# Population effects of acute oil spill events on seabirds

# Simulations using population models linked with colony-specific non-breeding distribution

Kjell Einar Erikstad, Tone Kristin Reiertsen, Kate Layton-Matthews, Manuel Ballesteros, Tycho Anker-Nilssen, Malin Johansen, Svein-Håkon Lorentsen, Hanno Sandvik, Hallvard Strøm, Geir Helge Rødli Systad





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COVER PICTURE Colour-ringed common guillemots used for estimating the annual survival rate of adult breeding birds, as inputs for the matrix population models. © Tone Kristin Reiertsen

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# Abstract

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Seabirds are particularly vulnerable to acute population reductions because of their slow pace of life, explaining their limited capacity for population growth and ability to recover from population losses. Acute events like disease, extreme weather or oil spills can cause acute mass mortality events with large impacts on breeding population sizes.

In this report, we first propose and compare two modelling approaches to estimate the population impact of an acute population reduction. One approach is based on count data as input to a Brownian population model, the other is based on demographic data as input to a matrix-based population projection model. The comparison of the two approaches is limited to three species from four breeding populations. We then present a case study on the use of geolocation (GLS) data from four common guillemot populations, under two oil spill simulations and during two time periods of the non-breeding season. This case study illustrates how the season an oil spill occurs in can alter the overall impact on seabird populations. Finally, this report also discusses potential challenges and pitfalls regarding e.g., sample sizes of GLS loggers and how this can affect the representativeness of estimates of seabirds' marine space use.

The two modelling approaches differ in both the type of input data needed and the type of output data produced. While matrix-based models rely on more detailed demographic data of fecundity and age-specific survival, the Brownian modelling approach only requires population counts. Both models provide a measure of population recovery time or change in time to reach quasi-extinction. However, an advantage of matrix models is that impacts of acute event on age-specific demographic rates (e.g., immature or adult survival) can be simulated directly. However, demographic data are available for fewer colonies and species, and with fewer years of data, than count data. Both modelling approaches presented here have advantages and disadvantages, but since most time series of demographic data and age-specific survival are short at this stage, we recommend the use of the Brownian modelling approach.

The degree of overlap between the simulated oil spill events and seabird population distributions differed between oil spill locations (western versus eastern Barents Sea) and between seasons (autumn versus winter). In autumn, the eastern oil spill simulation affected more guillemot populations compared to the western oil spill simulation, with the biggest impact on Bjørnøya and Hjelmsøya colonies. There was no, or a negligible, overlap with any of the four population distributions and the simulated oil spill in the western Barents Sea. In winter, the western oil spill event hit more populations compared to the eastern oil spill event in the same season, with an overlap for Bjørnøya and Hjelmsøya guillemot distributions. In autumn, only the distribution of guillemots from Hornøya overlapped with the eastern oil spill.

A test of the representativeness of estimates of birds' space use given varying sample sizes of GLS locations showed that the size of core areas (50% kernel) varies greatly with the number of loggers, and small samples may be insufficient to capture the total variation in a population's space use. This applies across species and seasons. An average of 20 loggers needs to be included to achieve representative estimates of space use, capturing at least 95% of the total variance.

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# Sammendrag

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Sjøfugler er på grunn av sin langsomme livshistoriestrategi og lave bestandsvekst spesielt sårbare for akutte bestandsreduksjoner (massedød). Akutte hendelser som sykdommer, ekstremvær og oljesøl kan føre til akutt massedød og store konsekvenser for sårbare hekkebestander.

I denne rapporten foreslår og sammenligner vi to ulike modellerings-tilnærminger for å estimere populasjonseffekter av akutte bestandsreduksjoner. Den ene tilnærmingen er en brownsk populasjonsmodell og baserer seg på å benytte telle-data som inndata, mens den andre er en matrisebasert populasjonsmodell og baserer seg på demografiske data som inndata. Sammenligningen mellom disse modellene er begrenset til tre arter (fra fire hekkepopulasjoner totalt).

I tillegg presenterer vi en GLS-basert enkeltstudie fra fire lomvibestander (Bjørnøya, Hornøya, Hjelmsøya og Sklinna) og to simuleringer av oljesøl (i det vestlige og østlige Barentshavet) i to forskjellige tidsperioder utenom hekkesesongen (høst og vinter). Studien viser hvordan oljeutslipp på ulike årstider påvirker sjøfuglbestander med kjent opprinnelse i ulik grad.

Rapporten diskuterer også noen mulige utfordringer og fallgruver når det gjelder antallet GLSloggere som benyttes. Representativiteten av utbredelsesestimater av sjøfugl til havs avhenger av antallet loggere som brukes.

De to modellerings-tilnærmingene er forskjellige i 1) hvilken type inndata som kreves, og 2) hvilken informasjon og resultater de gir. Den matrisebaserte modellen er avhengig av mer detaljerte demografiske data, som hekkesuksess og aldersspesifikk overlevelse, sammenlignet med den brownske modelleringsmetoden, som er avhengig av antall hekkende par eller individer. Fra begge modellerings-tilnærmingene vil man få informasjon om effekten på populasjoners evne til å restituere eller endringer i forventet tid til utdøing (kvasi-ekstinksjon). Men fra matrisemodellene er det i tillegg mulig å angi populasjonseffekter av akutte reduksjoner i aldersspesifikk overlevelse eller reproduksjon. Imidlertid eksisterer det færre tidsserier med demografiske data, og disse tidsseriene er ofte kortere enn de tellingsbaserte dataene. Selv om begge modelltilnærmingene har fordeler og ulemper, anbefaler vi at den brownske tilnærmingen benyttes inntil lengden på tidsserier med demografiske data og aldersspesifikk overlevelse blir lange nok.

Overlappet mellom de simulerte oljeutslippshendelsene og de fire sjøfuglbestandenes høst- og vinterutbredelse varierte både med oljeutslippets plassering (vest eller øst for den norske økonomiske sonen i Barentshavet) og med hendelsens tidspunkt (høst eller vinter). På høsten traff den østlige simuleringen av oljesøl flere lomvibestander sammenlignet med den vestlige simuleringen av oljesøl og hadde størst innvirkning på fugl fra Bjørnøya og Hjelmsøya. Den vestlige simuleringen av oljesøl viste ingen eller kun mindre overlapp med de fire lomvibestandene i august. Om vinteren rammet det vestlige oljeutslippet flere bestander sammenlignet med det østlige oljeutslippet og overlappet med lomvier fra Bjørnøya og Hjelmsøya. Det østlige oljesølet fikk en overlapp med lomvi fra Hornøya, mens ingen av de tre andre lomvibestandene ble rammet av denne hendelsen.

Ved å teste hvor representative estimater på utbredelsen av sjøfugler er ut ifra ulike utvalgsstørrelser av GLS-loggere, viser resultatene at størrelsen på kjerneområdene (50 %-kjerne) varierer sterkt med antall loggere. Bruker man for få loggere, kan det gi utilstrekkelig representativitet, slik at den totale variasjonen i lomvienes utbredelse ikke fanges opp. Dette gjelder både for ulike arter og årstider. For å oppnå at utbredelsesestimatet skal representere mer enn 95 % av den totale variansen, er det behov for å inkludere data fra gjennomsnittlig 20 loggere. Kjell Einar Erikstad, Tone Kristin Reiertsen, Kate Layton-Matthews, Manuel Ballesteros. Norsk institutt for naturforskning, Framsenteret, Postboks 6606 Langnes, 9296 Tromsø. E-post: <u>kjell.e.erikstad@nina.no</u>

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# Foreword

The Norwegian Environment Agency has been requested by the Ministry of Climate and the Environment to provide new input on methods to estimate the vulnerability of seabirds during the non-breeding season in the open sea. In Norwegian areas, many populations are strongly declining and 60% of all species are on the Norwegian red list. There is therefore a need for further development of a framework, at the population level, to estimate the impact of acute mass mortality events in relation to petroleum operations on seabird populations. The motivation of this study has therefore been to compare two modelling approaches to identify colony-specific impacts of acute population reductions on seabirds. Seabirds in general have a "slow life history strategy" with low yearly reproduction and high adult survival, resulting in a slow recovery from acute mass mortality events. For stable or increasing populations, given a large reduction in numbers of birds, their time to recovery will therefore be long. For populations already in decline, any acute populations reductions will accelerate their downward trend towards critically low populations sizes.

