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**Preparatory work to assist in the delivery of a pilot OSPAR
indicator B5 Marine Bird Bycatch**

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Summary

Commercial fisheries impact marine ecosystems in various ways. While some impacts may be positive (e.g. discards providing feeding opportunities) others are deleterious; bycatch of sensitive species – including marine birds – is one such pressure. Marine bird bycatch has been well-studied, although many gaps in knowledge are still present, including how bycatch may affect a given population.

In the North-east Atlantic, where many commercial fisheries operate, the OSPAR Convention provides a forum for neighbouring countries to collaborate on addressing impacts on marine biodiversity, such as bycatch. OSPAR Contracting Parties adopted in 2025 a Common Indicator on Marine Bird Bycatch (B5) that will be used internationally to assess bycatch impacts on marine birds across the North-east Atlantic. As part of the development of the OSPAR Common Indicator the UK's Joint Nature Conservation Committee let a contract to investigate possible datasets, propose methods and run some pilot analyses. The main findings are presented in this report.

Different sources of data were examined to compile a comprehensive picture of the potential data availability on fishing effort and marine bird bycatch rate sampling within each of the five Regions within the OSPAR Maritime Area, which covers the NE Atlantic. Starting with a bycatch survey inventory kindly made available by the ICES Working Group on Bycatch of Protected Species (WGBYC), other potential sources of bycatch and fishing effort data were then added.

To assess the impact of plausible bycatch scenarios on marine bird populations we ran a pilot Population Viability Analyses (PVA). We constructed pilot PVAs for Cory's shearwater *Calonectris borealis* and common guillemot *Uria aalge* breeding in OSPAR Regions IV (Bay of Biscay and Iberian Coast), and III (Celtic Seas), respectively. Due to the lack of comprehensive bycatch data for fisheries operating in any OSPAR region and taking into consideration the timeline of the present study, we defined seabird bycatch based on plausible hypothetical scenarios. We then used the ratio of the impacted to unimpacted final population size after three generations to compare changes in population growth. We propose that this ratio could inform the OSPAR Common Indicator I on Marine Bird Bycatch.

Data on marine bird bycatch is being collected – to some degree – throughout the OSPAR Maritime Area. However, serious paucity of data was found across all OSPAR regions, especially in the Wider Atlantic (OSPAR Region V). The main factors limiting data quality included the temporal resolution available and the coverage of observation effort. However, other deficiencies were also identified, including the occurrence of few observer programmes directed to monitor bycatch of protected species, very low observer coverage of small-scale fisheries and a lack of accurate estimates of fishing effort for most fleets.

The PVA demonstrated that small reductions in adult survival, caused by bycatch mortality, resulted in large population responses for both Cory's shearwater and

common guillemot. In the long term, this effect could reverse positive population trends. The analyses presented in this report suggest that PVA based on Leslie Matrix models provide a valuable tool for evaluating the impact of bycatch-driven marine bird mortality in OSPAR regions.

We provide several recommendations to support future developments of the OSPAR Common Indicator on Marine Bird Bycatch. This includes appraising data owner restrictions and using bycatch and PVA Minimum Criteria to assess data quality prior to assessment.

Contents

1	Background.....	1
2	Methods.....	5
2.1	Sources of data	5
2.2	Minimum quality criteria.....	5
2.3	Data preparation and candidate pilots.....	6
2.4	Bycatch analysis of candidate pilot regions.....	7
2.4.1	Cory's shearwater	7
2.4.2	Common guillemot	8
2.5	Demographic parameters	12
2.5.1	Cory's shearwater	12
2.5.2	Common guillemot	12
2.6	Population Viability Analysis.....	15
2.7	Population model assumptions.....	16
3	Results.....	18
3.1	Cory's shearwater.....	18
3.2	Common guillemot.....	22
4	Conclusions/recommendations.....	29
4.1	Availability of bycatch data in the Northeast Atlantic.....	29
4.2	Performance of PVA models to assess impact of bycatch.....	30
4.3	Recommendations for the assessment of OSPAR indicator B5 – marine bird bycatch	31
	References.....	33
	Appendix 1. Terms used to search published and grey literature on seabird bycatch in the OSPAR area	40
	Appendix 2. List of sources of bycatch data (in addition to the WGBYC inventory).....	41
	Appendix 3. Bycatch survey inventory	47
	Appendix 4. Bycatch quality criteria	48
	Appendix 5. PVA quality criteria.....	59
	Appendix 6. Matrix containing the results of available bycatch data.....	70
	Appendix 7. Overview of data availability for a Pilot assessment marine bird bycatch indicator	70
	Appendix 8. Results of the models assuming density independence	71
	Appendix 9. Programming scripts	76

1 Background

Commercial fisheries can impact marine ecosystems in multiple ways, including fish stock depletion and mortality of non-target species (Pauly *et al.* 2005). Broadly, marine birds and fisheries are attracted to the same productive habitats, resulting in high levels of temporal and spatial overlap. In terms of positive interactions between marine birds and fisheries, fisheries may provide an additional source of food through discards and bait setting. However, high levels of spatial overlap may also result in negative interactions, such as the incidental catch of non-target species, or bycatch. Bycatch is one of the main threats to profitable and sustainable fisheries (Patrick & Benaka 2013) and represents a significant threat to marine biodiversity and the conservation and welfare of vulnerable marine species (Lewison *et al.* 2004). Bycatch of marine birds has been reported in several species (Croxall 2008; Żydelis *et al.* 2009; Tuck *et al.* 2011; Dias *et al.* 2019), however many gaps in data and knowledge are still present. For example, there is no comprehensive and quantitative calculation of fishing effort, or an accompanying register of bycatch for marine birds, or a comprehensive assessment of how bycatch affects population demography and trends. As long-lived species, marine birds are highly sensitive to changes in adult mortality. Furthermore, many of the species threatened by bycatch are already of conservation concern (Dias *et al.* 2019).

In the European Union, several initiatives have been put in place to understand and address the impacts of marine bird bycatch. These include the EU Marine Strategy Framework Directive (MSFD – 2008/56/EC), the EU Action Plan for reducing incidental catches of seabirds in fishing gears (COM (2012) 665) and the Regulation (EU) 2019/1241 on the conservation of fisheries resources and the protection of marine ecosystems through technical measures. The MSFD requires the assessment of bycatch mortality under criterion D1C1 “the long-term viability of marine bird populations is not threatened by deaths caused by incidental bycatch in mobile and static fishing gear” (see Commission Decision 2017/848/EU).

In the North-east Atlantic, where many commercial fisheries operate, the OSPAR Convention provides a forum for EU Member States and other neighbouring countries (e.g. UK, Norway), to collaborate on addressing impacts on marine biodiversity such as bycatch. In 2024 [OSPAR Contracting Parties agreed Recommendation 2024/02 on reducing bycatch of marine birds in the maritime area](#). Under the Recommendation, Contracting Parties should consider to develop, adopt and implement a National Plan of Action to minimise, and where possible eliminate, incidental bycatch of marine birds in fisheries. They should also act collectively to collate data, conduct bycatch assessments, exchange best practice and identify “instances where fishing activities constitutes a threat to species and habitats”. In order to assess the effectiveness of these measures, OSPAR Contracting Parties adopted in 2025 a Common Indicator on Marine Bird Bycatch (B5) that will be used internationally to assess bycatch impacts on marine birds across the North-east Atlantic. EU Member States will be able to use the common indicator to report on marine bird bycatch as part of their obligations under Article 8 of the MSFD (see above).

To assist the development of the OSPAR’s Common Indicator, the UK’s Joint Nature Conservation Committee (JNCC) led a small contract – which this report is the product of – to investigate possible datasets, propose methods and run pilot analyses. The main aims of this work are:

- 1) Examine the availability of data on marine bird bycatch mortality across the OSPAR Maritime Area (Figure 1). This will include a bycatch survey inventory made available by WGBYC (ICES 2020), as well as published information from scientific and grey literature.

- 2) Run Population Viability Analysis (PVA) to examine the marine bird population response to different scenarios of bycatch for those areas identified as having sufficient bycatch data under Aim 1. Successful completion of this Aim will support the identification of an indicator.

In this report, we present a review of bycatch data availability, two candidate pilot analyses and the associated model assumptions, as well as detailing recommendations for future work.

The results of this project were used to conduct a pilot assessment of marine bird bycatch within [OSPAR's Quality Status Report in 2023](#).

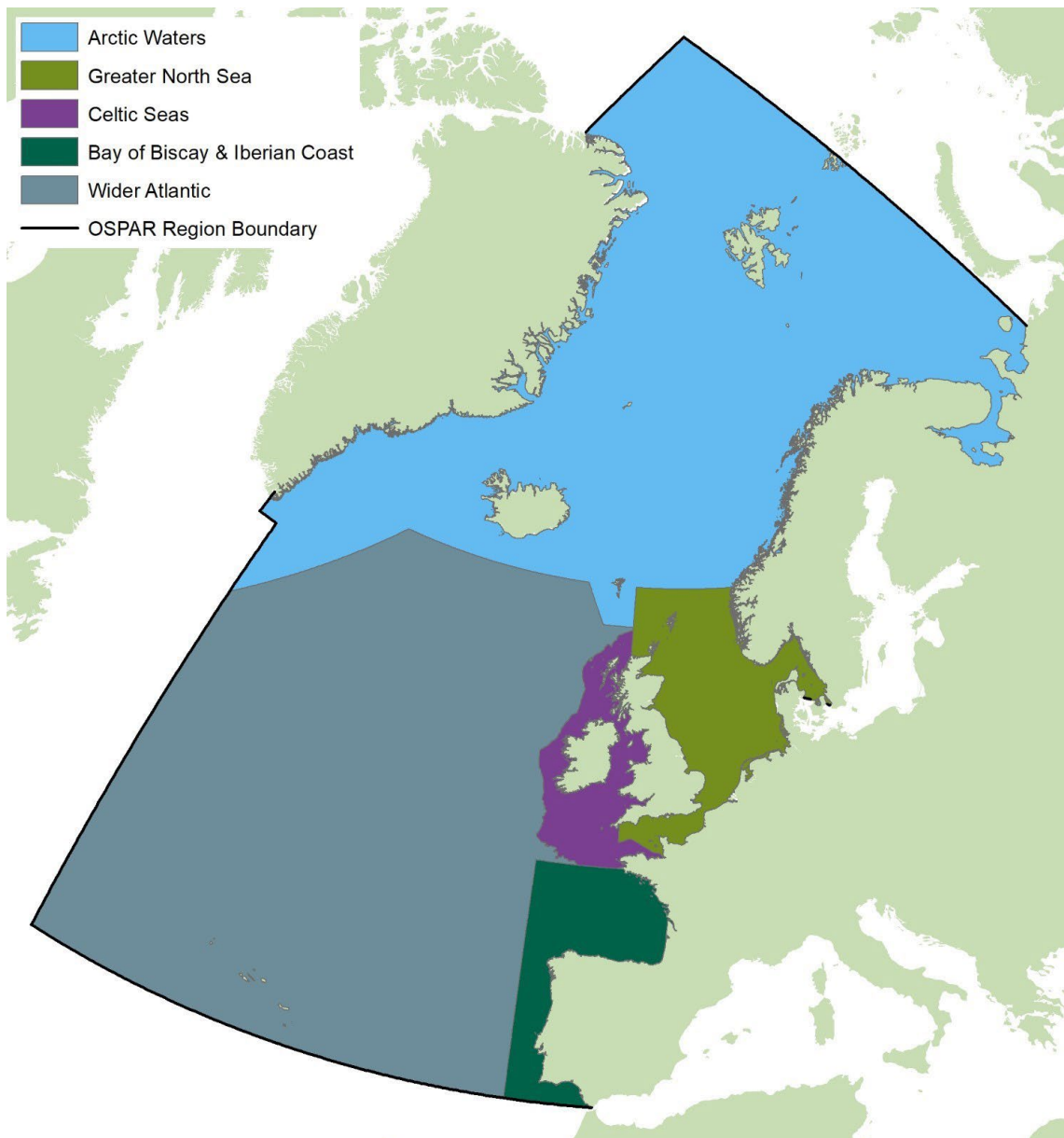


Figure 1. The OSPAR Maritime Area and the five assessment units used in this pilot assessment (Arctic Waters – Region I; Greater North Sea – Region II; Celtic Seas – Region III; Bay of Biscay and Iberian coast – Region IV; Wider Atlantic – Region V).

Providing actual estimates of bycatch mortality is considered outside the scope of this preliminary work. However, it is expected that the bycatch rate scenarios used in the PVA (Aim 2) sufficiently reflect true levels. These analyses are intended to be the first, exploratory parts of the workflow for the B5 marine bird bycatch indicator (as illustrated by the schematic indicator workflow, Figure 2). The schematic indicator workflow was developed following the outcome of the “OSPAR-HELCOM workshop to examine possibilities for developing indicators for incidental by-catch of birds and marine mammals” (OSPAR-HELCOM 2019, Copenhagen).

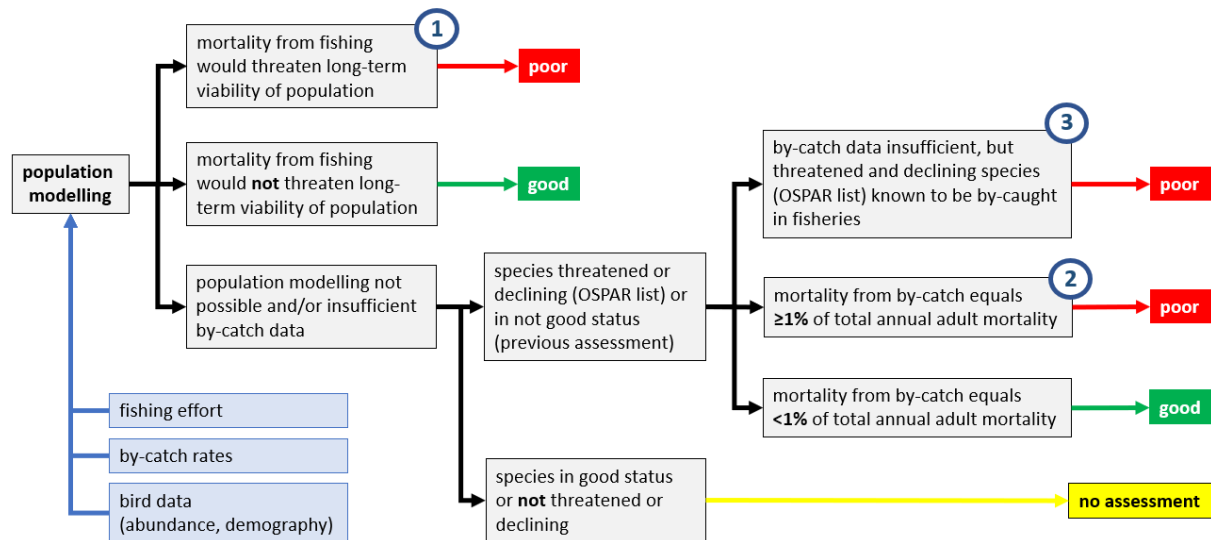


Figure 2. Workflow for the marine bird bycatch indicator from the threshold proposal of the indicator B5 Marine Bird Bycatch, based on the outcome of the OSPAR/HELCOM bycatch workshop held in Copenhagen in September 2019. “Poor” and “good” assign the conservation status on a species/population. Numbers indicate the sequence of assessment, according to data availability (where 1 = highest).

There are two main challenges to assessing the population response of marine birds to bycatch mortality. Firstly, there is a significant lack of data on fishing effort and bycatch rates for several fleets within the OSPAR regions. Even for the regions where more information is collected, quantitative data on bycatch are lacking for some fleets which are known to accidentally catch considerable numbers of marine birds. Such data gaps are more evident in fleets operating in international or foreign waters, where data may be stored in non-public and unknown databases, thus putting constraints on their accessibility, as well as small-scale fisheries where the small size of those vessels makes it difficult to accommodate observers. In other fisheries, data are either not readily available or are dispersed over several databases that have different data owners and contact points. These datasets can also be closed and not publicly accessible. Secondly, there is a considerable spatial and taxonomic imbalance in data availability for bird demographic rates, such as survival, breeding success and recruitment (Horswill & Robinson 2015; Horswill *et al.* 2021). Robust estimates of these processes are essential for parameterising reliable Population Viability Analyses (PVA). Some bird species are well studied at key sites, however a complete picture of spatial variation in their demography is typically unavailable.

Additional challenges associated assessing the population response of marine birds to bycatch mortality include linking individuals caught as bycatch to specific populations. During the breeding season, marine birds are limited in their movements by their need to regularly provision offspring. However, outside the breeding season many species of marine bird have wide ranging distributions. Even non true-migratory species, such as European herring gull

Larus argentatus or yellow-legged gull *Larus michahellis*, occupy vast areas during the non-breeding period (Coulson 2015; Bosch *et al.* 2019). Adults from different breeding colonies spaced hundreds of kilometres apart, may also concentrate on the same non-breeding sites, thereby showing a higher spatial overlap compared to the breeding period (e.g. Davies *et al.* 2021). Finally, as long-lived species, marine birds have delayed recruitment and the spatial distribution of this age class is often unknown (Péron & Grémillet 2013), making it difficult to also assess potential impacts across different life stages.

2 Methods

2.1 Sources of data

Different sources of data were examined to compile an inventory of data availability for fishing effort and marine bird bycatch rates within each of the five OSPAR regions (Figure 1). Although an exhaustive search of data was not foreseen in the initial proposal, the easy access of the contractor to several sources of information culminated in a very complete picture of available information. An initial bycatch survey inventory was kindly made available by the ICES Working Group on Bycatch of Protected Species (WGBYC) (ICES 2020). We then supplemented this with new data sources following three main approaches:

1. Members of OSPAR's ICG-COBAM (Coordination of Biodiversity Assessment and Monitoring) and JWGBIRD (the joint OSPAR/HELCOM/ICES Working Group on Seabirds) were contacted. Several data gaps were filled via this initial approach.
2. An online search using Google scholar was conducted to identify published and grey literature on seabird bycatch in the OSPAR regions. Relevant keywords broadly used in bycatch studies were used, first in English and then in the different languages of the OSPAR Contracting Parties and potential data owners (see Appendix 1 for a full list of search terms). Search terms included "seabird bycatch", fishing gear terms, OSPAR Regions, the Contracting-party countries and relevant Regional Fisheries Management Organisations (RFMOs – e.g. the International Commission for the Conservation of Atlantic Tunas – ICCAT) (Appendix 1).
3. Open-access datasets were consulted. These included the database held by the Sociedade Portuguesa para o Estudo das Aves ([Projects and bibliography on seabird bycatch at European waters](#)) and the European Union (EU) report, "[The Annual Reports on the implementation of the Data Collection Framework](#)".

In total, 41 sources of data (Appendix 2) were added to the initial bycatch survey inventory, resulting in 265 data sets (Appendix 3). The list included data from 11 of the 16 OSPAR Contracting Parties (Denmark including Greenland, France, Germany, Iceland, Ireland, Netherlands, Norway, Portugal including Azores, Spain, Sweden and United Kingdom) and three non-member states (Japan, Poland and Taiwan).

Finally, to obtain information on potential fishing activity within each OSPAR region, including origin of fleets and gears used, several sources were consulted. This included The N2K Group 2012, ICES 2013, OSPAR 2020, STECF 2020. Furthermore, to identify populations of marine birds with local estimates of demographic rates (Evans 2021) was firstly consulted. Then, the original publications were consulted to clarify any detail on methodology or the general assumptions stated in a given study.

2.2 Minimum quality criteria

A set of data quality criteria were developed to inform the selection of candidate species and regions that might be used for pilot PVAs. These data quality criteria were applied to both the bycatch data and the demographic data for marine birds. The Bycatch Quality Criteria (Appendix 4) and the PVA Quality Criteria (Appendix 5) included 18 and 19 criteria, respectively. Criteria included measures of quantity and quality of the available data. For our study, the Bycatch Quality Criteria were not intended to exclude any OSPAR Region from assessment (which might result in a serious limitation to demonstrate a "proof of concept" approach to a pilot), but instead to highlight the best candidate regions and species for constructing pilot models. Additionally, minimum criteria were used as a tool to assess the quality of available data and inform recommendations for future data collection.

For the Bycatch Quality Criteria, the selected categories were based on a literature search of best practice for bycatch assessment (Desfosse *et al.* 2012; Wolfaardt & Debski 2019). The criteria and thresholds for assigning quality scores to bycatch data are detailed in Appendix 4. The criteria for assigning quality scores included the purpose of the data collection (directed versus opportunistic), geographical and temporal scope, availability of fishing effort data, details on bycatch rate estimates and units, availability of associated error estimates, availability of data on gears known to cause substantial seabird bycatch. The PVA Quality Criteria were designed to identify relevant populations with high quality data. As bycatch is highly dependent on seabird occurrence and density in a certain area, relevant data would include the main temporal periods and geographical areas where a certain species are likely to occur. The criteria and thresholds for assigning quality scores to marine bird demographic data are detailed in Appendix 5. The criteria for assigning quality scores included the propensity for bycatch, data availability, demographic data coverage, population trend, conservation status, range area/geographical scope and temporal scope. Depending on the region or the species, the pilot assessment may address breeding populations, wintering populations or both.

2.3 Data preparation

Following the Bycatch Quality Criteria, the quality of the bycatch data for assessing bycatch were scored based on the origin of the fishing fleet (flag) and the gear type or ‘metier’ (following the classification reported in the Appendix IV of [Commission Decision 2010/93/EU](#) (full evaluation available in the Appendix 6 of the present report). We also categorised each fishing gear type according to the likelihood of it accidentally catching marine birds. Bycatch was assumed to occur in a certain fishing gear if at least one report was found in the literature or the bycatch survey inventory. In this approach, fishing gear was classified based on the gear/fleet combination (following the classification of metier level 3 or higher from FAO/ICES) and the country of origin. Finally, the percentage of data for each fishing gear category in the bycatch survey inventory, was calculated as the ratio of the number of datasets in the survey inventory and the total number of gear/fleet combinations like to cause bycatch within each OSPAR Region (Table 1). This analysis was run independently of the minimum quality criteria assessment.

Table 1. Overview of bycatch data available in the survey inventory (Appendix 7) per OSPAR Region. Two candidate regions (III – Celtic Seas; IV – Bay of Biscay and Iberian Coast) for the pilot models are shaded grey (i.e. have the highest percentage of gear/fleet data covered by the survey inventory).

OSPAR Region	Number of gear/fleet combinations likely to cause bycatch	Number of gear/fleet datasets in survey inventory	% of gear/fleet data covered by the survey inventory
I – Arctic Waters	22	15	68%
II – Greater North Sea	25	18	72%
III – Celtic Seas	21	17	81%
IV – Bay of Biscay and Iberian Coast	21	16	76%
V – Wider Atlantic	12	4	33%

According to the percentage of data for each fishing gear category in the bycatch survey inventory, Region III (Celtic Seas) and Region IV (Bay of Biscay and Iberian Coast), were identified as having the highest amount of available data (Table 1). Therefore, these areas

were selected pilot assessment (of potential impacts of bycatch on marine bird populations). However, it is notable that OSPAR Regions II (Greater North Sea) and I (Arctic Waters) also have high gear/fleet coverage in the survey inventory.

Following the advice of this project's steering group, Cory's shearwater *Calonectris borealis* and common guillemot *Uria aalge* in OSPAR Regions IV and III, respectively, were selected as candidate populations for the pilot PVAs. Cory's shearwater was assumed to represent the least complex example, with a single main breeding population in OSPAR Region IV. The population dynamics, breeding success and year-round distribution of this population is also well documented (Pereira *et al.* 2020). By contrast, common guillemot was considered to represent a more complex example species, where breeding populations are spread among different OSPAR regions and different colonies may overlap during the non-breeding season (Cadiou *et al.* 2004; Carroll *et al.* 2019). We focused the examination of impact to common guillemots on OSPAR Region III due to the availability of robust colony-specific demographic data (Mitchell *et al.* 2004; Meade *et al.* 2013; Anker-Nilssen *et al.* 2015; Horswill & Robinson 2015; Newell *et al.* 2016; Anker-Nilssen *et al.* 2020; Miles 2020; Dunn *et al.* 2022).

