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Marked population reduction in Antarctic fur seals challenges their *Least Concern* category

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ABSTRACT

Abundant species listed as *Least Concern* on the IUCN Red List may receive limited conservation attention if this classification reflects insufficient data rather than genuine population stability. The Antarctic fur seal, currently the world's most abundant otariid, remains listed as *Least Concern* despite documented regional declines within its core range in the Southern Ocean's South Atlantic region. To reassess this classification, we analysed population trends for South Georgia, the South Orkney and the South Sandwich Islands, which together comprise ca. 97% of the global population, using long-term survey data. Monitoring over 47 years revealed rapid, synchronous declines at South Georgia and South Orkney Islands, with a sustained downturn since 2000 which outlasted sub-decadal fluctuations. At South Georgia, annual change averaged −3.93% [95% CI: −2.73; −5.13] since 2007, reducing the estimated population by ca 1.5 million to ca 1.98 million seals in 2022. Over three generations (26 years), the population reduction was −0.57 [−0.65; −0.48], with a 0.92 probability of exceeding 50%. This meets the IUCN A2 criterion for listing the subpopulation as *Endangered*, as the underlying causes remain unresolved and are unlikely to be reversible in the near-term. By contrast, the South Sandwich Islands population increased annually by 3.12% [2.59–3.66]. Given that South Georgia alone (ca. 96% of global abundance) disproportionately influences species-level trends, and considering that the next largest subpopulations, Bouvetøya and the South Shetland Islands, are also declining, our findings indicate that the current *Least Concern* category is inaccurate and warrants a global reassessment of the species' conservation status.

1. Introduction

Species that are abundant are classified as 'Least Concern' on the IUCN Red List unless they experience a significant range contraction, a rapid population decline, or face substantial extinction threats (IUCN, 2024). However, when this classification arises from perceived abundance and limited data, it can result in reduced conservation attention (Baker et al., 2019; Redford et al., 2013; Virtanen and Moilanen, 2023), especially when compared to categories associated with higher extinction risk (Cardillo et al., 2023; Mace et al., 2007; Miller et al., 2006; Murray et al., 2014). This discrepancy highlights a potential oversight in conservation prioritization, where data-deficient but seemingly common species may be under-protected. In reality, even modest declines in abundant species can lead to substantial losses of individuals, biomass, and ecological interactions, ultimately affecting biodiversity and ecosystem function (Dupont and Dobson, 2025; Gaston et al., 2018; Gaston and Fuller, 2008; Säterberg et al., 2013). This risk is especially pronounced for abundant species that are also large-bodied and wide-ranging, as these traits make them particularly vulnerable to extinction (Ripple et al., 2017).

Among marine mammals, the Antarctic fur seal (*Arctocephalus gazella*) is the second most abundant pinniped in the Southern Hemisphere and the most numerous otariid worldwide (Costa et al., 2006; Forcada et al., 2023b; Wickens and York, 1997). It was driven to commercial extinction by the early 20th century through systematic overharvesting, but after cessation of sealing operations populations rebounded rapidly thanks to high reproductive success, low mortality, and a wide distribution range which includes the most productive

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regions of the Southern Ocean (Bonner, 1968; Forcada et al., 2023b; Hofmeyr et al., 2005; Hucke-Gaete et al., 2004; Payne, 1977; Shaughnessy et al., 1998). Since at least 1990, the species has been classified as *Lower Risk* or *Least Concern* (Hofmeyr, 2016; Reijnders et al., 1993), despite very limited attempts at surveying the entire species range.

Recent genetic analyses identified four distinct subpopulations (Humble et al., 2018; Paijmans et al., 2020), with the three largest located in the South Atlantic region of the Southern Ocean (Fig. 1; hereafter South Atlantic region). These three subpopulations together comprise approximately 98% of the species abundance (Forcada and Staniland, 2018), with South Georgia alone accounting for 96–98% of global pup production in 2009 and supporting an estimated 3.5 million seals [3.1–3.9 million] (Forcada et al., 2023b). In contrast to the smaller East Antarctica subpopulation (approximately 2% of total; Fig. 1), the other subpopulations are thought to be declining rapidly (Forcada, 2021; Forcada and Hoffman, 2014; Forcada et al., 2023b; Hofmeyr, 2016; Krause et al., 2022; Krause et al., 2024), a trend that may not be appropriately reflected in the current IUCN Red List classification.

