

Spatial scales of marine conservation management for breeding seabirds

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1. Introduction

Decision makers often have to select among a suite of management actions that might benefit a given species, and management options can range from small-scale solutions that protect a local area from outside disturbance or destruction, to large-scale or global actions that regulate human activities which are considered detrimental. In the marine realm, the unambiguous delineation of important areas for the protection of biodiversity is complicated by the lack of obvious habitat boundaries [1-3], and in many cases the spatial scale of marine protected areas is inadequate to fully protect the species of interest [4, 5]. Selecting the most appropriate conservation management option will therefore benefit from accurate knowledge about the spatial scale at which management is required to protect highly mobile species [6].

Seabirds are distributed across all of the world's oceans and adjacent coastlines and islands [7, 8]. They face multiple threats on land and at sea, and are more threatened than other groups of birds [9-11]. Because many seabirds feed on fish and are near the apex of the marine food chain, they are useful indicator species for the health of the marine environment and for marine spatial planning [12-14]. To protect seabirds at sea it is essential to understand their spatial distribution and potential exposure to anthropogenic threats. During the breeding season, seabirds are constrained to marine areas which they can reach from their nest while maintaining parental duties of incubating eggs or feeding chicks. The areas exploited during the breeding season are therefore important for the persistence of populations, and may be more feasible to manage than areas used during other life stages. However, some seabird species can travel thousands of kilometres even during the breeding season [e.g. 8, 15, 16], and the spatial scale of appropriate management may therefore vary.

Currently available approaches for seabird conservation at sea can be implemented across a range of spatial scales and within a variety of regulatory frameworks [5, 17]. Area-based management approaches such as marine protected areas can be based on a broad variety of management frameworks that range from complete protection from all extractive and destructive activities ('marine reserves') to multiple use areas that permit and regulate economic activity [18-20]. For seabirds, area-based measures range from the protection of

34 breeding colonies at the very local scale, to marine foraging areas around colonies and further
36 offshore where significant seabird concentrations occur [21-23]. At larger spatial scales,
38 additional conservation management options exist for seabirds that are not based on the
40 protection of a specific area [17]. For example, regulations that reduce or eliminate the
42 incidental mortality (bycatch) of seabirds in industrial or artisanal fishing operations [11, 24,
25], or regulations that limit the extraction of food resources [26, 27], can be implemented
across all spatial scales and may therefore mitigate key threats to widely dispersed species
[28-30]. Deciding which of these policy instruments may be most appropriate for a given
seabird species of conservation concern can be informed by a better understanding of the
species' broad spatial distribution and aggregation patterns.

44 The distribution of seabird species was often inferred from observations at sea, until
the development of small tracking devices in recent decades [31-33]. By 2017, more than 100
46 of the 360 species of seabirds had been equipped with tracking devices [34]; hence, sufficient
seabird tracking data exist on the spatial scales of foraging to inform effective management at
48 a broad taxonomic level [6, 35, 36]. To synthesize the existing information for management
planning, two complementary aspects of seabird distribution patterns are particularly
50 important, albeit not entirely independent: (1) the distance a species travels and the size of the
marine area that birds of a given colony exploit; and (2) to what extent individuals of the
52 same colony use the same areas at sea, which is referred to as 'spatial aggregation'. Even very
mobile species can show high spatial aggregation at sea, and areas in which they congregate
54 may be in national or international waters depending on the distance the birds travel from the
colony [37, 38]. Here, seabird space-use with respect to these two aspects is quantified to
56 indicate appropriate spatial scales for conservation management of breeding seabirds at the
family level.

58 Existing tracking data from 52 species of ten different families collected in the
Atlantic Ocean basin over the past two decades were used. These data were analysed with
60 previously established methods [1, 39, 40] to quantify the broad space-use requirements and
spatial aggregation patterns of adult seabirds during the breeding season, and variation among
62 families was tested. This approach allowed an assessment of whether the patterns of
taxonomically coherent groups of species are sufficiently consistent to provide guidance for
64 marine management.