In this report we compare two different population models using population viability analyses (PVA). PVAs are widely applied in conservation biology to estimate the effect of acute events on populations. Such analyses are also used internationally for assessing the threat status of species according to the International Union for Conservation of Nature (IUCN). Monitoring data from SEAPOP and SEATRACK were used in these analyses.

The project has been financed by Offshore Norge and SEAPOP, and we acknowledge Egil Dragsund and Valborg Øverland Birkenes from Offshore Norway and Cathrine Stephansen from Akvaplan-niva for discussions and follow-up during the process of producing this report.

December 2023, Kjell Einar Erikstad

# 1 Introduction

Human pressure on marine ecosystems has increased strongly over the last decades (Halpern et al. 2008), with concurrent global-scale declines in diversity and abundance of large vertebrate predators (Lewison et al. 2005). For seabirds, the threats are many, such as competition and bycatch from fisheries, contaminants, marine oil pollution and climate change, both indirect effects through bottom-up processes and direct effects through e.g. extreme weather (Camphuysen and Heubeck 2001, Frederiksen et al. 2004, Votier et al. 2008, Croxall et al. 2012, Erikstad et al. 2013a, 2013b, Dias et al. 2019). Specific incidents, for instance extreme weather or an oil spill, can result in acute mass mortality events. This can lead to dramatic declines in seabirds' population sizes, through reductions in juvenile, immature and adult survival (e.g., Votier et al. 2005, Frederiksen et al. 2008, Votier et al. 2008, Munilla et al. 2011, Quintana et al. 2022). Oil spills have been directly responsible for the deaths of hundreds of thousands of marine birds worldwide (González-Solís and Shaffer 2009) and are a widely known anthropogenic cause of seabird mass mortality events during the non-breeding season. The consequences can be dramatic, with even small oil spills killing thousands of birds (Barrett 1979, Anker-Nilssen et al. 1981, Castege et al. 2007, Munilla et al. 2011). Accurate tools to assess the risk of acute oil spill events for seabird population viability are therefore needed. Seabirds are vulnerable to exposure to marine oil pollution as they spend much of their lives at sea. Furthermore, their breeding colonies are concentrated in coastal and offshore habitats, which are also at risk from build-up of oil during acute spill events (Irons et al. 2000, Wiese and Robertson 2004). Diving species, such as auks, which spend most of their time on water, are considered an especially high-risk seabird group (Moe et al. 1999).

Seabirds are also particularly vulnerable to acute mortality events because of their slow life-history strategy (Sandvik et al. 2008). Consequently, seabird population growth is highly sensitive to changes in adult survival, compared to changes in other demographic rates such as recruitment of new breeders. Seabird populations only have the capacity to grow slowly and, hence, recover slowly from an acute population reduction (Erikstad et al. 1998, Weimerskirch et al. 2001). Therefore, acute population declines may greatly affect and change the status and vulnerability of seabird populations. The severity of impact on a given population, and the potential for that population to recover, depend on its long-term trend, i.e., whether it is declining, stable or increasing.

A study simulating acute population declines of 14 populations of 4 different seabird species breeding along the Norwegian coastline in Lofoten and the Barents Sea, showed that, after a simulated acute event that reduced population sizes, in all populations that were originally in decline prior to the event, the time to extinction was shortened (Reiertsen et al. 2019). Additionally, this study showed that for stable or increasing populations, a simulated acute reduction would have serious impacts on population size, increasing the populations' risk of extinction (Reiertsen et al. 2019). However, this study was based on direct reductions in population sizes of breeding birds, not accounting for possible differential mortality among age classes of birds, e.g. immatures versus adults. Previous studies of beached birds have shown that immature birds are more sensitive to the effects of oil spills than adults (Votier et al. 2008). Because seabirds have a long period of immaturity, spending several years at sea before returning to breeding colonies (Croxall 1991), little is known regarding their survival, space use or recruitment probabilities to natal breeding colonies. Immature birds (prior to recruitment at breeding colonies) may represent more than half of the total numbers of beached birds (e.g., Votier et al. 2008) and may also be especially sensitive to environmental change (Porter and Coulson 1987). Consequently, their response to an acute event can act to mitigate or accentuate the total effect on a population. Additionally, changes in the numbers of "floaters" (non-breeders present around the colony that can occupy empty breeding spaces) can mask increased mortality of adult breeding birds because count data, which reflect numbers of breeding adults, do not distinguish between 'floaters' and true breeders (Kokko et al. 2004). Matrix-based population models are based on estimates of age-dependent survival and fecundity and so provide the potential to assess population impacts at a finer scale, as they can account for differential mortality among age classes. Matrix-based population models can assess the impacts of oil spills on population sizes and extinction risk based on differential mortality among age classes. This approach therefore presents an important advance by allowing for estimation of the consequences of loss of immature birds prior to recruitment to breeding populations. However, such approaches rely on demographic data of survival and productivity, which are less widely monitored that population counts.

Methods to quantify the population-level effects of acute events such as oil spills on seabirds outside the breeding season have been largely constrained by a lack of knowledge of colony-specific origins of seabirds exposed to oil spills. Previous risk assessments of seabirds to oil pollution have mainly been restricted to ship survey data. Such data can indicate important areas for foraging birds and the density of seabirds in those areas and thereby potential 'high risk' areas for oil spills. However, since seabirds migrate over vast ocean areas, especially in the non-breeding season, identifying the origin of seabirds can be challenging, and thus colony-specific population impacts have rarely been dealt with (but see Stephansen et al. 2021). Through the SEATRACK program and, specifically, large-scale use of miniature geolocator loggers (Global Location Sensor loggers, GLS) we now have extensive knowledge of many seabirds' colony-specific non-breeding distribution and migratory patterns across the North Atlantic (Frederiksen et al. 2016, Fauchald et al. 2021). Such detailed knowledge of year-round distributions of birds from different colonies, together with long-term colony-specific annual demographic data and population counts and their use in population modelling approaches, is essential to understand how oil spills and other acute events can impact seabirds' population trajectories (Webster et al. 2002, Tranquilla et al. 2013).

In the present study we further developed the count-based approach developed by Reiertsen et al. (2019), applied a demographic matrix-based model and compared the two approaches. The method in Reiertsen et al. (2019) is a count-based Brownian model, which assesses seabird population changes in vulnerability after acute population reductions using a population viability analysis (Morris and Doak 2002). This study has two main aims. First, we compare the approach from Reiertsen et al. (2019) with the matrix-based approach that accounts for differential oil spillrelated mortality of immature and adult birds. The two population modelling approaches both have their respective advantages regarding the output from the analysis and data accessibility used as input to the models. The count-based population modelling approach only requires count data, which are often more extensively available and provide estimates of direct effects of acute events on breeding populations. Conversely, matrix-based population models require more detailed demographic data but, in turn, provide more detailed outputs by incorporating age-specific mortality rates and reproductive success. Both methods, however, provide the possibility to predict the probable future status of populations of conservation concern, based on the spatio-temporal distribution of birds outside the breeding season and where and when an acute oil-spill event may occur. Secondly, we link colony-specific population effects to their non-breeding spatial use (based on GLS data) and quantify seabird oil spill overlap in non-breeding areas under simulated oil spill scenarios. The spatio-temporal resolution of GLS data allows us to document differences in exposure probability to oil spills for different seasons and colony-specific populations. Here, we provide examples of how exposure probabilities may vary between seasons outside the breeding season and the importance of colony-specific data. Additionally, we reflect on the challenges and potential pitfalls that need to be considered.