At Bird Island, in the northwest of South Georgia (Fig. 2b), fur seal pup production declined from 60,500 to 27,900 between 2009 and 2017, an average annual decrease of 9.2%, and the mature female population declined annually by 7.2% (Forcada et al., 2023b). At Bouvetøya (Fig. 1; 5), the second largest subpopulation with approximately 66,000 seals in 2002 (Hofmeyr et al., 2005), pup counts declined annually by 5.6% between 2001 and 2007 (Hofmeyr, 2016). At the South Shetland Islands (Figs. 1, 4; Fig. 2a), with approximately 41,000 seals in 2002 (Krause et al., 2022), annual pup counts at monitoring sites in the southwest declined by 90.9% between 2008 and 2023 (Krause et al., 2024), corresponding to an annual rate of decline of approximately 5.6%.

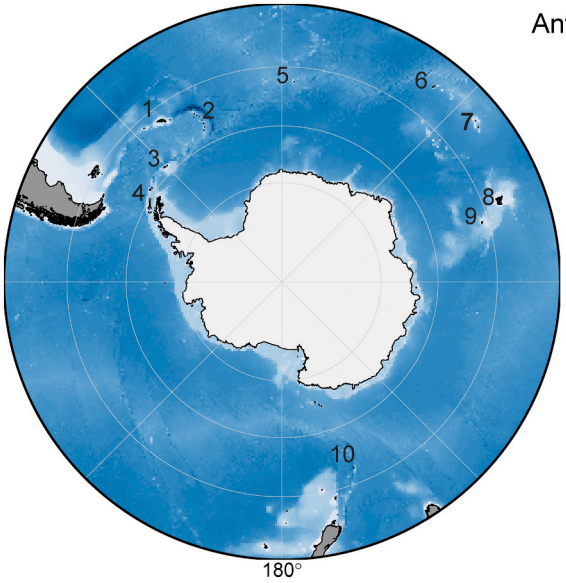
In the South Atlantic region, subpopulations are declining mainly because of ongoing environmental change, particularly at South Georgia (Forcada and Hoffman, 2014; Forcada et al., 2023b; Forcada et al., 2008). There, coupled climate and sea surface temperature cycles associated with low regional krill availability correlate with declines in fur seal juvenile survival, longevity and recruitment, delayed sexual maturation and increased generation length, while population growth is expected to remain mostly negative and highly variable (Forcada et al., 2023b).

Additional pressures include local top-down control (Krause et al., 2024; Schwarz et al., 2013), and potentially, the competitive exclusion from staple prey by increasing whale populations (e. g., Baines et al., 2022; Biuw et al., 2024; Savoca et al., 2024) and expanding commercial fisheries (CCAMLR, 2025; Lowther et al., 2020; Watters et al., 2020). Further threats arise from emerging pollutants (e.g., Aznar-Alemany et al., 2019), including microplastics (Garcia-Garin et al., 2020), with concerns over their persistence and toxicity (Brault et al., 2013), as well as outbreaks of new epizootic diseases such as highly pathogenic avian influenza (H5N1) (Bennison et al., 2024).

Given the rapid regional declines, environmental change, and rising threats, and despite their high global abundance, we investigate if Antarctic fur seals can still be classified as Least Concern. A higher-risk classification would have important implications for conservation objectives affecting the species and its ecosystems, particularly in resource-management contexts. Based on regional population and demographic trends, and the high population synchrony observed between distant locations which responds to common environmental drivers (Forcada et al., 2023b), we predict that the rapid declines observed in the South Georgia subpopulation extend across the wider archipelago and region, including the South Sandwich Islands and the South Orkney Islands. To test this, we evaluated overall population changes across the region using the best available survey data from representative locations. We then assessed the current regional status of the species against IUCN Red List criteria. Finally, given the disproportionate influence of the large South Georgia subpopulation on species-level assessments, we examined the implications of our findings for the global conservation status of the species.