66 2. Methods

2.1. Data collation and aggregation

68 Seabird tracking data were collated for adult birds during the breeding season, when
 individuals are most constrained in their space-use due to the need to return to the nesting site
70 on land. This constraint to return to the nest will likely accentuate differences between
 families and therefore facilitate a greater contrast in the space-use across the taxonomic
72 spectrum. While protecting juvenile, immature and adult life-stages outside the breeding
 season is equally important for the conservation of long-lived species [41, 42], the movement
74 patterns of seabirds when they are not breeding may be more affected by their latitudinal
 distributions than by taxonomic differences [43, 44]. In addition, a broad taxonomic
76 comparison of distribution patterns of juvenile, immature, and adult life stages outside the
 breeding season is currently difficult due to the paucity of suitably high-resolution tracking
78 data for these stages.

 Seabird tracking data from the Atlantic Ocean basin were available from the BirdLife
80 Seabird Tracking Database [34] or through institutional repositories or collaborators. The
 selection of data used for this analysis was opportunistic and taxonomically imbalanced
82 because seabird tracking efforts have so far focused on species and families of larger body
 size. However, the data represent a broad taxonomic spectrum of seabird movements during
84 the breeding season from a large geographical region and are therefore useful to inform
 spatial scales for management.

86 Only tracking data from Global Positioning System (GPS) loggers and Platform
 Terminal Transmitters (PTT) were used due to their high spatial accuracy, and only datasets
88 with at least five individuals were included to minimise erroneous conclusions based on small
 sample size [1, 37, 40]. During the breeding season, adult seabirds can be constrained to
90 forage within different distances from their nest depending on whether they are incubating
 eggs or feeding small or large chicks [16, 45-47]. All tracking data were therefore divided
92 into two stages, distinguishing the incubation period from the chick-rearing period when
 adults regularly return to feed the chick and therefore may not travel as far. Tracking data
94 were analysed separately for each combination of species, colony, and breeding stage, except
 for some species where the tracking period spanned separate breeding stages that were not
96 distinguished because of a lack of concurrent monitoring (classified as ‘unspecified

breeding', Table S1). Our analysis was based on 210 datasets of 52 species from ten seabird
98 families (Tables 1 and S1).

100 *2.2. Rationale for space-use quantification*

The analysis to support the selection of appropriate spatial scales for conservation
102 management was designed to quantify seabird space-use in terms of (1) the distance that birds
travel from their colony and the extent of the overall area that was exploited, and (2) the
104 spatial aggregation at sea and the size of areas where a significant proportion of the
population concentrated.

106 Although tracking data were collated from a 20-year time period, and it is possible that
seabirds may have shifted their distribution in response to environmental changes over that
108 time period [48, 49], the coarse metrics of space-use, which are based on evolutionary
differences among families, were unlikely to have changed over two decades. Hence, the year
110 in which data were collected was not considered in the analysis, and the analysis was based
on the assumption that travel capabilities of the ten seabird families have not fundamentally
112 changed between 1998 and 2017.

114 <<<< TABLE 1 here >>>>

116 *Quantifying the travel distance and size of exploited area*

First, unrealistic locations were removed based on a species-specific speed filter [50] and
118 PTT data were linearly interpolated to a regular 1 hr interval to reduce differences between
GPS and PTT data due to their different temporal sampling resolution [51]. Mean sampling
120 schemes were one location every 17 ± 32 minutes (standard deviation, range 0.5 – 156) for
GPS and one location every 65 ± 34 minutes (2.4 – 188) for PTT datasets. Tracking data
122 were then divided into discrete foraging trips either manually or using species- and device-
specific cut-off values for minimum distances and durations implemented with standard
124 processing routines [1]. For each foraging trip the maximum distance from the colony
(foraging range) and the total travel distance as the sum of all straight-line distances between

126 all subsequent locations were calculated. The median (and range) of these trip characteristics
are presented for each species, based on all foraging trips from all colonies and breeding
128 stages, to provide a general overview of travel capabilities across seabird species [52-54].
These summaries were also calculated using just the first trip of any given individual to
130 reduce pseudo-replication [55, 56], but this data reduction did not alter the broad taxonomic
pattern (Table S2).

132 Because single-dimension trip characteristics do not capture the range of
directionality across foraging trips from individuals in a colony, the area used by each species
134 at each colony was also quantified. This area was calculated as the minimum convex polygon
of 95% of all locations for each tracking dataset and is hereafter referred to as 'exploited
136 area'. A minimum convex polygon was chosen to encompass less frequently used areas, and
95% of locations were selected to avoid identifying an excessively large area due to some
138 erratic trips or low-quality location estimates; this approach is deemed appropriate for
similarly large-scale taxonomic comparisons [57, 58].