2.4 Bycatch analysis

2.4.1 Cory's shearwater

Cory's shearwater interact with three main fishing gear types: set longlines operated by vessels less than 12 m, set longlines operated by vessels greater than or equal to 12 m, and coastal gillnets operated by vessels greater than or equal to 12 m. Annual bycatch of Cory's shearwater off Portugal mainland waters was collated for these three gear types from Oliveira *et al.* (2015a, 2018, 2021) and Alexandre (2019). This included estimates of total annual bycatch mortality (Oliveira *et al.* 2018, 2021) and bycatch rate (Oliveira *et al.* 2015a, Alexandre 2019) (Table 2). Bycatch rates (for those studies that estimated total mortality) for set longlines operated by vessels less than 12 m, or greater than or equal to 12 m length, were reported at 0.090 and 0.045 birds per trip, respectively. Additionally, bycatch rates for coastal gillnets (only vessels greater than or equal to 12 m) was estimated at 0.042 birds per trip. The main population of Cory's shearwater using OSPAR Region IV – Bay of Biscay and Iberian Coast – breeds in Berlengas archipelago, with an estimate at 800–975 breeding pairs (Oliveira *et al.* 2020). Breeding in smaller numbers is also known for other sites within OSPAR Region IV (e.g. on the Peniche coast (Portugal, < 10 breeding pairs; Equipa-Atlas 2022) and Cies Islands (Galicia, Spain, ~ 50 breeding pairs; Molina *et al.* 2022)). Evidence points to high bycatch mortality of Cory's shearwater in OSPAR Region IV (Oliveira *et al.* 2015, 2018, 2020b, Alexandre 2019). For example, previous studies suggest that bycatch of Cory's shearwater in OSPAR Region IV goes beyond the reported population size of Cory's shearwater using this Region (Oliveira *et al.* 2020). The annual estimated mortality of Cory's shearwater in this previous study could be overestimated (Oliveira *et al.* 2021), however the potential effect on local population dynamics in the Berlengas archipelago is still a conservation concern (Oliveira *et al.* 2020).

The year-round distribution of Cory's shearwater from Berlengas archipelago are well described (Figure 3). In addition to using OSPAR Region IV during the breeding season, birds also use the southern half of OSPAR Region V – Wider Atlantic – at a lower density (Paiva *et al.* 2010a). Bycatch is less likely to occur in OSPAR Region V (Cooper *et al.* 2003; Parra *et al.* 2023), although bycatch in the small-scale Azorean longline fisheries cannot be ruled out. By contrast, during the non-breeding period, birds migrate to the South Atlantic and South Indian Oceans. Fisheries in the South Atlantic and South Indian Oceans are mostly industrial longliners using large hooks, and bycatch of Cory's shearwater by these fleets is unrecorded and considered unlikely due to their body size (Yeh *et al.* 2013; Paterson *et al.* 2019; Jiménez *et al.* 2020; Da *et al.* 2021).

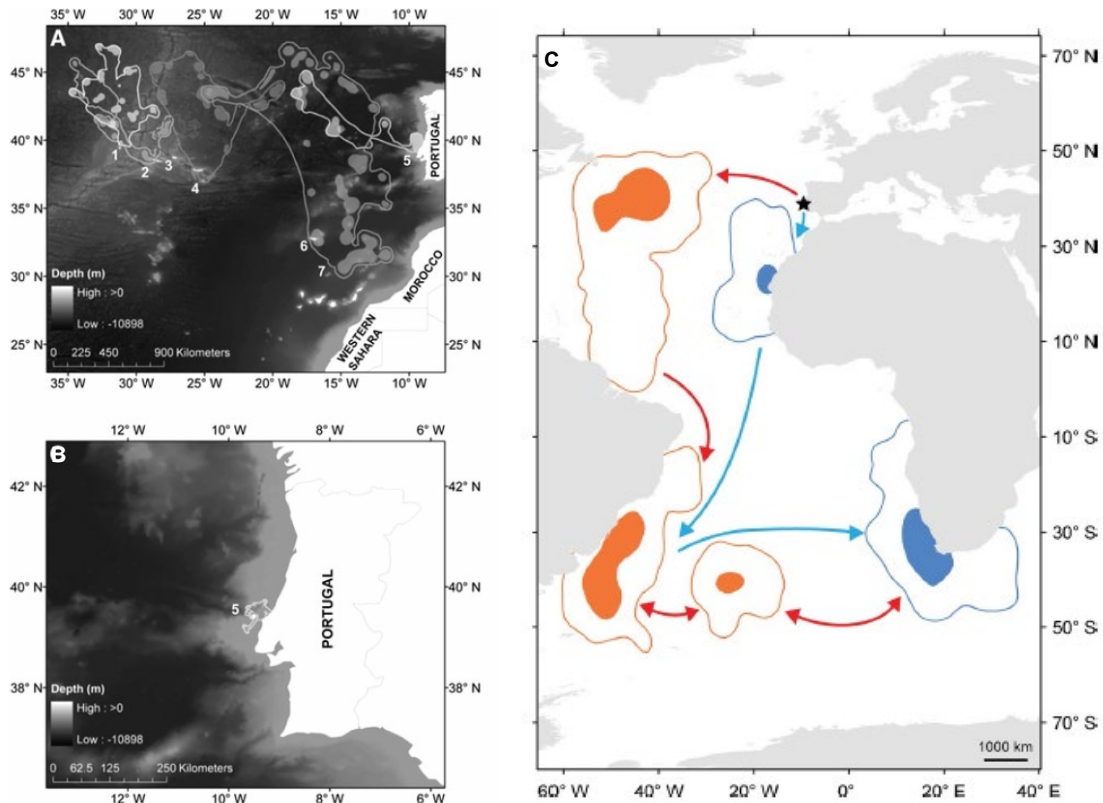


Figure 3. Distribution of Cory's shearwater breeding in the archipelagos of Azores (1, 2, 3 and 4), Berlengas (5) and Madeira during long (A) and short foraging trips (B) made during incubation period, resulted from individual tracking of breeding adults (extracted from Paiva *et al.* 2010). Also, home ranges and core foraging areas of experienced (blue) and non-experienced breeders from Berlengas archipelago during the non-breeding period is presented (C, extracted from Missagia *et al.* 2015).

2.4.2 Common guillemot

Annual bycatch mortality estimates for common guillemot in OSPAR Region III – the Celtic Seas – were taken from Northridge *et al.* (2020) (Table 2). Total bycatch mortality estimates were available for the main UK fishing fleets operated in this OSPAR Region; coastal gillnets, offshore gillnets, longlines and midwater trawls (Table 2). However, fishing fleets from Denmark, France, Ireland, the Netherlands and Spain also operate in OSPAR Region III (see Appendix 7). Some of these fleets operate fishing gears that are likely to pose additional mortality at relevant levels to the known estimates, namely gillnets, as it is the case of French, Irish and Spanish fleets. However, it was not possible to identify bycatch rates from those fleets for this species. Reported estimates of total bycatch mortality in UK fishing fleets were considerably higher in coastal and offshore gillnets (Table 2).

During the breeding season when birds need to regularly provision offspring, the average foraging range of common guillemots is 10.5 km (interquartile range = 3.2 to 19.1 km, Wakefield *et al.* 2017). However, during the non-breeding period, birds from the Celtic Seas colonies disperse widely to other parts of OSPAR Region III (Celtic Seas) and into OSPAR Regions II (Greater North Sea) and IV (Bay of Biscay and Iberian Peninsula) (SEAPOP 2021). Additionally, common guillemots breeding in other OSPAR Regions (I – Arctic Waters – and II – Greater North Sea), are documented to use OSPAR Region III (Celtic Seas) during the non-breeding season. The varying degree of spatial overlap between common guillemots from different colonies during the non-breeding season brings serious challenges to evaluating bycatch impact on colony or regional population viability. Therefore, for the PVA

analyses, only populations using OSPAR Region III – Celtic Seas – during at least part of their annual cycle were considered (i.e. we also considered birds breeding in OSPAR Regions I – Arctic Waters – and II – Greater North Sea).

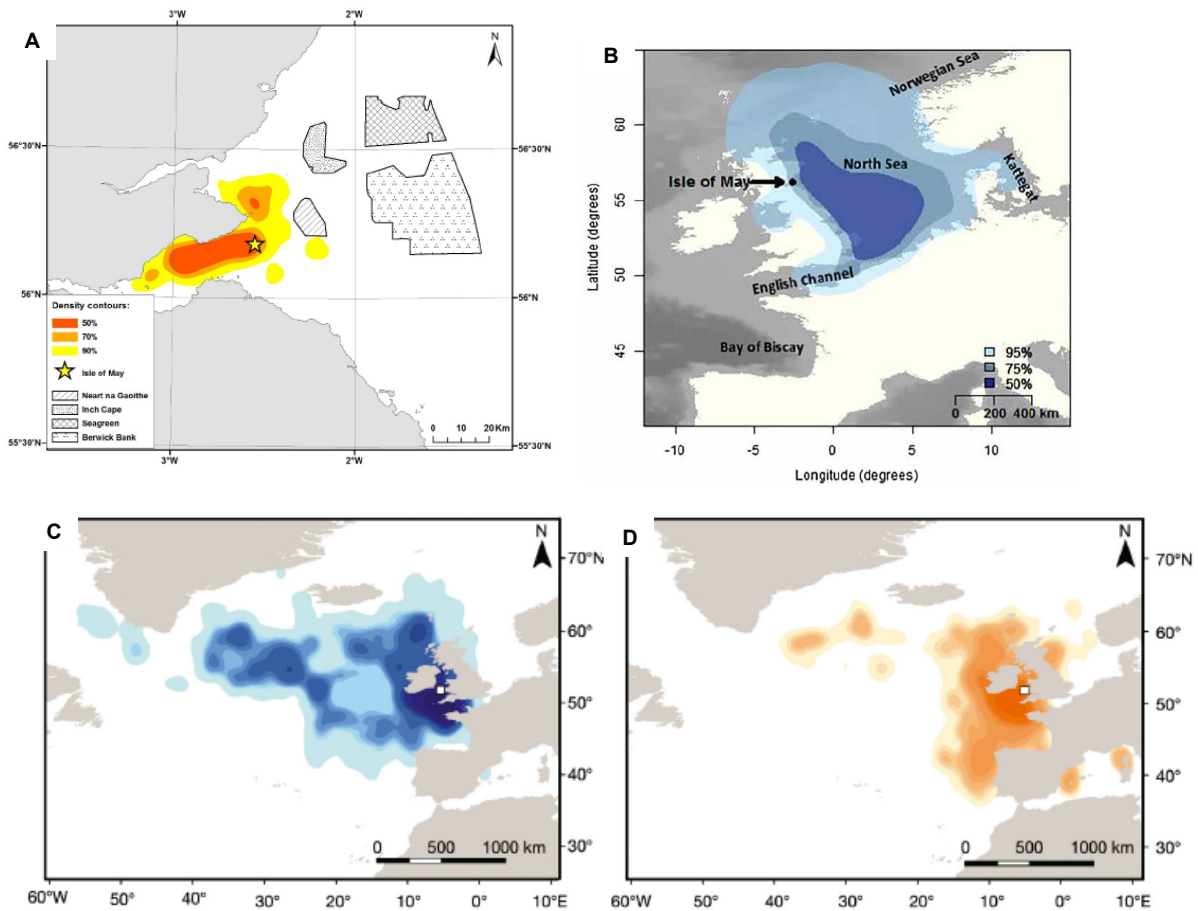


Figure 4. Distribution kernels of common guillemots during breeding (A; extracted from Bogdanova *et al.* 2022) and non-breeding season (B; extracted from Harris *et al.* 2015) based on individual tracking of adult birds, and representing an example of a colony located in OSPAR Region II – Greater North Sea – (Isle of May). Colony location is represented with a star and a black dot in the panel A and B, respectively. Panel C and D depict non-breeding distribution of male and female common guillemots, respectively, from Skomer Island (extracted from Fayet *et al.* 2017), a colony from OSPAR Region III – Celtic Seas. Colony location is represented with a white square.

Table 2. Bycatch mortality rates reported for Cory's shearwater and common guillemot per fishing gear operating in the candidate OSPAR Regions. Bycatch mortality is presented as birds per year \pm standard deviation (or \pm 95% confidence intervals, CI) unless unavailable, in those cases bycatch rate as birds per trip was given. The year of estimate and source are also given.

Study species	OSPAR Region	Area	Fishing gear	Study duration	Bycatch mortality (birds per year) \pm SD (95% CI)	Bycatch rate (birds per trip) \pm SD	Source of data
Cory's shearwater	IV	Portugal – Peniche and SPA Ilhas Berlengas	Set longlines (vessels < 12 m)	2016–2017	1,634 \pm 586	-	Oliveira <i>et al.</i> 2021
		Portugal – Peniche and SPA Ilhas Berlengas	Set longlines (vessels \geq 12 m)	2016–2017	616 \pm 221	-	Oliveira <i>et al.</i> 2018
		Portugal – Peniche and SPA Ilhas Berlengas	Coastal gillnets (vessels \geq 12 m)	2016–2017	1,100 \pm 517	-	Oliveira <i>et al.</i> 2018
		Portugal – Natural Park Sudoeste Alentejano e Costa Vicentina	Set longlines	2018	-	0.0003 \pm 0.05	Alexandre 2019
		Portugal Mainland	Purse seine	2010–2012	-	0.005	Oliveira <i>et al.</i> 2015b
		Portugal Mainland	Bottom trawl	2010–2012	-	bycatch recorded – quantity unknown	

Study species	OSPAR Region	Area	Fishing gear	Study duration	Bycatch mortality (birds per year) \pm SD (95% CI)	Bycatch rate (birds per trip) \pm SD	Source of data
Common guillemot	III	All area	Coastal gillnets (UK fleet)	2016	983 (717 – 1,267)	-	Northridge <i>et al.</i> 2020
				2017	839 (614 – 1,092)	-	
			Offshore gillnets (UK fleet)	2016	47 (22 – 75)	-	
				2017	41 (22 – 63)	-	
			Longlines (UK fleet)	2016–2017	0	-	
			English Channel	Midwater trawls	2016	3 (0 – 9)	
		2017			5 (0 – 12)	-	

2.5 Demographic parameters

2.5.1 Cory's shearwater

The most up-to-date estimates of population size and breeding success for the breeding population of Cory's shearwater from Berlengas archipelago were collated from Oliveira *et al.* (2020). The breeding success of Cory's shearwater in Berlengas archipelago shows large variation between colonies that can be attributed to different conservation strategies. For example, artificial nests are used by a considerable portion of the colony on Berlenga Island resulting in higher rates of breeding success (mean \pm standard deviation; 0.775 ± 0.028) compared to the remaining archipelago (0.397 ± 0.016). The mean of these two estimates (0.586) is considered to represent the minimum potential breeding success that could be expected if artificial nests were supplied across the archipelago (Oliveira *et al.* 2020). Steep terrain and cliffs on the smaller islets would prevent the deployment of artificial nests across the archipelago, such that elevating the regional rate to match Berlenga Island is unlikely.

We ran three baseline PVA scenarios for Cory's shearwater to reflect the three estimates of breeding success (Table 3). We also adjusted the initial population sizes for each of these scenarios accordingly (see Section 3.7 for further details). As rates of immature survival, adult survival and age at first breeding were not available for this colony, we used values for Cory's shearwaters breeding on Selvagem Grande (located off Madeira archipelago) (Mougin *et al.* 2000) (Table 3). Bycatch mortality is expected to be minimal at Selvagem Grande because this population does not forage within the coastal waters off mainland Portugal (Paiva *et al.* 2010b; Dias *et al.* 2012; Ramos *et al.* 2013; Beal *et al.* 2023). Therefore, adult and immature rates of survival on Selvagem Grande are considered not to include bycatch and therefore be higher than the likely rates of survival at Berlengas archipelago. Rates of immature survival were only available for the total period from fledging to breeding (i.e. 0–7 years, Mougin *et al.* 2000), therefore we estimated an annual mean survival rate for this age class (i.e. 0.85, Table 3).

2.5.2 Common guillemot

The demographic traits of common guillemots are well studied in the UK. Local estimates of breeding success for multiple colonies in OSPAR Region III are available ([Seabird Monitoring Programme Database](#)), however local estimates of survival are limited to Skomer Island (Meade *et al.* 2013). Therefore, to minimise biases associated with combining demographic data from different colonies (e.g. Horswill *et al.* 2021), we assume the demographic profile for common guillemots breeding on Skomer Island to be representative of the wider area. Age of first breeding has not been quantified for this population and therefore we applied the value for common guillemots breeding on the Isle of May (UK, North Sea; Halley & Harris 1993). There are two monitoring plots for common guillemots on Skomer Island that report different rates of breeding success (Meade *et al.* 2013; Newman *et al.* 2021) (Table 3). Therefore, we ran PVA scenarios based on each value. Population size was obtained from Mitchell *et al.* (2004) and Miles (2020) for the population breeding on the UK (318,156 breeding pairs) and Irish (138,108 breeding pairs) coast of the Celtic Seas.

We ran an additional two PVAs to capture guillemot colonies from other OSPAR regions that use the Celtic seas during at least part of their annual cycle (i.e. OSPAR Regions I – Arctic Waters – and II – Greater North Sea). For the Arctic Waters (OSPAR Region I), we assigned a local demographic profile using information from Jan Mayen (Anker-Nilssen *et al.* 2020) (Table 3). Therefore, this PVA scenario also reflects the potential impact of bycatch in OSPAR Region III to common guillemots breeding outside the UK. For the Greater North Sea (OSPAR Region II), we used local demographic information from the Isle of May (Horswill & Robinson 2015; Newell *et al.* 2016; Dunn *et al.* 2022). We assigned the

population size for the Greater North Sea using colonies breeding on the North Sea coast of UK from Mitchell *et al.* (2004) and Miles (2020) (i.e. 631,905 breeding pairs).

Table 3. Demographic parameters of Cory's shearwater and common guillemot populations using OSPAR region IV and III, respectively, during their annual cycle. Breeding success is given as mean \pm standard deviation.

Species	Population	Description	Population size (breeding pairs)	Breeding success	Age at recruitment	Immature survival	Adult Survival
Cory's shearwater	Baseline profile 1	Berlengas archipelago, excluding Berlenga Island	520–675 (Oliveira <i>et al.</i> 2020)	0.397 \pm 0.016 (Oliveira <i>et al.</i> 2020)	9 years (Mougin <i>et al.</i> 2000)	0.328 (0–7y) (Mougin <i>et al.</i> 2000)	0.935 (females) Mougin <i>et al.</i> 2000)
	Baseline profile 2	All archipelago, excluding Berlenga Island and assuming artificial nests were widely available	520–675 (Oliveira <i>et al.</i> 2020)	0.586 \pm 0.016			
	Baseline profile 3	Berlenga Island	280–300 (Oliveira <i>et al.</i> 2020)	0.775 \pm 0.028 (Oliveira <i>et al.</i> 2020)			
Common guillemot	Baseline profile 1	UK & IE (Celtic Seas)	456,264 (Miles 2020)	0.82 \pm 0.05 (Meade <i>et al.</i> 2013)	6 years (Horswill & Robinson 2015)	0.43 \pm 0.10 (0–3 y) (Meade <i>et al.</i> 2013)	0.930 \pm 0.04 (Meade <i>et al.</i> 2013)
	Baseline profile 2			0.71 \pm 0.08 (Newman <i>et al.</i> 2021)			
	Baseline profile 3	UK (North Sea)	631,905 (Mitchell <i>et al.</i> 2004)	0.73 \pm 0.11 (Newell <i>et al.</i> 2016)		0.560 (0–1 y) 0.792 (1–2 y) 0.917 (2–3 y) (Horswill & Robinson 2015)	0.930 \pm 0.07 (Dunn <i>et al.</i> 2022)
	Baseline profile 4	Jan Mayen (Arctic Waters)	< 1,000 (Anker-Nilssen <i>et al.</i> 2015)	0.65 \pm 0.10 (Anker-Nilssen <i>et al.</i> 2020)		-	-

2.6 Population Viability Analysis

To examine the population response of Cory's shearwaters and common guillemots to different levels of bycatch mortality ('bycatch scenarios'), we used a stochastic population viability analysis (PVA) based on a Leslie matrix approach. The stage-structured matrix model accommodated species-specific age at first breeding, breeding success and age-specific survival estimates (Table 3). We assumed an even sex ratio and modelled the number of females in each age-class. To define the initial age structure, we assumed a stable age structure with mean demographic rates equal to the reported values (Table 3). Population dynamics were projected over three generations for each species. A generation was assumed to be 19.3 and 15.1 years for Cory's shearwater and common guillemot, respectively (BirdLife International 2024). We chose to examine the population response over three generations to reflect the time frame used by the IUCN Red List of Threatened Species in threat assessment (BirdLife International 2024).

To compare changes in population dynamics, we examined the projected final population sizes under each scenario. The ratio of impacted (including various levels of bycatch mortality) to unimpacted (baseline scenarios excluding bycatch mortality) population size (hereafter referred as RI:UGL) is considered to be a metric that overcomes uncertainty in demographic rates and population trends (Cook & Robinson 2016). RI:UGL is the same as the counterfactual of population size (Miles 2020). We present RI:UGL as the percentage change from unimpacted to impacted scenarios over three generations and present the mean RI:UGL and its 95% confidence interval.

The baseline PVA scenarios were built using species-specific demographic values (Table 3). To incorporate temporal variation in annual rates of survival and breeding success, we sampled each demographic parameter from normal distributions assigning a standard deviation of 1 for juvenile and immature survivals, 0.1 for adult survival and the specific values given on table 3 for breeding success (e.g. Cook & Robinson 2016). The model was run 1,000 times to give a mean trajectory for the study population and a measure of corresponding uncertainty.

Density dependence operates to stabilise population dynamics by adjusting demographic parameters in relation to population size. For example, in its compensatory form (Beverton & Holt 1957) a reduction in seabird bycatch that increases rates of survival could generate increased competition for food resources and nesting sites that decreases rates of breeding success and prevents exponential population growth (e.g. Miles *et al.* 2020). To avoid generating falsely inflated predictions of future seabird population size, we included a formulation of compensatory density dependence in the PVA following Cook and Robinson (2016) using Weibull function (Eq.1) because it was found to suit a variety of species (Cury *et al.* 2011).

$$\text{Equation 1. } D = \text{max}D * \exp(-a * N^b)$$

Where D is the estimated demographic parameter, $\text{max}D$ is the biologically plausible maximum value for this parameter, N is the population size, a is a scale parameter and b is a shape parameter (assumed as $b = 1$). a is estimated with reference to b , $\text{max}D$ and number of adults in the population. For increasing population trajectories, incorporating compensatory density-dependence in the PVA will result in smaller future population sizes than a density-independent model. For scenarios generating increasing population trajectories, we applied a simple density dependent regulation to rates of breeding success, assuming a maximum breeding success ($\text{max}D$) of 0.95 combined with a shape (b) parameter of 1. This demographic parameter (given as the ratio between the number of fledged chicks and the number of nests with an egg) is most likely to demonstrate a compensatory response to a change in adult survival associated with bycatch reduction. For

scenarios generating stable or declining populations, we assumed density independence. All density independent models are presented in the Appendix 8.

The lack of comprehensive bycatch data for fisheries operating in the OSPAR regions meant that we employed three hypothetical bycatch scenarios. These scenarios were generated by adjusting rates of adult and immature survival by 1%, 5% and 10%, depending on whether the reported survival estimates (Table 3) were assumed to include bycatch mortality. For Cory's shearwater, adult and immature survival estimates were taken from an independent population where bycatch mortality is considered minimal (Selvagem Grande, Mougín *et al.* 2000). Therefore, mortality was added to the baseline scenarios. By contrast, estimates of adult and immature survival for common guillemot were assumed to include bycatch mortality, and therefore mortality was subtracted from the baseline scenarios to alter impact levels. Here, we assumed that bycatch is already reducing rates of survival by 5% and 10%. We selected an adjustment of 1% following the concept of "small numbers" defined by Article 9 of the Birds Directive, whereby this is not expected to impact population dynamics, although this is not a consensus view (Schippers *et al.* 2020). The 5% and 10% figures were used to reflect possible bycatch mortalities. The additional number of birds that died following adjustments in immature and adult mortality (1%, 5% or 10%) was then estimated for each scenario to support comparison with reported bycatch mortalities found in the literature. The absolute number of birds that died due to bycatch was calculated for each age class assuming a 1:1 sex ratio as follows:

$$\text{Equation 2. } M = (1 - S) * \Delta M$$

$$\text{Equation 3. } Y = N/\Phi * M$$

Here, rates of mortality (M) are estimated from equation 1 as a function of survival (S) and the change in mortality ($\Delta M = 1\%$, 5% or 10%), and the total amount of birds that died due to bycatch (Y) is estimated in equation 2 using the estimate of mortality rate, the initial population size (N) and the sex ratio (Φ). The 95% confidence interval for population size was used to account for uncertainty in this value.