2. Methods

To assess whether observed rapid declines at South Georgia and the South Orkney Islands extended across the wider subpopulation, we analysed regional population change using the best available visual count data from representative sites at South Georgia, the South Sandwich and South Orkney Islands (Fig. 2a). We reanalysed long term demographic data from Bird Island (Fig. 2b) to adjust visual counts and derived life tables for estimating generation length and population change. We reassessed population size and change over the entire subpopulation, and based on the estimated change over three generations,



Antarctic fur seal breeding distribution

Genetic subpopulation

South Georgia
South Shetland
Bouvetøya
East Antarctica

	Location	Pup production
1	South Georgia	≤ 1,200,000
2	South Sandwich *	≤ 1750
3	South Orkney *	≤ 500
4	South Shetland	≤ 7600
5	Bouvetøya	≤ 11,000
6	Marion–Pr.Edward	≤ 1600
7	Crozet	≤ 520
8	Kerguelen	≤ 6400
9	Heard–McDonald	≤ 1300
10	Macquarie	≤ 200

Fig. 1. Distribution of breeding populations of Antarctic fur seals with information on the four genetic subpopulations. The table shows estimated pup production up to 2010 or before, for remote locations not recently surveyed. Colours correspond to the genetic subpopulations. Locations with asterisk could hold admixed breeding colonies, but the genetic identity is unresolved.

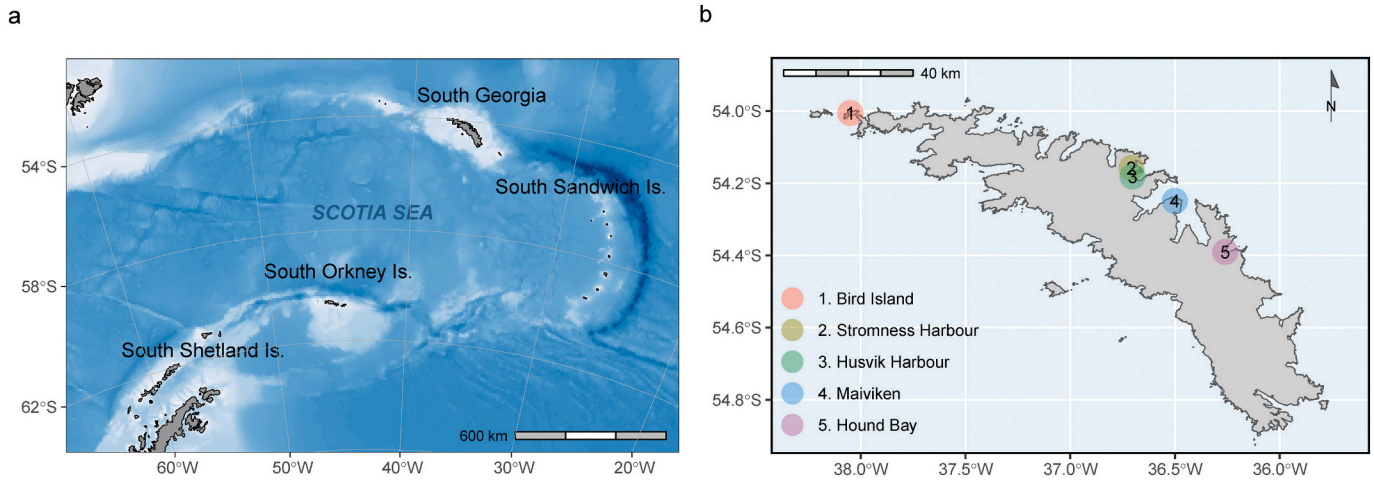


Fig. 2. a) Scotia Sea, with breeding locations of the subpopulation of South Georgia, including the South Sandwich and South Orkney Islands, and the subpopulation of the South Shetland Islands. b) Locations of five sites around the coast of South Georgia where population surveys were obtained in 2021–22. In locations 2–5, seal counts were obtained with high resolution images from Remotely Piloted Aerial Systems (RPAS).

we assigned Red List categories under IUCN criteria for South Georgia, the South Orkney Islands, and the South Sandwich Islands.