140

2.2.1. Quantifying the spatial aggregation and size of area with concentrated use

142 Foraging areas may range from widely dispersed to highly concentrated in a relatively
restricted area. First, the 'core area' for each individual was calculated as the 50% kernel
144 utilization distribution, and the extent of overlap between core areas of all individuals of a
given species at a colony in a given breeding stage was then quantified. To identify the core
146 area, the scale of the area-restricted search derived from first-passage time analysis was used
as the smoothing factor in the kernel density estimator [1, 59, 60]. Because the core area size
148 is dependent on the smoothing factor, and area-restricted search may be difficult to detect for
some species or data resolutions [61], an alternative approach was also used in which the
150 smoothing factor was scaled to the median foraging range of a colony. Results from both
approaches were highly correlated and did not affect our conclusions (Table S3), and only
152 results from the former approach are presented. The overlap in core areas of individuals was
quantified using Bhattacharyya's Affinity index (BA), a non-directional measure of home-
154 range overlap that ranges between 0 (complete separation) and 1 (completely matching
probability distributions), and is considered the most appropriate index for quantifying the
156 similarity between utilisation distributions [39, 62]. Because the BA is calculated between
pairs of individuals, the BA across all pairwise comparisons was averaged for a given dataset.

158 Individuals for which <10 locations were available were excluded from the estimation of
spatial aggregation.

160 To compare the size of the core areas of each population (hereafter ‘area of
concentrated use’), the 50% kernel utilisation distribution of each individual was delineated,
162 and areas where the 50% kernels of at least 20% of tracked individuals of that population
overlapped were identified [1].

164 To provide a scale of reference for the marine area requirements of seabirds, the sizes
of existing marine protected areas were downloaded from the World Database on Protected
166 Areas (www.protectedplanet.net, accessed 15 Aug 2017), and filtered to include only marine
and coastal protected areas.

168 *2.3. Assessing representativeness of datasets with varying sample size*

Sample size can affect quantitative metrics of space-use based on tracking data [40, 51, 63].
170 Because datasets ranged from 5 to 119 individuals per colony and breeding stage, the
representativeness of each dataset was quantified to characterise the distribution at the level
172 of the colony. Following the approach of Lascelles et al. [1], each dataset was iteratively sub-
sampled to randomly select tracking data from 3 to $n-1$ individuals, where n is the number of
174 individuals tracked in that dataset. During each iteration, the 50% kernel utilisation
distribution was calculated from the randomly selected data, and the proportion of the un-
176 sampled locations that fell within the 50% isopleth was assessed. If the proportion of un-
sampled locations contained within the 50% isopleth of the randomly selected individuals
178 (hereafter referred to as the ‘inclusion value’) was $\geq 50\%$, then the dataset was considered
representative for the colony because the un-sampled individuals were already properly
180 represented by the sampled individuals [1]. For each simulated sample size of every dataset
30 iterations were performed and the mean inclusion value across the 30 iterations was
182 calculated for each sample size. A non-linear least-squares regression was then fitted to
inclusion values to estimate the asymptote of each dataset based on the 30 iterations for each
184 simulated sample size.

The representativeness of each dataset is reported as the proportion of the estimated
186 asymptote that the mean inclusion value of a dataset achieved at the highest sample size. If
this representativeness was $>70\%$, a dataset was adequate to describe the space-use of the
188 population [1, 40]. If the non-linear regression could not identify an asymptote due to a

singular gradient (i.e. the area expansion had not levelled off with increasing sample size),
190 the mean inclusion value for the largest sample size of that dataset was used. The level of
representativeness was then tested for a positive correlation with the number of individuals
192 that had been tracked by calculating the Pearson correlation coefficient. The proportion of
datasets for each family where the tracking data were considered not representative for the
194 spatial distribution of a given colony is presented (Table S4).

