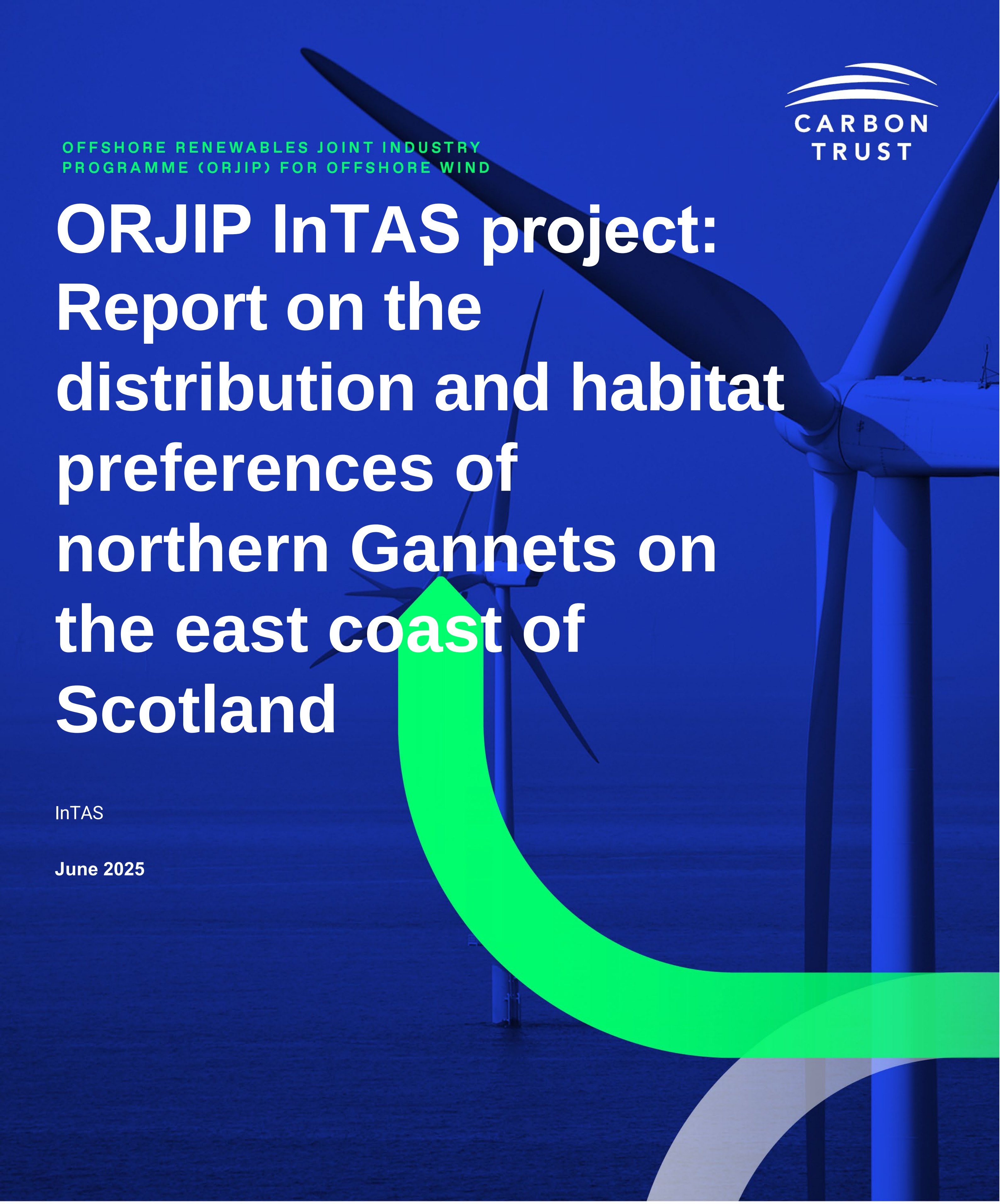

CARBON TRUST

OFFSHORE RENEWABLES JOINT INDUSTRY PROGRAMME (ORJIP) FOR OFFSHORE WIND

ORJIP InTAS project: Report on the distribution and habitat preferences of northern Gannets on the east coast of Scotland

InTAS

June 2025

orjip
working to accelerate
offshore consenting

CARBON TRUST
Crown Estate Scotland
Oighreachd a' Chrùin Alba
Offshore Wind Evidence + Change Programme
THE CROWN ESTATE
EDF renewables
equinor
Ørsted
OW OCEAN WINDS
RWE
Scottish Government
Riaghaltas na h-Alba
sse Renewables
TotalEnergies

ORJIP InTaS project: Report on the distribution and habitat preferences of northern Gannets on the east coast of Scotland

Jason Matthiopoulos, Paul Blackwell, Chris Thaxter, Kelly Macleod, Aonghais Cook

2023-12-02

Abstract

The results in this report represent the application of the modelling framework developed under WP2 of the InTaS project funded by the Carbon Trust as part of the broader ORJIP initiative. The framework combines, for the first time, the statistical inference methods traditionally used in isolation for survey and telemetry data. It aims to accurately and precisely apportion the exposure of particular seabird colonies and age stages, to anthropogenic offshore disturbance. Atlantic Gannets (*Morus bassanus*) were identified as one of four priority species during the literature survey undertaken in WP1 of the same project. A large-scale proof of concept was agreed for the east coast of Scotland. Survey and telemetry data (from both adults and juveniles) were collated for similar spatial and temporal extents. The locations and sizes of gannet colonies were provided and used to guide the habitat modelling and apportionment algorithm. Model selection was carried out to explore combinations of nine environmental covariates that most parsimoniously explained the pooled telemetry and survey data sets. Using the best model, a comparison of survey-only, telemetry-only and joint survey-telemetry analyses confirmed the conclusions of simulation experiments from WP2 suggesting that the convergence and precision of joint analyses are superior to the single-data analyses. The covariates retained in the selected model indicated avoidance of gravelly and muddy substrates, and attraction towards highly stratified pelagic environments as indicated by features such as potential energy and thermal fronts. We present results on the spatial distribution of usage by different colonies and size ages and present an illustrative calculation of apportionment for an exemplar off-shore region, along with a software tool that can use the results of our modelling for any area of interest for potential offshore development.