This report will therefore present:

- 1) A comparison of the two population modelling approaches, to estimate the vulnerability of seabird populations, following simulated acute mass-mortality events. This comparison is limited to three species (four populations in total) where data were sufficient to gain precise estimates of demographic rates for parameterising matrix population models.
- 2) A description of how GLS data can be linked with the two approaches of population modelling, exemplified by a case study of two simulated oil spills in the Barents Sea, where overlap of simulated oil-spills with non-breeding distributions of colony-specific seabird populations was estimated. These analyses are a case study of common guillemots (*Uria aalge*) from four Norwegian colonies and two simulated acute surface oil spills in two areas of the Barents Sea.
- 3) A discussion of possible challenges and pitfalls when using spatial data based on GLS loggers, by analysing how different sample sizes of loggers affects the representativeness of estimates of seabirds' space use, based on an analysis of four seabird species.

# 2 Method

## 2.1 Selection of study populations

To compare the modelling approaches we selected four populations of three pelagic seabird species: Atlantic puffins *Fratercula arctica* breeding at Røst and Hornøya, and common guillemots and black-legged kittiwakes *Rissa tridactyla* breeding at Hornøya (**Figure 1, Table 1**). This selection was based on the following criteria:

- 1) to include both declining and stable or increasing populations,
- 2) to include populations where both count data and demographic data (adult survival and reproduction) were available.

Atlantic puffins (hereafter puffins) from Røst and Hornøya showed different population trends (**Table 2** and **3**), where the population of puffins breeding at Røst were declining (r = -0.04), while the Hornøya puffin population was increasing (r = 0.02). Black-legged kittiwakes (hereafter kittiwakes) from Hornøya showed a steep declining trend (r = -0.06) and common guillemots (hereafter guillemots) from Hornøya had an increasing trend (r = 0.08). Analyses were based on time series of annual count and demographic data from the SEAPOP monitoring programme. Time series were included until the year 2017, i.e., the year when an acute mass mortality event was modelled.



*Figure 1*. The three species used to compare the two population modelling approaches in this report: black-legged kittiwake, common guillemot and Atlantic puffin. Photos: Tone K. Reiertsen.

**Table 1**. Overview of the four populations included in this analysis.  $N_{2017}$  is the estimated population size of breeding birds in 2017 and 'Measure' describes how population size was quantified. The different species have different nesting strategies and estimates of population size therefore represent what entity has been used. For guillemots this is NAI = Number of Adult Individuals and for puffins and kittiwake this is AON = Apparent Occupied Nests. The population growth rate ( $\lambda$ ) and intrinsic rate of increase (r) are also reported.

Species	Colony	N <sub>2017</sub>	Measure	Status	λ (80% CI)	<i>r</i> (80% Cl)
Guillemot	Hornøya	18986	NAI	Increasing	1.07 (1.06, 1.08)	0.06 (0.05,0.07)
Puffin	Hornøya	11183	AON	Stable	1.00 (0.99, 1.00)	0.000 (-0.006, 0.008)
Puffin	Røst	316800	AON	Declining	0.96 (0.95, 0.97)	-0.038 (-0.05, -0.03)
Kittiwake	Hornøya	3870	AON	Declining	0.95 (0.94, 0.95)	-0.054 (-0.060, -0.047)

# 2.2 Estimating total population sizes

Since monitored plots where counts took place are just a sample of the whole breeding population, we converted these annual counts to total numbers of breeding pairs, for each colony and species. If we assume that birds counted in these monitoring plots are representative for the whole population, this can easily be done by estimating the yearly variance in growth rate by this formula log  $[N_t / N_{t-1}]$ , for each consecutive year of data. This requires a total count of the population, and then annual counts can be estimated forward, based on the initial total count and yearly variance. A total count of the population should be done at least every 10 years, which can then be used to project the total population size both forward and backward along the time series to get yearly total population estimates as input to the models. A total estimate of the breeding population is needed both for the Brownian and matrix model to project population sizes forward in time, based on an acute event scenario. It is also important to be aware that the target for any loss of birds during an acute event is the number of individuals and not the breeding population size, which is often counted in pairs.

Population counts represent the number of breeding pairs or breeding adults at a colony. Since the matrix models explicitly incorporate both immature and adult stages, we also needed an estimate of the total population size ( $N_{tot}$ ), including both immature and adult birds, for this modelling approach. One output of a matrix model is the stable age structure of a given population, i.e., the proportion of individuals in each pre-defined age group, assuming the population is at its equilibrium state. We therefore assumed each population was at this stable state and then calculated the proportion of immature birds versus adult birds in each population, thus obtaining a total *N* for 2017, based on which the populations were projected forward in time.

Species	Colony	N <sub>2017</sub> (adults only)	% immature	% adults	N <sub>2017</sub> (adults + immatures)
Guillemot	Hornøya	18986	0.56	0.44	42751
Puffin	Hornøya	11183	0.56	0.44	25585
Puffin	Røst	316800	0.36	0.64	493507
Kittiwake	Hornøya	3870	0.46	0.54	7573

**Table 2.** The estimates of total breeding population size  $N_{2017}$  for the four different populations.

# 2.3 Demographic data

Puffin and guillemot demographic rates were estimated using an Integrated Population Model (IPM) framework, which jointly estimates immature survival, adult survival and breeding success in a single modelling framework. Estimates for kittiwakes were modelled using a Bayesian mark–recapture model for survival, and a generalised linear model for breeding success. An estimate of immature survival was taken from Reiertsen et al. (2013). Estimates are shown in **Table 3**.

<b>Table 3.</b> Demographic data used to parameterise the matrix models (mean and standard deviation, SD)
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Species	Species Colony		ature vival	Ad surv	ult ⁄ival	Bree succ	ding :ess	Data source
		Mean	SD	Mean	SD	Mean	SD	
Puffin	Røst	0.83	0.78	0.90	0.51	0.30	3.42	IPM
Puffin	Hornøya	0.84	0.78	0.89	0.58	0.74	0.88	IPM
Guillemot	Hornøya	0.83	1.18	0.96	0.49	0.79	0.42	IPM
Kittiwake	Hornøya	0.75	0.66	0.87	0.56	0.69	1.10	Reiertsen et al. 2013

# 2.4 Scenarios of acute events

#### 2.4.1 Scenarios for the Brownian population modelling approach

Using the Brownian population model, we performed scenarios for the four populations (**Table 3**). The population model was initially run without an acute event (i.e., the baseline model). We then simulated an acute event for each study population. We implemented a (1) 10%, (2) 25% and (3) 50% reduction in population size, occurring in 2017 (see Appendix, **Table S1**). This resulted in 3 scenarios per study population, in addition to the baseline scenario. We simulated 10,000 runs of the population model, projecting each simulated population 100 years into the future. The baseline model was used to compare to the acute-scenario models. For the increasing populations (puffins as well as guillemots from Hornøya), we estimated the number of years before the population returned to the population size immediately prior to the acute event (i.e., recovery time), given each of the three scenarios. For declining populations (puffins from Røst and kittiwakes from Hornøya), we estimated the change in the number of years until they reached quasi-extinction, i.e., until the population halved in size after a 10% and 25% reduction scenario.