196 *2.4. Statistical analysis*

To examine whether there was evidence for variation in space-use patterns at a higher
198 taxonomic level [64, 65], the effect of seabird family on maximum travel distance from the
colony, spatial aggregation (BA), the size of an area of concentrated use, and the size of the
200 exploited area was tested. Generalised linear mixed models that included colony size and the
stage of the breeding cycle as fixed effects were used. These two factors affect the space-use
202 patterns of seabirds [66-68], but the analysis did not aim to investigate the relative
importance of these factors and no inference was drawn from those parameters. The sampling
204 rate of the tracking device was also included as a fixed effect because it can affect the extent
and shape of home-range areas [51]. In addition, variation at the species and colony level was
206 accounted for by including these two variables as random intercepts to avoid
pseudoreplication [69]. Because some datasets had small sample sizes, each dataset was
208 weighted based on the level of representativeness that was attained in the sensitivity analysis
to reduce the influence of small and possibly unrepresentative datasets on the overall
210 conclusions.

The data collation of all individual foraging trips was used to test the effect of seabird
212 family on maximum travel distance from the colony. The effect of seabird family on spatial
aggregation, the size of an area of concentrated use, and the size of the exploited area was
214 tested at a population level because the latter three measures were calculated for each unique
combination of species, colony, and breeding stage.

216 For each of these four response variables, two models were fitted that differed only by
the inclusion of seabird family as a fixed factor in one of the pair of models, while all other
218 fixed and random factors were identical. A likelihood-ratio test was used to infer whether
seabird family explained a significant amount of variation in space-use variables that was not
220 already accounted for by other fixed or random effects [70]. All analytical steps were

conducted in R 3.4.2 [71], and code to replicate the analyses is provided at
222 <https://github.com/steffenoppel/seabirds>.

224 3. Results

Seabird tracking data from 52 species across ten families were collected between 1998 and
226 2017 in 210 unique combinations of species, colony, and breeding stage (Table S1). The data
contained a total of 12,039 distinct foraging trips from 5419 individual birds, with a mean of
228 21 tracked individuals (range 5 - 119) per dataset, and included >10% of the species in each
family that breed in the Atlantic Ocean basin (Table 1).

230 As expected, seabird species varied enormously in foraging trip characteristics, with single
foraging trips ranging from <1 km to >12,000 km (Table 2). There was considerable variation
232 within species and families in the foraging range, and some of this variation was explained by
the breeding stage (Fig. 1). Despite substantial variation among breeding stages, species and
234 colonies, there was clear evidence that foraging range varied at the family level (LR-Test χ^2_9
= 55.57, $p < 0.001$), with cormorants having the shortest ranges, and albatrosses the largest
236 (Table 2, Fig. 1). This pattern remained equally strong if only a single trip per individual was
used in the analysis (Table S2).

238

<<<< FIGURE 1 here >>>>

240

Seabirds also varied markedly in the extent to which they congregated at sea. The average
242 Bhattacharyya's Affinity index for a given dataset ranged from virtually no overlap (BA <
0.001 for four datasets; Adélie Penguin *Pygoscelis adeliae*, European Shag *Phalacrocorax*
244 *aristotelis*, Common Guillemot *Uria aalge*, Tristan Albatross *Diomedea dabbenena*) to very
high overlap (BA = 0.91; Magellanic Penguin *Spheniscus magellanicus*). Due to the high
246 variation in overlap among species and between breeding stages, there was no significant
variation among families (LR-Test $\chi^2_9 = 12.22$, $p = 0.20$). For most families there was higher
248 overlap during chick-rearing than during incubation (Fig. 2). Cormorants, gulls and auks had
consistently high overlap in both breeding stages, while albatrosses and frigatebirds showed
250 consistently low overlap (Fig. 2).

Owing to variability in travel distance and aggregation, the size of the marine area exploited
252 by seabird populations during the breeding season varied by six orders of magnitude among
families (Table 2; LR-Test $\chi_9^2 = 57.91$, $p < 0.001$), with cormorants and penguins having
254 generally the smallest exploited areas and albatrosses and Great Shearwaters (*Ardenna*
gravis) the largest (Table 2).

256

<<<< FIGURE 2 here >>>>

258

Low overlap of individual core ranges can frequently lead to unrepresentative tracking data,
260 as the foraging behaviour of untracked individuals is poorly captured by those already
tracked. There were 101 (48%) datasets that did not meet the criteria for representativeness
262 that would be required to designate marine important bird areas following Lascelles et al.
(2016), with 100% of the frigatebird datasets ($n = 3$) and 80% of albatross datasets ($n = 20$)
264 not representative at the population level. For gulls, penguins and gannets, >60% of datasets
were representative (Table S3). There was a positive correlation between the number of
266 individuals tracked and representativeness ($r_s = 0.332$, $p < 0.01$, $n = 210$), and of the datasets
that included >50 individuals only three were not representative (all from albatrosses, Fig.
268 S1).