Figure 1: An adult Northern Gannet (Morus bassanus). By Andreas Trepte - Own work

Contents

1 Overview

Different types of data carry more or less information about particular aspects of a seabird species' distribution. If the interest is in broad-scale maps of distribution representing the aggregate usage of particular regions of space by all birds of a given species, then survey data can be an effective source of information. These may provide estimates about the usage within a region of interest (if the surveys are targeted geographically), or they may provide wider comparisons between the region of interest and the rest of the distribution of the species. Integration of data from multiple surveys, particularly if combined with environmental covariates into habitat models (Jason Matthiopoulos, Fieberg, and Aarts 2020) can provide spatial breadth and the ability for such comparisons. Taking further steps along the path of data integration (J. Matthiopoulos et al. 2022) is essential if we wish to apportion usage by colony or breeding stage. This requires folding into the analysis individually-referenced data, the prime example of which are telemetry data on individual movement.

1.1 Study objectives

Here we aimed to:

1. Analyse patterns of spatial utilisation of the Scottish north sea by gannet.
2. Deduce which environmental variables are primarily driving this distribution.
3. Generate reconstructions of spatial usage by different colonies and age classes.
4. Demonstrate apportionment results with associated credible intervals for a particular area of development.
5. Encode the above in reproducible code so that the data, covariates and areas of interest can be altered, allowing the analysis to be re-run expediently.

Objective 1 aims to generate the best possible description of distribution. To this end, we have used survey and telemetry data that combine breadth and resolution. Objective 2 uses model selection among an extensive array of candidate models, to decide which environmental variables are covariates of this species distribution. We visualise the spatial effect of all the variables retained in the final model. We also present a comparison of the results of fitting the two single data models with the results of the best joint model selected under Objective 2. A comprehensive graphical view of all colonies and both age stages is produced under Objective 3, using the best joint model only. In the case of gannet, telemetry data were available for both adults and juveniles. So, the modelling task is considerably simpler compared to cases where the utilisation parameters for juveniles need to be indirectly inferred from the combination of aggregate survey data and adult telemetry only. Under objective 4, using the best joint model only, we demonstrate how to apportion the spatial overlap of marine installations with the distribution of animals belonging to different ages and colonies. Specifically, we consider exposure of different breeding stages and colonies, by calculating the amount of spatial usage by each population component that is enclosed in an arbitrary boundary at sea. Crucially for impact assessment purposes, this apportionment of effects is accompanied by spatially explicit measures of uncertainty. The Bayesian framework employed here is ideal for this purpose because parametric bootstrapping of the spatial uncertainty can be performed directly by sampling from the posterior distribution of the fitted models. Finally, we provide instructions and appendices with code to facilitate running the apportionment functions from a given model object and within a given offshore area.

Table 1: Characteristics of the colonies included in this analysis (Based on Seabird2000 survey data).

Colony	Longitude	Latitude	Breeding pairs
Fair Isle	-1.63	59.53	1123
Forth Islands - Bass Rock to Haystack	-3.14	56.03	44110
Foula	-2.07	60.12	723
Noss NNR	-1.02	60.15	8017
Rosehearty to Bay of Cullen	-2.41	57.67	1085
Sule Stack	-4.5	59.02	5137

1.2 Relevant facts about gannet natural history

Gannets (Figure 1) are a large seabird breeding in a few, mostly large, colonies around the North Atlantic though most birds breed around Britain and Ireland. They forage on a wide variety of pelagic fish prey which they mostly catch by plunge-diving into the sea from height. They also foraged on discards from fishing boats (Skov and Durinck 2001).The practice of discarding has been reduced since 2015 until a complete "discard ban" in the European Union was introduced [and enforced] in Jan 2019. Consequently, discards are no longer an important source of food and feeding strategies have had to adapt. Woodward et al. (2019) reported summary statistics for the foraging range of tracked gannets from their breeding colonies across multiple studies. The mean foraging range (± SD) was 120.4 km (± 50.0). However, the mean of the maximum foraging ranges across the studies was 315.2 km (± 194.2), showing the birds can, and do, forage much further than the mean value. Gannets from different breeding colonies forage in different areas of sea with little overlap in the areas used (Wakefield et al. 2013). Thus, foraging range can vary between colonies. In addition, there are sex differences in the foraging behaviour of gannets, with female birds foraging further and for longer from colonies than male birds (Stauss et al. 2012).

In total, the analysis examined 6 colonies whose size ranged from 723 to 44110 breeding pairs (Table 1). The data originate from the Seabird2000 surveys in order to align with the CEF, however, these analyses are now automated and spatial predictions can be readily updated with new population data.

2 Environmental covariates

A total of nine environmental covariates were considered for this analysis (Figure 2). Their derivation and interpretation is described in detail in the Data report generated for this project under WP1. Briefly, the variables were: (1) depth, (2) minimum distance to coast, (3) seabed slope, (4) proportion of gravel, (5) sand:mud ratio, (6) potential energy anomaly (PEA), (7) sea surface temperature, (8) thermal front gradient density (TFGD), and (9) net primary production (alpha-chlorophyll - NPP). To facilitate comparisons between the magnitude of influence and to help with model convergence, all covariates were standardized to mean zero and standard deviation one.