#### 2.4.2 Scenarios for the demographic modelling approach

Using the matrix model, we performed scenarios for the same populations as in 2.4.1. Table 3 shows the estimated demographic rates used to parameterise the models for each study population. We first ran a baseline model and then simulated an acute event for each study population. We implemented a (1) 10%, (2) 25% and (3) 50% reduction in survival in the year 2017 (affecting the population size in 2018, since survival rate is estimated from the breeding season in year tto the breeding season in year t+1), which affected either (1) immature survival ( $\Phi_{im}$ ), (2) adult survival ( $\Phi_{ad}$ ) or (3) both  $\Phi_{im}$  and  $\Phi_{ad}$  (i.e., affecting the rates of all age classes). This resulted in nine scenarios per study population. As in 2.4.1, we simulated 10,000 runs of the population model, projecting each population 100 years into the future. For each simulation, we sampled demographic rates (immature survival, adult survival and breeding success), following their estimated means, variances and covariances (see Table 3). Differences among iterations arose from estimated variability in demographic rates and thereby different realizations of each population run. First, we ran a baseline model to calculate the long run population-growth rate ( $\lambda$ ) and the corresponding intrinsic rate of population increase (r). For the increasing populations (puffins as well as guillemots from Hornøya), we estimated the number of years before the population returned to the population size immediately prior to the acute event (i.e., recovery time), given each of the nine scenarios. For declining populations (puffins from Røst and kittiwakes from Hornøya), we estimated the change in the number of years until guasi-extinction, i.e., until the population halved in size after a 10% and 25% reduction scenario.

### 2.5 Methodological description of the two modelling approaches

#### 2.5.1 Predicting the impact of acute events using a Brownian population model

In cases where only count-based annual population-size data are available, a Brownian population model can be used to predict the impact of acute events. This is a density-independent model and enables the estimates of time to both quasi-extinction and recovery. Most seabird populations are below their populations' carrying capacity, and density dependent models are therefore not necessary (Sandvik et al. 2014). The main input to this model is population size and the yearly variation in population growth rate *r* before the acute event.

$$lnN_{t+1} = lnN_t + \bar{r} - \frac{1}{2}\sigma_d^2 N_t^{-1} + \sum \beta_i X_{i.t} + \varepsilon_t$$

 $N_t$  is the population size in year t,  $\bar{r}$  is the longterm population growth rate,  $\sigma_d^2$  is the demographic variance,  $\beta_i$  is the slope of the *i*<sup>th</sup> environmental covariate  $X_{i,t}$ ,  $\varepsilon_t$  is environmental noise (i.e., an independent variable with zero mean and environmental variance  $\sigma_e^2$ . The parameters  $\beta_i$ ,  $\bar{r}$  and  $\sigma_e^2$  are estimated from the population time series using maximum likelihood, optimizing the log-likelihood

$$\ln L = -\frac{1}{2} \sum_{k=2}^{n} \{ [\ln N_k - E(\ln N_k)]^2 \sigma^{-2} + \ln(2\pi\sigma^2) \}$$

over *n* elements of time series (Sæther et al. 2009), where  $E(\ln N_k)$  is the predicted log-population size based on the observed population size  $N_{k-1}$ , and  $\sigma^2 = \sigma_e^2 + \sigma_d^2 N_t$ . In the absence of estimates of lifetime reproductive success, demographic variance is assumed to be 0.1 in all colonies, which is a realistic value for long-lived birds (Lande et al. 2003).

#### 2.5.2 Predicting the impact of acute events using matrix models

The second approach of predicting impact of acute mass mortality events on future population trajectories was based on a matrix population model. This is a demographic approach to understand population-level changes based on available information of vital rates rates such as birth and death rates (Leslie 1945). Matrix population models represent convenient tools to summarise survival and reproductive rates (collectively 'demographic rates') of a population, to calculate an asymptotic finite population growth rate ( $\lambda$ ), generation time and sensitivities of  $\lambda$  to the underlying demographic rates (Caswell 1978, 2001). This information can be used for determining the status of a threatened species and the potential effect of scenarios on population trajectories. The use of matrix population models as a conservation tool has become widespread in ecology (Mills et al. 1999, Caswell and Kaye 2001, Fujiwara and Caswell 2001).

We constructed a matrix population projection model, which projects a population's size forward in time based on a matrix containing estimated demographic rates, constructed according to the life history of the species. We can then perform population viability analyses using matrix-based models, where we estimate the long-term population growth rate ( $\lambda$ , corresponding to  $\bar{r}$  in the previously used Brownian model), time to extinction and extinction probabilities.

Both the matrix model structure and the simulation of demographic rates can be of varying complexity. Here, we use a model with age-class structure (immature ages and an adult age class) and density-independence. At each time step in the simulation, we sample demographic rates from their estimated means and variances and assume a given temporal covariance between demographic rates. Covariation between demographic rates is important to account for, as demographic rates do not usually vary in time entirely independently (for example higher adult survival in year *t* would also likely lead to higher immature survival in year *t*). This covariation can have a big impact on population-growth trajectories. The structure of the matrix model, shown below, was used to calculate the effect of an acute mortality event on seabird population-size trajectories.



This is an example of the matrix model for a species with an age at maturity of 6 years (letters on the top represent age classes: *im* = immatures of age 1–5 years, *ad* = adults of age 6 years or more). *F* is the breeding success (i.e., proportion of chicks which fledge per breeding pair),  $\Phi_{im}$  is annual immature survival, and  $\Phi_{ad}$  is annual adult survival. This matrix then projects the population vector (**N**<sub>*t*-1</sub>) from one time step to the next (**N**<sub>*t*</sub>). In doing so, we can then estimate the long-term population growth rate and other useful values such as sensitivities of the population growth rate to underlying demographic rates (i.e., retrospective analyses, Caswell 2000).

# 2.6 Quantifying damage: MIRA's environmental risk assessment

In order to quantify the extent of the damage of an acute mass mortality event, we have used the damage keys from MIRA (*metode for miljørettet risikoanalyse*). Damage keys define how a given population loss is considered in terms of environmental damage (expected recovery time given in intervals of numbers of years), categorised in damage categories denoted:

- Minor (< 1 year recovery time),
- Moderate (1–3 years recovery time),
- Considerable (3–10 years recovery time) or
- Serious (>10 years recovery time)

According to the MIRA classification, recovery time is given as the median and 80% confidence intervals. However, according to Morris and Doak (2002), the recommendation for such analyses is to base classifications on the worst-case scenario. In this report we therefore use the worst-case scenario classifications: where recovery is possible (i.e., stable or increasing populations), the higher 80% confidence interval was reported, while for populations declining prior to the acute event, the lower 80% confidence interval was reported.

Damage classifications have only been developed for populations able to recover, i.e., to reach the original population level prior to the acute event. In practice, this means, however, that this approach is not relevant for most seabird populations, because they are decreasing. An approach to assess damage of population that are not able to recover (population in decline prior to the acute event) has been proposed by Reiertsen et al. (2019). An assessment of the use of damage classifications should also be applied to this approach and for populations in decline which lack the potential to recover.

# 2.7 Spatially non-breeding distribution data

#### 2.7.1 Geolocators and data processing

Geolocation data (GLS) from Hornøya were used to 1) identify colony-specific non-breeding distributions of seabirds in autumn and winter, 2) calculate the overlap between seabird distributions and simulated oil spills in the Barents Sea, and to 3) analyse the breakpoint where the sample size of number of loggers is sufficient to provided representative estimates of non-breeding distributions.

For the breakpoint analysis, GLS-logger data of three species were used: kittiwakes and puffins were tracked using MK4083 and common guillemots using MK3006 geolocators provided by the Lotek British Antarctic Survey (BAS, Cambridge, UK). For the case study of overlap between simulated oil-spill and seabird non-breeding distribution, only GLS data of common guillemots (from four different colonies) were used. Loggers were attached by cable ties to colour rings on breeding birds during the breeding season. These loggers measure light levels every minute and store the maximum value within a 10-minute interval.

