for newer population data, and potentially new covariates, the use of the MSS tool would be valuable. Using GLS data, such as those available for guillemot and razorbill, should be considered for apportioning in the non-breeding season, in order to move away from some of the key assumptions regarding colony provenance that are made in BDMPS.

Table 2. Summary of the main data requirements, and strengths and weaknesses of each approach.

Method	Season	Data inputs	Data availability	Analytical Complexity	Biological realism	Advantages	Disadvantages	References
SNH Tool	Breeding	Foraging range (e.g. from tracking data)	High	Low	Low	Very simple to understand, quick to apply and produce results	Linear distance is not realistic for species that cannot cross land; decay occurs homogenously in radii, species foraging ranges may become outdated, or be less reliable given lack of data; does not account for uncertainty	SNH (2014)
SNH Tool 'plus'	Breeding	Foraging range (e.g. from tracking data)	High	Low	Low, but better than previous	Advantage over previous tool in not assuming linear distance, but distance by sea	As with previous tool i.e. radii; species foraging range criticisms; lack of uncertainty	SNH (2018)
MSS Tool	Breeding	Tracking data, population size, covariates Non-breeding BNB model	Medium, if starting from scratch	Very high, if running models from scratch	High	Good inclusion of biological realism, capturing environmental association and population competition effects; R code	Existing species maps become outdated, new populations may be tracked over new time periods, or new species may be studied requiring re-running of models; relies on covariate	Butler et al. (2020)

Method	Season	Data inputs	Data availability	Analytical Complexity	Biological realism	Advantages	Disadvantages	References
		includes at-sea aerial/boat data for distributions	High, if using existing data	Medium, if using existing models, but still with computational cost		available to implement the method; can include non-breeding birds; explicitly includes partial uncertainty assessment; flexible for three different 'versions' of the tool	data availability; imputation of colony counts carries uncertainty in UCC variant; assumptions made on covariate drivers and ratio of breeding/non-breeding birds in BNB method variant; currently uses all behaviours not just foraging; does not account for uncertainty in colony size or foraging distribution	
TDF	Breeding	Tracking data; foraging range	Medium, requires initial tracking data if parameterising High, if using existing TDF for a given species	Medium, if running from scratch Low, if using existing species' TDF	Medium	Simple, likely rapid on the whole, and brings in temporal component for greater realism beyond just distance metrics	Largely untested. Processing of large amounts of tracking data but likely still at relatively low computational costs; simple method to understand; still based on foraging ranges if applied to unobserved colonies; assumes TDF is generalizable	Sage (2022)
BDMPS	Non-breeding	Population sizes; for	Medium, may be many sources	Low	Low	Currently the 'main' approach for non-	BDMPS for each species, is large, homogenous and	Furness (2015)

Method	Season	Data inputs	Data availability	Analytical Complexity	Biological realism	Advantages	Disadvantages	References
		BDMPS various data used for defining, e.g. ringing, tracking; EIA, further data for specific effects, such as likely mortality data, CRM data	but data quality and amounts vary by species and source			breeding data, simple to use and based on a comprehensible spreadsheet	within each contains the same apportioning proportions; expert judgement made in defining areas; time static; assumption of temporal breeding phases; decisions taken on further effects from wind farms in EIAs, such as mortality rates, and further lacks integration of demographic realism; does not account for uncertainty.	
GLS methods	Non-breeding	GLS data, population size	Low to medium, dependent on species' having available data	Likely medium	Medium, not directly linked to covariates, but improves on BDMPS	Potential use of actual data on non-breeding distribution rather than estimated spatial units as in BDMPS; potential to include uncertainty within the modelling workflow	Untested; limited by GLS data available for species, that may also be limited to certain colonies constituting potential sampling/geographical bias; requires further definition of the precise analytical tools to be used.	-

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