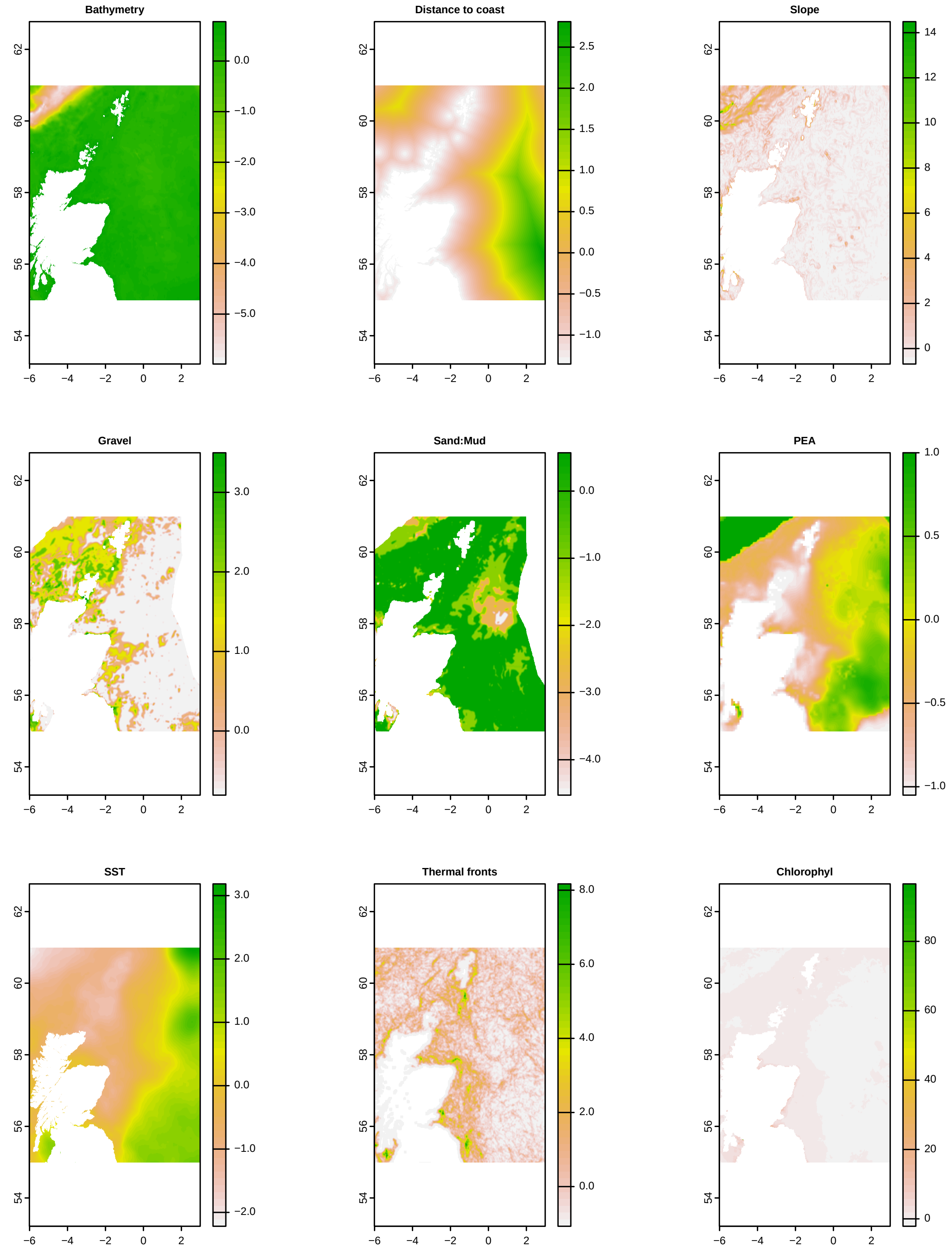

Figure 2: The candidate covariate layers considered in this analysis. All covariates are standardised to mean zero and sd=1.

2.1 Derived covariates

The main derived covariates required for models of central-place foragers are the maps of distance-to-colony. A stack of rasters is required, one raster for every colony to be included in the modelling. The nominal positions of the colonies are approximate, and recorded in (Table 1). This is a requirement regardless of whether a particular colony is associated with tagging data or not. The distances were calculated but not standardised. A synoptic view of the accessibility of different points at sea can be obtained by weighting the accessibility of each colony by its relative population size (Figure 3). Note that this accessibility model is for illustrative purposes only, but it is numerically based on the parameter value retrieved for adults in the final model selected in this analysis (Table 4).

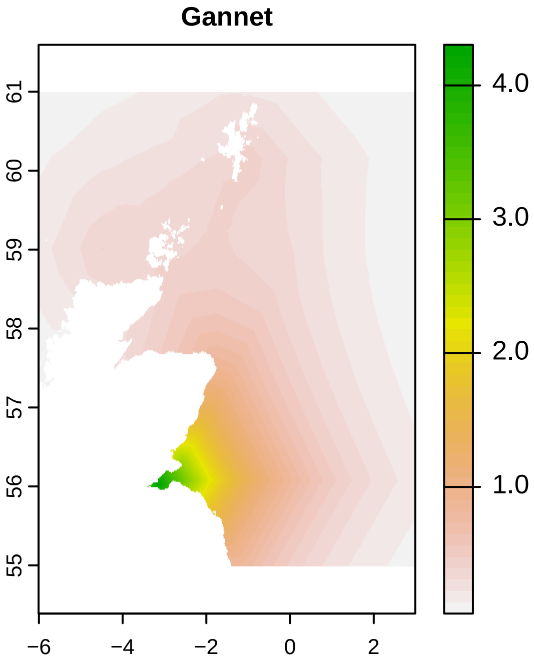

Figure 3: A visualisation of a possible accessibility surface for the gannet metapopulation in the east coast of Scotland. Here, we used a negative exponential distance function for each colony and weighted the accessibility of each colony by its relative population size. The rate of decay with distance is the corresponding parameter retrieved for adults in the final model (see below).

2.2 Survey transects

A total of 8 survey projects were combined into the pooled data set, comprising 45 surveys from 2012 to 2017. These were slightly different from the surveys described in the data report of WP1. Despite there being more surveys close to the east coast of mainland Scotland, these had specifically excluded seabird records. In contrast, additional survey transects were acquired for a large offshore area east of Aberdeenshire (Figure 4). The detections of gannets were made at the level of individual birds, so it was possible to get accurate counts for particular transect locations. The resulting span and resolution of the survey data provided both contrast and detail for the models to work on.

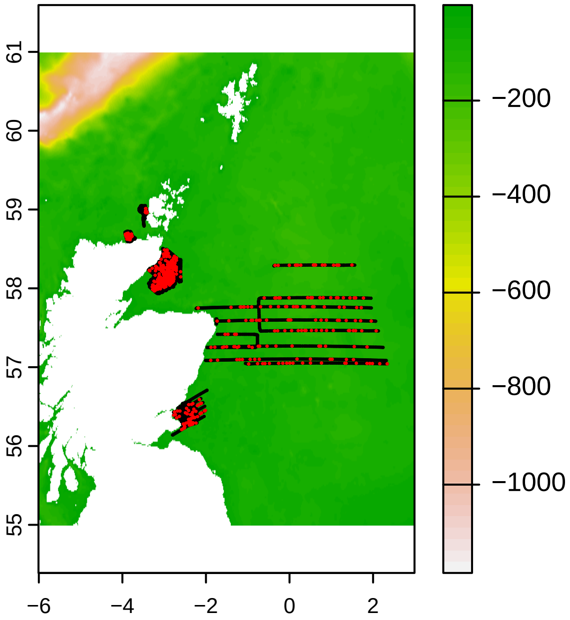

Figure 4: The survey transects considered in the analysis (black lines) and the detections of individuals from the study species (red dots).