2.1. Study population, distribution and abundance

South Georgia is the largest Antarctic fur seal subpopulation globally (Fig. 1). There are small breeding groups in the South Orkney and South Sandwich Islands archipelagos (Fig. 2a), but the genetic identity of their breeders and pups remains unverified. The South Orkney population comprises primarily non-resident juvenile and adult males, which mainly originate from South Georgia as confirmed from tagging and telemetry studies (Boyd et al., 1998; Jones et al., 2021; Kightley and Caldwell, 1982; Laws, 1973), with occasional temporary migrants from the nearby South Shetland Islands (Lowther et al., 2020; Ouled-Cheikh et al., 2024). Juveniles and adult males from South Georgia and South Shetland Islands undertake post-breeding seasonal migrations along the northwestern Weddell Sea and west Antarctic Peninsula and some reach as far south as the Bellingshausen Sea (Jones et al., 2021; March et al., 2021).

Numbers of pups born at the South Orkney Islands have remained extremely low since the early 1970s, when fewer than 70 were recorded across the archipelago (Laws, 1981). At Signy Island, monitored annually since 1977 (Kightley and Caldwell, 1982), counts exceeded 20,000 individuals between 1994 and 2000, yet no more than five pups were recorded in any given year. Pups have been nearly absent post-2000 (Dunn et al., 2025; Waluda et al., 2010), with the last one seen in 2018. At Laurie Island, only four pups were observed from 1996 to 2005, despite a maximum of 16,610 individuals counted in early 2005 (Carlini et al., 2006).

At the South Sandwich Islands, pup counts have been limited due to access constraints, but increased to ≥1,750 by 1997/98, including 500 at Zavodovski Island (Convey et al., 1999), which was resurveyed in 2023/24. More recent data for other islands are from 2011 only (Lynch et al., 2016).

2.2. Data

Different datasets were required for each part of the analysis (Appendix 1, and below). At South Georgia, abundance estimates at targeted survey sites were based on counts of breeding males and females collected during the pupping season. These counts were scaled to total abundance using data from a representative study site at Bird Island, which provided: (1) demographic and vital rate estimates from individual capture–recapture data resolved by age, sex, and reproductive stage; (2) a total pup production estimate from comprehensive daily counts of newborn pups; and (3) haul-out curves derived from daily counts of males and females across the breeding season. Datasets (1–3) informed integrated population models (IPMs) that estimated the proportion of total abundance represented by a count on any given survey day at the study location. This proportion was then used as a population correction to scale survey counts at other sites lacking long-term individual data and haul-out records (Forcada et al., 2023b).

2.2.1. Individual data collection at a special study location of Bird Island, South Georgia

Capture-recapture (electronic and plastic tags, and genetic markers), and count data for Antarctic fur seals representative of South Georgia were collected at Bird Island's Special Study Beach (SSB; 54.0116°S, 38.0507°W; location 1, Fig. 2b) from 1979 to 2025 (Croxall and Prince, 1979; Doidge et al., 1984; Duck, 1990; Forcada et al., 2023b; Forcada et al., 2008). Capture-mark-recapture, pup production monitoring, and individual counts at SSB began in 1979 (Doidge et al., 1984) and have been conducted annually since 1984 (Duck, 1990; Forcada et al., 2008). Hereafter, a breeding season is referred to by the second year of the split-year austral summer, e.g., 2023–24 is 2024.