Light data were processed using the BAS Trak software (Fox 2010) and the Geo Light package (Lisovski and Hahn 2012). Data were decompressed and corrected for clock drift that possibly occurred during deployment. We carefully inspected daily light curves and estimated the timing of dawn and dusk. Latitude (derived from day and night length) and longitude (derived from the timing of local midday and midnight) were calculated using sun elevation angles ranging from  $-2^{\circ}$  to  $-3,35^{\circ}$ . The geolocators provide two locations per day with an average error of ±186 km (Phillips et al. 2004). These two daily positions were averaged and smoothed twice using a two-point running mean. We filtered out locations around autumnal and vernal equinoxes (approximately 2–3 weeks on either side) and discarded obvious unrealistic locations (short term locations, one or two days, with deviation >750 km from the core distribution of an individual's location or track).

To get an average core distribution area per population, kernel densities were used. Kernel density maps were produced in R studio 2023.09.01 (R Core Team 2023). Kernel utilization distributions (KUD) were estimated with the kernel.area function in the adehabitatHR package version 0.4.21 (Calenge 2009) using least square cross validation (LSCV) smoothing. 50% KUD estimates were used to represent the core areas of the different species' foraging distributions during the non-breeding season.

#### 2.7.2 Estimation of the sample size needed for defining seabird core distributions

In general, GLS loggers have a low accuracy (Phillips et al. 2004). A common procedure to overcome this problem is to estimate core areas based on all GLS positions (50% kernel distribution) (Lascelles et al. 2016). Another problem that needs to be considered is how large sample sizes (number of birds) are needed in such analyses of core areas. Only a very small fraction of a population is tracked yearly with GLS loggers. It is therefore important to examine the validity and representativeness of such data before scaling the data for the use of examining acute population level effects (Lindberg and Walker 2007, Lascelles et al. 2016).

To assess whether data were representative and allow inferences to be drawn about the spatial patterns of a population, we examined how seabirds' core distribution (50% kernel areas) changed with increasing sample size. To do so, we randomly selected individual GLS tracks iteratively for two time periods (autumn: August–September, and winter: December–February) and calculated the 50% KUD (in km<sup>2</sup>) from four different species. The sample size was increased incrementally from one logger until the maximum was reached (i.e., total number of individuals). KUDs were generated 50 times at increasing random sample sizes. Then, average areas of the 50% KUD and standard deviation were plotted for each combination of species and period, and a nonlinear least-squares regression model was fitted to the data [Michaelis-Menten model: nls(y ~ a \* x / (b + x)); Lascelles et al. 2016]. To estimate the sample size needed for a data group to be considered, we used regression models with breakpoint estimation in the package segmented (Muggeo 2003), which is an estimation and inference of regression models with piecewise linear relationships, also known as segmented regression models.

#### 2.7.3 Estimation of overlap between seabird distributions and oil-spill events

From a previous collaborative study between NINA and SINTEF, simulations of oil drift and overlap with the non-breeding distribution of four different common guillemot populations, using the Barents Sea to varying extents, enabled us to illustrate seasonal and population-specific overlaps as a case study. This highlights how tracking technology (GLS loggers) and simulated oil drift models can be used to assess overlap with marine bird space use, at different times during the non-breeding season, and the associated potential population impacts.

A stochastic oil spill model (OSCAR) was combined with the non-breeding spatial distribution of Common Guillemots as an example to provide a measure of impact of a simulated acute oil spill

event on birds from different breeding colonies during their non-breeding season. For details about the oil spill model simulation set-up see Lundmark-Daae (2014) and **Table 4**.

Parameter	West Barents Sea	East Barents Sea
Latitude	71º18.66'N	71°24.4'N
Longitude	22°15.15'E	30°6.8'E
Release depth	Surface Release	Surface Release
Release rate	4000 m <sup>3</sup>	4000m <sup>3</sup>
Release duration	7 days	7 days
Total release	28000m <sup>3</sup>	28000m <sup>3</sup>
Duration of each simu- lation	15 days	15 days
Number of simulations per year	25	25
Period of oil spill	February and August	February and August

**Table 4.** Information from the two different oil spills. For more information about these oil spills see also Lundmark-Daae (2014).

This case study was developed for two locations in the Barents Sea (**Table 4**). For each location, two scenarios were set up: one for an oil spill release in February and the other in August. One of the selected locations was in an area where oil production was planned to commence in 2015 (western Finnmark), and the other selected location where an exploration well was planned (eastern Finnmark). The two locations are shown on the maps in **Figure 10 A–D**. The reference oil used is from the Barents region, and the release rate and duration are chosen to reflect a blowout situation in the selected months. The input parameters are summarised in **Table 4**. The current and wind data sets used cover the period 2012–2013.

The logger data (GLS) used to estimate common guillemots' core non-breeding distribution are from the year 2011–2014. During this period, we have sufficient sample sizes of GLS data (see **Table 10**) to reflect the core autumn and winter areas of the different colonies. Winter was defined as the months December–February, and autumn as August–September. Overlap between oil spills and core autumn and winter distributions of the four guillemot populations was estimated using a home range approach to quantify static overlap. Home ranges of the bird distribution and oil distribution are overlaid and quantified in percent (following the notation from Kernohan et al. 2001): HR<sub>i,j</sub> =  $A_{i,j} / A_i$ , where  $A_i$  is the area of animal *i*'s core area, and  $A_{i,j}$  is the area of overlap between the *j*<sup>th</sup> oil area and the *i*<sup>th</sup> bird core area.

# 3 Results

# 3.1 Results of the Brownian population modelling

For the stable population (puffins from Hornøya), all three population reductions lead to serious damage (according to MIRA classification), since the higher 80% CI provides recovery times of > 10 years. For the increasing population (guillemots from Hornøya), 10% and 25% population reductions lead to considerable damage and 50% population reduction leads to serious damage. The number of years until population sizes return to the level prior to the acute population reduction are given in **Table 5**, and population trajectories are visualised in **Figure 2**. For both declining populations, all acute population reduction scenarios led to serious damage, since neither ever reach recovery. Furthermore, the projected time to quasi-extinction (halved population size) was considerable reduced (**Table 6, Figure 3**).

**Table 5.** Results of the Brownian modelling approach for stable or increasing populations. For each acute event scenario 10%, 25% and 50% reduction), the table shows the time to recovery (i.e., the number of years until the population returns to the population size prior to the acute population reduction). Time to recovery is given as median estimate (lower and upper 80% confidence interval). The degree of damage is given in parentheses according to MIRA classification and is based on the upper 80% confidence interval (based on recommendations by Morris and Doak 2002 for increasing populations).

					Time to recovery	
Species	Colony	Pop. size	Pop. status	10% reduction	25% reduction	50% reduction
Puffin	Hornøya	11 183	Stable ( <i>r</i> = 0.02)	3 (1, 95) (Serious)	8 (2, ∞) (Serious)	23 (6, ∞) (Serious)
Guillemot	Hornøya	18 986	Increasing ( <i>r</i> = 0,08)	2 (1, 4) (Considerable)	4 (2, 8) (Considerable)	9 (6, 15) (Serious)

**Table 6.** Results of the Brownian modelling approach for declining populations. For each acute event scenario (10% and 25% reduction), the table shows the decrease in time to quasi-extinction (i.e., the number of years until the estimated population size is halved compared to 2017). Decrease in time to quasi-extinction is given as median estimate (lower and upper 80% confidence interval). The degree of damage is given in parentheses according to MIRA classification and is based on the lower 80% confidence interval. To calculate the change in time, we compared the time to quasi-extinction for each scenario with the time to quasi-extinction in the baseline population projection (i.e., no acute event).