Table 2: Telemetry locations by colony and breeding stage

	Adults	Juveniles
BASS	90503	184905

2.3 Tracking data

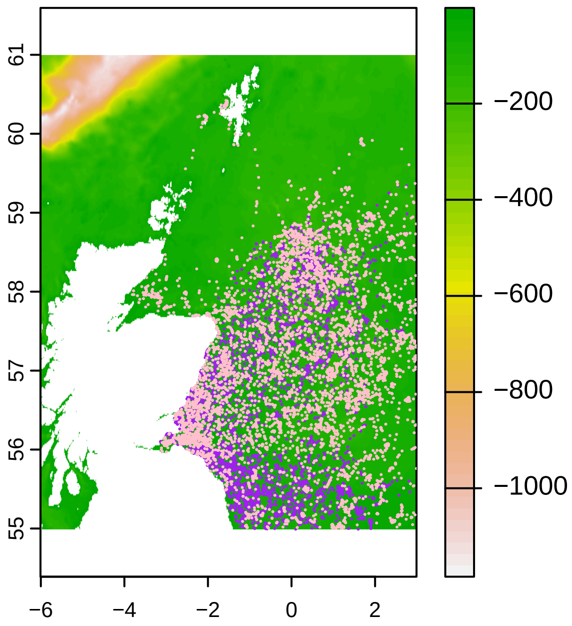

Figure 5: The telemetry data from adult individuals (shown in purple) and juveniles (shown in pink).

The telemetry dataset comprised locations from 241 tagged individuals, and the distribution of data by colony and breeding stage is shown in (Table 2). Importantly, not all colonies will be associated with tagged individuals and the number of individuals tagged in each colony will not be proportional to that colony's size (as reported in (Table 1)). Similarly, the tags were deployed on a sample of individuals that is not representative of population structure (males/females, adults/juveniles). These imbalances in sampling effort are accounted for in the modelling and prediction stage so that spatial apportioning results are unbiased, but of course, colonies and breeding stages with more data will be characterised with more precision in these results.

3 Inference

The telemetry and survey data were modelled under a joint likelihood in the Bayesian framework described and validated in the report from WP2 of this project. The objective of the joint model was to better reconcile the aggregate usage (as observed via survey data) with the colony and age-specific data (as observed via the tagging data). The JAGS code for the model (see Appendix I for code) is a direct extension of the basic model outlined in WP2, using more than two candidate covariates and more than two colonies. We have additionally made the assumption that both juveniles and adults respond in the same direction to different covariates (i.e., they prefer or avoid them), although the strength of those preferences can be very different for the two breeding stages.

3.1 Model selection on Joint model

Unlike the proof-of-concept analyses presented in the WP2 report, with real data, we cannot know a-priori which of the candidate covariates are relevant for the seabirds. We therefore followed a forward addition model selection approach using the Deviance Information Criterion to balance goodness of fit with parsimony. Each model was given a unique code indicating how many and which covariates were included. For example, `3.568` indicates a model with the three covariates `SandMud`, `PEA` and `Thermal` included in that order. All models had an intercept and distance from the colony was retained by default, since it is known (at least for provisioning adults) that they will have an association with their colony. This association is likely to be weaker for juveniles, so that was encoded in the prior for the juvenile parameter for distance to colony (see priors for parameters `aD[1]` and `aD[2]` in Appendix I).

A total of 36 models were examined (Table 3) and the best model was 4.6584.

The selected model showed avoidance of gravel and mud. We found preference for thermal fronts and high values of potential energy anomaly, indicating that gannets have a preference for highly stratified pelagic environments (Table 4).

3.2 Comparison with single-datatype models

Since the main methodological contribution of this project is the combination of survey and telemetry data, we examined the two single-datatype models corresponding to the best joint model (4.6584). We were interested in examining first, whether these models would converge, second, whether they would arrive at similar parameter estimates and third, if these estimates would be characterised by similar precision as those delivered by the joint model. In the present area of application, a model that does not converge indicates overparameterisation, i.e. data insufficiency, for the number of variables included. We decided to plot posteriors for parameters, even if the single-datatype models did not converge. These information-rich comparisons are illustrated in (Figure 6). In addition to parameters for the three models examined, we also plot the priors provided to the model as way of examining relative increases in parameter precision in the final results. Compared to the prior distributions, all three models resulted in posteriors with higher precision but different median estimates. The three models yielded different posteriors, although all three of them were more precise than the priors. The joint model often, but not always, gave estimates intermediate to the other two models'.

Table 3: The different models compared in the study. For each model, asterisks indicate the participating covariates. Models are sorted by increasing delta-DIC value (the best model is at the top). Wherever an NA value is cited in place of a delta-DIC, the model failed to converge.

	Mod	Dpth	DCst	Slp	Grvl	SndMd	PEA	SST	Thrml	NPP	DCol	DDIC
29	4.6584				*	*	*		*		*	0
36	5.65849				*	*	*		*	*	*	0
32	5.65841	*			*	*	*		*		*	1
33	5.65842		*		*	*	*		*		*	1
30	4.6587					*	*	*	*		*	19
31	4.6589					*	*		*	*	*	32
26	4.6581	*				*	*		*		*	33
24	3.658					*	*		*		*	39
27	4.6582		*			*	*		*		*	39
22	3.654				*	*	*				*	174
23	3.657					*	*	*			*	199
20	3.652		*			*	*				*	201
25	3.659					*	*			*	*	206
21	3.653			*		*	*				*	208
15	2.65					*	*				*	223
19	3.651	*				*	*				*	223
11	2.61	*					*				*	433
14	2.64				*		*				*	498
12	2.62		*				*				*	534
16	2.67						*	*			*	534
13	2.63			*			*				*	542
17	2.68						*		*		*	562
18	2.69						*			*	*	562
7	1.6						*				*	566
4	1.3			*							*	576
8	1.7							*			*	830
5	1.4				*						*	847
10	1.9									*	*	1101
3	1.2		*								*	1200
9	1.8								*		*	1212
1	0.0										*	1254
2	1.1	*									*	NA
6	1.5					*					*	NA
28	4.6583			*		*	*		*		*	NA
34	5.65843			*	*	*	*		*		*	NA
35	5.65847				*	*	*	*	*		*	NA

Table 4: Parameter median estimates from the posteriors of the joint model, accompanied by their 95% credible intervals.