Daily surveys from November to mid-January recorded numbers of females, pups, and territorial males. Female breeding status was tracked via flipper tags and PIT-tags (Passive Integrated Transponder tags, since 1997), while male territory tenure was monitored using temporary paint marks and microsatellite genotyping (Hoffman et al., 2006). A sample of females was aged via post-canine tooth sectioning and marked for long-term identification, most years. Newborn pups have been tagged since 1984, with PIT-tags added from 2001; genetic samples were collected from pups and breeding females during capture. Territorial males were sampled annually via remote biopsy using a modified crossbow syringe (Forcada et al., 2023b). Genetic samples were collected during daily surveys of nearly all the territorial individuals observed at SSB since 1995, and between-year genetic recaptures are available from 1995 to 2021 inclusive. Early pup mortality was estimated from daily carcass recovery prior to tagging at approximately 6 weeks of age. Both sexes exhibit strong philopatry, returning to breed nearly every year once established (Hoffman and Forcada, 2012; Hoffman et al., 2006; Lunn and Boyd, 1991).

For genetic identification, DNA was extracted from tissue samples using a modified phenol-chloroform protocol and genotyped at between nine and 39 polymorphic microsatellite loci (Hoffman et al., 2003). All loci conformed to Hardy–Weinberg and linkage equilibrium, with a low genotyping error rate (<0.005) and identity probability (1.354 ×

10^{-12}), suggesting that identical genotypes correspond to individuals who were resampled within and/or among years. Genetic recaptures were identified by screening for duplicate genotypes using program Identity (Allen et al., 1995), following Hoffman et al. (2006).

2.2.2. Survey count data

Survey counts at South Georgia were conducted as close as possible to the peak pupping day of the respective season. The pupping season, from mid-November to mid-January, peaks with high spatial synchrony across the South Atlantic region between the 6th and 10th of December, when numbers of newborn pups, breeding females, and territorial males at each location reach their maximum daily values and show lower day-to-day variability than at earlier or later dates (Duck, 1990; Forcada et al., 2005; Goebel et al., 2009; Hofmeyr et al., 2007). This continues to be the case, as observed in the more recent daily counts (see Results, Section 2.3.1.1).

Complete counts of the entire Bird Island population were obtained in nine seasons, including visual counts in December 1988, 1989, 1990, 1994, and 1997, and photographic counts in December 2003, 2008, 2016, and 2023. Counts were conducted from elevated vantage points in all the breeding beaches by trained field scientists. Visual counts were conducted by two observers working independently and their counts had a difference of less than 1–2%. In a pilot survey (data not presented), visual counts were within 98–99% of the counts from high-definition images from hand-held digital cameras, and RPAS (Remotely Piloted Aerial System). Therefore, biases due to survey method were likely to be very low.

Comprehensive aerial photographic data of the South Georgia mainland were obtained during two helicopter surveys of all the fur seal breeding beaches conducted in December 2006 and 2008 (Forcada et al., 2023b), available at doi:https://doi.org/10.5061/dryad.2rbnzs7tc (Forcada et al., 2023a). Surveys of four of the locations (Fig. 2b) were repeated in December 2021 using an eBee X (AgEagle, Switzerland) RPAS, a fixed-wing, autonomous mapping drone, equipped with an Aeria X sensor (24 M-pixel (6000 × 4000 pixels), APS-C, RGB, 18.5 mm focal length). Data are available at doi:https://doi.org/10.5285/978f67ee-8d89-444b-8ea2-e2871a233d90, doi:https://doi.org/10.5285/b65acd94-09 cd-4fd9-809c-e44b4b51f8c7, doi:https://doi.org/10.5285/72553ef2-8566-4160-95e6-ab2bcd072a8f, doi:https://doi.org/10.5285/249af89f-be4a-4ed7-9dbd-a767a614febf. RPAS and hand-held cameras from vantage points and aerial surveys produced comparably accurate counts (error $\leq$ 1%).

Additional alternate-day haulout counts throughout the breeding season were conducted at Maiviken (54.2435°S, 36.5033°W; location 4, Fig. 2b), approximately 105 km east of Bird Island, to provide haulout curves in addition to those obtained at SSB. Several colonies (Burnet 1–3, Little, Poa 1–3, Tortula) were monitored with high resolution images every other day throughout the breeding season, from November to February (Hollyman et al., 2021), between 2009 and 2025. Data are available at: https://data.bas.ac.uk/request.php?id=GB/NERC/BAS/PDC/01192. This produced a second set of haul-out counts, independent from SSB.