				Time to quasi-extinction			
Species	Colony	Pop size	Pop status	Baseline	10% reduction	25% reduction	
Puffin	Røst	316 800	Declining (r= -0,04)	19 (12, 29)	16 (8, 48) (Serious)	14 (6, 40) (Serious)	
Kittiwake	Hornøya	3 870	Declining (r= -0,06)	15 (10, 24)	12 (6, 30) (Serious)	10 (5, 25) (Serious)	

#### Atlantic puffin, Hornøya



**Figure 2.** Population projections of a stable and an increasing population, the puffin (top) and common guillemot (bottom) populations at Hornøya, using a Brownian population model. In addition to the baseline model (without acute event), three different scenarios (10%, 25% and 50% reduction in population size in 2017) have been modelled. The black lines for the projections represent the median, upper and lower 80% confidence intervals and quartiles.

#### Black-legged kittiwake, Hornøya



**Figure 3.** Population trajectories of two declining populations, the kittiwake population from Hornøya and the puffin population from Røst, using a Brownian population model. In addition to the baseline model (without acute event) three different acute event scenarios have been modelled, 10%, 25% and 50% reduction in population size in 2017 respectively. The black lines for the projections represent the median, upper and lower 80% confidence intervals and quartiles. The dotted horizontal line is the quasi-extinction threshold (half population size of 2017).

# 3.2 Results of the demographic modelling approach

For stable populations, a reduction in survival rates of immatures and/or adults lead to serious damage when the worst-case scenario (upper 80% guantile of the simulations) was considered. However, time to recovery was lower for reductions in immature survival than reductions in adult survival. A 10% reduction in immature survival gave a time to recovery of 37 years compared to 48 years for a 10% reduction of adult survival and 48 years for a 10% reduction in both. Table 7 and **Figure 4** summarise and illustrate time to recovery for the stable population, puffins from Hornøya. The damage assessment of guillemots from Hornøya used as an example of an increasing population in this report, varied from moderate to serious. A 10% reduction in immature or adult survival showed a moderate damage, with 2 and 3 years of recovery time, respectively, while a reduction in survival of both age classes gave a considerable damage with a time to recovery of 4 years. Table 7 and Figure 5 summarise and illustrate time to recovery for the increasing population, guillemots from Hornøya. For both populations used as examples of declining populations, puffins from Røst and kittiwakes from Hornøya, neither ever recoverred to the population size prior to the reduction in immature and/or adult survival. There are no damage keys to assess time to extinction, and all scenarios are therefore considered as serious damage. However, the decrease in time to quasi-extinction is higher for reductions in adult survival than for reductions in immature survival, when compared to the baseline model. A summary of the effects of each acute event scenario for the two populations in decline is given in Table 8 and visualised in Figures 6 and 7.

**Table 7.** Results of the demographic modelling approach for stable or increasing populations. For each acute event scenario 10%, 25% and 50% reduction), the table shows the time to recovery (i.e., the number of years until the population returns to the population size prior to the acute population reduction). Time to recovery is given as median estimate (lower and upper 80% confidence interval). The degree of damage is given in parentheses according to MIRA classification and is based on the upper 80% confidence interval (based on recommendations by Morris and Doak 2002 for increasing populations).

				Time to recovery	
Species	Colony	Rates affected	10% reduction	25% reduction	50% reduction
Puffin	Hornøya	Immature survival	3 (0, 37) (serious)	7 (1, 47) (serious)	11 (3, 49) (serious)
Puffin	Hornøya	Adult survival	4 (0, 43) (serious)	13 (3, 57) (serious)	22 (8, 73) (serious)
Puffin	Hornøya	Both	8 (2, 48) (serious)	29 (11, 85) (serious)	68 (34, ∞) (Never)
Guillemot	Hornøya	Immature survival	1 (1, 2) (moderate)	2 (1, 3) (moderate)	2 (2, 3) (moderate)
Guillemot	Hornøya	Adult survival	1 (1, 3) (moderate)	3 (2, 5) (considerable)	5 (3, 9) (considerable)
Guillemot	Hornøya	Both	2 (1, 4) (considerable)	5 (4, 7) (considerable)	12 (9, 14) (serious)

**Table 8.** Results of the demographic modelling approach for declining populations. For each acute event scenario (10% and 25% reduction), the table shows the decrease in time to quasi-extinction (i.e., the number of years until the estimated population size is halved compared to 2017). Decrease in time to quasi-extinction is given as median estimate (lower and upper 80% confidence interval). The degree of damage is given in parentheses according to MIRA classification and is based on the lower 80 % confidence interval. To calculate the change in time, we compared the time to quasi-extinction for each scenario with the time to quasi-extinction in the baseline population projection (i.e., no acute event).

			Ti	me to quasi-extincti	on
Species	Colony	Rates affected	10% reduction	25% reduction	50% reduction
Puffin	Røst	Immature survival		18 (12, 27) (serious)	16 (10, 25) (serious)
Puffin	Røst	Adult survival	19 (12, 29)	16 (10, 26) (serious)	13 (7, 22) (serious)
Puffin	Røst	Both		15 (9, 23) (serious)	10 (6, 18) (serious)
Kittiwake	Hornøya	Immature survival		15 (10, 24) (serious)	15 (9, 23) (serious)
Kittiwake	Hornøya	Adult survival	15 (10, 24)	14 (9, 22) (serious)	11 (6, 18) (serious)
Kittiwake	Hornøya	Both		14 (8, 21) (serious)	9 (5, 16) (serious)



**Figure 4**. Population projections (apparently occupied nests) of Atlantic puffins from Hornøya, using a demographic modelling approach, and based on different acute event scenarios (1–9). Red lines correspond to the period 2017–2018 when the acute event occurred. The black lines for the projections represent the median (solid) and upper and lower 80% confidence intervals (hatched).



**Figure 5.** Population projections (apparently occupied nests) of common guillemots from Hornøya, using a demographic modelling approach, and based on different acute event scenarios (1–9). Red lines correspond to the period 2017–2018 when the acute event occurred. The black lines for the projections represent the median (solid) and upper and lower 80% confidence intervals (hatched).



**Figure 6**. Population projections (apparently occupied nests) of Atlantic puffins from Røst, using a demographic modelling approach, and based on different acute event scenarios (1–6). Red lines correspond to the period 2017–2018 when the acute event occurred. The black lines for the projections represent the median (solid) and upper and lower 80% confidence intervals (hatched).



**Figure 7**. Population projections (apparently occupied nests) of black-legged kittiwakes from Hornøya, using a demographic modelling approach, and based on different acute event scenarios (1–6). Red lines correspond to the period 2017–2018 when the acute event occurred. The black lines for the projections represent the median (solid) and upper and lower 80% confidence intervals (hatched).



# 3.3 Comparison of the two modelling approaches

The comparison of the two approaches is performed with the 25% simulated acute population reduction, and the differences between the two models are presented in Table 9. In the case of the matrix-based model approach, the acute event was assumed to affect both immature and adult individuals equally (i.e., all age classes in the population). The general finding is that matrix population models give a more pessimistic results than the Brownian population models, when considering the median time to extinction or time to recovery. Considering the worst-case scenarios, both approaches for the two populations in decline (puffins from Røst and kittiwakes from Hornøya) estimate the same time to extinction (6 and 5 years for puffins and kittiwakes, respectively). For the stable population (puffin from Hornøya), the times to recovery differ considerably between the two approaches when using the worst-case scenario to assess the differences. The recovery time is 85 years for the matrix approach and much less pessimistic, compared with never for the Brownian population modelling approach. But the results for the puffin show very large uncertainties (confidence intervals shown in parenthesis in Table 9), due to an increase in annual variability in both population size and adult survival the last decade. Time to recovery was also more pessimistic according to the matrix approach (7 years) compared to the Brownian model (4 years) for the increasing population (guillemots from Hornøya).