Description	2.5%	Median	97.5%
Intercept Juveniles	-23.664984	-17.681116	-14.822085
Intercept Adults	-12.355127	-12.223362	-12.093638
Bathymetry Juveniles	0	0	0
Bathymetry Adults	0	0	0
Distance from Coast Juveniles	0	0	0
Distance from Coast Adults	0	0	0
Slope Juveniles	0	0	0
Slope Adults	0	0	0
Gravel Juveniles	-0.410399	-0.24765	-0.11437
Gravel Adults	-0.299867	-0.225707	-0.161517
Mud:Sand Juveniles	-0.316775	-0.211082	-0.105572
Mud:Sand Adults	-0.653345	-0.604089	-0.547394
PE Anomaly Juveniles	0.401083	0.701439	1.10396
PE Anomaly Adults	0.851008	1.021483	1.190405
SST Juveniles	0	0	0
SST Adults	0	0	0
Therm Fronts Juveniles	0.33164	0.488126	0.647656
Therm Fronts Adults	0.199661	0.246695	0.286109
Chlorophyl Juveniles	0	0	0
Chlorophyl Adults	0	0	0
Dist to colony Juveniles	0.001729	0.008376	0.014921
Dist to colony Adults	0.009176	0.016793	0.024455

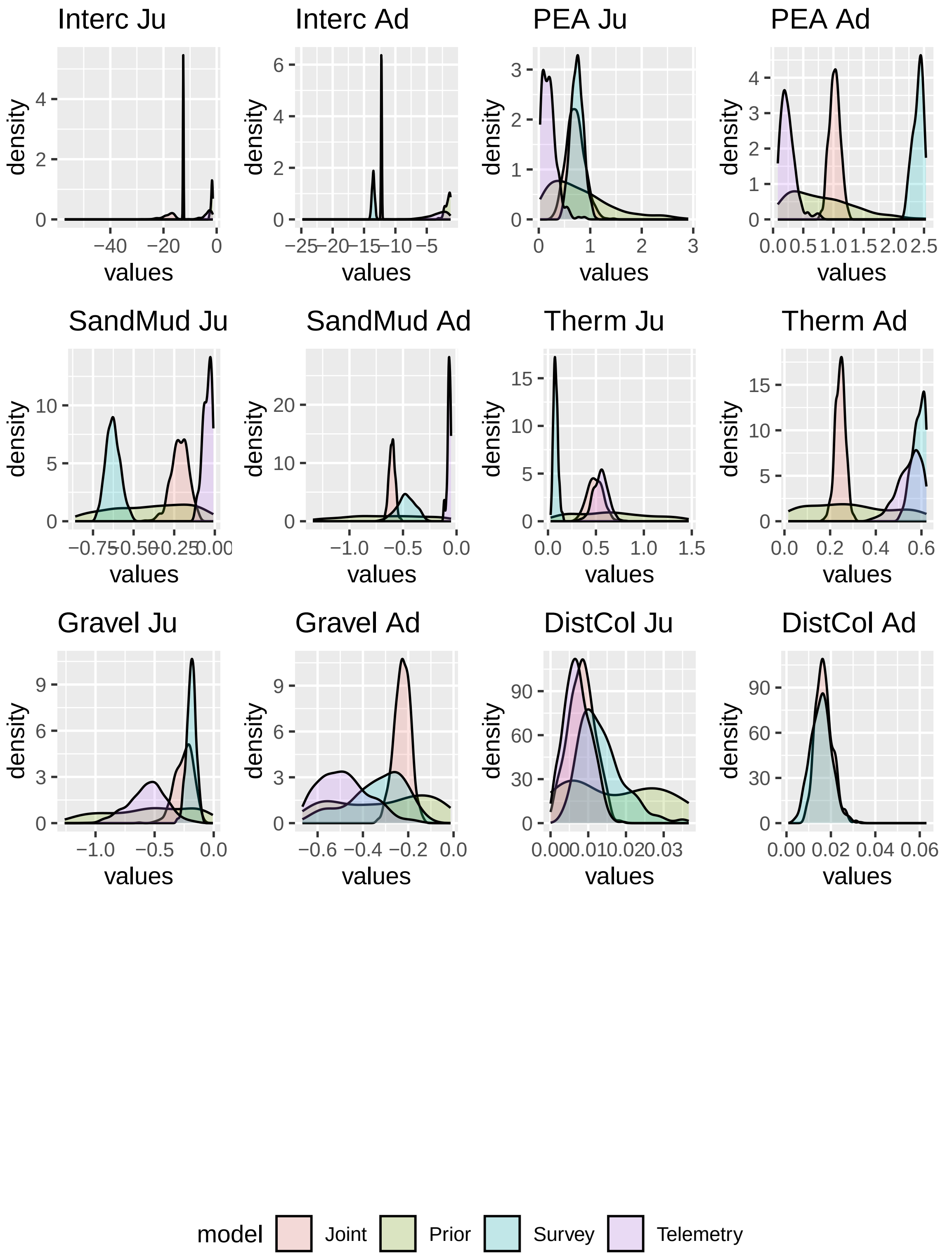

Figure 6: Comparison of the Prior distributions for each parameter, with the posteriors generated from two single-datatype models (Survey and Telemetry) and the Joint model. Posteriors from any non-converging models are also shown for comparison

Table 5: Exposure to development area by colony and age stage. This is unweighted exposure, representing the percentage of usage by this particular age class from the given colony.