Where counting imagery was used, one or two observers working independently using consistent training and methodology produced counts from digital images, classifying seals according to four categories: pups, breeding females, territorial males and non-territorial males. Altogether, with a maximum straight-line (geodesic) distance between any two counting locations of 125 km, the data obtained in 2022 provide a representative sample of population variation over space and time at South Georgia.

At Signy Island (SI; 60.34°S, 45.00°W; Fig. 2a), South Orkney Islands, count data were collected around the entire island as part of a long-term monitoring programme which started in 1977 (Kightley and Caldwell, 1982), and continues to date, with only a few interruptions due to weather or logistic constraints (Dunn et al., 2025). Single ground counts from vantage points by two trained observers using consistent methodology took place between mid-February and early March every year, when fur seal numbers peak at SI. Counts of the whole island were completed in the minimum possible time (see also Appendix 2).

Ground count surveys of the South Sandwich Islands (Fig. 2a) were conducted in January of 1997 and 1998 (Convey et al., 1999) and in January 2011 (Lynch et al., 2016), providing minimum fur seal pup numbers. RPAS surveys of Zavodovski Island (56.30°S, 27.58°W) were conducted in December 14–15 of 2023, using a Mavic 3 Pro Quadcopter (DJI, Shenzhen, China) flown at an altitude of 70 m (CMOS ½ in. 48Mp; 24 mm lens).

2.3. Analysis

2.3.1. Population modelling

2.3.1.1. South Georgia. We assessed Antarctic fur seal abundance at Bird Island and other South Georgia sites using the latest data and the integrated population modelling (IPM) analysis of Forcada et al. (2023b). Two IPMs, one for females and one for males, jointly analysed age-at-count and pup production data, along with capture–mark–recapture (CMR) data from tagging and genetic sampling obtained at a long-term study site (SSB) to estimate key demographic rates, and derive absolute abundance estimates by stage and sex: pre-breeders and mature individuals, the latter including breeding females, territorial males, immigrants and mature non-breeders. These absolute estimates were then combined with daily counts of adult females and males at SSB to estimate a population correction for any given survey day. This correction reflected the fraction of total abundance represented by the number of females or males counted on that date. The IPM formulation and estimation methods, including implementation, assessment, and model selection are detailed in Appendix 1 (Supplementary Information).

An age-stage-structured population projection model was the main IPM building block, assuming a birth pulse and a pre-breeding census (Forcada et al., 2023b). In a female IPM, it described apparent survival (ϕ) and accession to breeding (α; recruitment) for immature females (pre-breeders; P) of ages 3 to 7^{+} (ages older than 7), and the transition of individuals through breeding states, breeder (B) and mature non-breeder (N), with probabilities ψ^{BN}, and ψ^{NB}. In a male IPM, it described survival (ϕ) and accession to first breeding territory tenure (α) for pre-territorial males; (P) of ages 7 to 11^{+}; and the transition of individuals between breeding states including territorial (T) and mature non-territorial males (N), with probabilities ψ^{TN}, and ψ^{NT}.

We modelled temporal variation in vital rates when possible to reflect the population state at the time of data collection. For males, sample size precluded temporal variation in most cases (Appendix 1). For females, we used temporal random effects for ϕ^{P} and α^{P}, immigration ($log(\iota)$), recapture (p), and correlated temporal random effects for ϕ^{B}, ϕ^{N}, ψ^{BN} and ψ^{NB}, where $\varepsilon^{\theta}_{i,t} \sim MVNormal(0, \Sigma_{\theta,t})$ and $\Sigma_{\theta,t}$ is a temporal variance-covariance matrix (Forcada et al., 2023b; Link and Barker, 2005).