Accounting for the level of representativeness of each dataset, and simulating the size of an
270 area of concentrated use across a range of sample sizes, there was a strong effect of family on
the size of areas of concentrated use (LR-Test $\chi_8^2 = 57.91$, $p < 0.001$). The largest areas of
272 concentrated use were found in albatrosses and gannets, and the smallest in cormorants and
gulls, but within each family, the size of the area of concentrated use varied by two to four
274 orders among species and breeding stages (Fig. 3).

276 <<<< FIGURE 3 here >>>>

278 There was a negative correlation between the level of spatial aggregation at sea and the size
of the area exploited during the breeding season ($r_s = -0.285$, $p < 0.001$, $n = 210$), resulting in
280 a gradient of space-use that can inform the relevant scales for conservation management (Fig.

4). Species with large ranges generally had low spatial aggregation (bottom right in Fig. 4),
282 and were mostly albatrosses, petrels, shearwaters, storm petrels, frigatebirds and tropicbirds.
Short-ranging species were mostly cormorants, auks and gulls, and tended to show higher
284 aggregation at sea (top left in Fig. 4). For most species, tracked birds had smaller ranges and
showed greater aggregation during the chick-rearing than during the incubation stage.

286

<<<< FIGURE 4 here >>>>

288

4. Discussion

290 Seabird species range from those that congregate at sea and can be efficiently protected
within a small area, to those that disperse widely and range over areas that can encompass
292 millions of square kilometres. For the study species in the Atlantic Ocean basin, there were
consistent differences among families in both maximum foraging range and the size of areas
294 used at sea. Within this spectrum, albatrosses, petrels, storm petrels, frigatebirds, and
tropicbirds travelled on average farther and dispersed more widely at sea during the breeding
296 season than cormorants, penguins, auks, and gulls, although there was considerable variation
within each family. Although some species may have recently shifted or expanded their
298 foraging ranges due to climate-induced changes in the marine environment [48, 72], these
shifts in spatial location are unlikely to be a result of fundamental changes to the species'
300 travel capabilities, and our broad conclusions are therefore robust to climatic changes in the
near future.

302 Our synthesis can be used to identify the management approaches likely to be most
effective given the geographic scale over which the threats to a certain species need to be
304 addressed. For some species, this broad-scale information at the family level may be
sufficient to implement certain conservation actions without the need for further detailed data
306 on individual movements from a given colony [6, 35, 73]. Some of the widely dispersing
species use areas at sea that may be considered too large for the establishment and
308 enforcement of strict marine reserves that ban all economic activity that negatively affect
birds and other biodiversity [4, 19, 20]. However, other management approaches that reduce
310 threats such as bycatch in fishing gear or depletion of prey resources can be implemented
across very large spatial scales – either within appropriately managed protected areas that

312 regulate rather than ban economic activities, or in the framework of other effective area-based
management measures or sustainable-use regulations that apply to large marine regions
314 without the designation of protected areas [74-77]. All management approaches should also
consider that not only seabirds, but also their threats may disperse at sea and occur only in
316 certain areas or at certain times. Static structures such as wind turbines or gillnets will affect
seabirds only at one location, whereas oil, plastics and other pollutants disperse freely with
318 currents and therefore need to be managed at different spatial scales [5]. Threats from
fisheries will only occur where a particular fishery operates, and regulation of such fisheries
320 is most important where fisheries and species vulnerable to interactions co-occur [30]. Hence,
multiple management mechanisms addressing various threats in time and space may be
322 required to safeguard particular species.

Our data represent some families better than others, and our results may not be fully
324 representative of species-rich families such as gulls and terns, or storm petrels. For some
families there may also be significant intra-family variation, which our data collation may not
326 capture appropriately: penguins, for example, include both migrant and resident species, but
our tracking data encompassed mostly migrant species, which have greater foraging ranges
328 even during the breeding season [78]. Nonetheless, for families that encompass few species,
such as the tropicbirds and the frigatebirds, the information provided here is likely more
330 accurate and transferrable than for the gull family which encompasses >40 species in the
Atlantic Ocean basin with a diverse range of body sizes and travel capabilities [79, 80].
332 Because high-resolution GPS tracking devices have only recently become small enough to
track small seabirds [81], our data are biased towards larger-bodied species, with many storm
334 petrels, small auks, and diving petrels not yet represented in tracking databases. Hence, while
our study is a useful first step towards synthesizing seabird tracking data, there are some
336 knowledge gaps where strategic tracking of certain families and species groups will advance
our understanding of the space-use of smaller seabirds in the future.