Colony	Med Juv %	95% CI	Med Adult %	95% CI
Fair Isle	1.12	(0.49 - 2.02)	0.18	(0.09 - 0.29)
Forth Islands - Bass Rock to Haystack	6.03	(2.47 - 10.74)	7.04	(3.82 - 10.64)
Foula	0.97	(0.36 - 1.84)	0.12	(0.05 - 0.22)
Noss NNR	0.93	(0.34 - 1.78)	0.11	(0.05 - 0.2)
Rosehearty to Bay of Cullen	2.3	(1.36 - 3.17)	0.93	(0.86 - 1.01)
Sule Stack	1.24	(0.54 - 2.2)	0.21	(0.1 - 0.34)

Table 6: Exposure to development area by colony and age stage. This is weighted exposure, representing the usage of the area inside boundary of interest by this particular age class from the given colony as a percentage of total population usage.

Colony	Med Juv %	95% CI	Med Adult %	95% CI
Fair Isle	0.01	(0 - 0.02)	0	(0 - 0)
Forth Islands - Bass Rock to Haystack	2.21	(0.9 - 3.93)	2.58	(1.4 - 3.9)
Foula	0.01	(0 - 0.01)	0	(0 - 0)
Noss NNR	0.06	(0.02 - 0.12)	0.01	(0 - 0.01)
Rosehearty to Bay of Cullen	0.02	(0.01 - 0.03)	0.01	(0.01 - 0.01)
Sule Stack	0.05	(0.02 - 0.09)	0.01	(0 - 0.01)

4 Spatial prediction

4.1 Usage maps

The joint model can be used to generate spatial predictions for the marine usage of individuals (both breeders and non-breeders) from all colonies individually, or together. Since the model also estimates the relative proportion of adults and juveniles across the sea, the results can be weighted and aggregated in different ways. Any such visualisations are possible, but in (Figure 7) we show individual plots for only two colonies, aggregate plots for Adults and Juveniles and combined plots for the whole population.

4.2 Apportioning impact

The final step in producing the necessary results is to estimate the usage of a given region in space, by colony and population component. For the purposes of illustration, we introduce an arbitrary (and large) region (Figure 8). The use of functionality in the `TrackTrans` package for generating apportioning estimates is straightforward, and explained in Appendix II.

The package uses parametric bootstrapping from the posterior of the joint model to generate median and 95% CIs for the usage of the candidate area by different individuals from different colonies. These can be formulated as two types of exposure. First, we can extract the **unweighted exposure**

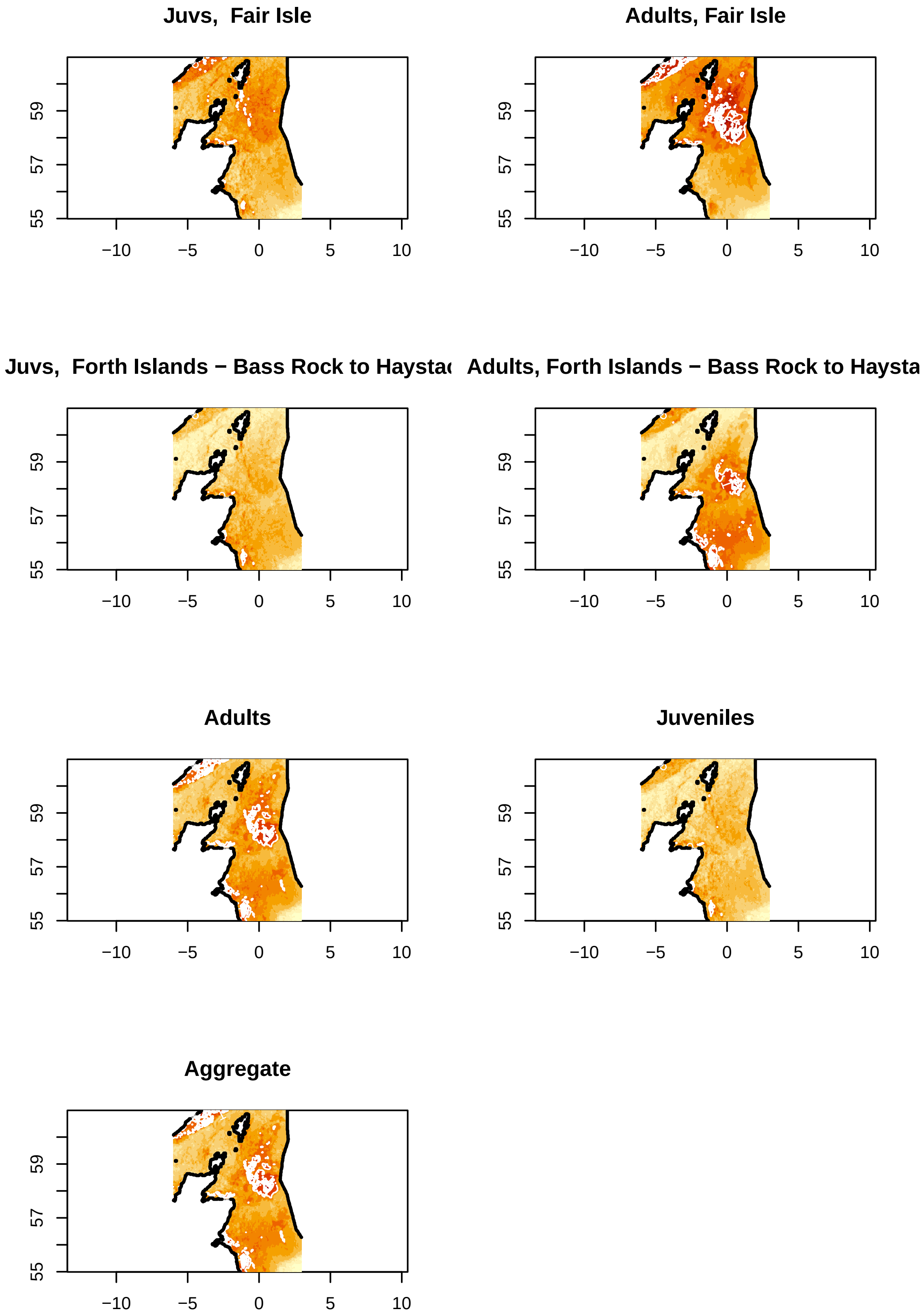

Figure 7: Predictions of spatial usage from the joint model. We show juvenile and adult maps for two colonies, total juvenile and adult usage maps, and the aggregate map from all colonies and both breeding stages. To facilitate visualisation, colours are in logarithmic scale.White contours indicate the hotspots of expected usage in linear scale.