We tested for density-dependence modelling ϕ^{B}, ϕ^{N}, ψ^{BN}, and ψ^{NB} as functions of standardised population density. For example,

$$logit\left(\phi^{B}_{i,t}\right) = \mu_{i}^{N_B} + d^{B}\left(N_{B,t}/\overline{N}_{B}\right) + \varepsilon^{B}_{i,t}$$

where $\varepsilon^{B}_{i,t}$ was a temporal random effect, and d^{B} was a regression slope for density, measured as number of breeders at time t, $(N_{B,t})$, standardised by mean number of breeders over time $(\overline{N}_{B})$. A significantly negative slope (d^{B}) would indicate negative density-dependence on survival, which would decrease as population density increased.

The female IPM likelihood produced two main quantities based on absolute abundance of mature females (M) at SSB (S), $N^{S}_{M,t}/E\left(n^{S}_{j}\right)$ and $N^{S}_{B,t}/E\left(n^{S}_{j}\right)$, where $M = N + B$, N are mature non-breeding and B mature

breeding females respectively; and $E\left(n_j^S\right)$ is the predicted female count at SSB on the *jth* day of a breeding season. These multipliers scale up observed counts to total numbers of mature, $\widehat{N}_M = \frac{\sum_c n_j^c \widehat{N}_M^S}{E\left(n_j^S\right)}$, and breeding females, $\widehat{N}_B = \frac{\sum_c n_j^c \widehat{N}_B^S}{E\left(n_j^S\right)}$, at other locations, where n_j^c is the female count at colony c on day j. Note that $\widehat{N}_B$ is equivalent to annual pup production, and the number of mature individuals ($\widehat{N}_M$) is a main parameter of interest for Red List assessments (IUCN, 2024).

These equations assume that the dynamics of daily counts at SSB and other locations are highly correlated, which is accurate within Bird Island and across the region when counts are conducted at or near the peak pupping date, and is due to the species' high regional synchrony in pupping (Forcada et al., 2023b). However, due to segregation in foraging range among breeding females at locations far away from SSB (Staniland et al., 2011), geographical differences in hauling out dynamics increase throughout the season, and the spatial correlation in counts with SSB may decay rapidly after the first six days following peak. This is shown in Fig. 3 for serial haul-out counts at Maiviken (MVK; Fig. 2b) conducted during 2022, which is the only other intensively sampled location at South Georgia, apart from SSB. As the South Georgia survey counts of many locations away from SSB in 2022 occurred later than peak pupping, they would probably not represent the same proportion of the total abundance as a count on the same day at SSB, according to the ratios $N_{M,t}^S / E\left(n_j^S\right)$ and $N_{B,t}^S / E\left(n_j^S\right)$, which relate specifically to SSB. To mitigate some of this potential bias and incorporate uncertainty due to hauling out differences, we also used alternate-day counts throughout the breeding season at MVK.

For this, we fitted Poisson GAMs to daily data and obtained predicted counts at both locations. To make the haul-out curves comparable, predictions were rescaled to range between 0 and 1; i.e., $z_i = \frac{n_i - min(n_i)}{max(n_i) - min(n_i)}$, for day i.

An adjusted MVK count on the ith day assumed a difference of size κ_i in $E(n_i)$ between locations, which at the transformed scale is $\kappa = \frac{n_i^M \delta_i}{z_i^M}$, where δ_i^- is $z_i^M - z_i^S$ when $z_i^M > z_i^S$, and δ_i^+ is $z_i^S - z_i^M$ when $z_i^M < z_i^S$ (e.g., Fig. 3, lower panels). Thus, a rescaled MVK count with respect to SSB, was $n_i^M K_i$, where

$$K_i = \begin{cases} 1, & \text{if } z_i^M = z_i^S \\ 1 + \frac{\delta_i^-}{z_i^M} = 2 - \frac{z_i^S}{z_i^M}, & \text{if } z_i^M > z_i^S \\ 1 - \frac{\delta_i^+}{z_i^M} = 2 - \frac{z_i^M}{z_i^S}, & \text{if } z_i^M < z_i^S \end{cases}$$