All analyses were run in the open-source software package "R" (v.3.5.3, R Core Team 2022). PVA code was customised from the stochastic population model described by Cook and Robinson (2016). Additional functionality included creating outputs for each candidate species. The full script can be found in Appendix 9.

2.7 Population model assumptions

Several assumptions were made during the construction of the models that could influence the interpretation of outputs. These include:

- The applied estimates of bycatch related mortality remained constant across the projected three generations. Adjustments to immature and adult survival follow the same level, reflecting constant fishing effort and fleet composition.
- Other sources of mortality remain constant along the projected three generations. We do not consider other sources of mortality that may change over the study period.
- Bycatch per age class is proportional to the frequency of a given age-class in the population in any given year.
- Bycatch is not sex-specific, and the population follows a 1:1 sex ratio.
- Bycatch of birds from a given population is proportional to the size of that population in relation to a metapopulation.

- The initial population size figure from the literature was assumed to represent the actual situation of the population, such that no substantial change has occurred since the date of the population estimates.
- Mean demographic parameters and uncertainty in these values remained constant from the time they were estimated and throughout the projected three generations.
- The population is closed to immigration and emigration.
- The current level of bycatch explicitly encompassed by specific populations is unknown. 10% change in survival of one population may not be comparable to a 10% change in another population, but we assume the same level of impact.

3 Results

For each species, we considered population specific baseline demographic profiles that were subsequently examined under three scenarios of bycatch mortality (1%, 5% or 10%).

3.1 Cory's shearwater

The baseline demographic profile 1 modelled for Cory's shearwater (Figure 5) used the breeding success estimates and population size of the Berlengas archipelago breeding population, excluding Berlenga Island (Table 3). This baseline profile 1 showed a decreasing population trajectory over three generations with no bycatch occurring. The extent of the decrease became more pronounced with higher levels of bycatch mortality (Figure 5). The baseline demographic profile 2 (Figure 6) assumed a higher breeding success (0.586, i.e. the mean value for managed and unmanaged colonies, Oliveira *et al.* 2020) for the Berlengas archipelago population, excluding Berlenga Island. This baseline profile showed an increasing population trajectory, although bycatch mortality of up to 5% removed this population growth and the population declined if bycatch mortality was increased to 10% (Figure 6). Finally, in the baseline demographic profile 3 (Figure 7), we used the breeding success estimates (i.e. breeding success = 0.775) and size of the Berlenga Island population only. This baseline scenario showed an increasing population trajectory. Furthermore, increasing bycatch mortality to 1%, 5% and 10% did not reverse this positive trend (Figure 7).

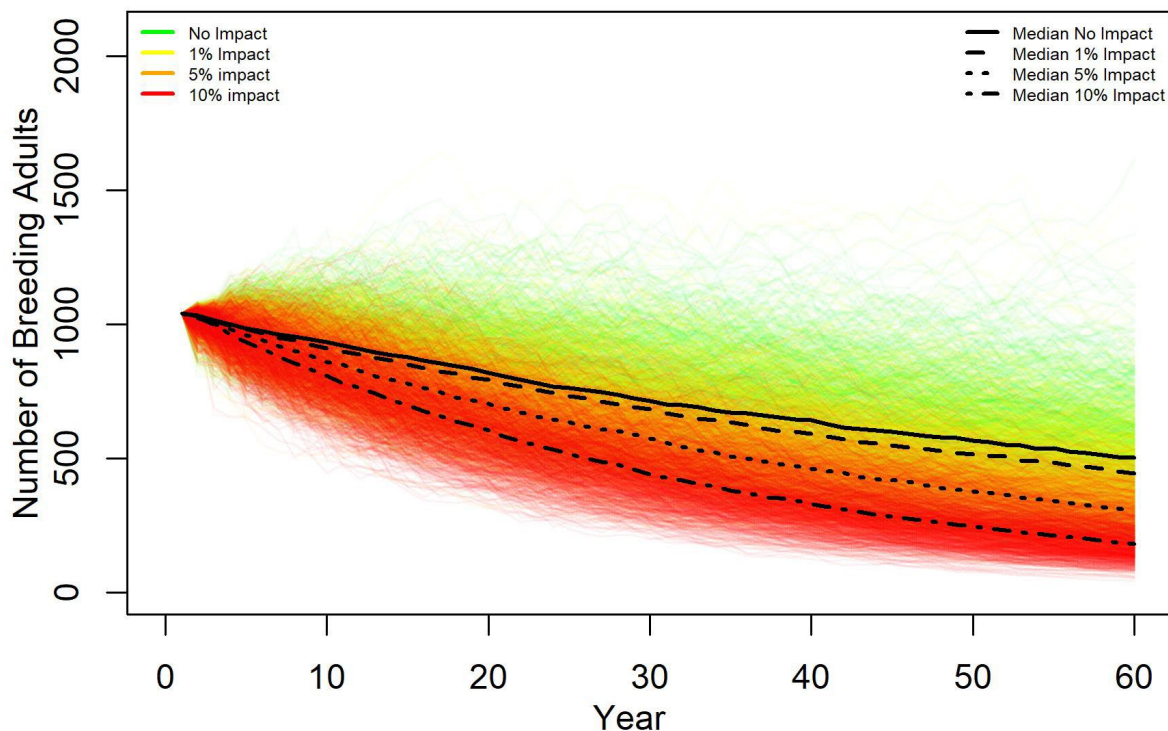


Figure 5. The PVA demonstrated that the population of Cory's shearwater breeding in Berlengas archipelago, excluding Berlenga Island (baseline profile 1), declined under all scenarios of bycatch mortality (i.e. from no bycatch to a 10% reduction in immature and adult survival). The different lines represent the 1,000 iterations of the stochastic PVA and colours reflect the different bycatch scenarios. The median population trajectory for each scenario is shown as a black line. Model assumes density-independent breeding success because population is in decline.

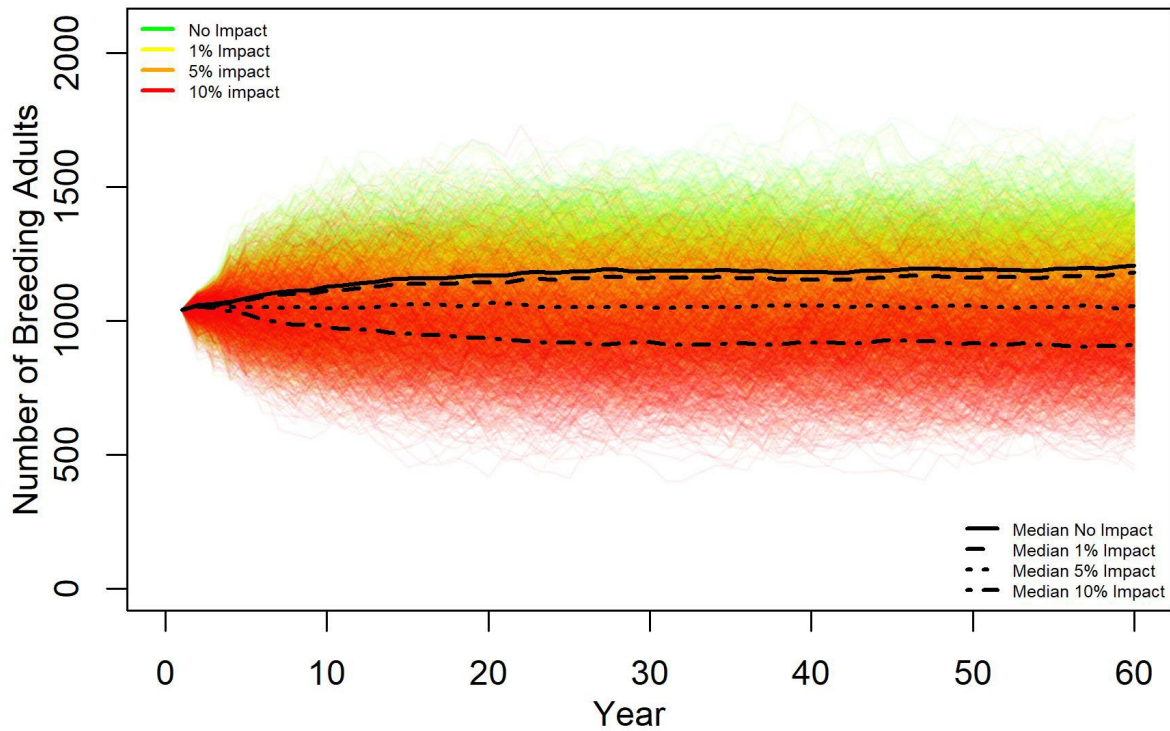


Figure 6. The PVA demonstrated that the population of Cory's shearwater breeding in Berlengas archipelago, excluding Berlenga Island but assuming a higher breeding success (0.586, baseline profile 2), has a different response depending on the scenario of bycatch mortality. Assuming a 1% reduction in survival has no significant impact on the mean population trajectory, while assuming a 5% or 10% decrease in survival alters the direction of the mean population trajectory. The different lines represent the 1,000 iterations of the stochastic PVA, and colours reflect the different bycatch scenarios. The median population trajectory for each scenario is shown as a black line. Model assumes compensatory density-dependent breeding success because some simulations show an increasing trajectory.

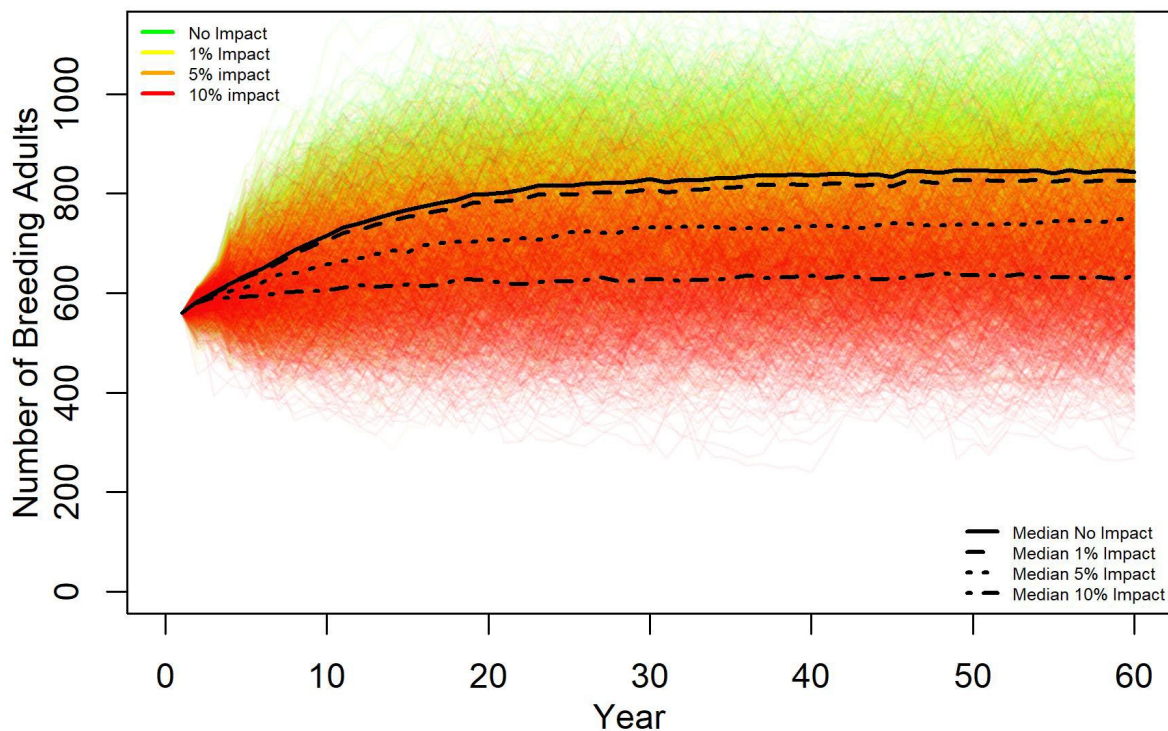


Figure 7. The PVA demonstrated that the population of Cory's shearwater breeding on Berlenga Island only (baseline profile 3), increased under all scenarios of bycatch mortality (i.e. from no bycatch to a 10% reduction in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes compensatory density-dependent breeding success because some simulations show an increasing trajectory.

Although the negative impact from higher bycatch mortality may be compensated by an increase in breeding success in the Berlengas archipelago population, excluding Berlenga Island (baseline profile 1), such balance is reversed when bycatch mortality reached levels of up to 5% or 10%. This same baseline profile shows that a 10% increase in mortality due to bycatch, which represents 8 to 10 birds each year, would result in a reduction in population size of 72% (i.e. 1 to 0.276×100) when compared to the same population with no bycatch mortality, after three generations (Table 4). By contrast, assuming the baseline profile 2 or 3, a 10% increase in bycatch mortality would result in a reduction in population size of 24 and 25%, respectively.

Table 4. Impact of 1%, 5% and 10% increase in mortality on the ratio of the population size after three generations for the impacted and unimpacted (RI:UGL) population of Cory's shearwater breeding in Berlengas archipelago derived from stochastic models (95% CIs given within brackets). The range of total annual bycatch is given for each scenario as number of birds, assuming 1%, 5% and 10% increases to bycatch mortality. RI:UGL ranges between 0 and 1; 0 assuming a high impacted population and 1 assuming a low impacted population. The reduction in population size after three generations under a scenario of a 10% increase in bycatch mortality (compared with the baseline level which assumes bycatch is not already happening) is also presented.

Population	Actual trend	RI:UGL			Total annual bycatch (number of birds, from simulations)			Population size (breeding pairs)	Reduction in population size after 3GT (10%)
		1%	5%	10%	1%	5%	10%		
Baseline profile 1 (Figure 5)	Decrease	0.883 (0.871–0.896)	0.532 (0.491–0.571)	0.276 (0.234–0.317)	~ 1	4–5	8–10	520–675	72%
Baseline profile 2 (Figure 6)		0.977 (0.967–0.984)	0.881 (0.834–0.922)	0.756 (0.653–0.834)	~ 1	4–5	8–10	520–675	24%
Baseline profile 3 (Figure 7)	Increase	0.976 (0.966–0.984)	0.878 (0.824–0.920)	0.754 (0.653–0.835)	< 1	~ 2	~ 5	280–300	25%

The annual number of birds estimated to have died due to bycatch (i.e. 1 to 10 birds, Table 4), considering the different levels of impact in mortality, represented a very low proportion of the current breeding populations from Berlengas archipelago, where the population size was estimated at 800–975 pairs. Assuming a 1% increase in mortality due to bycatch resulted in only one additional bird dying per year, while a 10% increase would represent 13 to 15 birds (resulted from the sum of profiles 1 or 2 with profile 3) removed every year from Berlengas archipelago population due to bycatch, corresponding to approximately 5 birds from Berlenga Island and 8 to 10 birds from the remaining population. Artificial nesting sites could help buffer this species from bycatch. However, without additional conservation measures this population is rapidly declining even without bycatch impacts. The latest estimates of Cory's shearwater bycatch in Portugal mainland (Table 2) far exceed the limit that the population is likely to be capable of supporting (Oliveira *et al.* 2020). However, Oliveira *et al.* (2021) highlighted those bycatch estimates are potentially overestimated, and reflect variability in bycatch data, suggesting that the published estimates of annual mortality should be viewed as an indication of a likely strong effect of fisheries on the Cory's shearwater population breeding in the Berlengas archipelago. Refinement of bycatch rates would help to quantify the number of birds caught as bycatch annually. However, the PVA results presented here demonstrate that the Berlengas population is sensitive to small amounts of additional mortality due to bycatch, whereby – with only 13 to 15 adult birds removed every year – could result in a decline of the population.

3.2 Common guillemot

The impact of bycatch on the population dynamics of common guillemots was examined against three baseline demographic profiles. In contrast to the baseline profiles used for Cory's shearwater, we assumed the baseline profiles for guillemot already included reductions in adult survival due to bycatch mortality.

The baseline profile 1 (Figure 8) was based on the population that breeds in the Celtic Seas (OSPAR Region III), showing a high breeding success (0.82 ± 0.05 ; Table 3). This profile generated an increasing population trajectory over three generations (Figure 8). By contrast, using the lower estimate of breeding success (0.71 ± 0.08) from Skomer Island in baseline profile 2 resulted in a stable population trajectory (Figure 9). Similarly, the baseline demographic profile 3 (Figure 10), based on the population that breeds in the Greater North Sea (OSPAR Region II), that has a comparable rate of breeding success (0.73 ± 0.11) to baseline profile 2, generated a stable population trajectory (Figure 10). Finally, the baseline demographic profile 4 (Figure 11) reflecting common guillemots breeding on Jan Mayen (OSPAR Region I – Arctic Waters), where breeding success and adult survival are lower than in the other profiles (Table 3), generated a declining population trajectory.

As the survival rates of common guillemot most likely include impacts of bycatch mortality, we increased adult survival by 1%, 5% and 10% (i.e. the reverse approach to the impact adjustments we applied to Cory's shearwater). This approach is assumed to reflect the effect of removing bycatch pressures. Compared to the baseline demographic profiles, all three scenarios for reducing levels of bycatch either increased population growth (Figures 8 to 10) or reduced rates of population decline (Figure 11).

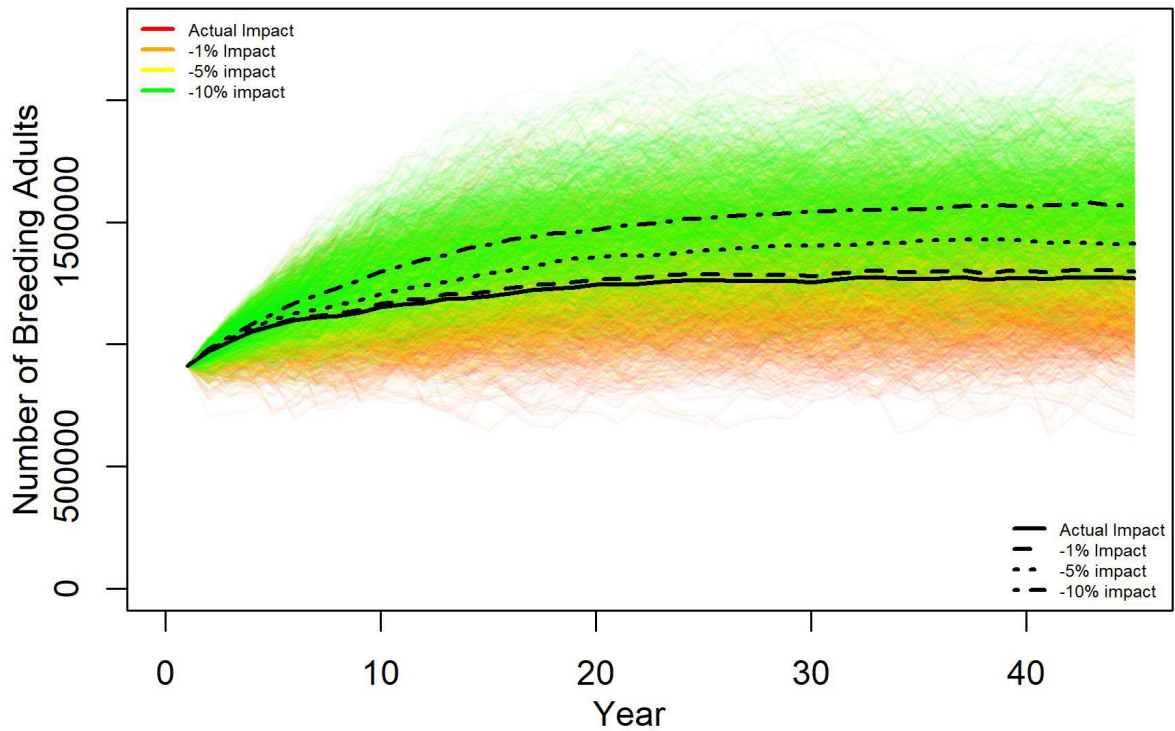


Figure 8. The PVA demonstrated that the population of common guillemots breeding in Celtic Seas colonies assuming a high value of breeding success (0.82; baseline profile 1), including UK and Ireland, increased under all scenarios of bycatch mortality (i.e. from a baseline that is assumed to *include* bycatch mortality to reduced levels of bycatch resulting in 1%, 5% and 10% increases in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes compensatory density-dependent breeding success because some simulations show an increasing trajectory.

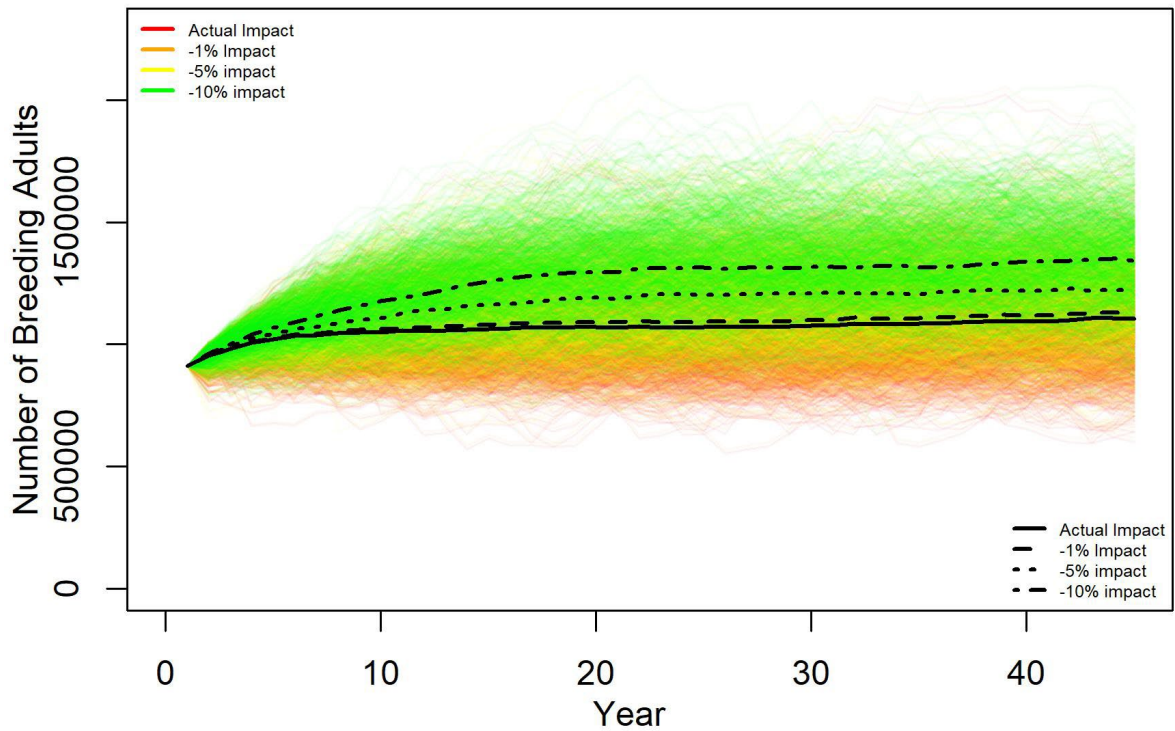


Figure 9. The PVA demonstrated that the population of common guillemots breeding in Celtic Seas colonies assuming a low value of breeding success (0.71; baseline profile 1), including UK and Ireland, increased under all scenarios of bycatch mortality (i.e. from a baseline that is assumed to *include* bycatch mortality to reduced levels of bycatch resulting in 1%, 5% and 10% increases in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes compensatory density-dependent breeding success because some simulations show an increasing trajectory.