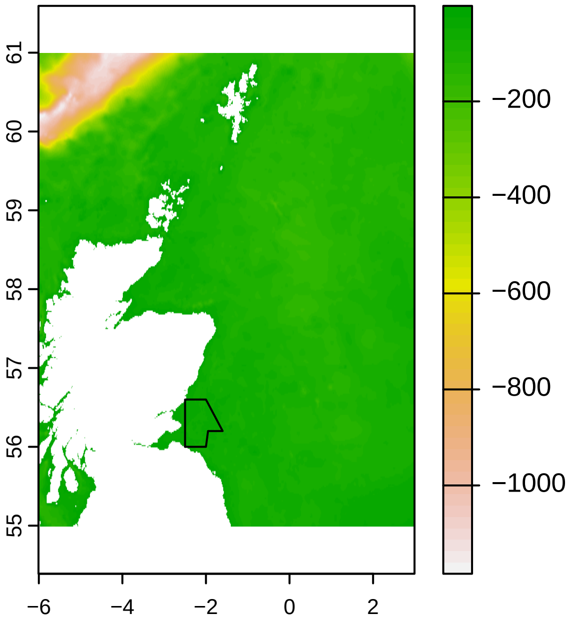

Figure 8: An example of a marine region that might be used to interrogate the model about apportioning usage.

(Table 5), representing the percentage of the usage of adults/juveniles from a given colony found inside the boundary. So, for example, the value 0.18 in (Table 5) indicates that adults from Fair Isle spend 0.18% of their marine foraging usage inside the area of interest.

Second, we can extract the **weighted exposure** (Table 6), representing the percentage of the usage of adults/juveniles from a given colony found inside the boundary. So, for example, the value 0 in (Table 6) indicates that 0% the total usage of the population is attributable to adults from Fair Isle spending their time inside the area of interest.

Note that the accompanying 95% credible intervals in the above tables need to be recalculated by boostrapping every time the boundaries of the region are changed since, due to spatial auto-correlation, the individual CIs that may be generated for any given two cells in the map are not independent, and therefore not additive (in the way that median predictions are). Given a file with the post processing data from a fitted model object, the necessary code for recalculating exposure for any given boundary is given in Appendix II. The necessary data files for running this code will be provided along with the outputs of this project for use by other agencies such as CEH and BIOSS.

5 Appendix I: JAGS implemetation of joint model for telemetry & survey data

```
jointJAGS <- "model{

### MAIN LOOP ###

# Survey data part
for(i in 1:nn) # Data row loop
  {
  for(s in 1:2) # Age-stage loop
  {
  lambLoc[i,s]<-exp(a0[s]+
                    a1[s]*DepthTr[i]+
                    a2[s]*SlopeTr[i]+
                    a3[s]*DistCoastTr[i]+
                    a4[s]*GravelTr[i]+
                    a5[s]*SandMudTr[i]+
                    a6[s]*PEATr[i]+
                    a7[s]*SSTTr[i]+
                    a8[s]*ThermalTr[i]+
                    a9[s]*NPPTr[i])

  for(c in 1:nC) # Colony loop
    {
      diLa[i,s,c]<-popS[c]*exp(-aD[s]*DistTr[i,c])
    }
  }
  # labda
```

```
  lambda[i]<- lambLoc[i,2]*sum(diLa[i,2,1:nC])+lambLoc[i,1]*sum(diLa[i,1,1:nC])
  Count[i]~dpois(lambda[i])
  }

# Telemetry data part
for(j in 1:pts)
  {
  btilde[j,1]<- a1[St[j]]*Depth.x[j]+
                a2[St[j]]*Slope.x[j]+
                a3[St[j]]*DistCoast.x[j]+
                a4[St[j]]*Gravel.x[j]+
                a5[St[j]]*SandMud.x[j]+
                a6[St[j]]*PEA.x[j]+
                a7[St[j]]*SST.x[j]+
                a8[St[j]]*Thermal.x[j]+
                a9[St[j]]*NPP.x[j]-
                aD[St[j]]*ColonyDist.x[j]
  btilde[j,2]<- a1[St[j]]*Depth.y[j]+
                a2[St[j]]*Slope.y[j]+
                a3[St[j]]*DistCoast.y[j]+
                a4[St[j]]*Gravel.y[j]+
                a5[St[j]]*SandMud.y[j]+
                a6[St[j]]*PEA.y[j]+
                a7[St[j]]*SST.y[j]+
                a8[St[j]]*Thermal.y[j]+
                a9[St[j]]*NPP.y[j]-
                aD[St[j]]*ColonyDist.y[j]
  mu[j,1]<-xy0[j,1]+(thinTg)*Ga^2/2*btilde[j,1]
  mu[j,2]<-xy0[j,2]+(thinTg)*Ga^2/2*btilde[j,2]

  xy1[j,1]~dnorm(mu[j,1],1/(thinTg*Ga^2))
  xy1[j,2]~dnorm(mu[j,2],1/(thinTg*Ga^2))
  }

# Priors

  a0[2]~dnorm(0,0.1)
  a1[2]~dnorm(0,0.1)
  a2[2]~dnorm(0,0.1)
  a3[2]~dnorm(0,0.1)
  a4[2]~dnorm(0,0.1)
  a5[2]~dnorm(0,0.1)
  a6[2]~dnorm(0,0.1)
  a7[2]~dnorm(0,0.1)
  a8[2]~dnorm(0,0.1)
  a9[2]~dnorm(0,0.1)
```

```
  for(i in 1:10) {sc[i]~dgamma(10,10)}

  a0[1]<-sc[1]*a0[2]
  a1[1]<-sc[2]*a1[2]
  a2[1]<-sc[3]*a2[2]
  a3[1]<-sc[4]*a3[2]
  a4[1]<-sc[5]*a4[2]
  a5[1]<-sc[6]*a5[2]
  a6[1]<-sc[7]*a6[2]
  a7[1]<-sc[8]*a7[2]
  a8[1]<-sc[9]*a8[2]
  a9[1]<-sc[10]*a9[2]


aD[1]~dgamma(1,1) # Distance coefficient for juvs
aDdummy~dgamma(1,1)
aD[2]<-aD[1]+aDdummy # Distance coefficient for adults

Ga~dgamma(10,0.007)

#data# nn,nC, popS,Count,DepthTr,SandMudTr,SlopeTr,DistCoastTr,GravelTr,
#data# DistTr, PEATr, SSTTr, ThermalTr, NPPTr
#data# pts, xy0, xy1, Depth.x, Depth.y, SandMud.x, SandMud.y, DistCoast.x,DistCoast.y
#data# Gravel.x,Gravel.y,Slope.x,Slope.y,ColonyDist.x,ColonyDist.y
#data# PEA.x, PEA.y, SST.x, SST.y, Thermal.x, Thermal.y, NPP.x, NPP.y
#data# thinTg, St

#monitor#  a0,a1,a2, a3, a4, a5, a6, a7, a8, a9, aD,  Ga, dic
}"
```