**Table 9**. Summary comparison of the two population models (Brownian model and matrix population model) to estimate the population viability of 4 populations. Colony names, species, population trend and population effects are given. The population effects are given as either time to quasi-extinction or time to recovery, depending on whether the populations are declining or being stable/increasing. The results for both models are given in years (median and upper and lower 80% confidence intervals). For simplicity and comparisons, we only show the 25% simulated acute population reduction in this table. Note that, in the matrix models, the simulated acute mortality event was implemented on both immature and adult birds.

Colony	Species	Population trend	Population effects	Brownian model	Matrix model
Røst	Puffin	Declining	Time to quasi-extinction	14 (6,40)	10 (6, 18)
Hornøya	Kittiwake	Declining	Time to quasi-extinction	10 (5,25)	9 (5, 16)
Hornøya	Puffin	Stable (+)	Time to recovery	8 (2, ∞)	29 (11,85)
Hornøya	Guillemot	Increasing	Time to recovery	2 (1,4)	5 (4,7)

# 3.4 Relationship between simulated oil spills and guillemot nonbreeding distribution

#### 3.4.1 Sample sizes needed for representative estimates of core distribution areas

The results show that the size of core areas (50% kernel) varies a lot with the number of loggers, and small samples may be insufficient to capture the total variation of a population's space use. This applies both to different species and seasons. The analyses are carried out on species from Hornøya with high sample sizes for all species. In order to get estimates of space use that represent more than 95% of the total variation, one needs to include an average of 20 loggers (**Table 10**). The range is large, from 11 loggers among guillemots during autumn and Atlantic puffin during winter to 28 loggers for kittiwakes during winter. Illustrations of the relationship between the core area, number of loggers and how representative the core area is, defined by a breakpoint, are given in **Figure 9** and **Table 10**.



**Figure 9.** The relationship between estimates of core distribution areas used by seabirds and the number of GLS loggers included in the model. The figures show average areas of the 50% kernel utilization distribution (black dots) and deviation (grey) for each species. A nonlinear least-squares regression (red) was fitted to the data. Breakpoints (blue hatched lines) were estimated using a regression model with change-points estimation. The red areas show the 95% confidence intervals from the model.

Table 10. Overview of the data used to estimate the effect of sample size (number of loggers) and
the representativeness (%) and breakpoint (number of loggers) of identifying the core areas used by
different species during autumn (August–September) and winter (December–February). All species
breeding at Hornøya colony.

Species	Season	Periods (years)	Sample size	Representative- ness (%)	Breakpoint (no loggers)
Common guillemot	Autumn	2011–2014	112	99.58	17
	Winter	2011–2015	97	99.68	11
Brünnich's guillemot	Autumn	2012–2014	85	98.32	25
	Winter	2012–2015	62	95.76	26
Kittiwake	Autumn	2012–2014	54	97.54	22
	Winter	2012–2015	79	95.81	28
Puffin	Autumn	2012–2013	45	96.95	11
	Winter	2012–2014	44	97.31	18

#### 3.4.2 Case study on space use of guillemots and overlap with simulated oil spills

**Figures 10 A–D** illustrate the spatial distribution of simulated oil spills and the potential overlap with the non-breeding distributions of common guillemots from Hjelmsøya and Hornøya. Estimates of overlap are provided in **Table 11**. The analyses show that simulated surface probability of oil spills may have different direct negative effects on different populations of common guillemots, depending on their non-breeding distribution and seasonality. Overall, the direct overlap between simulated oil spills and core distribution areas of guillemots were low. However, these analyses are stationary, and there are indications that birds from two of the populations (Hornøya and Hjelmsøya) are particularly susceptible to being hit by an oil spill occurring in February, resulting in negative effects on the populations (**Figure 10**).

	Seabird d	listribution	Oil spill west		Oil spill east	
Oil spill surface in August (km <sup>2</sup> )			12,178		10,743	
Oil spill surface in February (km <sup>2</sup> )			11,905		11,063	
	Core area (km <sup>2</sup> )		Overlap (%)		Overlap (%)	
	August	February	August	February	August	February
Bjørnøya	68,313	115,676	0.0	8.6	13.2	0.0
Hornøya	87,343	45,916	0.0	0.0	0.0	24.1
Hjelmsøya	107,940	49,619	0.2	23.8	7.4	0.0
Sklinna	157,765	250,234	0.0	0.0	0.2	0.0

**Table 11.** Overview of overlap between guillemot distribution (from four different breeding colonies) and oil spill surface distribution after two simulated oil spill scenarios (August and February) in two different locations in the Barents Sea, one in the west and one in the east.



# **Figure 10.** Oil spill areas and core areas (50% kernels) for four common guillemot colonies (**A**: Bjørnøya, **B**: Hornøya, **C**: Hjelmsøya, and **D**: Sklinna) in relation to simulated surface oil spills in the Barents Sea. Oil spills were simulated in two areas (west and east) and two time periods (August and February). The breeding colony is shown by a small, coloured circle, and core areas of spatial use by a larger shaded area of the same colour as the colour of the breeding colony. The probability of oil distribution is shown by the sharp red areas with green shading around depending on the density of oil. For more information about these oil spills see Lundmark-Daae (2014).

#### 29



66°N

50°E

10°E

30°E

20°E

40°E

50°E

#### B) Hornøya

(Figure 10 continued.)

20°E

30°E

40°E

66°N

10°E



68°N

66°N

10°E

20°E

30°E

40°E

50°E

50°E

#### C) Hjelmsøya

(Figure 10 continued.)

20°E

30°E

40°E

66°N

10°E





(Figure 10 continued.)

# 4 Discussion

Due to seabirds' vulnerability to acute mass mortality or acute population reductions, robust quantitative frameworks are needed to estimate their recovery potential, to aid population management and to provide accurate risk assessments. In this report we compare two modelling approaches, which estimate the population-level consequences of an acute event using population viability analyses (Morris and Doak 2002). The first is a Brownian population model based on yearly counts of numbers of breeding birds at specific colonies, while the other is a matrix population model which summarises population dynamics by important demographic rates (age-specific survival and fecundity).

# 4.1 Comparison of two models of population viability

The results from both the matrix and the Brownian model are shown in **Table 9** for a 25% simulated acute reduction in adult and immature survival or population size, respectively. The reduction in time to quasi-extinction was similar for two declining populations (puffins from Røst and kittiwakes at Hornøya) according to the Brownian population modelling approach (6 and 5 years, respectively, given the worst-case scenario). In comparison, according to the matrix-based model, a reduction in adult and immature survival led to a reduced time to quasi-extinction of 4 and 7 years for Røst puffins and Hornøya kittiwakes, respectively. For the two increasing populations (guillemots and puffins from Hornøya), the difference in recovery time was more variable (see **Table 9**), where puffins were estimated to never recover using the Brownian model and only after 85 years using the matrix-based approach.

The low viability of puffins from Hornøya can be explained to some extent by the inter-annual variability in demographic rates and population sizes (estimated from the monitoring data). Although the long-term trend of this population has been relatively stable over the study period, there has been large variability in populations sizes with strong increases from 1990 to 2013 but a decline thereafter, with increasing variance in not only population counts but also adult survival and breeding success (see Layton-Matthews et al. in prep).