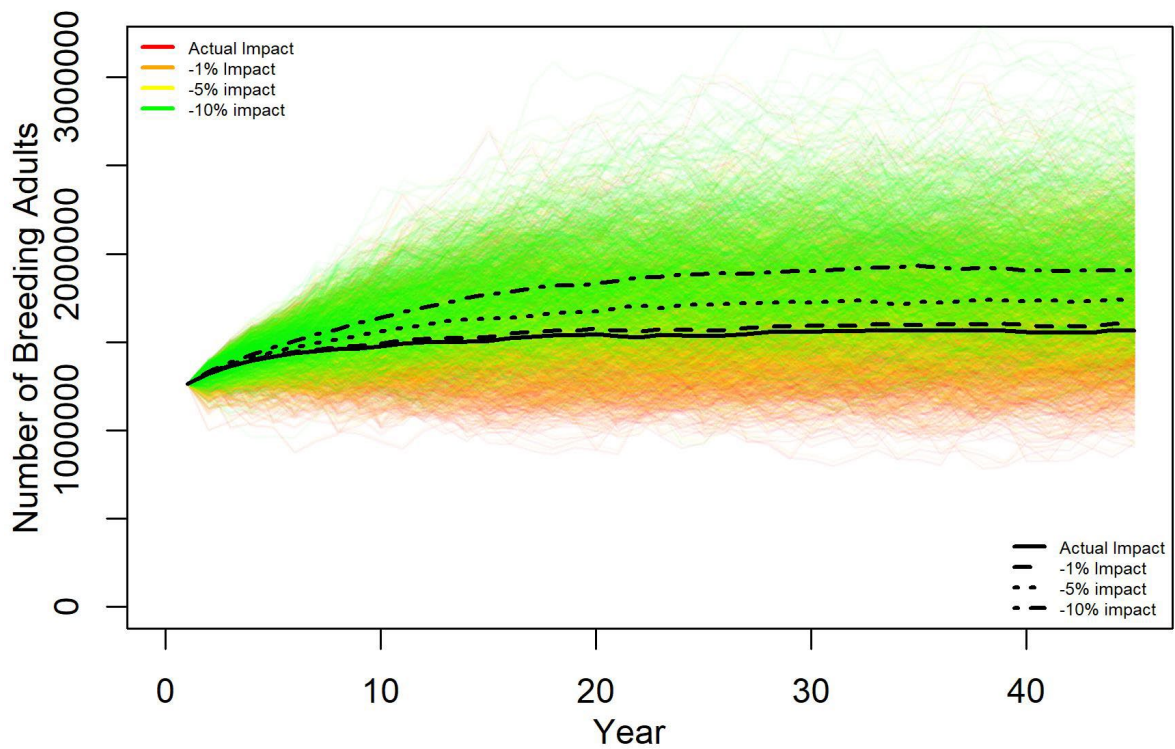


Figure 10. The PVA demonstrated that the population of common guillemots breeding in North Sea colonies from UK only, increased under all scenarios of bycatch mortality (i.e. from a baseline that is assumed to *include* bycatch mortality to reduced levels of bycatch resulting in 1%, 5% and 10% increases in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes compensatory density-dependent breeding success because some simulations show an increasing trajectory.

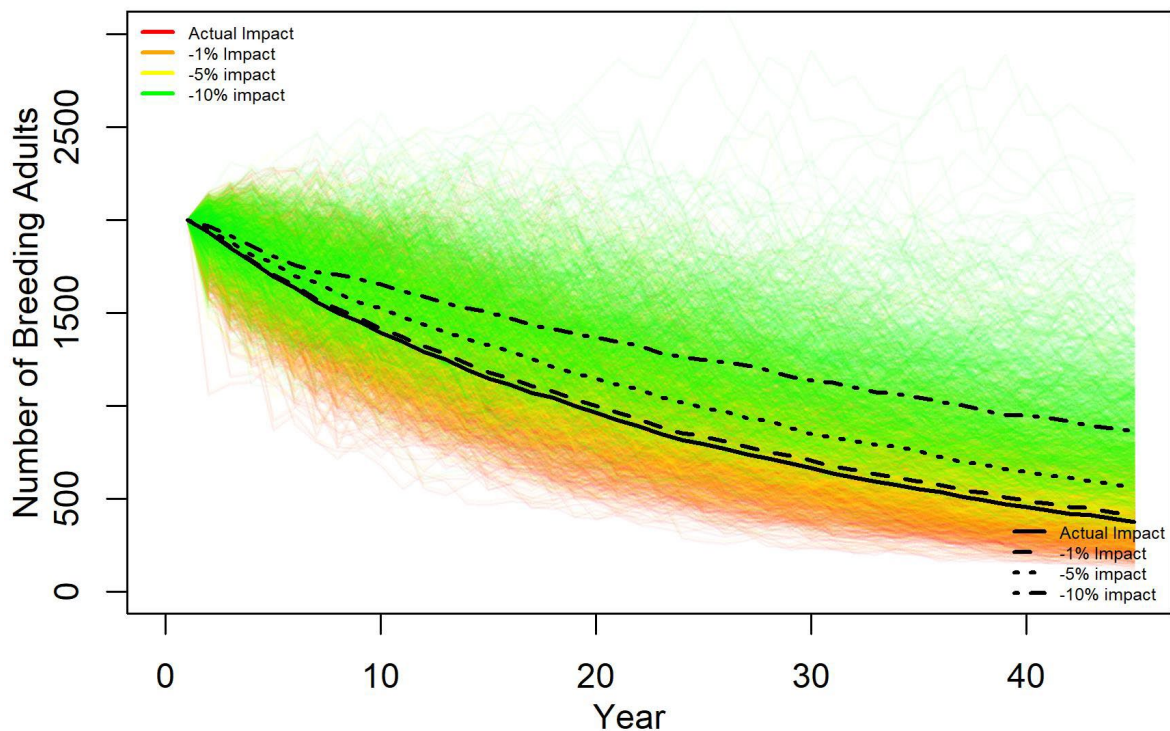


Figure 11. The PVA demonstrated that the population of common guillemots breeding on Jan Mayen, located in the Arctic Waters, declined under all scenarios of bycatch mortality (i.e. from a baseline that is assumed to *include* bycatch mortality to reduced levels of bycatch resulting in 1%, 5% and 10% increases in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes density independent breeding success.

The population profiles for common guillemots in the Celtic Seas region (Figures 8, 9 and 10) were similar to those of Cory's shearwater breeding in Berlengas archipelago (Figures 5, 6 and 7): increasing rates of mortality resulted in larger negative population responses. Such a pattern has been thoroughly explored in previous studies, where variation in survival showed stronger effects on population size or trend, than variations in breeding success for long-lived species (e.g. Cook & Robinson 2016). The models for common guillemot above show that changes in survival affects population trend more than changes in breeding success. Baseline profile 1 and 2 (Figures 8 and 9) show that a 10% decrease in mortality due to reducing bycatch, which represents an extra ~ 4,724 birds surviving each year, would result in an increase in population size of 18% after three generations, when compared to the same population with current assumed levels of bycatch mortality, regardless of whether high (0.82) or lower (0.71) estimates of breeding success are used (Table 5). Likewise, for baseline profile 3 (Figure 10), a 10% decrease in mortality would result in the same population size increase of 18%, although a higher number of birds (7,709) would survive under this profile.

The positive effect from reducing bycatch mortality and increasing survival is more noticeable for a population exhibiting a negative trend (i.e. baseline profile 4 for Jan Mayen – Figure 11). Here, a decrease in adult mortality of 10% compared with current levels (~ 28 more birds surviving each year) resulted in an increase in population size of 58% after three generations, (Table 5).

Table 5. Impact of 1%, 5% and 10% increase in mortality on the ratio of the population size after three generations for the impacted and unimpacted (RI:UGL) population of common guillemots breeding in the Celtic Seas (UK & IE), UK North Sea and Jan Mayen (Arctic Waters) that use the Celtic Seas during their life cycle. Estimates were derived from stochastic models (95% CIs given in brackets). Also, a value of total annual bycatch (number of birds) is given for each scenario, assuming 1%, 5% and 10% increases to bycatch mortality. RI:UGL ranges between 0 and 1; 0 assuming a high impacted population and 1 assuming a low impacted population. The increase in population size after three generations that would be a consequence of a 10% decrease in bycatch mortality (compared with the baseline level which assumes bycatch is already happening) is also presented.

Baseline population	Actual trend	RI:UGL			Total annual bycatch (number of birds, from simulations)			Population size (breeding pairs)	Increasing in population size after 3GT (10%)
		1%	5%	10%	1%	5%	10%		
1: Celtic Seas (UK & IE) (Figure 8)	Stable	0.978 (0.972 – 0.983)	0.900 (0.872 – 0.925)	0.817 (0.772 – 0.856)	~ 472	~ 2,517	~ 4,724	456,264	18%
2: Celtic Seas (UK & IE) (Figure 9)		0.979 (0.973 – 0.984)	0.901 (0.871 – 0.924)	0.818 (0.772 – 0.860)					
3: UK North Sea (Figure 10)	Decreasing	0.978 (0.971 – 0.984)	0.898 (0.865 – 0.925)	0.813 (0.763 – 0.857)	~ 771	~ 4,487	~ 7,709	631,905	18%
4: Jan Mayen (Arctic Waters) (Figure 11)	Decreasing	0.916 (0.905 – 0.925)	0.647 (0.613 – 0.679)	0.423 (0.380 – 0.467)	~ 3	~ 14	~ 28	< 1,000	58%

Reported annual bycatch of common guillemots in the Celtic Seas from UK fleets was 1,033 birds (739–1,351) and 885 birds (636–1,167) in 2016 and 2017, respectively (Northridge *et al.* 2020). These observed levels of bycatch are similar to the predicted number of birds that would survive if there was 1% reduction in total annual mortality (Table 5). However, guillemots visiting the Celtic Seas from breeding colonies in other OSPAR Regions (i.e. North Sea (OSPAR Region II) and Jan Mayen (OSPAR Region I)) may also experience additional bycatch pressures occurring near their breeding colonies. It may be possible to examine this further using molecular analysis or ringing data to assign the origin of bycaught birds. Alternatively, seasonal stratification of bycatch data (i.e. splitting birds by breeding phenology (breeding versus non-breeding), might allow some spatial separation of origin because breeding birds are typically more concentrated at their respective breeding colonies during the breeding season). However, such stratification might bring little insights when dealing with the wintering distribution of birds. Furthermore, quantifying bycatch from non-UK fleets operating in the Celtic Sea is an important evidence gap.

4 Conclusions/recommendations

4.1 Availability of bycatch data in the Northeast Atlantic

Data on marine bird bycatch is being collected – to some degree – throughout the OSPAR Maritime Area. However, serious paucity of data was found for all regions, especially in the Wider Atlantic (OSPAR Region V), where only 33% of fishing fleets are recording seabird bycatch data (considering all data, irrespective of their quality). The next lowest region was the Arctic Waters (OSPAR Region I) where 68% of fishing fleets are recording seabird bycatch data (Table 1 and Appendix 7). Both OSPAR Region V and OSPAR Region I include important breeding, feeding and resting habitats for several marine bird populations. They also include important fishing grounds for European and foreign fleets. In terms of data quality, many sources performed well against the minimum quality criteria developed (Appendix 4), namely the majority of the German fleet, the Icelandic gillnets targeting cod, the Norwegian set longlines targeting Greenland halibut, part of the Portuguese fleet (those operating set gillnets, bottom longlines and purse seines), all Swedish fleet except for longliners, part of the Spanish fleet (those operating bottom trawls and purse seines) and the UK pelagic trawls (Appendix 6).

Key limitations in data quality were attributed to:

- Temporal coverage of observation effort. Given that bycatch is, in essence, incidental, a good coverage of fishing activity data with a greater amount of observation effort, together with high standards on data collection and bycatch reporting are important. Previous studies indicate that observation coverage needs to be above 20% of fleet effort to reduce uncertainty in bycatch rate estimates and total bycatch mortality (Lawson 2006; Wolfaardt & Debski 2019). This is particularly important for those gears where bycatch is more likely to occur, namely pelagic trawls, gillnets, longlines and purse seines.
- The occurrence of few observer programmes directed to monitor bycatch of protected, endangered and threatened species (PETS). At the European level, the majority of data on PETS bycatch is coming from the already set Data Collection Framework under the Common Fisheries Policy of EU Member States to collect data on catches and discards of target species. Such a framework was not designed to collect data on PETS, and commonly, the tasks developed by observers aboard are completely incompatible with bycatch monitoring needs.
- Low observer coverage of small-scale fishing fleets. Many small vessels are fishing in the vicinity of important breeding colonies or feeding sites, which could potentially be responsible for serious numbers of marine bird bycatch (Bærum *et al.* 2019; Christensen-dalsgaard *et al.* 2019; Northridge *et al.* 2020; Oliveira *et al.* 2021). Capacity in these fisheries is sometimes limited, however, because small vessels often cannot easily fit an extra member on the crew solely to undertake PET observations. Therefore, alternative monitoring tools might be valuably implemented in such circumstances (e.g. electronic monitoring using CCTV cameras, logbooks and reference fleets).
- Accurate estimates of fishing effort are needed to obtain total bycatch numbers from bycatch rates, but data is not easily available. Fishing effort from the EU fishing fleet is collected and managed under the Data Collection Framework – DCF (STECF 2020). Annual reports are made available from the [DCF website](#). UK maintained reporting to DCF at least until 2019, but some changes might occur after BREXIT enforcement. Other non-EU fleets of concern are mainly the ones managed by ICCAT. All countries or fishing entities that target tuna and/or shark are requested to submit fisheries data related with those operations. [ICCAT statistical databases](#) are also made available online.

4.2 Performance of PVA models to assess impact of bycatch

The analyses presented in this report suggest that a stochastic population viability analysis (PVA) based on a Leslie matrix approach is a valuable tool to evaluate the impact of bycatch-driven mortality in marine bird populations occurring in the OSPAR Maritime Area. However, the reliability of using PVA to examine management or impact scenarios depends on the quality of the input data. Similar to the case of bycatch data, some paucity of marine bird demographic information was found. Across the OSPAR Maritime Area, data on immature rates of survival and breeding success are limited, for example 54% and 31% of marine bird species (not only Cory's shearwater and common guillemot) with evidence of being bycaught, are lacking information on these demographic processes, respectively (Evans 2021). This limitation may become more serious when dealing with certain seabird populations in a given OSPAR region (e.g. if a species is poorly monitored and at high risk of bycatch).

PVAs were conducted separately for populations breeding in specific geographical areas, with the assumption made that the individuals within each population are exposed to the same level of bycatch threat within the respective OSPAR region. For the Cory's shearwater case study, this assumption is likely to be valid. However, for the common guillemot case study, the three populations are unlikely to utilise OSPAR Region III equally. For example, common guillemots breeding in the Celtic Sea can stay in this region year-round, whilst only a small proportion of birds from the colonies at Jan Mayen or the Greater North Sea region are expected to be found in the Celtic Sea during the non-breeding season. Plus, those populations might experience additional bycatch in their breeding OSPAR Region. To overcome such limitations, marine bird bycatch assessment might be developed in two separated approaches. A first approach might target only breeding populations (in case of migrant species as the case of common guillemot) or resident populations (in case of non-migratory species, e.g. European shag). Migratory species have more restricted and localized movements during the breeding period that is centralized to their colonies. The same might be assumed for resident and non-migratory populations along the entire life cycle. In those cases, local or national bycatch estimates and population size numbers obtained from colony-based counts are easily linked to a given colony in each region, resulting in higher accuracy on estimates and stronger confidence in the final bycatch assessment. To deal with migratory species in wintering grounds, other methods to estimate bird population size might be desirable. Assessments using counts at sea and counts from coastal points have shown a good performance to estimate bycatch scale (Marchowski 2023). An alternative method to take into account such complex dynamics might be to assess population viability for multiple occurrences (i.e. taking into consideration individuals from breeding colonies located outside the OSPAR region in analysis) at the metapopulation level through a multi-site extinction analysis (Morris *et al.* 1999), or by adapting apportioning tools developed to establish the colonies of origin for birds that may be affected by offshore wind energy developments (Butler *et al.* 2020). Further analysis is required to assess suitability to these approaches.

The analysis detailed in the report generated several important insights. Firstly, small adjustments to adult mortality, following the concept of "small numbers" defined by the Birds Directive and assuming the 1% figure, resulted in a small, albeit potentially significant, change in population dynamics. By contrast, higher adjustments (5% and 10%) in adult mortality considerably affected the population trend, sometimes inverting the directional trend.

The metric used to compare population trajectories under different scenarios of bycatch impact (RI:UGL) was easy to interpret in a population context. A clear link between this relative metric and the impact level supported a straightforward understanding of impact at the population level. Also, it allowed us to explore relative changes in each population under

different impact scenarios, which may be more informative than examining absolute projected population sizes.

Density-independent PVA do not account for compensatory changes in demographic rates as populations change size and therefore for increasing populations this formulation could lead to more inflated rates of population growth. However, the reverse is true for declining populations, where not accounting for compensatory regulation will underestimate rates of population growth. Little information is available for parameterising the shape of density-dependent regulation for different species and populations of seabirds (Horswill *et al.* 2017). At present, we recommended including compensatory density dependence in a broad-scale indicator such as B5 (Marine Bird Bycatch), for increasing populations, and exploring options for incorporating density-dependent mechanisms in small populations experiencing decline.

4.3 Recommendations for the assessment of OSPAR indicator B5 – marine bird bycatch

1. Generally, the workflow presented in Figure 1 represents a suitable approach for developing assessment of the OSPAR indicator B5 Marine Bird Bycatch. For regions and species where data are available to support a PVA, the method presented in the present study can be followed to support an indicator assessment. For PVA, two different approaches can be followed. For migratory species during the breeding season, as well as for non-migratory species during the full annual cycle, estimates of population size obtained from colony counts and local/national bycatch estimates can be used to define initial population sizes and marine bird bycatch impacts. Estimating bycatch impacts for migratory species during non-breeding season is more complicated because it is difficult to assign bycatch during the non-breeding season to a colony of origin. Here, combining tracking data (to identify a colony's non-breeding distribution) with counts at sea or from coastal points offers an alternative for obtaining estimates of regional population size. We also recommend exploring options for adapting apportioning tools developed to establish the colonies of origin for birds that may be affected by offshore wind energy developments. For colonies where data cannot support PVA assessment, a precautionary approach should be followed as shown in Figure 1 (i.e. "population modelling not possible and/or insufficient bycatch data").
2. Three sets of data are needed to run an assessment on marine bird bycatch. These are fishing effort, bycatch rates, and marine bird demographic data. Ensuring comparable spatial scales for these data is key. However, neither fishing effort nor seabird monitoring are spatially ubiquitous. Bycatch data is more informative when given at a finer scale, at temporal, spatial and fishing effort levels.
3. Fishing effort data is important for scaling up bycatch rates for an entire fleet operating in an OSPAR region. These data are available on EU and ICCAT platforms. Data should be used at the same resolution as the finest spatial scale set by the bycatch data.
4. For bycatch data, there is a need to address any concerns about data ownership rights as soon as possible. The full ICES database was not freely available for this study, and a special request would need to be presented to WGBYC members. Also, that database should be seen as a work in progress where evidence gaps need to be filled. These evidence gaps include a lack of information on most small-scale fisheries, a lack of data for fleets where marine bird bycatch was reported before or is known to occur, insufficient detail on the unit used to measure fishing effort (e.g. longline fleets report number of fishing trips per year, as well as hooks per year). The list of sources added during the development of the present study

(Appendix 2) is intended to be a good complement to the ICES bycatch survey inventory, which the WGBYC itself could explore in the near future.

5. There should be a focus to collate marine bird species-specific demographic data from the same colony and study period where possible. For species where multiple estimates of demographic rates are available within a region, it is important to use scenario testing to examine the sensitivity of the population response to different demographic profiles, as well as mean values.
6. Although not intended to narrow options by way of eliminating data from any possible indicator analysis, the Bycatch and PVA Minimum Criteria tools should be used to evaluate bycatch and marine bird data before assessment. This will provide a suitable overview of data quality under analysis.
7. The ratio between final population sizes predicted by PVA under impacted and unimpacted scenarios allows the effect of bycatch to be quantified. We define this ratio (R) between impacted (I) and unimpacted (U) populations after three generations (GL) as $RI:UGL$. This can be interpreted as the percentage difference in population size from the baseline scenario compared with a scenario that encompasses alterations in survival due to bycatch mortality after three generations. Here, three generations was chosen to reflect the time frame used for in threat assessment in the IUCN Red List of Threatened Species. The $RI:UGL$ ratio could also be used to inform the assessment of bycatch mortality under criterion D1C1 (EU Marine Strategy Framework Directive, MSFD - 2008/56/EC).
8. The spatial scale of the OSPAR indicator B5 Marine Bird Bycatch requires careful consideration. Many marine birds are migratory and utilise more than one OSPAR region during their annual cycle. Consequently, next steps might consider examining the sensitivity of outputs to varying the spatial coverage of analyses. Furthermore, other marine bird populations and species should be examined using the approach outlined in this report.
9. We projected PVAs over three generations. This approach follows assessment methods used by the IUCN Red List of Threatened Species. Unless future changes in fishing effort is known and therefore a different time scale of impact is required, we recommend using three generations to evaluate the OSPAR indicator B5 Marine Bird Bycatch.

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Appendix 1. Terms used to search published and grey literature on seabird bycatch in the OSPAR area

Fishing gear	OSPAR Regions	Contracting-party countries	RFMOs (Regional Fisheries Management Organisations)	Languages of search
Gillnet	Arctic Waters	Belgium	International Commission for the Conservation of Atlantic Tunas – ICCAT	Danish
Hand lines	Greater North Sea	Denmark	North East Atlantic Fisheries Commission – NEAFC	English
Hooks	Celtic Seas	European Union		French
Longline	Bay of Biscay and Iberian	Finland		German
Pole and	Wider Atlantic	France		Icelandic
Pots		Germany		Norwegian
Purse seine		Iceland		Portuguese
Seine		Ireland		Spanish
Set nets		Luxembourg		Swedish
Trammel net		Netherlands		
Traps		Norway		
Trawl		Portugal		
		Spain		
		Sweden		
		Switzerland		
		United Kingdom		

Appendix 2. List of sources of bycatch data (in addition to the Working Group on Bycatch of Protected Species (WGBYC) inventory)

Name	Country / region	Organization	Type of publication	Year of data
A contribution to reducing bycatch in a high priority area for seabird conservation in Portugal	Portugal	SPEA	Paper	2015–2018
An assessment of seabird – fishery interactions in the Atlantic Ocean	I, III, IV, V	ICCAT	Paper	2003–2006
Annual Report for data collection in the fisheries and aquaculture sectors	Poland	National Marine Fisheries Research Institute	Report	2017
Assessing incidental bycatch of seabirds in Norwegian coastal commercial fisheries: Empirical and methodological lessons	Norway	Norwegian Institute for Nature Research	Paper	2009
Attendance of scavenging seabirds at trawler discards off Galicia, Spain	IV	Instituto Español de Oceanografía	Paper	1998–1999
Best practices to mitigate seabird bycatch in longline, trawl and gillnet fisheries — efficiency and practical applicability	Norway	Fish Capture Division, Institute of Marine Research	Paper	-
Ólafsson, H.G. 2015. Bird bycatch in the Icelandic Gillnet Lumpfish Fishery. BioPol	Iceland	BioPol	Report	2015
Bycatch in gillnet fisheries – An overlooked threat to waterbird population	II	DHI Water-Environment-Health	Paper	< 2009
By-catch of Cory's shearwater in the commercial longline fisheries based in the Mediterranean coast and operating in East Atlantic waters: First approach to incidental catches of seabird in the area.	Spain, Azores	Instituto Español de Oceanografía	Paper	2004–2011

Name	Country / region	Organization	Type of publication	Year of data
Bycatch of high sea longline fisheries and measures taken by Taiwan: Actions and challenges	V	Fisheries Agency and the Overseas Fisheries Development Council of the ROC	Paper	2002–2008
Bycatch of seabirds and marine mammals in lumpsucker gillnets 2014-2017	Iceland	Marine and Freshwater Research Institute	Report	2014–2017
Bycatch of the European purse seine tuna fishery in the Atlantic Ocean for the 2003-2007 period	IV	IRD/IEO/AZTI scientists.	Paper	2003–2007
Common methodology for assessing the impact of fisheries on marine Natura 2000		N2K group	Project/ technical report	2012
Contribution to the preparation of a Plan of Action for Seabirds	III (Gran Sol and Netherlands)	MRAG Ltd	Report	2010
Determination of the level of bird mortality in the static net fishery in 2002-2003, execution of experiments with alternative fishing techniques and evaluation of measures for the 2003-2004 season	Netherlands	Ministerie van LNV	Report	2002–2003
Distribution of seabird by-catch using data collected by Japanese observers in 1997-2009 in the ICCAT area	I, V	National Research Institute of Far Seas Fisheries, Ordo ICCAT	Paper	1997–2009
Estimation of discards in Norwegian coastal gillnet fisheries	Norway	Norwegian Institute for Nature Research	Report	2012–2018
Gillnet bycatch of seabirds in Southwest Greenland, 2003 - 2008	Greenland	Greenland Institute of Natural Resources	Report	2003–2008