6 Appendix II: Usage of R functions for the generation of apportioning predictions for a given marine boundary

The key function for going this is `TrackTrans::rApportion()` which uses parametric bootstrapping from the model's posterior to generate an arbitrary number of realisations of usage. The number of bootstraps is specified by the parameter `dr`. The necessary samples from the posterior, and environmental covariates are stored on the file `SpeciesPostData.rda` The boundary of the area of interest also needs to be specified and, in the example of the main text we use an arbitrary boundary (Figure 8).The results comprise weighted and unweighted proportions of usage (median and lower/upper credible intervals) for each of the colonies and each of the two breeding stages.

```r
# Import and unpack the post-processing data files for the species
load("GannetPostData.rda")
covariates<-list()
for(i in 1:length(postData$wrappedCovs))
  {covariates[[i]]<-rast(postData$wrappedCovs[[i]])}
```

```r
dis<-list()
for(i in 1:length(postData$wrappedDis))
  {dis[[i]]<-rast(postData$wrappedDis[[i]])}

# Define or import polygon of interest
polLong<-c(-1.5,-1,-0.95,-0.6,-1,-1.5,-1.5)
polLat<-c(56,56,56.2,56.2,56.6,56.6,56)
polCRS<-crs(bath)
polLongLat<-cbind(polLong,polLat)
pol<-vect(polLongLat, type="polygons",crs=polCRS)

# Call apportioning function and look at results
app<-rApportion(dr=postData$dr, pars=postData$pars, covariates=covariates, dis=dis,
           pop=postData$pop, boundary=pol)

app
```

```
## $`Median Unweighted`
##              [,1]         [,2]
## [1,] 0.005776201 0.0011847663
## [2,] 0.022064220 0.0224309157
## [3,] 0.004893933 0.0007660225
## [4,] 0.004987244 0.0008069882
## [5,] 0.011774893 0.0059506226
## [6,] 0.006261400 0.0013353925
##
## $`Lower Unweighted`
##              [,1]         [,2]
## [1,] 0.003074746 0.0006434873
## [2,] 0.013169178 0.0155379229
## [3,] 0.002038293 0.0003176335
## [4,] 0.002175628 0.0003558156
## [5,] 0.009243820 0.0055126617
## [6,] 0.003284843 0.0006507369
##
## $`Upper Unweighted`
##              [,1]        [,2]
## [1,] 0.008597900 0.001925633
## [2,] 0.030420978 0.029095110
## [3,] 0.007752509 0.001413193
## [4,] 0.007796234 0.001462169
## [5,] 0.013827633 0.006400966
## [6,] 0.009323247 0.002189096
##
## $`Median Weighted`
##               [,1]         [,2]
## [1,] 5.388050e-05 1.105152e-05
```

```
## [2,] 8.084166e-03 8.218521e-03
## [3,] 2.939043e-05 4.600335e-06
## [4,] 3.321101e-04 5.373889e-05
## [5,] 1.061198e-04 5.362925e-05
## [6,] 2.671718e-04 5.698074e-05
##
## $‘Lower Weighted‘
##               [,1]         [,2]
## [1,] 2.868129e-05 6.002460e-06
## [2,] 4.825089e-03 5.692979e-03
## [3,] 1.224093e-05 1.907542e-06
## [4,] 1.448793e-04 2.369444e-05
## [5,] 8.330878e-05 4.968218e-05
## [6,] 1.401631e-04 2.776672e-05
##
## $‘Upper Weighted‘
##               [,1]         [,2]
## [1,] 8.020136e-05 1.796234e-05
## [2,] 1.114602e-02 1.066023e-02
## [3,] 4.655755e-05 8.486907e-06
## [4,] 5.191661e-04 9.736866e-05
## [5,] 1.246198e-04 5.768792e-05
## [6,] 3.978197e-04 9.340797e-05
```

References

Matthiopoulos, Jason, John Fieberg, and Geert Aarts. 2020. *Species-Habitat Associations: Spatial Data, Predictive Models, and Ecological Insights.* University of Minnesota Libraries Publishing. Retrieved from the University of Minnesota Digital Conservancy, https://hdl.handle.net/11299/217469.

Matthiopoulos, J, E. Wakefield, J. W. E. Jeglinski, R. W. Furness, M. Trinder, G. Tyler, A. McCluskie, S. Allen, J. Braithwaite, and T. Evans. 2022. “Integrated Modelling of Seabird-Habitat Associations from Multi-Platform Data: A Review.” *Journal of Applied Ecology* 59 (4): 909–20. https://doi.org/DOI: 10.1111/1365-2664.14114.

Skov, Henrik, and Jan Durinck. 2001. “Seabird Attraction to Fishing Vessels Is a Local Process.” *Marine Ecology Progress Series* 214: 289–98. https://doi.org/10.3354/meps214289.

Stauss, C, S Bearhop, Tw Bodey, S Garthe, C Gunn, Wj Grecian, R Inger, et al. 2012. “Sex-Specific Foraging Behaviour in Northern Gannets Morus Bassanus: Incidence and Implications.” *Marine Ecology Progress Series* 457 (June): 151–62. https://doi.org/10.3354/meps09734.

Wakefield, Ewan D., Thomas W. Bodey, Stuart Bearhop, Jez Blackburn, Kendrew Colhoun, Rachel Davies, Ross G. Dwyer, et al. 2013. “Space Partitioning Without Territoriality in Gannets.” *Science* 341 (6141): 68–70. https://doi.org/10.1126/science.1236077.

Woodward, I, Chris B Thaxter, Ellie Owen, and Aonghais S C P Cook. 2019. “Desk-Based Revision of Seabird Foraging Ranges Used for HRA Screening.” BTO.