338 Besides the incomplete coverage of all species within each family, there was large
variation in the number of colonies from which tracking data for a given species were
340 available. Seabird foraging ranges are known to vary within species, with respect to colony
size and environmental factors such as ocean productivity and the foraging habitat available
342 within a given radius [56, 66, 82-84]. The inclusion of tracking data from either a very small
or a very large colony may therefore have misrepresented the typical space-use of particular
344 species [85]. While such differences need to be considered for the implementation of specific

protection measures, our broad scale analysis indicated that the differences in space-use
346 among families were generally larger than differences within species, and our overall
conclusions are unlikely to be affected by a few atypical datasets.

348 Our results also highlight that for some families the space-use patterns vary
substantially between incubation and the chick-rearing stage (Figs 1 and 2, Table 2), which
350 may be relevant for seasonal site protection or other dynamic area-based management
measures that aim to regulate certain activities during discrete periods [86]. However, some
352 of the apparent variation between breeding stages might be a consequence of varying data
coverage and inter-specific differences. For example, among gannets and boobies our results
354 seem to indicate that birds have extremely low spatial aggregation during incubation
compared to brood-guard (Fig. 2). This pattern is potentially because the largest gannet in our
356 dataset, the Northern Gannet (*Morus bassanus*), which forages in temperate and productive
waters, has mostly been tracked while feeding chicks [87-89], whereas the available data
358 during incubation were from the smaller, tropical boobies, which forage in less productive
waters and may therefore disperse more widely at sea [90-92]. Nonetheless, our data clearly
360 indicate that most seabirds have smaller foraging ranges and show greater aggregation at sea
during the chick-rearing than the incubation period, which could be used to inform
362 appropriate management approaches at different times of the breeding cycle .

The dataset and space-use metrics that was collated could also be used with various
364 explanatory variables to understand the causes of variation and predict the likely movement
scales of other species of seabirds for which no tracking data exist. Such extrapolations have
366 been applied successfully to separate colonies within species [83], but if space-use
requirements can also be predicted across species then some conservation management may
368 proceed on that basis rather than await species-specific local tracking data [93, 94]. The
generality of the patterns of space use found among families could be tested with data from
370 additional species, regions and marine systems, or life-history stages. Nonetheless,
researchers considering which seabirds to track for the purpose of improving conservation
372 management are encouraged to first critically examine the value that the collected data will
add to existing knowledge [35, 36, 95].

374 Our review focussed on adult birds during the breeding season to facilitate a broad
taxonomic comparison. However, in long-lived seabirds, immature or adult birds not actively
376 breeding may comprise a larger proportion of the total population, and may have

fundamentally different space-use patterns and distributions than breeding adults [96-98].

378 Seabird conservation therefore requires not only the protection of breeding adults, but also of
other life stages, which may not occur in the same spatial area. The broad scales of space-use
380 that are summarised here for breeding adults will not be sufficient to evaluate all potential
spatial overlaps with threats that may lead to population declines, and further tracking of
382 highly threatened species or different life stages may be required to facilitate effective
management [35].

384 In summary, seabirds are well-known indicators for the health of the marine
environment [12-14], and may therefore constitute a useful tool for marine spatial planning.
386 Many seabirds, especially cormorants, penguins, auks, and gulls congregate in certain areas at
sea which are useful candidates for area-based management approaches such as marine
388 protected areas. Marine protected areas can be managed in a variety of ways that may permit
and regulate certain economic activities, and for marine protected areas of very large size, the
390 complete exclusion of all economic activities may neither be practical nor desirable [18, 19,
99]. Our results show that some families, especially albatrosses, petrels, storm petrels and
392 highly pelagic tropical species such as frigatebirds and tropicbirds, disperse widely at sea,
and require management approaches that are implemented at large scales such as bycatch
394 regulations, compliance monitoring and other fisheries observer programmes, or large-scale
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396

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