Name	Country / region	Organization	Type of publication	Year of data
Global seabird bycatch in longline fisheries	III, V	RSPB, SEO/BirdLife	Paper	2006–2007
Incidental bycatch of northern fulmars in the small-vessel demersal longline fishery for Greenland halibut in coastal Norway 2012–2014	Norway	Norwegian Institute for Nature Research (NINA)	Paper	2012–2014
Interactions of marine protected species with artisanal fisheries in the Parque Natural do Sudoeste Alentejano e Costa Vicentina (PNSACV) and adjacent classified áreas (SPAs and SACs)	Portugal	CCMAR-UAIg, FCUL	Thesis	2018
Longline fisheries in the NE Atlantic, a threat for seabirds?	Spain	Instituto Español de Oceanografía	Conference paper	-
Lunneryd, S.G., Königson, S., Sjöberg., N.B., 2004. By-catch of seals, harbour porpoises and birds in Swedish commercial fisheries. Fiskeriverket informerar 2004/8, Öregrund, Göteborg, Sweden.	Sweden	Fiskeriverkets kustlaboratorium	Report	2002
Observations on interaction between seabirds and the spanish surface longline fishery targeting swordfish in the Atlantic ocean during the period 1993-2017	Spain, Portugal, Azores	Instituto Español de Oceanografía	Paper	1993–2017
Portugal Annual Report for data collection in the fisheries and aquaculture sectors - 2019	Portugal (including Azores)	DGRM	Report	2019
Programa de Observação para as Pescas dos Açores - POPA - Relatório de actividades 2019	Portugal – Azores	IMAR – Instituto do Mar	Report	2019
Reducing Seabird Bycatch in Longline Fisheries by Means of Bird-Scaring Lines and Underwater Setting	Norway	Institute of Marine Research Bergen, Norway	Paper	1998

Name	Country / region	Organization	Type of publication	Year of data
Report of the 2018 ICCAT sub-committee on ecosystems meeting	I, III, IV, V	ICCAT, IPMA	Report	-
Report of the Workshop to Review and Advise on Seabird Bycatch (WKBYCS)	-	International Council for the Exploration of the Sea	Report	2000–2011
Review and evaluation of three mitigation measures - bird-scaring line, underwater setting and line shooter - to reduce seabird bycatch in the north Atlantic longline fishery	Norway	Norwegian Institute for Nature Research	Paper	1992, 1996, 1998, 1999
Seabird bycatch in fishing gear in Iceland	Iceland	Icelandic Institute of Natural History	Paper	< 2001
Seabird bycatch in Portuguese mainland coastal fisheries: An assessment through on-board observations and fishermen interviews	Portugal	SPEA	Paper	2010–2012
Seabird mortality from longline fishing in the Mediterranean Sea and Macaronesian waters: a review and a way forward	V		Paper	< 1999
SPAIN Annual Report for data collection in the fisheries and aquaculture sectors - 2017	Spain – North Sea (ICES IIIa, IV and VIId areas) and Eastern Arctic (ICES areas I, II)	Ministerio de Agricultura y Pesca, Alimentación y Medio Ambiente Secretaría General de Pesca & IEO	Report	2017
The impact of longline fishing on seabirds in the north-east Atlantic: recommendations for reducing mortality	I – Norway	RSPB, NOF, JNCC, BL	Report	1997–1998

Name	Country / region	Organization	Type of publication	Year of data
The incidental catch of seabirds in gillnet fisheries: A global review	Denmark UK	DHI, Agern Allé 5, DK-2970 Hørsholm, Denmark	Paper	1990–2002, 2009–2010
The status and trends of seabirds breeding in Norway and Svalbard	Norway and Svalbard	Norwegian Institute for Nature Research	Report	-
Trials using different hook and bait types in the configuration of the surface longline gear used by the Spanish swordfish (<i>Xiphias gladius</i>) fishery in the Atlantic Ocean	V	Instituto Español de Oceanografía	Paper	2005–2006
United Kingdom Annual Report for data collection in the fisheries and aquaculture sectors	UK (North Sea, Celtic Sea and Arctic waters)	Marine Management Organisation, England Agri-Food and Biosciences Institute, Northern Ireland Marine Scotland, Marine Laboratory, Scotland Centre for Environment, Fisheries & Aquaculture Science, England Environment Agency Natural Resources Wales Welsh Government	Report	2017

Name	Country / region	Organization	Type of publication	Year of data
What's the catch with lumpsuckers? A North Atlantic study of seabird bycatch in lumpsucker gillnet fisheries	Norway Iceland Denmark Sweden Greenland	Norwegian Institute for Nature Research	Paper	Norway – 2012, 2013, 2015 Iceland – 2014–2017 Denmark – 2010–2018 Greenland – 2013–2016
ZEPAMAR	Espanha Galiza	SEO/BirdLife	Project	2004, 2005, 2016–2018

Appendix 3. Bycatch survey inventory

Appendix 3 (Bycatch survey inventory) is provided in an accompanying spreadsheet:

[jncc-report-766-appendix-3-bycatch-survey-inventory-2020-update.xlsx](#).

Appendix 4. Bycatch quality criteria

Adequacy of bycatch data

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Importance of these fisheries compared to other fisheries that catch of birds	Perceived importance of these fisheries compared to other fisheries catch of birds	0 – not provided 1 – not observed 2 – observed but low 3 – medium 4 – high 5 – very high	0 – not provided	3 – medium	2 – observed but low
Monitoring type	Monitoring type	0 – data based on market observations, questionnaires or logbooks 1 – data based on at sea observations and/or electronic monitoring	0 – data based on market observations, questionnaires or logbooks	1 – data based on at sea observations and/or electronic monitoring	1 – data based on at sea observations and/or electronic monitoring

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Longevity of observer data	Longevity of observer data	0 – No observer program has ever been implemented 1 – Observer program conducted prior to 15 years ago 2 – Observer program conducted on one or more occasions along the period between 15 and 5 years ago, but not annually 3 – Observer program conducted annually along the period between 15 and 5 years ago and not subsequently 4 – Observer program conducted on one or more occasions along the past 5 years, but not annually 5 – Observer program conducted annually along the past 5 years	2 – Observer program conducted on one or more occasions along the period between 15 and 5 years ago, but not annually	4 – Observer program conducted on one or more occasions along the past 5 years, but not annually	5 – Observer program conducted annually along the past 5 years

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Does data derive from dedicated sampling for protected species or is it from commercial species monitoring	Main purpose of data collection	0 – No information on main purpose of data collection 1 – Data derives from commercial species monitoring 2 – Data derives from dedicated sampling	1 – Data derives from commercial species monitoring	2 – Data derives from dedicated sampling	2 – Data derives from dedicated sampling
Gear detail	Gear level	0 – No gear assigned 1 – Gear assigned up to level 3 2 – Gear assigned to level 4 or higher	1 – Gear assigned up to level 3	2 – Gear assigned to level 4 or higher	2 – Gear assigned to level 4 or higher
Are bycatch rates available on the basis of trips/days/hauls/net length/number of hooks	Metric of bycatch rates	0 – bycatch rates are not available 1 – bycatch rates given on the basis of days at sea 2 – bycatch rates given on the basis of hauls 3 – bycatch rates given on the basis of most descriptive metrics (e.g. length*time soaked for gillnets, number of hooks*time soaked for longlines, number of traps*time soaked for traps, number of hauls for towed gear)	1 – bycatch rates given on the basis of days at sea	2 – bycatch rates given on the basis of hauls	3 – bycatch rates given on the basis of most descriptive metrics (e.g. length*time soaked for gillnets, number of hooks*time soaked for longlines, number of traps*time soaked for traps, number of hauls for towed gear)

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Sampling Design	Sampling of vessels, permits, licenses	<p>0 – No information on sampling of vessels, permits, licenses</p> <p>1 – No observer program or sampling design does not support bycatch or total catch estimation</p> <p>2 – Opportunistic or haphazard sampling, including voluntary observer programs, to support bycatch or total catch estimation</p> <p>3 – Random sampling scheme or probability-based sampling with moderate observer coverage levels to support bycatch or total catch estimation</p> <p>4 – Random sampling scheme or probability-based sampling with adequate observer coverage levels to support bycatch or total catch estimation</p> <p>5 – Near-census of vessels with estimation required, or census of vessels with no estimation required</p>	2 – Opportunistic or haphazard sampling, including voluntary observer programs, to support bycatch or total catch estimation	3 – Random sampling scheme or probability-based sampling with moderate observer coverage levels to support bycatch or total catch estimation	5 – Near-census of vessels with estimation required, or census of vessels with no estimation required

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Sampling Design	Sampling of trips	0 – No information on sampling of trips 1 – No observer program, or sampling design does not support bycatch or total catch estimation 2 – Opportunistic or haphazard sampling, including voluntary observer programs, to support bycatch or total catch estimation 3 – Random sampling scheme or probability-based sampling with pilot/baseline observer coverage levels to support bycatch or total catch estimation 4 – Random sampling scheme or probability-based sampling with adequate observer coverage levels to support bycatch or total catch estimation 5 – Near-census of trips with estimation required, or census of trips with no estimation required	2 – Opportunistic or haphazard sampling, including voluntary observer programs, to support bycatch or total catch estimation	3 – Random sampling scheme or probability-based sampling with pilot/baseline observer coverage levels to support bycatch or total catch estimation	4 – Random sampling scheme or probability-based sampling with adequate observer coverage levels to support bycatch or total catch estimation

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Sampling Design	Sampling of hauls	0 – No information on sampling of hauls 1 – No observer program or sampling design does not support bycatch or total catch estimation 2 – Opportunistic or haphazard sampling, including voluntary observer programs, to support bycatch or total catch estimation 3 – Random sampling scheme or probability-based sampling to support bycatch or total catch estimation 4 – Near-census of hauls with estimation required 5 – Census of hauls with no estimation required	3 – Random sampling scheme or probability-based sampling to support bycatch or total catch estimation	4 – Near-census of hauls with estimation required	5 – Census of hauls with no estimation required
Are zero bycatch samples recorded, in order to be able to give confidence intervals?	Zero bycatch sampling	0 – zero bycatch samples are not recorded 1 – zero bycatch samples are recorded	1 – zero bycatch samples are recorded	1 – zero bycatch samples are recorded	1 – zero bycatch samples are recorded

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Observer coverage	Observer coverage	0 – observer coverage is not given 1 – observer coverage < 1% 2 – observer coverage 1–4% 3 – observer coverage 5–19% 4 – observer coverage 20–49% 5 – observer coverage ≥ 50%	1 – observer coverage <1%	3 – observer coverage 5–19%	4 – observer coverage 20–49%
Representativeness should be based on appropriate temporal stratification	Temporal stratification	0 – Temporal stratification is not given 1 – Year 2 – Quarter 3 – Month	2 – Quarter	2 – Quarter	3 – Month

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Temporal coverage of observation effort	Temporal coverage of observation effort	0 – No temporal information on observation effort 1 – Observation effort is seasonally biased and most important seasons (for seabirds) are less sampled than remained seasons 2 – Observation effort is seasonally biased but most important seasons (for seabirds) are not less sampled than remained seasons 3 – Observation effort is not seasonally biased	0 – No temporal information on observation effort	2 – Observation effort is seasonally biased but most important seasons (for seabirds) are not less sampled than remained seasons	3 – Observation effort is not seasonally biased
Spatial coverage of observation effort	Spatial coverage of observation effort	0 – No spatial information on observation effort 1 – Observation effort is spatially biased, and does not cover the main fishing grounds 2 – Observation effort is spatially biased but covers the main fishing grounds 3 – Observation effort is not spatially biased	0 – No spatial information on observation effort	2 – Observation effort is spatially biased but covers the main fishing grounds	3 – Observation effort is not spatially biased

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Observation effort includes coastal waters	Spatial coverage of observation effort	0 – No spatial information on observation effort 1 – Observation effort does not include coastal areas and waters around main breeding colonies 2 – Observation effort includes coastal areas and waters around main breeding colonies	0 – No spatial information on observation effort	2 – Observation effort includes coastal areas and waters around main breeding colonies	2 – Observation effort includes coastal areas and waters around main breeding colonies
Data quality control	Data quality control	0 – No information on data quality 1 – No observer program or no data quality control 2 – Limited or incomplete observer training, no debriefing or other quality control 3 – One-time observer training, no debriefing or other quality-control measures 4 – Periodic observer training, minimal quality-control measures 5 – One-time observer training, comprehensive quality-control measures 6 – Periodic observer training, comprehensive quality-control measures	0 – No information on data quality	3 – One-time observer training, no debriefing or other quality-control measures	6 – Periodic observer training, comprehensive quality-control measures

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Taxonomic group detail	Taxonomic group detail	0 – No information on taxonomic group detail 1 – Seabirds are not included in the sampling 2 – Seabirds are included but not identified to species level 3 – Seabirds are included and identified to species level	3 – Seabirds are included and identified to species level	3 – Seabirds are included and identified to species level	3 – Seabirds are included and identified to species level
Peer reviewed/published	Observer program sampling design	0 – No information on the observer program sampling design 1 – Not peer reviewed, or sampling design found to be seriously flawed during peer review 2 – Internally peer reviewed, or problems found during a peer review not fully addressed 3 – Externally peer reviewed (and passed)	0 – No information on the observer program sampling design	2 – Internally peer reviewed, or problems found during a peer review not fully addressed	3 – Externally peer reviewed (and passed)

Analytical methodology

Criteria	Indicator	Scores	Minimum quality	Medium quality	High Quality
Peer reviewed/ published	Observer program sampling design	0 – No information on the observer program sampling design 1 – Not peer reviewed, or sampling design found to be seriously flawed during peer review 2 – Internally peer reviewed, or problems found during a peer review not fully addressed 3 – Externally peer reviewed (and passed)	0 – No information on the observer program sampling design	2 – Internally peer reviewed, or problems found during a peer review not fully addressed	3 – Externally peer reviewed (and passed)

Appendix 5. PVA quality criteria

Criteria	Indicator	Scores	Minimum quality	High Quality
Subdivision meets the minimum quality criteria for bycatch data	Bycatch quality criteria	0 – Minimum quality criteria for bycatch data not achieved 1 – Minimum quality criteria for bycatch data achieved	Minimum quality criteria for bycatch data achieved	Minimum quality criteria for bycatch data achieved
Species abundance in the region	Species status	0 – Species is rare or vagrant 1 – Species is regular (defined as likely to be encountered at sea in small numbers) or common (defined as likely to be encountered at sea in relatively large numbers)	Species is regular (defined as likely to be encountered at sea in small numbers) or common (defined as likely to be encountered at sea in relatively large numbers)	Species is regular (defined as likely to be encountered at sea in small numbers) or common (defined as likely to be encountered at sea in relatively large numbers)

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Availability of data on species abundance</p>	<p>Data on species abundance</p>	<p>0 – Data on species abundance is not available</p> <p>1 – Data on species abundance is available for a period prior to 20 years ago, and not subsequently</p> <p>2 – Data on species abundance is available for one occasion within the past 20 years</p> <p>3 – Data on species abundance is available for each year along the past 5 years</p> <p>4 – Data on species abundance is available for two occasions within the past 20 years, spaced less than 10 years apart</p> <p>5 – Data on species abundance is available for two occasions within the past 20 years, spaced 10 or more years apart</p> <p>6 – Data on species abundance is available for two to 9 occasions within the past 20 years</p> <p>7 – Data on species abundance is available for ≥ 10 occasions within the past 20 years</p>	<p>Data on species abundance is available for two occasions within the past 20 years, spaced less than 10 years apart</p>	<p>Data on species abundance is available for ≥ 10 occasions within the past 20 years</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Reference population for data on species abundance</p>	<p>Data on species abundance</p>	<p>0 – Abundance data is not available 1 – Abundance data refers to the global population 2 – Abundance data refers to part of global population, and not including the region population 3 – Abundance data refers to part of global population, including the region population 5 – Abundance data refers to part of region population 6 – Abundance data refers only to the region population with no temporal stratification 7 – Abundance data refers only to the region population with temporal stratification</p>	<p>Abundance data refers only to the region population with no temporal stratification</p>	<p>Abundance data refers only to the region population with temporal stratification</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Methodology to estimate species abundance targets the main portion of the population that occurs in the region</p>	<p>Data on species abundance</p>	<p>0 – Abundance data is not available 1 – Abundance data comes only from breeding colony counts 2 – Abundance data comes from breeding colony counts (for the regions where species mainly breeds) or from wintering counts (for the regions where species mainly winters, but no more details on the methodology used) 3 – Abundance data comes from both breeding colony counts and at sea counts (for the regions where species mainly breeds or is resident) or only at sea counts (for the regions where species mainly winters)</p>	<p>Abundance data comes from breeding colony counts (for the regions where species mainly breeds) or from wintering counts (for the regions where species mainly winters, but no more details on the methodology used)</p>	<p>Abundance data comes from both breeding colony counts and at sea counts (for the regions where species mainly breeds or is resident) or only at sea counts (for the regions where species mainly winters)</p>
<p>Availability of data on species annual survival of immatures</p>	<p>Data on immature survival</p>	<p>0 – Data on species immature survival is not available 1 – Data on species immature survival is available for a period prior to 15 years ago 2 – Data on species immature survival is available for a period within 15 and 5 years ago and not subsequently 3 – Data on species immature survival is available for a period within the past 5 years</p>	<p>Data on species immature survival is available for a period within 15 and 5 years ago and not subsequently</p>	<p>Data on species immature survival is available for a period within the past 5 years</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Reference population for data on species annual survival of immatures</p>	<p>Data on immature survival</p>	<p>0 – Data on immature survival is not available 1 – Data on immature survival refers to one population with little or no distribution in the region 2 – Data on immature survival refers to two or more populations with little or no distribution in the region 3 – Data on immature survival refers to one population with knowing distribution in the region 4 – Data on immature survival refers to two or more populations with knowing distribution in the region</p>	<p>Data on immature survival refers to one population with little or no distribution in the region</p>	<p>Data on immature survival refers to two or more populations with knowing distribution in the region</p>
<p>Availability of data on species annual survival of breeders</p>	<p>Data on breeders' survival</p>	<p>0 – Data on species breeders' survival is not available 1 – Data on species breeders' survival is available for a period prior to 15 years ago 2 – Data on species breeders' survival is available for a period within 15 and 5 years ago and not subsequently 3 – Data on species breeders' survival is available for a period within the past 5 years</p>	<p>Data on species breeders' survival is available for a period within 15 and 5 years ago and not subsequently</p>	<p>Data on species breeders' survival is available for a period within the past 5</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Reference population for data on species annual survival of breeders</p>	<p>Data on breeders' survival</p>	<p>0 – Data on species breeders' survival is not available 1 – Data on species breeders' survival refers to one population with little or no distribution in the region 2 – Data on species breeders' survival refers to two or more populations with little or no distribution in the region 3 – Data on species breeders' survival refers to one population with knowing distribution in the region 4 – Data on species breeders' survival refers to two or more populations with knowing distribution in the region</p>	<p>Data on species breeders' survival refers to one population with little or no distribution in the region</p>	<p>Data on species breeders' survival refers to two or more populations with knowing distribution in the region</p>
<p>Availability of data on species reproductive rate or productivity (as breeding success or number of fledglings per breeding pair for one egg only species or more than one egg species, respectively)</p>	<p>Data on species productivity</p>	<p>0 – Data on species productivity is not available 1 – Data on species productivity is available for a period prior to 15 years ago 2 – Data on species productivity is available for a period within 15 and 5 years ago and not subsequently 3 – Data on species productivity is available for a period within the past 5 years</p>	<p>Data on species productivity is available for a period within 15 and 5 years ago and not subsequently</p>	<p>Data on species productivity is available for a period within the past 5 years</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Reference population for data on species reproductive rate or productivity (as breeding success or number of fledglings per breeding pair for one egg only species or more than one egg species, respectively)</p>	<p>Data on species productivity</p>	<p>0 – Data on species productivity is not available 1 – Data on species productivity refers to one population with little or no distribution in the region 2 – Data on species productivity refers to two or more populations with little or no distribution in the region 3 – Data on species productivity refers to one population with knowing distribution in the region 4 – Data on species productivity refers to two or more populations with knowing distribution in the region</p>	<p>Data on species productivity refers to one population with little or no distribution in the region</p>	<p>Data on species productivity refers to two or more populations with knowing distribution in the region</p>
<p>Availability of data on age of recruitment</p>	<p>Data on age recruitment</p>	<p>0 – Data on species age recruitment is not available 1 – Data on species age recruitment is available for a period prior to 15 years ago 2 – Data on species age recruitment is available for a period within 15 and 5 years ago and not subsequently 3 – Data on species age recruitment is available for a period within the past 5 years</p>	<p>Data on species age recruitment is available for a period within 15 and 5 years ago and not subsequently</p>	<p>Data on species age recruitment is available for a period within the past 5 years</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Reference population for data on age of recruitment</p>	<p>Data on age recruitment</p>	<p>0 – Data on species age recruitment is not available 1 – Data on species age recruitment refers to one population with little or no distribution in the region 2 – Data on species age recruitment refers to two or more populations with little or no distribution in the region 3 – Data on species age recruitment refers to one population with knowing distribution in the region 4 – Data on species age recruitment refers to two or more populations with knowing distribution in the region</p>	<p>Data on species age recruitment refers to one population with little or no distribution in the region</p>	<p>Data on species age recruitment refers to two or more populations with knowing distribution in the region</p>
<p>Availability of data on species bycatch</p>	<p>Data on species bycatch</p>	<p>0 – Data on species bycatch is not available for the region 1 – Data on species bycatch is available for a period prior to 15 years ago in the region 2 – Data on species bycatch is available for a period within 15 and 5 years ago and not subsequently in the region 3 – Data on species bycatch is available for a period within the past 5 years in the region</p>	<p>Data on species bycatch is available for a period within 15 and 5 years ago and not subsequently in the region</p>	<p>Data on species bycatch is available for a period within the past 5 years</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
Bycatch is reported or suspected for the species	Species bycatch occurrence	0 – No bycatch estimates nor any suspected 1 – Species bycatch was recorded or is likely to be null 2 – Species bycatch was recorded or is likely to occur	Species bycatch was recorded or is likely to occur	Species bycatch was recorded or is likely to occur
Gear types are sampled, of those that are expected to cause significant bycatch in a particular sub-region	Gear types by fleet flag expected to cause significant bycatch in a particular region	0 – none of the gear types suspect or known to cause bycatch are sampled in the region 1 – > 0 to 50% of gear types suspect or known to cause bycatch are sampled in the region 2 – 51 to 80% of gear types suspect or known to cause bycatch are sampled in the region 3 – 81 to 100% of gear types suspect or known to cause bycatch are sampled in the region	51 to 80% of gear types suspect or known to cause bycatch are sampled in the region	81 to 100% of gear types suspect or known to cause bycatch are sampled in the region

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Bycatch estimate assumptions identified, tested, and deemed appropriate</p>	<p>Bycatch estimate assumptions</p>	<p>0 – No bycatch estimation methodologies 1 – Assumptions not identified or tested 2 – Assumptions identified and tested, but no assumptions resolved 3 – Minor assumptions identified, tested, and determined to be appropriate or resolved 4 – Critical assumptions identified, tested, and determined to be appropriate or resolved 5 – All assumptions identified, tested, and determined to be appropriate or resolved</p>	<p>Critical assumptions identified, tested, and determined to be appropriate or resolved</p>	<p>All assumptions identified, tested, and determined to be appropriate or resolved</p>
<p>Statistical bias of bycatch estimates</p>	<p>Statistical bias</p>	<p>0 – No bycatch estimation methodologies or statistical bias unknown 1 – Estimators have high statistical bias 2 – Estimators have negligible statistical bias or not statistically biased, or census sampling</p>	<p>Estimators have high statistical bias</p>	<p>Estimators have negligible statistical bias or not statistically biased, or census sampling</p>

Criteria	Indicator	Scores	Minimum quality	High Quality
<p>Measures of uncertainty on bycatch estimates</p>	<p>Measures of uncertainty</p>	<p>0 – No bycatch estimation methodologies 1 – Measures of uncertainty not calculated 2 – Measures of uncertainty calculated, but not at all levels (vessel/permit/license, trip and haul) 3 – Measures of uncertainty calculated at all levels (vessel/permit/license, trip and haul)</p>	<p>Measures of uncertainty calculated, but not at all levels (vessel/permit/license, trip and haul)</p>	<p>Measures of uncertainty calculated at all levels (vessel/permit/license, trip and haul)</p>

Appendix 6. Matrix of Quality Criteria Bycatch Assessment

Appendix 6 (matrix of Quality Criteria Bycatch Assessment) is provided in an accompanying spreadsheet:

[jncc-report-766-appendix-6-quality-criteria-bycatch-assessment.xlsx](#).