The advantage of matrix models is that they also explicitly model the non-breeding proportion of the population, which can constitute up to 50% of the total population (Votier et al. 2005), compared to the Brownian model, which only considers the breeding portion. However, estimating age-specific survival requires mark-recapture data of different age classes, for which we do not have direct data from these populations, and so estimates were taken from the literature or estimated using other data sources (Layton-Matthews et al. 2023). This lack of age-specific data on survival is also a general limitation for most seabird species and locations. Another major problem is that we know little about the behaviour (or distribution) of these immature birds during the non-breeding period, which may differ compared to breeding birds. Most likely, this part of the population has a different foraging distribution and thus a different exposure to acute mass-mortality events than breeding adults. A good study documenting the importance of immature seabird distributions is from Skomer Island, where Votier et al. (2008) showed that all age classes of common guillemots were potentially at risk from 4 major oil spill. However, the youngest age class (0-3 years) was far more widely spread than birds aged 4-6 years, which were again more spread out than older breeding birds. Therefore, the chance of encountering an oil spill was strongly age dependent. From SEAPOP key site populations, little knowledge exist on survival of immature birds and their at-sea distribution that could be used to parametrise matrix models. Given the importance of such data, however, SEATRACK and SEAPOP are prioritizing the collection of such data in the coming years. This study emphasises the importance of detailed demographic to estimate, e.g., age-class specific survival.

Another challenge with matrix models is the length of the demographic time series, which are often shorter than count-based timeseries, because demographic data are more time-consuming

to collect. Seabirds' general life history strategy, with high survival and low reproduction rates and young recruiting as breeders after 4–5 years, requires a certain length of demographic time series to estimate impacts. Applications of the matrix population modelling approach thus require long time series, and we recommend testing how sensitive outcomes of matrix-based PVAs are to time-series length. Nevertheless, despite these limitations, matrix models are an advance on Brownian models, which use count data that must be understood as integrating changes across demographic rates. Yearly population counts also incorporate immature birds, but Brownian models cannot separate variation in numbers of different age classes.

# 4.2 Use of tracking data to estimate overlap in oil spills and seabird distributions

Understanding the extent and importance of marine areas for seabird populations of known origin should be given priority for comprehensive conservation planning (Croxall et al. 2012). By using tracking technology (GLS), we show differences in habitat use during autumn and winter for four populations of guillemots (Bjørnøya, Hornøya, Hjelmsøya and Sklinna) in the Barents Sea. This differential use of non-breeding areas led to different overlaps and, thus, risk of damage from the two simulated oil spills which occurred at different sites and times during the non-breeding season. Overlap was low in general. The highest overlap occurred for the Hjelmsøya population in winter with the simulated oil-spill in the western Barents Sea, and for the Hornøya population in winter with the simulated oil-spill in the eastern Barents Sea (Table 11 and Figure 10). The degree of overlap between seabird distributions and oil-spill surface distributions can be used to estimate the densities of seabirds impacted by an oil-spill event, for a given species, colony and month throughout the year, following methods described in Fauchald et al. (2021). This highlights the importance of identifying seabird populations' non-breeding distributions from known colonies, so that this can be linked to monitoring data (counts, demographic data) collected at the respective colonies, through which we can estimate population consequences of acute events. However, the sample size of tracking devices may represent a challenge regarding how representative the estimates of seabirds non-breeding distributions are. We show that the ability to provide representative estimates of non-breeding distributions and core foraging areas is highly dependent on the number of loggers. We show that, during the non-breeding period (excluding spring migration), an average sample size of 20 loggers per population would be necessary to limit uncertainty.

# 4.3 Long term effects of acute oil pollution

Although oil spills may have acute effects on seabirds, there is now an increasing number of studies showing that oil spills may have longer-term population effects that should be explored further. Prior to the Exxon Valdez oil spill, it was generally believed that impacts on seabirds resulted exclusively from direct, acute mortality (Dunnet 1982), with no effects on populations in the years after the spill (Votier et al. 2008). Later research has challenged this traditional view, however, suggesting that, due to ecosystem-driven effects, the effect of oil spills may be complex and longlasting (Peterson et al. 2003, Barros et al. 2014). In 2002, the *Prestige* oil tanker wrecked and about 63,000 tons of heavy oil were released into the marine environment. By using temporal and spatial replicated data (before–after–control–impact design), it was shown that the European shag (*Phalacrocorax aristotelis*) experienced reduced breeding success (up to 45%) in oiled colonies compared to non-oiled colonies, over at least 10 years after the oil spill. This indicates that acute oil spills can have large, long-term effects on the whole ecosystem. This rare documentation of long-term effects after a major oil spill highlights the need for long-term monitoring of demographic parameters for seabirds, before and after acute events occur, to assess the true impact of this type of acute disturbance on marine organisms (Barros et al. 2014).

# 5 Conclusion

Population viability analyses (PVAs) are widely used in conservation biology to simulate population trajectories and estimate the status of populations of conservation concern (Brook et al. 2000). There are relatively few studies testing the accuracy of PVAs. However, Brook et al. (2000) tested such models in a retrospective analysis of 21 long-term ecological studies and concluded that their predictability was high. The life history of seabirds raises some specific challenges in implementing PVAs. Matrix-based population models require knowledge of age-specific survival rates, whereas data from immature individuals are generally lacking. There is also a lack of data on seabirds' year-round distribution for Norwegian colonies, although studies indicate that immatures have a wider distribution than established breeders. Brownian models only require data reflecting year-to-year changes in breeding bird numbers at the colonies. Fluctuations in breeding population size encompass changes in several demographic rates, including recruitment of immature birds to the population at a time lag of 4-5 years. However, it is not possible to isolate changes in recruitment from other parameters like adult survival as drivers of changes in population size. Although both approaches have advantages and disadvantages, as discussed in this report, we recommend the use of Brownian models, as count data are more widely available, with count datasets often spanning longer time periods. However, in the future, when more of these data are available, including data of immature survival and non-breeding distributions, matrix-based models will become an increasingly favourable approach.

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# 7 Appendix

**Table S1.** The reductions in population size the year directly after the acute event. The acute event was implemented in year 2017 and becomes apparent in population size in 2018. Reduction in population size was measured as the difference between projected population size in 2018 for the baseline scenario and each acute event scenario. Reduction in population size is given as the mean with 80% confidence intervals (in parentheses).

			Reduction in population size after acute event				
Species	Colony	Rates affected	10% reduction	25% reduction	50% reduction		
Puffin	Hornøya	Immature survival	926 (802, 1119)	2036 (1991, 2341)	3072 (2360, 3005)		
Puffin	Hornøya	Adult survival	1331 (1252,1440)	3144 (2557, 3998)	5632 (5310, 6267)		
Puffin	Hornøya	Both	2452 (2478, 2601)	6352 (6110, 6714)	12971 (12275, 13569)		
Guillemot	Hornøya	Immature survival	1352 (750, 1864)	3221 (1514, 4505)	4381 (2384, 6134)		
Guillemot	Hornøya	Adult survival	2920 (3836, 2417)	6492 (8448, 5668)	11141 (9836, 14093)		
Guillemot	Hornøya	Both	4822 (4725, 4828)	11490 (10742, 11856)	22947 (21708, 24038)		
Puffin	Røst	Immature survival	8022 (4028, 19973)	18536 (12564,39856)	-		
Puffin	Røst	Adult survival	37684 (28801, 43325)	84675 (63653, 98638)	-		
Puffin	Røst	Both	49116 (48329, 53360)	119248 (112728, 128491)	-		
Kittiwake	Hornøya	Immature survival	162 (111, 243)	352 (334, 457)	-		
Kittiwake	Hornøya	Adult survival	456 (443, 472)	1248 (1204, 1131)	-		
Kittiwake	Hornøya	Both	682 (611, 744)	1664 (1525, 1767)	-		

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