Appendix 7. Overview of data availability for a Pilot assessment marine bird bycatch indicator

Appendix 7 (Overview of data availability for a Pilot assessment marine bird bycatch indicator) is provided in an accompanying spreadsheet:

[jncc-report-766-appendix-7-data-availability-pilot-assessment-overview.xlsx](#).

Appendix 8. Results of the models assuming density independence

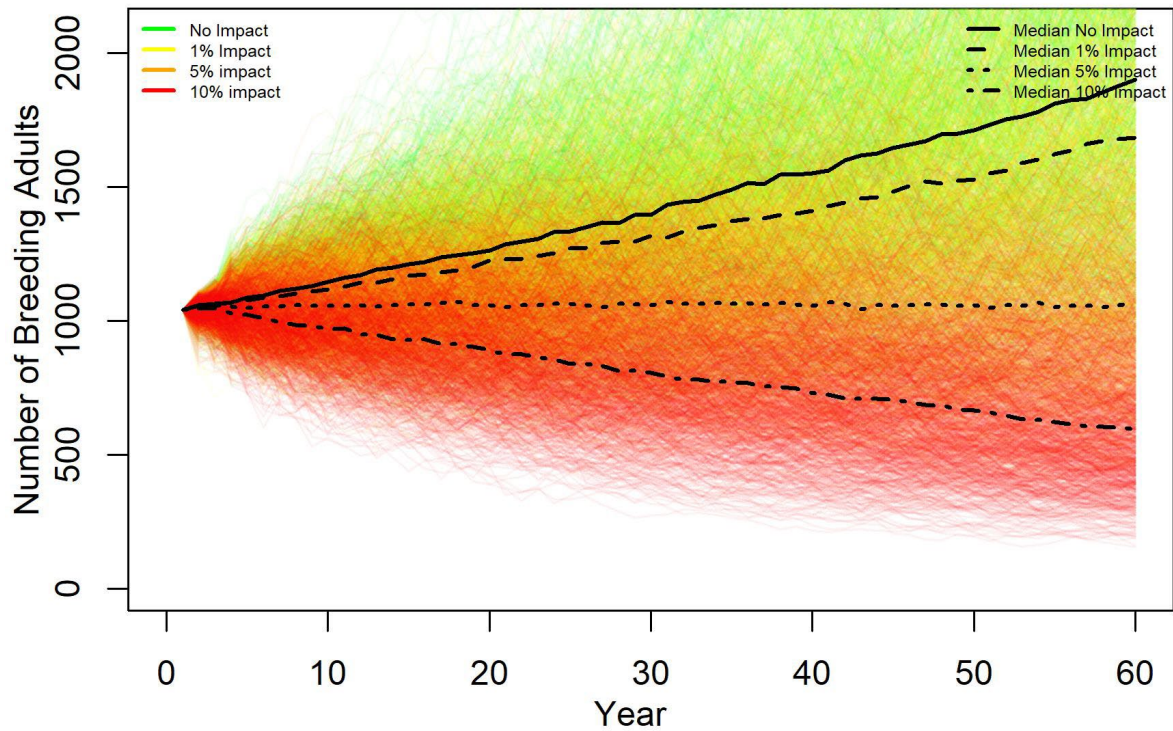


Figure 12. To compare with Figure 6 in the main report. The PVA demonstrated that the population of Cory's shearwater breeding in Berlengas archipelago, excluding Berlenga Island but assuming a higher breeding success (0.586, baseline profile 2), has a different response depending on the scenario of bycatch mortality. Assuming a 1% reduction in survival has no significant impact on the mean population trajectory, while assuming a 5% or 10% decrease in survival alters the direction of the mean population trajectory. The different lines represent the 1,000 iterations of the stochastic PVA, and colours reflect the different bycatch scenarios. The median population trajectory for each scenario is shown as a black line. Model assumes density-independent breeding success.

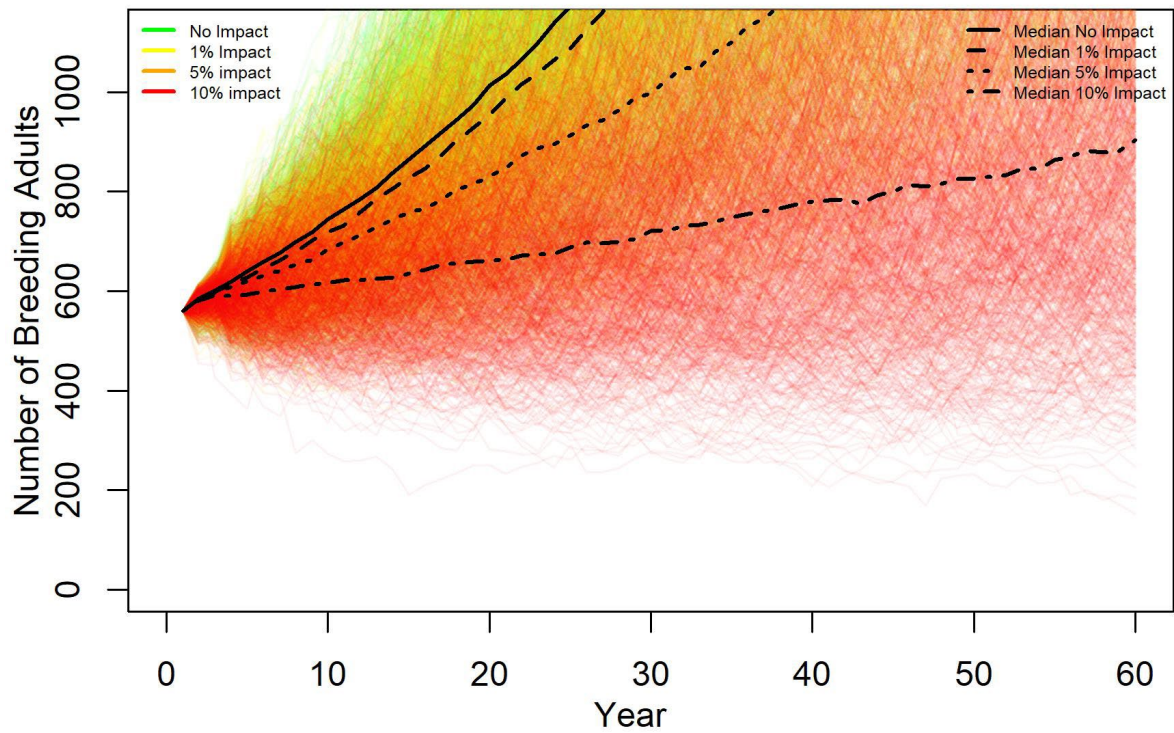


Figure 13. To compare with Figure 7 in the full report. The PVA demonstrated that the population of Cory's shearwater breeding on Berlenga Island only (baseline profile 3), increased under all scenarios of bycatch mortality (i.e. from no bycatch to a 10% reduction in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes density-independent breeding success.

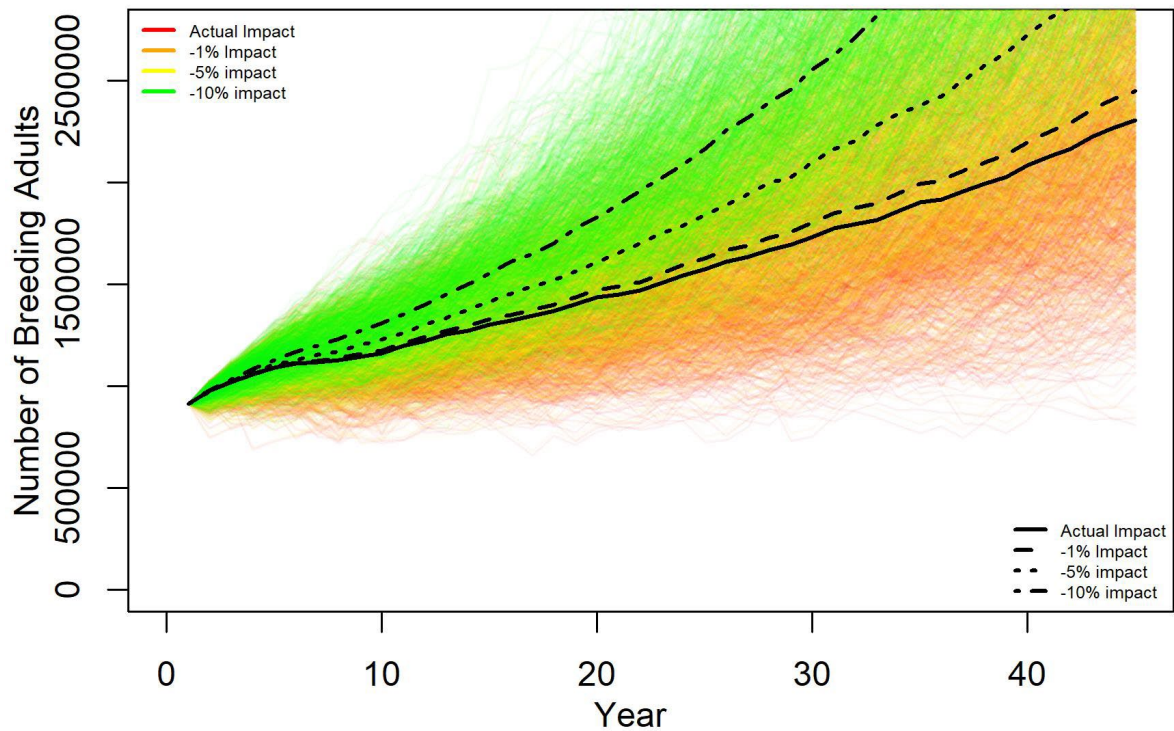


Figure 14. To compare with Figure 8 in the full report. The PVA demonstrated that the population of common guillemots breeding in Celtic Seas colonies assuming a high value of breeding success (0.82; baseline profile 1), including UK and Ireland, increased under all scenarios of bycatch mortality (i.e. from a baseline that is assumed to *include* bycatch mortality to reduced levels of bycatch resulting in 1% ,5% and 10% increases in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes density-independent breeding success.

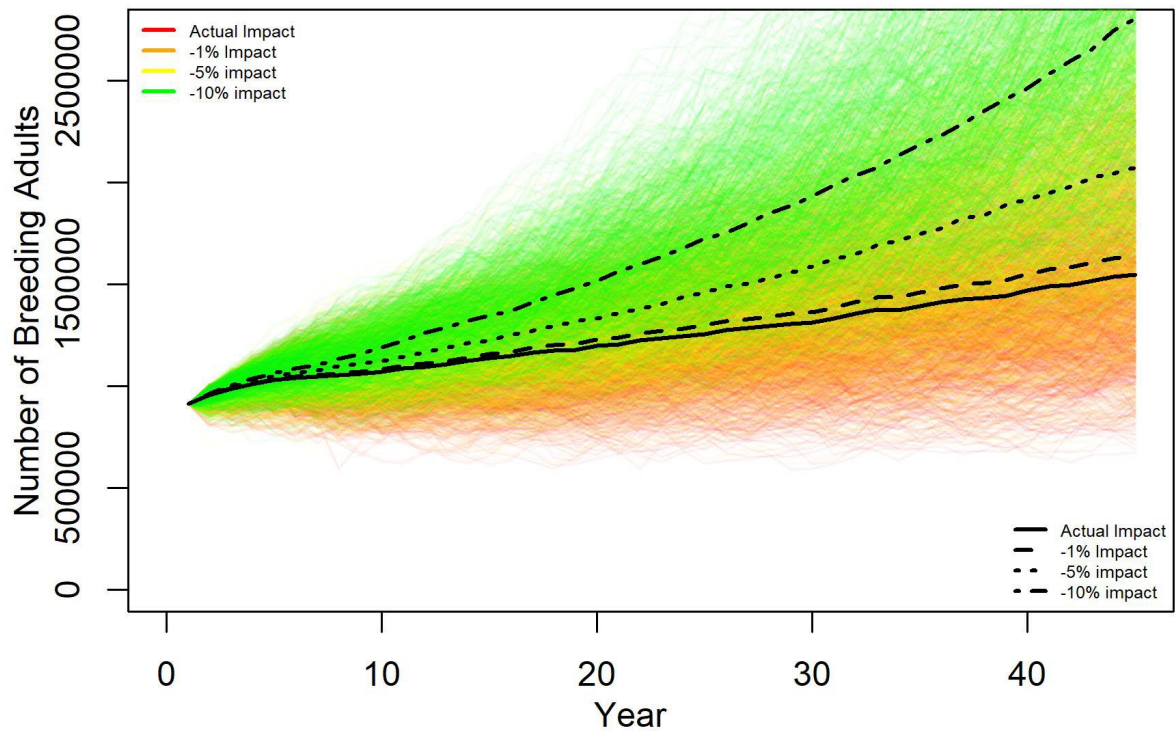


Figure 15. To compare with Figure 9 in the full report. The PVA demonstrated that the population of common guillemots breeding in Celtic Seas colonies assuming a low value of breeding success (0.71; baseline profile 1), including UK and Ireland, increased under all scenarios of bycatch mortality (i.e. from a baseline that is assumed to *include* bycatch mortality to a reduced level of bycatch resulting in 1%, 5% and 10% increases in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes density-independent breeding success.

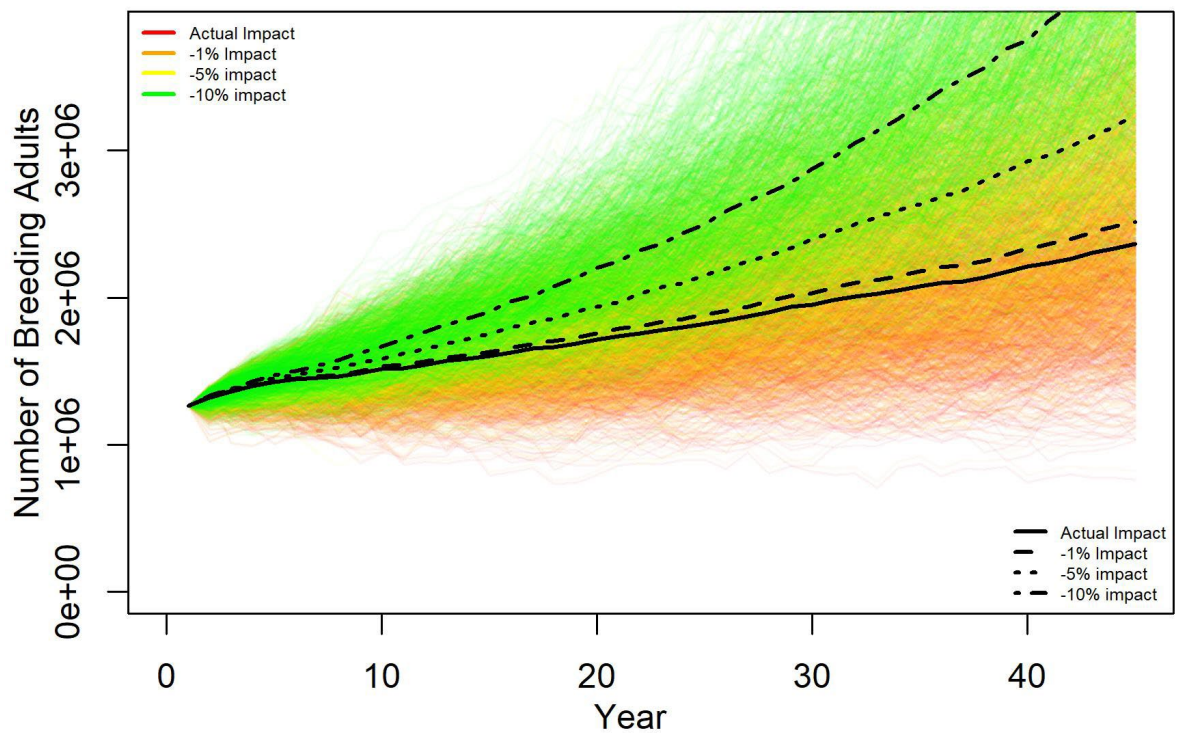


Figure 16. To compare with Figure 10 in the full report. The PVA demonstrated that the population of common guillemots breeding in North Sea colonies from UK only, increased under all scenarios of bycatch mortality (i.e. from a baseline that is assumed to *include* bycatch mortality to reduced levels of bycatch resulting in 1%, 5% and 10% increases in survival). The different colours represent the 1,000 iterations of the stochastic PVA for each scenario of bycatch. The median population trajectory for each scenario shown as a black line. Model assumes density-dependent breeding success.


```

#Figure 10_Density dependent_guillemot_north sea
#Figure 11_Sochastic_guillemot_Jan_Mayen
#Figure 14_Sochastic_guillemot_Celtic_seas_prod_082_skomer
#Figure 15_Sochastic_guillemot_Celtic_seas_prod_071_skomer
#Table 4_Pop_size_ratio_stochastic_Corys
#Table 4_Pop_size_ratio_density_dependence_Corys
#Table 6_Pop_size_ratio_guillemot

# GENERAL FUNCTIONS

##### functions need to set logit-link for sampling survivalexpit <-
function(x){exp(x)/(1+exp(x))}

logit <- function(x){log(x/(1-x))}

##### Weibull function to calculate density dependent survival/productivity rates
Weibull = function(maxF,a,N,b) { maxF * exp(-a * N^b) }

# POPULATION MODELS

##### function to test sensitivity of metrics to input parameters in an r-selected
species with 4 age classes

##### This function runs simulations of increases in mortality or decrease in
productivity of varying

##### magnitudes. Inputs should be "prod" or "surv" for an impact on productivity or
survival

##### impact.mag which should be a vector of magnitudes of varying impact levels
(e.g. 1%-25%)

##### needs to be matched runs (i.e same unimpacted values for
survival/productivity)

population.impact = function(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err,
nyears, niter,

                                impact.param, impact.mag) {

```

```

FirstYr = init * prod * SexRatio
SecYr = FirstYr * age1.surv
ThirdYr = SecYr * juv.surv
Ad = init

##### matrix for population sizes (all individuals & number of breeding adults)
base.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)
impact.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)

base.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)
impact.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)

##### start looping through iterations
pb <- winProgressBar(title = "progress bar", min = 0, max = niter, width = 300)

for (i in 1:niter){

##### matrices to output N birds in each age class to
iterations = matrix(data=0, nrow = 4, ncol = nyears)
iterations[,1] = c(FirstYr, SecYr, ThirdYr, Ad)

base.iterations = iterations
impact.iterations = iterations

## do population model for each iteration
for (j in 1:(nyears-1)) {

age1.logit = expit(rnorm(1, logit(age1.surv), 1)) ## SD selected using trial & error
comparison to published estimates

```

```

    juv.logit = expit(rnorm(1, logit(juv.surv), 1)) ## SD selected using trial & error
comparison to published estimates

    ad.logit = expit(rnorm(1, logit(ad.surv), 0.5)) ## SD selected using trial & error
comparison to published estimates

    prod.random = exp(rnorm(1,log(prod),prod.err)) * SexRatio ## multiply random
estimate of productivity by sex ratio to get chicks fledged/female

    # generate leslie matrix for unimpacted population

    leslie.mat = matrix(c(0,0,0, prod.random, age1.logit,0,0,0, 0,juv.logit,0,0,
0,0,juv.logit,ad.logit), nrow=4,ncol=4, byrow=TRUE)

    # do matrix multiplication to get population estimate in year n+1 for unimpacted
population

    population = matrix(base.iterations[,j])

    base.iterations[j+1] = leslie.mat %*% population

    # repeat for impacted population(s)

if (impact.param == "prod") leslie.mat.impact = matrix(c(0,0,0, prod.random-
(prod.random*impact.mag), age1.logit,0,0,0, 0,juv.logit,0,0, 0,0,juv.logit,ad.logit),
nrow=4,ncol=4, byrow=TRUE)

if (impact.param == "surv") leslie.mat.impact = matrix(c(0,0,0, prod.random, age1.logit - ((1-
age1.logit)*impact.mag),0,0,0, 0,juv.logit - ((1-juv.logit)*impact.mag),0,0, 0,0,juv.logit - ((1-
juv.logit)*impact.mag),ad.logit - ((1-ad.logit)*impact.mag)), nrow=4,ncol=4, byrow=TRUE)

    # do matrix multiplication to get population estimate in year n+1 for unimpacted
population

    population = matrix(impact.iterations[,j])

    impact.iterations[j+1] = leslie.mat.impact %*% population

    }

## get number of birds in each year from each simulation

base.population.sim[i,] = colSums(base.iterations)

```

```

impact.population.sim[i,] = colSums(impact.iterations)

base.population.AD[i,] = base.iterations[4,]
impact.population.AD[i,] = impact.iterations[4,]

setWinProgressBar(pb, i, title=paste( round(i/niter*100, 0), "Time left to make cup of tea!!!"))
    }
close(pb)

return(list(base = base.population.sim, impact = impact.population.sim, base.ad =
base.population.AD, impact.ad = impact.population.AD))
}

```

```
#####
```

```
#####
```

```
##### Function for a density dependent impact on productivity
```

```
##### same as for density independent but includes additional
parameters
```

```
##### maxF (maximum productivity rate) & b (shape function)
```

```
#####
```

```
#####
```

```
population.impact.ddprod = function(init, SexRatio, age1.surv, juv.surv, ad.surv, prod,
prod.err, b, maxF, nyears, niter,
```

```
    impact.param, impact.mag) {
```

```
    FirstYr = init * prod * SexRatio
```

```
    SecYr = FirstYr * age1.surv
```

```
    ThirdYr = SecYr * juv.surv
```

```
    Ad = init
```

```

##### matrix for population sizes

base.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)
impact.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)

base.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)
impact.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)

##### start looping through iterations

pb <- winProgressBar(title = "progress bar", min = 0, max = niter, width = 300)

for (i in 1:niter){

##### matrices to output N birds in each age class to

iterations = matrix(data=0, nrow = 4, ncol = nyears)
iterations[,1] = c(FirstYr, SecYr, ThirdYr, Ad)

base.iterations = iterations
impact.iterations = iterations

##### estimate base productivity & use this to calculate a in Weibull function

prod.random = exp(rnorm(1,log(prod),prod.err)) * SexRatio ## multiply random
estimate of productivity by sex ratio to get chicks fledged/female

a = -(log(prod.random/maxF) / Ad^b)

## do population model for each iteration
for (j in 1:(nyears-1)) {

```

```
age1.logit = expit(rnorm(1, logit(age1.surv), 1)) ## SD selected using trial & error
comparison to published estimates
```

```
juv.logit = expit(rnorm(1, logit(juv.surv), 1)) ## SD selected using trial & error
comparison to published estimates
```

```
ad.logit = expit(rnorm(1, logit(ad.surv), 0.5)) ## SD selected using trial & error
comparison to published estimates
```

```
##### calculate adult survival rates for impacted and unimpacted populations
```

```
prod.unimp = Weibull(maxF,a,base.iterations[4,j],b)
```

```
prod.imp = Weibull(maxF,a,impact.iterations[4,j],b)
```

```
# generate leslie matrix for unimpacted population
```

```
leslie.mat = matrix(c(0,0,0, prod.unimp, age1.logit,0,0,0, 0,juv.logit,0,0,
0,0,juv.logit,ad.logit), nrow=4,ncol=4, byrow=TRUE)
```

```
# do matrix multiplication to get population estimate in year n+1 for unimpacted
population
```

```
population = matrix(base.iterations[,j])
```

```
base.iterations[,j+1] = leslie.mat %*% population
```

```
# repeat for impacted population(s)
```

```
if (impact.param == "prod") leslie.mat.impact = matrix(c(0,0,0, prod.imp-
(prod.random*impact.mag), age1.logit,0,0,0, 0,juv.logit,0,0, 0,0,juv.logit,ad.logit),
nrow=4,ncol=4, byrow=TRUE)
```

```
if (impact.param == "surv") leslie.mat.impact = matrix(c(0,0,0, prod.imp, age1.logit - ((1-
age1.logit)*impact.mag),0,0,0, 0,juv.logit - ((1-juv.logit)*impact.mag),0,0, 0,0,juv.logit - ((1-
juv.logit)*impact.mag),ad.logit - ((1-ad.logit)*impact.mag)), nrow=4,ncol=4, byrow=TRUE)
```

```
# do matrix multiplication to get population estimate in year n+1 for unimpacted
population
```

```
population = matrix(impact.iterations[,j])
```

```
impact.iterations[,j+1] = leslie.mat.impact %*% population
```

```
}
```

```

## get number of birds in each year from each simulation
base.population.sim[i,] = colSums(base.iterations)
impact.population.sim[i,] = colSums(impact.iterations)

base.population.AD[i,] = base.iterations[4,]
impact.population.AD[i,] = impact.iterations[4,]

setWinProgressBar(pb, i, title=paste( round(i/niter*100, 0), "Time left to make cup of tea!!!"))
    }

close(pb)

return(list(base = base.population.sim, impact = impact.population.sim, base.ad =
base.population.AD, impact.ad = impact.population.AD))
}

##### function to test sensitivity of metrics to input parameters in a k-selected
species with 7 age classes

#population.impactK = function(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err,
nyears, niter,

#
        impact.param, impact.mag) {

population.impactK = function(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv,
ad.surv, prod, prod.err, nyears, niter,

        impact.param, impact.mag) {

FirstYr = init * prod * SexRatio
SecYr = FirstYr * juv.surv
ThirdYr = SecYr * age1.surv
FourthYr = ThirdYr * age2.surv

```

```

FifthYr = FourthYr * age3.surv
Sixth = FifthYr * age3.surv
Ad = init

#### matrix for population sizes
base.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)
impact.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)

base.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)
impact.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)

##### start looping through iterations
pb <- winProgressBar(title = "progress bar", min = 0, max = niter, width = 300)

for (i in 1:niter){

##### matrices to output N birds in each age class to
iterations = matrix(data=0, nrow = 7, ncol = nyears)
iterations[,1] = c(FirstYr, SecYr, ThirdYr, FourthYr, FifthYr, Sixth, Ad)

base.iterations = iterations
impact.iterations = iterations

## do population model for each iteration
for (j in 1:(nyears-1)) {

    juv.logit = expit(rnorm(1, logit(juv.surv), 1)) ## SD selected using trial & error comparison
to published estimates

```

```
age1.logit = expit(rnorm(1, logit(age1.surv), 1)) ## SD selected using trial & error
comparison to published estimates
```

```
age2.logit = expit(rnorm(1, logit(age2.surv), 1)) ## SD selected using trial & error
comparison to published estimates
```

```
age3.logit = expit(rnorm(1, logit(age3.surv), 1)) ## SD selected using trial & error
comparison to published estimates
```

```
ad.logit = expit(rnorm(1, logit(ad.surv), 0.5)) ## SD selected using trial & error
comparison to published estimates
```

```
prod.random = exp(rnorm(1, log(prod), prod.err)) * SexRatio ## multiply random estimate
of productivity by sex ratio to get chicks fledged/female
```

```
# generate leslie matrix for unimpacted population
```

```
leslie.mat = matrix(c(rep(0,6), prod.random,
juv.logit,rep(0,7),age1.logit,rep(0,7),age2.logit,rep(0,7),
age3.logit,rep(0,7),age3.logit,rep(0,7),age3.logit,ad.logit), nrow=7,ncol=7, byrow=TRUE)
```

```
# do matrix multiplication to get population estimate in year n+1 for unimpacted
population
```

```
population = matrix(base.iterations[,j])
```

```
base.iterations[,j+1] = leslie.mat %*% population
```

```
# repeat for impacted population(s)
```

```
if (impact.param == "prod") leslie.mat.impact = matrix(c(rep(0,6), prod.random-
(prod.random*impact.mag), juv.logit,rep(0,7),age1.logit,rep(0,7),age2.logit,rep(0,7),
age3.logit,rep(0,7), age3.logit,rep(0,7), age3.logit,ad.logit), nrow=7,ncol=7, byrow=TRUE)
```

```
if (impact.param == "surv") leslie.mat.impact = matrix(c(rep(0,6), prod.random, juv.logit -
((1-juv.logit)*impact.mag),rep(0,7),age1.logit - ((1-age1.logit)*impact.mag),rep(0,7),age2.logit
- ((1-age2.logit)*impact.mag),rep(0,7), age3.logit - ((1-age3.logit)*impact.mag), rep(0,7),
age3.logit - ((1-age3.logit)*impact.mag), rep(0,7), age3.logit - ((1-age3.logit)*impact.mag),
ad.logit - ((1-ad.logit)*impact.mag)), nrow=7,ncol=7, byrow=TRUE)
```

```
# do matrix multiplication to get population estimate in year n+1 for unimpacted
population
```

```
population = matrix(impact.iterations[,j])
```

```

    impact.iterations[,j+1] = leslie.mat.impact %*% population
  }

  ## get number of birds in each year from each simulation
  base.population.sim[i,] = colSums(base.iterations)
  impact.population.sim[i,] = colSums(impact.iterations)

  base.population.AD[i,] = base.iterations[7,]
  impact.population.AD[i,] = impact.iterations[7,]

  setWinProgressBar(pb, i, title=paste( round(i/niter*100, 0), "Time left to make cup of
tea!!!"))
}

close(pb)

return(list(base = base.population.sim, impact = impact.population.sim, base.ad =
base.population.AD, impact.ad = impact.population.AD))

}

##### function to test sensitivity of metrics to input parameters in a k-selected
species with 7 age classes

##### This function runs simulations of increases in mortality or decrease in
productivity of varying

##### magnitudes. Inputs should be "prod" or "surv" for an impact on productivity or
survival

##### impact.mag which should be a vector of magnitudes of varying impact levels
(e.g. 1%-25%)

##### needs to be matched runs (i.e same unimpacted values for
survival/productivity)

```

```
#population.impactK.ddprod = function(init, SexRatio, age1.surv, juv.surv, ad.surv, prod,
prod.err, nyears, niter,
```

```
#           impact.param, impact.mag) {
```

```
population.impactK = function(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv,
ad.surv, prod, prod.err, b, maxF, nyears, niter,
```

```
           impact.param, impact.mag) {
```

```
FirstYr = init * prod * SexRatio
```

```
SecYr = FirstYr * juv.surv
```

```
ThirdYr = SecYr * age1.surv
```

```
FourthYr = ThirdYr * age2.surv
```

```
FifthYr = FourthYr * age3.surv
```

```
Sixth = FifthYr * age3.surv
```

```
Ad = init
```

```
##### matrix for population sizes
```

```
base.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)
```

```
impact.population.sim = matrix(data = 0, nrow = niter, ncol = nyears)
```

```
base.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)
```

```
impact.population.AD = matrix(data = 0, nrow = niter, ncol = nyears)
```

```
##### start looping through iterations
```

```
pb <- winProgressBar(title = "progress bar", min = 0, max = niter, width = 300)
```

```
for (i in 1:niter){
```

```

##### matrices to output N birds in each age class to
iterations = matrix(data=0, nrow = 7, ncol = nyears)
iterations[,1] = c(FirstYr, SecYr, ThirdYr, FourthYr, FifthYr, Sixth, Ad)

base.iterations = iterations
impact.iterations = iterations

##### estimate base productivity & use this to calculate a in Weibull function
prod.random = exp(rnorm(1,log(prod),prod.err)) * SexRatio ## multiply random estimate of
productivity by sex ratio to get chicks fledged/female

a = -(log(prod.random/maxF) / Ad^b)

## do population model for each iteration
for (j in 1:(nyears-1)) {

  juv.logit = expit(rnorm(1, logit(juv.surv), 1)) ## SD selected using trial & error comparison
to published estimates

  age1.logit = expit(rnorm(1, logit(age1.surv), 1)) ## SD selected using trial & error
comparison to published estimates

  age2.logit = expit(rnorm(1, logit(age2.surv), 1)) ## SD selected using trial & error
comparison to published estimates

  age3.logit = expit(rnorm(1, logit(age3.surv), 1)) ## SD selected using trial & error
comparison to published estimates

  ad.logit = expit(rnorm(1, logit(ad.surv), 0.5)) ## SD selected using trial & error
comparison to published estimates

##### calculate adult survival rates for impacted and unimpacted populations
prod.unimp = Weibull(maxF,a,base.iterations[7,j],b)

```

```

prod.imp = Weibull(maxF,a,impact.iterations[7,j],b)

# generate leslie matrix for unimpacted population

leslie.mat = matrix(c(rep(0,6), prod.unimp,
juv.logit,rep(0,7),age1.logit,rep(0,7),age2.logit,rep(0,7),
age3.logit,rep(0,7),age3.logit,rep(0,7),age3.logit,ad.logit), nrow=7,ncol=7, byrow=TRUE)

# do matrix multiplication to get population estimate in year n+1 for unimpacted
population

population = matrix(base.iterations[,j])

base.iterations[,j+1] = leslie.mat %*% population

# repeat for impacted population(s)

if (impact.param == "prod") leslie.mat.impact = matrix(c(rep(0,6), prod.imp-
(prod.random*impact.mag), juv.logit,rep(0,7),age1.logit,rep(0,7),age2.logit,rep(0,7),
age3.logit,rep(0,7), age3.logit,rep(0,7), age3.logit,ad.logit), nrow=7,ncol=7, byrow=TRUE)

if (impact.param == "surv") leslie.mat.impact = matrix(c(rep(0,6), prod.imp, juv.logit - ((1-
juv.logit)*impact.mag),rep(0,7),age1.logit - ((1-age1.logit)*impact.mag),rep(0,7),age2.logit -
((1-age2.logit)*impact.mag),rep(0,7), age3.logit - ((1-age3.logit)*impact.mag), rep(0,7),
age3.logit - ((1-age3.logit)*impact.mag), rep(0,7), age3.logit - ((1-age3.logit)*impact.mag),
ad.logit - ((1-ad.logit)*impact.mag)), nrow=7,ncol=7, byrow=TRUE)

# do matrix multiplication to get population estimate in year n+1 for unimpacted
population

population = matrix(impact.iterations[,j])

impact.iterations[,j+1] = leslie.mat.impact %*% population

}

## get number of birds in each year from each simulation

base.population.sim[i,] = colSums(base.iterations)

impact.population.sim[i,] = colSums(impact.iterations)

```

```

base.population.AD[i,] = base.iterations[7,]
impact.population.AD[i,] = impact.iterations[7,]

  setWinProgressBar(pb, i, title=paste( round(i/niter*100, 0), "Time left to make cup of
tea!!!"))

}

close(pb)

return(list(base = base.population.sim, impact = impact.population.sim, base.ad =
base.population.AD, impact.ad = impact.population.AD))

}

##### METRICS TO TEST
### Ratio of impacted to unimpacted population size
CPX = function(impact,base, x) {
  ratio = impact[,x]/base[,x]

  mean.cpx = mean(ratio)
  min.cpx = min(ratio)
  max.cpx = max(ratio)
  med.cpx = median(ratio)
  sd.cpx = sd(ratio)
  u95.cpx = quantile(ratio, 0.975)
  l95.cpx = quantile(ratio, 0.025)

  return(list(mean.cpx = mean.cpx, min.cpx = min.cpx, max.cpx = max.cpx, med.cpx =
med.cpx, sd.cpx = sd.cpx, boots = ratio, u95.cpx = u95.cpx, l95.cpx = l95.cpx))
}

```

```
##### CODE TO PRODUCE FIGURES AND TABLE VALUES
#####
##### this code should be completely self-contained and will reproduce figures
##### 5, 12 and 13 in JNCC Research Report Number 766 - Oliveira et al (2024)
#####
##### species: Cory's shearwater
##### model: stable stochastic model (density independent)
##### trend: stable/decreasing population

require(matrixStats) ## get matrixStats package, needed for colMedians function
require(scales)

##### Set working directory - R will look for input files & store outputs here

setwd("C:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/corys") #### Change
to appropriate directory on your computer

## Create folder to save files in

dir.create("Stochastic_Corys")

##### Bring in R functions necessary to run models

source("3 Stochastic Functions.txt") ##### this is a text file with R functions needed to run
models

##### it should be stored in the working directory set above
```

Now set values for model parameters

SexRatio = 0.5

age1.surv = 0.328 ### Demographic estimates refereed in the report - table 3

juv.surv = 0.935 ### Demographic estimates refereed in the report - table 3

ad.surv = 0.935 ### Demographic estimates refereed in the report - table 3

prod.vt = c(0.397,0.586,0.775) ### Demographic estimates refereed in the report - table 3

init.vt = c(1040,1040,560) ### Population size as number of breeders (2*minimum number of breeding pairs) refereed in the report - table 3

gf.names = c("Corys_non-Berlenga","Corys_non-Berlenga_BS-0.586","Corys_Berlenga")

prod.err.vt = c(0.016,0.016,0.028) ### Demographic estimates refereed in the report - table 3

nyears = 60 ### 3*Generation length extracted from BirdLife International 2024

niter = 1000

#####Run a routine to save the figures for all 3 different profiles

```
for(b in 1:length(prod.vt)){
```

```
  prod <- prod.vt[b]
```

```
  init <- init.vt[b]
```

```
  prod.err <- prod.err.vt[b]
```

```
  test.mod.stab <- Stoch.simul(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err, nyears, niter)
```

```
  ##### simulate 1%, 5% & 10% impact on survival
```

```
  surv.impact.stab.10 = population.impact(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err, nyears, niter, "surv", 0.01)
```

```
  surv.impact.stab.20 = population.impact(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err, nyears, niter, "surv", 0.05)
```

```
surv.impact.stab.30 = population.impact(init, SexRatio, age1.surv, juv.surv, ad.surv, prod,
prod.err, nyears, niter, "surv", 0.1)
```

```
#### plot simulations
```

```
jpeg(paste("Stochastic_Corys/",gf.names[b],".jpeg"),width = 15, height = 10, units = "cm",
res = 300)
```

```
par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))
```

```
plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*2), xlab = "Year", ylab = "Number of
Breeding Adults", main = "")
```

```
for (i in 1:nrow(test.mod.stab$adult)) { lines(seq(1,nyears,1), test.mod.stab$adult[i,], col =
alpha("green", 0.05))}
```

```
for (i in 1:nrow(surv.impact.stab.10$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.stab.10$impact.ad[i,], col = alpha("yellow", 0.05))}
```

```
for (i in 1:nrow(surv.impact.stab.20$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.stab.20$impact.ad[i,], col = alpha("orange", 0.05))}
```

```
for (i in 1:nrow(surv.impact.stab.30$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.stab.30$impact.ad[i,], col = alpha("red", 0.05))}
```

```
lines(seq(1,nyears,1), colMedians(test.mod.stab$adult), lty = 1, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.stab.10$impact.ad), lty = 2, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.stab.20$impact.ad), lty = 3, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.stab.30$impact.ad), lty = 4, lwd = 2)
```

```
legend("topleft", lwd = 2, bty = "n", col = c("green","yellow","orange","red"), legend = c("No
Impact", "1% Impact", "5% impact", "10% impact"),cex=0.5)
```

```
legend("topright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Median No Impact",
"Median 1% Impact", "Median 5% Impact", "Median 10% Impact"), cex = 0.5)
```

```
mtext(side = 1, "Year", outer = T)
```

```
mtext(side = 2, "Number of Breeding Adults", outer = T)
```

```

dev.off()
}

#####

##### this code should be completely self-contained and will reproduce figures
##### 6 and 7 in JNCC Research Report Number 766 - Oliveira et al (2024)
#####

##### species: Cory's shearwater
##### model: stable stochastic model (assuming compensatory density-dependent)
##### trend: increasing population

require(matrixStats) ## get matrixStats package, needed for colMedians function
require(scales)

##### Set working directory - R will look for input files & store outputs here

setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/corys")

## Create folder to put files in

dir.create("Density_dependent_Corys")

##### Bring in R functions necessary to run models

source("3 Stochastic Functions.txt") ##### this is a text file with R functions needed to run
models

##### it should be stored in the working directory set above

##### Now set values for model parameters for a stable population

```

```

#init = 10000

SexRatio = 0.5

age1.surv = 0.328    ### Demographic estimates refereed in the report - table 3

juv.surv = 0.935    ### Demographic estimates refereed in the report - table 3

ad.surv = 0.935          ### Demographic estimates refereed in the report - table 3

prod.vt = c(0.397,0.586,0.775) ### Demographic estimates refereed in the report - table 3

init.vt = c(1040,1040,560) ### Demographic estimates refereed in the report - table 3###
Population size as number of breeders (2*minimum number of breeding pairs) refereed in
the report - table 3

gf.names = c("Corys_non-Berlenga","Corys_non-Berlenga_BS-0.586","Corys_Berlenga")

prod.err.vt = c(0.016,0.016,0.028) ### Demographic estimates refereed in the report - table
3

nyears = 60 ### 3*Generation length extracted from BirdLife International 2024

niter = 1000

#####Run a routine to save the figures for all 3 different scenarios

for(c in 1:length(prod.vt)){

  prod <- prod.vt[c]

  init <- init.vt[c]

  prod.err <- prod.err.vt[c]

  ##### simulate 1%, 5% & 10% impact on survival

  surv.impact.stab.10 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv,
prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.01)

  surv.impact.stab.20 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv,
prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.05)

```

```
surv.impact.stab.30 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv,
prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.1)
```

```
#### plot simulations
```

```
jpeg(paste("Density_dependent_Corlys/",gf.names[c],"jpeg"),width = 15, height = 10, units
= "cm", res = 300)
```

```
par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))
```

```
plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*2), xlab = "Year", ylab = "Number of
Breeding Adults", main = "")
```

```
for (i in 1:nrow(surv.impact.stab.10$base)) { lines(seq(1,nyears,1),
surv.impact.stab.10$base.ad[i,], col = alpha("green", 0.05))}
```

```
for (i in 1:nrow(surv.impact.stab.10$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.stab.10$impact.ad[i,], col = alpha("yellow", 0.05))}
```

```
for (i in 1:nrow(surv.impact.stab.20$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.stab.20$impact.ad[i,], col = alpha("orange", 0.05))}
```

```
for (i in 1:nrow(surv.impact.stab.30$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.stab.30$impact.ad[i,], col = alpha("red", 0.05))}
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.stab.10$base.ad), lty = 1, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.stab.10$impact.ad), lty = 2, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.stab.20$impact.ad), lty = 3, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.stab.30$impact.ad), lty = 4, lwd = 2)
```

```
legend("topleft", lwd = 2, bty = "n", col = c("green","yellow","orange","red"), legend = c("No
Impact", "1% Impact", "5% impact", "10% impact"),cex=0.5)
```

```
legend("bottomright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Median No Impact",
"Median 1% Impact", "Median 5% Impact", "Median 10% Impact"), cex = 0.5)
```

```
mtext(side = 1, "Year", outer = T)
```

```
mtext(side = 2, "Number of Breeding Adults", outer = T)
```

```

dev.off()
}

#####

##### this code should be completely self-contained and will reproduce figure
##### 8 in JNCC Research Report Number 766 - Oliveira et al (2024)
#####

##### species: Common Guillemot
##### model: stable stochastic model (assuming compensatory density-dependent)
##### trend: increasing population

require(matrixStats) ## get matrixStats package, needed for colMedians function
require(scales)

##### Set working directory - R will look for input files & store outputs here
setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/guillemot")

##### Bring in R functions necessary to run models

source("Density dependent for K-species.R") ##### this is a text file with R functions needed
to run models

##### it should be stored in the working directory set above

##### Now set values for model parameters

init = 456264*2 ### Population size as number of breeders (2*minimum number of breeding
pairs) refereed in the report - table 3

SexRatio = 0.5

juv.surv = 0.75### Demographic estimates refereed in the report - table 3

```

```

age1.surv = 0.75      ### Demographic estimates refereed in the report - table 3
age2.surv = 0.75      ### Demographic estimates refereed in the report - table 3
age3.surv = 0.93      ### Demographic estimates refereed in the report - table 3
ad.surv = 0.93        ### Demographic estimates refereed in the report - table 3
prod = 0.82           ### Demographic estimates refereed in the report - table 3

prod.err = 0.05      ### Demographic estimates refereed in the report - table 3
nyears = 45          ### 3*Generation length extracted from BirdLife International 2024
niter = 1000

##### simulate 1%, 5% & 10% impact on survival

##### assuming default values of 1 for b & 0.95 for maxF -> For common guillemot maxF =
0.95

surv.impact.ddprod.01 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.01)

surv.impact.ddprod.05 = population.impactK ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.05)

surv.impact.ddprod.10 = population.impactK ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.1)

##### plot simulations

jpeg("Guillemot_Celtic_Seas_DDprod Stochastic_prod_082_skomer.jpeg",width = 15, height
= 10, units = "cm", res = 300)

par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))

plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*2.5), xlab = "Year", ylab = "", main = "")

for (i in 1:nrow(surv.impact.ddprod.01$base)) { lines(seq(1,nyears,1),
surv.impact.ddprod.01$base.ad[i,], col = alpha("red", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.01$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.01$impact.ad[i,], col = alpha("orange", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.05$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.05$impact.ad[i,], col = alpha("yellow", 0.05))}

```

```

for (i in 1:nrow(surv.impact.ddprod.10$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.10$impact.ad[i,], col = alpha("green", 0.05))}

lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.01$base.ad), lty = 1, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.01$impact.ad), lty = 2, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.05$impact.ad), lty = 3, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.10$impact.ad), lty = 4, lwd = 2)

legend("topleft", lwd = 2, bty = "n", col = c("red","orange","yellow","green"), legend =
c("Actual Impact", "-1% Impact", "-5% impact", "-10% impact"),cex=0.5)

legend("bottomright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Actual Impact", "-1%
Impact", "-5% impact", "-10% impact"), cex = 0.5)

mtext(side = 1, "Year", outer = T)
mtext(side = 2, "Number of Breeding Adults", outer = T)

dev.off()

#####
##### this code should be completely self-contained and will reproduce figure
##### 9 in JNCC Research Report Number 766 - Oliveira et al (2024)
#####
##### species: Common Guillemot
##### model: stable stochastic model (assuming compensatory density-dependent)
##### trend: increasing population

require(matrixStats) ## get matrixStats package, needed for colMedians function
require(scales)

##### Set working directory - R will look for input files & store outputs here

```

```
setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/guillemot")
```

```
##### Bring in R functions necessary to run models
```

```
source("Density dependent for K-species.R") ##### this is a text file with R functions needed to run models
```

```
##### Now set values for model parameters
```

```
init = 456264*2 #### Population size as number of breeders (2*minimum number of breeding pairs) refereed in the report - table 3
```

```
SexRatio = 0.5
```

```
juv.surv = 0.75#### Demographic estimates refereed in the report - table 3
```

```
age1.surv = 0.75    #### Demographic estimates refereed in the report - table 3
```

```
age2.surv = 0.75    #### Demographic estimates refereed in the report - table 3
```

```
age3.surv = 0.93    #### Demographic estimates refereed in the report - table 3
```

```
ad.surv = 0.93#### Demographic estimates refereed in the report - table 3
```

```
prod = 0.71    #### Demographic estimates refereed in the report - table 3
```

```
prod.err = 0.08    #### Demographic estimates refereed in the report - table 3
```

```
nyears = 45  #### 3*Generation length extracted from BirdLife International 2024
```

```
niter = 1000
```

```
##### simulate 1%, 5% & 10% impact on survival
```

```
## assume default values of 1 for b & 0.95 for maxF -> For common guillemot maxF = 0.95
```

```
surv.impact.ddprod.01 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.01)
```

```
surv.impact.ddprod.05 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.05)
```

```
surv.impact.ddprod.10 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.1)
```

```
##### plot simulations

jpeg("Guillemot_Celtic_Seas_DDprod Stochastic_prod_071_skomer.jpeg",width = 15, height
= 10, units = "cm", res = 300)

par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))

plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*2.5), xlab = "Year", ylab = "", main = "")

for (i in 1:nrow(surv.impact.ddprod.01$base)) { lines(seq(1,nyears,1),
surv.impact.ddprod.01$base.ad[i,], col = alpha("red", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.01$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.01$impact.ad[i,], col = alpha("orange", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.05$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.05$impact.ad[i,], col = alpha("yellow", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.10$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.10$impact.ad[i,], col = alpha("green", 0.05))}

lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.01$base.ad), lty = 1, lwd = 2)

lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.01$impact.ad), lty = 2, lwd = 2)

lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.05$impact.ad), lty = 3, lwd = 2)

lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.10$impact.ad), lty = 4, lwd = 2)

legend("topleft", lwd = 2, bty = "n", col = c("red","orange","yellow","green"), legend =
c("Actual Impact", "-1% Impact", "-5% impact", "-10% impact"),cex=0.5)

legend("bottomright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Actual Impact", "-1%
Impact", "-5% impact", "-10% impact"), cex = 0.5)

mtext(side = 1, "Year", outer = T)

mtext(side = 2, "Number of Breeding Adults", outer = T)

dev.off()

#####

##### this code should be completely self-contained and will reproduce figure
```

```

##### 10 in JNCC Research Report Number 766 - Oliveira et al (2024)
#####
##### species: Common Guillemot
##### model: stable stochastic model (assuming compensatory density-dependent)
##### trend: increasing population

require(matrixStats) ## get matrixStats package, needed for colMedians function
require(scales)

##### Set working directory - R will look for input files & store outputs here
setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/guillemot")

##### Bring in R functions necessary to run models

source("Density dependent for K-species.R") ##### this is a text file with R functions needed
to run models

##### Now set values for model parameters

init = 631905*2 ### Population size as number of breeders (2*minimum number of breeding
pairs) refereed in the report - table 3

SexRatio = 0.5

juv.surv = 0.560    ### Demographic estimates refereed in the report - table 3
age1.surv = 0.792  ### Demographic estimates refereed in the report - table 3
age2.surv = 0.917  ### Demographic estimates refereed in the report - table 3
age3.surv = 0.93   ### Demographic estimates refereed in the report - table 3
ad.surv = 0.93     ### Demographic estimates refereed in the report - table 3
prod = 0.73        ### Demographic estimates refereed in the report - table 3

```

```

prod.err = 0.11      ### Demographic estimates refereed in the report - table 3
nyears = 45  ### 3*Generation length extracted from BirdLife International 2024
niter = 1000

##### simulate 1%, 5% & 10% impact on survival

## assume default values of 1 for b & 0.95 for maxF -> For common guillemot maxF = 0.95

surv.impact.ddprod.01 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.01)

surv.impact.ddprod.05 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.05)

surv.impact.ddprod.10 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.1)

##### plot simulations

jpeg("Guillemot_North_Sea_DDprod Stochastic.jpeg",width = 15, height = 10, units = "cm",
res = 300)

par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))

plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*2.5), xlab = "Year", ylab = "", main = "")

for (i in 1:nrow(surv.impact.ddprod.01$base)) { lines(seq(1,nyears,1),
surv.impact.ddprod.01$base.ad[i,], col = alpha("red", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.01$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.01$impact.ad[i,], col = alpha("orange", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.05$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.05$impact.ad[i,], col = alpha("yellow", 0.05))}

for (i in 1:nrow(surv.impact.ddprod.10$impact)) { lines(seq(1,nyears,1),
surv.impact.ddprod.10$impact.ad[i,], col = alpha("green", 0.05))}

lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.01$base.ad), lty = 1, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.01$impact.ad), lty = 2, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.05$impact.ad), lty = 3, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.ddprod.10$impact.ad), lty = 4, lwd = 2)

```

```
legend("topleft", lwd = 2, bty = "n", col = c("red", "orange", "yellow", "green"), legend =
c("Actual Impact", "-1% Impact", "-5% impact", "-10% impact"), cex=0.5)
```

```
legend("bottomright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Actual Impact", "-1%
Impact", "-5% impact", "-10% impact"), cex = 0.5)
```

```
mtext(side = 1, "Year", outer = T)
```

```
mtext(side = 2, "Number of Breeding Adults", outer = T)
```

```
dev.off()
```

```
#####
```

```
##### this code should be completely self-contained and will reproduce figure
```

```
##### 11 in JNCC Research Report Number 766 - Oliveira et al (2024)
```

```
#####
```

```
##### species: Common Guillemot
```

```
##### model: stable stochastic model (density independent)
```

```
##### trend: stable/decreasing population
```

```
require(matrixStats) ## get matrixStats package, needed for colMedians function
```

```
require(scales)
```

```
##### Set working directory - R will look for input files & store outputs here
```

```
setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/guillemot")
```

```
##### Bring in R functions necessary to run models
```

```
source("Stochastic Function for K-species.R") ##### this is a text file with R functions needed
to run models
```

```
##### it should be stored in the working directory set above
```

Now set values for model parameters

init = 1000*2 ### Population size as number of breeders (2*minimum number of breeding pairs) refereed in the report - table 3

SexRatio = 0.5

juv.surv = 0.560 ### Demographic estimates refereed in the report - table 3

age1.surv = 0.792 ### Demographic estimates refereed in the report - table 3

age2.surv = 0.917 ### Demographic estimates refereed in the report - table 3

age3.surv = 0.939 ### Demographic estimates refereed in the report - table 3

ad.surv = 0.861 ### Demographic estimates refereed in the report - table 3

prod = 0.65 ### Demographic estimates refereed in the report - table 3

prod.err = 0.10 ### Demographic estimates refereed in the report - table 3

nyears = 45 ### 3*Generation length extracted from BirdLife International 2024

niter = 1000

simulate 1%, 5% & 10% impact on survival

assuming default values of 1 for b & 0.95 for maxF -> For common guillemot maxF = 0.95

surv.impact.K.01 = population.impactK(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.01)

surv.impact.K.05 = population.impactK(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.05)

surv.impact.K.10 = population.impactK(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.1)

plot simulations

jpeg("guillemot/Stochastic k selected_Jan_Mayen.jpeg", width = 15, height = 10, units = "cm", res = 300)

par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))

```
plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*1.5), xlab = "Year", ylab = "", main = "")
```

```
for (i in 1:nrow(surv.impact.K.01$base.ad)) { lines(seq(1,nyears,1),
surv.impact.K.01$base.ad[i,], col = alpha("red", 0.05))}
```

```
for (i in 1:nrow(surv.impact.K.01$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.01$impact.ad[i,], col = alpha("orange", 0.05))}
```

```
for (i in 1:nrow(surv.impact.K.05$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.05$impact.ad[i,], col = alpha("yellow", 0.05))}
```

```
for (i in 1:nrow(surv.impact.K.10$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.10$impact.ad[i,], col = alpha("green", 0.05))}
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.01$base.ad), lty = 1, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.01$impact.ad), lty = 2, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.05$impact.ad), lty = 3, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.10$impact.ad), lty = 4, lwd = 2)
```

```
legend("topleft", lwd = 2, bty = "n", col = c("red","orange","yellow","green"), legend =
c("Actual Impact", "-1% Impact", "-5% impact", "-10% impact"),cex=0.5)
```

```
legend("bottomright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Actual Impact", "-1%
Impact", "-5% impact", "-10% impact"), cex = 0.5)
```

```
mtext(side = 1, "Year", outer = T)
```

```
mtext(side = 2, "Number of Breeding Adults", outer = T)
```

```
dev.off()
```

```
#####
```

```
##### this code should be completely self-contained and will reproduce figure
```

```
##### 14 in JNCC Research Report Number 766 - Oliveira et al (2024)
```

```
#####
```

```
##### species: Common Guillemot
```

```
##### model: stable stochastic model (density independent)
```

```
##### trend: stable/decreasing population
```

```
require(matrixStats) ## get matrixStats package, needed for colMedians function  
require(scales)
```

```
##### Set working directory - R will look for input files & store outputs here  
setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/guillemot")
```

```
##### Bring in R functions necessary to run models
```

```
source("Stochastic Function for K-species.R") ##### this is a text file with R functions needed  
to run models
```

```
##### it should be stored in the working directory set above
```

```
##### Now set values for model parameters
```

```
init = 456264*2 #### Population size as number of breeders (2*minimum number of breeding  
pairs) refereed in the report - table 3
```

```
SexRatio = 0.5
```

```
juv.surv = 0.750    #### Demographic estimates refereed in the report - table 3
```

```
age1.surv = 0.75   #### Demographic estimates refereed in the report - table 3
```

```
age2.surv = 0.75   #### Demographic estimates refereed in the report - table 3
```

```
age3.surv = 0.93   #### Demographic estimates refereed in the report - table 3
```

```
ad.surv = 0.93 #### Demographic estimates refereed in the report - table 3
```

```
prod = 0.82  #### Demographic estimates refereed in the report - table 3
```

```
prod.err = 0.05    #### Demographic estimates refereed in the report - table 3
```

```
nyears = 45  #### 3*Generation length extracted from BirdLife International 2024
```

```
niter = 1000
```

```
##### simulate 1%, 5% & 10% impact on survival

##### assuming default values of 1 for b & 0.95 for maxF -> For common guillemot maxF =
0.95

surv.impact.K.01 = population.impactK(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.01)

surv.impact.K.05 = population.impactK(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.05)

surv.impact.K.10 = population.impactK(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.1)

##### plot simulations

jpeg("Stochastic k selected _Celtic _Seas _prod _082 _skomer.jpeg",width = 15, height = 10,
units = "cm", res = 300)

par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))

plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*3), xlab = "Year", ylab = "", main = "")

for (i in 1:nrow(surv.impact.K.01$base.ad)) { lines(seq(1,nyears,1),
surv.impact.K.01$base.ad[i,], col = alpha("red", 0.05))}

for (i in 1:nrow(surv.impact.K.01$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.01$impact.ad[i,], col = alpha("orange", 0.05))}

for (i in 1:nrow(surv.impact.K.05$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.05$impact.ad[i,], col = alpha("yellow", 0.05))}

for (i in 1:nrow(surv.impact.K.10$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.10$impact.ad[i,], col = alpha("green", 0.05))}

lines(seq(1,nyears,1), colMedians(surv.impact.K.01$base.ad), lty = 1, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.K.01$impact.ad), lty = 2, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.K.05$impact.ad), lty = 3, lwd = 2)
lines(seq(1,nyears,1), colMedians(surv.impact.K.10$impact.ad), lty = 4, lwd = 2)

legend("topleft", lwd = 2, bty = "n", col = c("red","orange","yellow","green"), legend =
c("Actual Impact", "-1% Impact", "-5% impact", "-10% impact"),cex=0.5)

legend("bottomright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Actual Impact", "-1%
Impact", "-5% impact", "-10% impact"), cex = 0.5)
```

```
mtext(side = 1, "Year", outer = T)
```

```
mtext(side = 2, "Number of Breeding Adults", outer = T)
```

```
dev.off()
```

```
#####
```

```
##### this code should be completely self-contained and will reproduce figure
```

```
##### 15 in JNCC Research Report Number 766 - Oliveira et al (2024)
```

```
#####
```

```
##### species: Common Guillemot
```

```
##### model: stable stochastic model (density independent)
```

```
##### trend: stable/decreasing population
```

```
require(matrixStats) ## get matrixStats package, needed for colMedians function
```

```
require(scales)
```

```
##### Set working directory - R will look for input files & store outputs here
```

```
setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/guillemot")
```

```
##### Bring in R functions necessary to run models
```

```
source("Stochastic Function for K-species.R") ##### this is a text file with R functions needed to run models
```

```
##### it should be stored in the working directory set above
```

```
##### Now set values for model parameters
```

init = 456264*2 #### Population size as number of breeders (2*minimum number of breeding pairs) refereed in the report - table 3

SexRatio = 0.5

juv.surv = 0.750 #### Demographic estimates refereed in the report - table 3

age1.surv = 0.750 #### Demographic estimates refereed in the report - table 3

age2.surv = 0.750 #### Demographic estimates refereed in the report - table 3

age3.surv = 0.93 #### Demographic estimates refereed in the report - table 3

ad.surv = 0.93#### Demographic estimates refereed in the report - table 3

prod = 0.71 #### Demographic estimates refereed in the report - table 3

prod.err = 0.08 #### Demographic estimates refereed in the report - table 3

nyears = 45 #### 3*Generation length extracted from BirdLife International 2024

niter = 1000

simulate 1%, 5% & 10% impact on survival

assuming default values of 1 for b & 0.95 for maxF -> For common guillemot maxF = 0.95

surv.impact.K.01 = population.impactK(init, SexRatio, juv.surv, age1.surv, age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.01)

surv.impact.K.05 = population.impactK(init, SexRatio, juv.surv, age1.surv, age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.05)

surv.impact.K.10 = population.impactK(init, SexRatio, juv.surv, age1.surv, age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.1)

plot simulations

jpeg("Stochastic k selected_Celtic_Seas_prod_071_skomer.jpeg",width = 15, height = 10, units = "cm", res = 300)

par(mfrow = c(1,1), mar = c(2,2,2,1), oma = c(1,1,0,0))

plot(0,0, type = "n", xlim = c(0,nyears), ylim = c(0,init*3), xlab = "Year", ylab = "", main = "")

```
for (i in 1:nrow(surv.impact.K.01$base.ad)) { lines(seq(1,nyears,1),
surv.impact.K.01$base.ad[i,], col = alpha("red", 0.05))}
```

```
for (i in 1:nrow(surv.impact.K.01$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.01$impact.ad[i,], col = alpha("orange", 0.05))}
```

```
for (i in 1:nrow(surv.impact.K.05$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.05$impact.ad[i,], col = alpha("yellow", 0.05))}
```

```
for (i in 1:nrow(surv.impact.K.10$impact.ad)) { lines(seq(1,nyears,1),
surv.impact.K.10$impact.ad[i,], col = alpha("green", 0.05))}
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.01$base.ad), lty = 1, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.01$impact.ad), lty = 2, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.05$impact.ad), lty = 3, lwd = 2)
```

```
lines(seq(1,nyears,1), colMedians(surv.impact.K.10$impact.ad), lty = 4, lwd = 2)
```

```
legend("topleft", lwd = 2, bty = "n", col = c("red","orange","yellow","green"), legend =
c("Actual Impact", "-1% Impact", "-5% impact", "-10% impact"),cex=0.5)
```

```
legend("bottomright", bty = "n", lwd = 2, lty = c(1,2,3,4), legend = c("Actual Impact", "-1%
Impact", "-5% impact", "-10% impact"), cex = 0.5)
```

```
mtext(side = 1, "Year", outer = T)
```

```
mtext(side = 2, "Number of Breeding Adults", outer = T)
```

```
dev.off()
```

```
#####
```

```
##### Outputs for the ratio of impacted to unimpacted Pop Size
```

```
##### this code should be completely self-contained and will reproduce
```

```
##### the values in table 4
```

```
##### in JNCC Research Report Number 766 - Oliveira et al (2024)
```

```
#####
```

```
##### species: Cory's shearwater
```

```
##### model: stable stochastic model (density independent)
```

```
##### trend: stable/decreasing population
```

```
##### profile: baseline profile 1
```

```
##### Set working Directory
```

```
setwd("C:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/corys")
```

```
require(scales)
```

```
source("3 Stochastic Functions.txt")##### this is a text file with R functions needed to run models
```

```
##### it should be stored in the working directory set above
```

```
##### setting starting values for demographic parameters
```

```
SexRatio = 0.5 # Sex ratio males:females
```

```
age1.surv = 0.328 ### Demographic estimates taken from Cory's Shearwater in Technical Report for OSPAR & Helcom updated in 25/02/2021
```

```
juv.surv = 0.935 ### Demographic estimates taken from Cory's Shearwater in Technical Report for OSPAR & Helcom updated in 25/02/2021
```

```
ad.surv = 0.935 ### Demographic estimates taken from Cory's Shearwater in Technical Report for OSPAR & Helcom updated in 25/02/2021
```

```
prod = 0.397 ### Demographic estimates refereed in the report - table 3
```

```
init = 1040### Population size as number of breeders (2*minimum number of breeding pairs) refereed in the report - table 3
```

```
prod.err = 0.016 ### Demographic estimates refereed in the report - table 3
```

```
nyears = 60 ### 3*Generation length extracted from BirdLife International 2024
```

```
niter = 1000
```

```
#impact.mag = seq(0,0.03,0.01) ## magnitude for impact scenarios
```

```
##### simulate 1%, 5% & 10% impact on survival
```

```
## assume default values of 1 for b & 0.95 for maxF -> For Cory's Shearwater maxF = 0.95
```

```
surv.impact.01 = population.impact(init, SexRatio, age1.surv, juv.surv, ad.surv, prod,
prod.err, nyears, niter, "surv", 0.01)
```

```
surv.impact.05 = population.impact(init, SexRatio, age1.surv, juv.surv, ad.surv, prod,
prod.err, nyears, niter, "surv", 0.05)
```

```
surv.impact.10 = population.impact(init, SexRatio, age1.surv, juv.surv, ad.surv, prod,
prod.err, nyears, niter, "surv", 0.1)
```

```
CPX(surv.impact.01$impact.ad,surv.impact.01$base.ad,nyears)[c(1,7,8)]
```

```
CPX(surv.impact.05$impact.ad,surv.impact.05$base.ad,nyears)[c(1,7,8)]
```

```
CPX(surv.impact.10$impact.ad,surv.impact.10$base.ad,nyears)[c(1,7,8)]
```

```
#####
```

```
##### Outputs for the ratio of impacted to unimpacted Pop Size
```

```
##### this code should be completely self-contained and will reproduce
```

```
##### the values in table 4
```

```
##### in JNCC Research Report Number 766 - Oliveira et al (2024)
```

```
#####
```

```
##### species: Cory's shearwater
```

```
##### model: stable stochastic model (assuming compensatory density-dependent)
```

```
##### trend: increasing population
```

```
##### profile: baseline profile 2 and 3
```

```
##### Set working Directory
```

```
setwd("C:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/corys")
```

```
require(scales)
```

```
source("3 Stochastic Functions.txt")##### this is a text file with R functions needed to run
models
```

```
##### it should be stored in the working directory set above
```

setting starting values for demographic parameters

SexRatio = 0.5 # Sex ratio males:females

age1.surv = 0.328 ### Demographic estimates refereed in the report - table 3

juv.surv = 0.93### Demographic estimates refereed in the report - table 3

ad.surv = 0.935 ### Demographic estimates refereed in the report - table 3

nyears = 60 ### 3*Generation length extracted from BirdLife International 2024

niter = 1000

simulate 1%, 5% & 10% impact on survival

assume default values of 1 for b & 0.95 for maxF -> For Cory's Shearwater maxF = 0.95

##Baseline Profile 2

prod = 0.586 ### Demographic estimates refereed in the report - table 3

prod.err = 0.016 ### Demographic estimates refereed in the report - table 3

init = 1040 ### Population size as number of breeders (2*minimum number of breeding pairs) refereed in the report - table 3

surv.impact.ddprod.1 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.01)

surv.impact.ddprod.5 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.05)

surv.impact.ddprod.10 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.1)

CPX(surv.impact.ddprod.1\$impact.ad,surv.impact.ddprod.1\$base.ad,nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.5\$impact.ad,surv.impact.ddprod.5\$base.ad,nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.10\$impact.ad,surv.impact.ddprod.10\$base.ad,nyears)[c(1,7,8)]

##Baseline Profile 3

prod = 0.775 #### Demographic estimates refereed in the report - table 3

prod.err = 0.028 #### Demographic estimates refereed in the report - table 3

init = 560 #### Population size as number of breeders (2*minimum number of breeding pairs)
refereed in the report - table 3

surv.impact.ddprod.1 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv,
prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.01)

surv.impact.ddprod.5 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv, ad.surv,
prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.05)

surv.impact.ddprod.10 = population.impact.ddprod(init, SexRatio, age1.surv, juv.surv,
ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", 0.1)

CPX(surv.impact.ddprod.1\$impact.ad,surv.impact.ddprod.1\$base.ad,nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.5\$impact.ad,surv.impact.ddprod.5\$base.ad,nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.10\$impact.ad,surv.impact.ddprod.10\$base.ad,nyears)[c(1,7,8)]

#####

Outputs for the ratio of impacted to unimpacted Pop Size

this code should be completely self-contained and will reproduce

the values in table 5

in JNCC Research Report Number 766 - Oliveira et al (2024)

#####

species: Common Guillemot

profile: baseline profile 1, 2, 3 & 4

Set working Directory

setwd("c:/wksp/2021_OSPAR_bycatch_pilot/2024_analysis_after_CH/guillemot")

do stochastic models with density dependent effects on productivity

source("Density dependent for K-species.R")#### this is a text file with R functions needed to run models

it should be stored in the working directory set above

#####

Baseline Profile 1

UK Celtic Seas prod = 0.82

#####

setting starting values for demographic parameters

init = 456264

SexRatio = 0.5

juv.surv = 0.75#### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age1.surv = 0.75 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age2.surv = 0.75 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age3.surv = 0.93 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

ad.surv = 0.93 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

prod = 0.82 ### productivity value is that presented for Common Guillemot in Mitchell et al 2004

prod.err = 0.05

nyears = 45

niter = 1000

```
surv.impact.ddprod.01 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.01)
```

```
surv.impact.ddprod.05 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.05)
```

```
surv.impact.ddprod.10 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv,
age2.surv,age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.1)
```

```
CPX(surv.impact.ddprod.01$base.ad,surv.impact.ddprod.01$impact.ad,nyears)[c(1,7,8)]
```

```
CPX(surv.impact.ddprod.05$base.ad,surv.impact.ddprod.05$impact.ad,nyears)[c(1,7,8)]
```

```
CPX(surv.impact.ddprod.10$base.ad,surv.impact.ddprod.10$impact.ad,nyears)[c(1,7,8)]
```

```
#####
```

```
##### Baseline Profile 2
```

```
##### UK Celtic Seas prod = 0.71
```

```
#####
```

```
##### setting starting values for demographic parameters
```

```
init = 456264
```

```
SexRatio = 0.5
```

```
juv.surv = 0.75#### Demographic estimates taken from Common Guillemot in Mitchell et al 2004
```

```
age1.surv = 0.75    ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004
```

```
age2.surv = 0.75    ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004
```

```
age3.surv = 0.93    ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004
```

```
ad.surv = 0.93      ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004
```

```
prod = 0.71         ### productivity value is that presented for Common Guillemot in Mitchell et al 2004
```

prod.err = 0.08

nyears = 45

niter = 1000

surv.impact.ddprod.01 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.01)

surv.impact.ddprod.05 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.05)

surv.impact.ddprod.10 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.1)

CPX(surv.impact.ddprod.01\$base.ad, surv.impact.ddprod.01\$impact.ad, nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.05\$base.ad, surv.impact.ddprod.05\$impact.ad, nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.10\$base.ad, surv.impact.ddprod.10\$impact.ad, nyears)[c(1,7,8)]

#####

Baseline Profile 3

UK GREATER NORTH SEA

#####

setting starting values for demographic parameters

init = 631905

SexRatio = 0.5

juv.surv = 0.560 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age1.surv = 0.792 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age2.surv = 0.917 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age3.surv = 0.93 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

ad.surv = 0.93 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

prod = 0.73 ### productivity value is that presented for Common Guillemot in Mitchell et al 2004

prod.err = 0.11

nyears = 45

niter = 1000

surv.impact.ddprod.01 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.01)

surv.impact.ddprod.05 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.05)

surv.impact.ddprod.10 = population.impactK.ddprod(init, SexRatio, juv.surv, age1.surv, age2.surv, age3.surv, ad.surv, prod, prod.err, b= 1, maxF = 0.95, nyears, niter, "surv", -0.1)

CPX(surv.impact.ddprod.01\$base.ad, surv.impact.ddprod.01\$impact.ad, nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.05\$base.ad, surv.impact.ddprod.05\$impact.ad, nyears)[c(1,7,8)]

CPX(surv.impact.ddprod.10\$base.ad, surv.impact.ddprod.10\$impact.ad, nyears)[c(1,7,8)]

#####

do stochastic models with density independent effects

#####

source("Stochastic Function for K-species.R")##### this is a text file with R functions needed to run models

it should be stored in the working directory set above

#####

Baseline Profile 4

JAN MAYEN - ARCTIC SEAS

#####

setting starting values for demographic parameters

init = 1000

SexRatio = 0.5

juv.surv = 0.560 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age1.surv = 0.792 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age2.surv = 0.917 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

age3.surv = 0.939 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

ad.surv = 0.861 ### Demographic estimates taken from Common Guillemot in Mitchell et al 2004

prod = 0.65 ### productivity value is that presented for Common Guillemot in Mitchell et al 2004

prod.err = 0.1

nyears = 45

niter = 1000

#####

Change in population Pop Size through time

#####

#####

Stochastic Model

```
surv.impact.K.01 = population.impactK(init, SexRatio, juv.surv, age1.surv,  
age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.01)
```

```
surv.impact.K.05 = population.impactK(init, SexRatio, juv.surv, age1.surv,  
age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.05)
```

```
surv.impact.K.10 = population.impactK(init, SexRatio, juv.surv, age1.surv,  
age2.surv,age3.surv, ad.surv, prod, prod.err, nyears, niter, "surv", -0.1)
```

```
CPX(surv.impact.K.01$base.ad,surv.impact.K.01$impact.ad,nyears)[c(1,7,8)]
```

```
CPX(surv.impact.K.05$base.ad,surv.impact.K.05$impact.ad,nyears)[c(1,7,8)]
```

```
CPX(surv.impact.K.10$base.ad,surv.impact.K.10$impact.ad,nyears)[c(1,7,8)]
```

```
### THE END
```