This adds prediction uncertainty to counts away from SSB, which are more likely to follow a MVK haul out pattern as the seals would forage in the same areas as MVK seals; and for counts closer to SSB uncertainty can be reduced by obtaining an average corrected count at colony c, $\overline{n}_j^c$, weighted by the inverse of the distance in km from c to SSB and to MVK. This is

$$\overline{n}_j^c = \frac{\left(w_{1,j} n_j^c + w_{2,j} n_j^c K_j\right)}{\sum w_j}$$

where $w_{1,j} = \frac{1}{d_j^{SSB}}$ and $w_{2,j} = \frac{1}{d_j^{MVK}}$, with d as geodesic distance in km. Thus, a count closer to SSB will assume a more similar daily haul out pattern to this location, with $\overline{n}_j^c \to n_j^c$, whereas a count closer to MVK will have a stronger influence of K_j, with $\overline{n}_j^c \to n_j^c K_j$.

It follows that an estimate of total number of mature females at a survey area is

$$\widehat{N}_{F_M} = \frac{\widehat{N}_M^S}{E\left(n_j^S\right)} \sum_c \frac{w_1 n_j^c + w_2 n_j^c K_j}{w_1 + w_2}$$

and to account for pre-breeders and obtain an estimate of total number of females we use

$$\widehat{N}_{F_{All}} = \left(1 + \frac{\sum_k \widehat{N}_{P_k}^S}{\widehat{N}_M^S}\right) \frac{\widehat{N}_M^S}{E\left(n_j^S\right)} \sum_c \frac{w_1 n_j^c + w_2 n_j^c K_j}{w_1 + w_2}$$

where $\widehat{N}_{P_k}^S$ is the estimated number of pre-breeders of age k, for $k = 1, \ldots, 7^+$, at SSB.

Similarly to females, the male IPM produced two multipliers of observed counts at locations different from SSB, from which estimates of total number of mature males were

$$\widehat{N}_M = \frac{\sum_c n_j^c \widehat{N}_M^S}{E\left(n_j^S\right)},$$

and of territorial males

$$\widehat{N}_T = \frac{\sum_c n_j^c \widehat{N}_T^S}{E\left(n_j^S\right)},$$

Here, mature males (M = N + T) are territorial males (T) and mature non-territorial (N) which have held territories before; and n_j^c is the male count at colony c on day j.

To estimate mature males at study areas (c) adjusting for differences in haul out between SSB and MVK we used

$$\widehat{N}_{M_M} = \frac{\widehat{N}_M^S}{E\left(n_j^S\right)} \sum_c \frac{w_1 n_j^c + w_2 n_j^c K_j}{w_1 + w_2}$$

An absolute estimate of total number of males at c was obtained adjusting for pre-territorial males,

$$\widehat{N}_{M_{All}} = \left(1 + \frac{\sum_k \widehat{N}_{P_k}^S}{\widehat{N}_M^S}\right) \frac{\widehat{N}_M^S}{E\left(n_j^S\right)} \sum_c \frac{w_1 n_j^c + w_2 n_j^c K_j}{w_1 + w_2}$$

where $\widehat{N}_{P_k}^S$ is the estimated number of pre-territorials of age k, for $k = 1, \ldots, 11+$, at SSB.

2.3.2. IUCN Red List criteria selection and assessment for South Georgia, South Orkney Islands, and the South Sandwich Islands

South Georgia is a distinct genetic group or subpopulation, which are defined by the IUCN (2024) as "geographically or otherwise distinct groups in the [global] population between which there is little demographic or genetic exchange". The genetic identity of pups from the South Orkney and South Sandwich Islands is unknown. Due to its close geographic proximity, the South Sandwich Islands could be part of the South Georgia genetic group, but we produced an independent assessment for completeness. In contrast, due to absence of complete surveys since the early 1970s, the highly probable origin from South Georgia of most of the counted population (Boyd et al., 1998), and the marginal numbers of pups counted at long-term study islands (Carlini et al., 2006; Dunn et al., 2025), we consider the South Orkneys Islands as *Data Deficient*.

Because population declines at South Georgia are ongoing, but the specific causes remain unclear and are likely to be irreversible in the near future (e.g., due to poor greenhouse warming mitigation), we focused on IUCN Red List Criteria A1–A4, and especially A2 (IUCN,

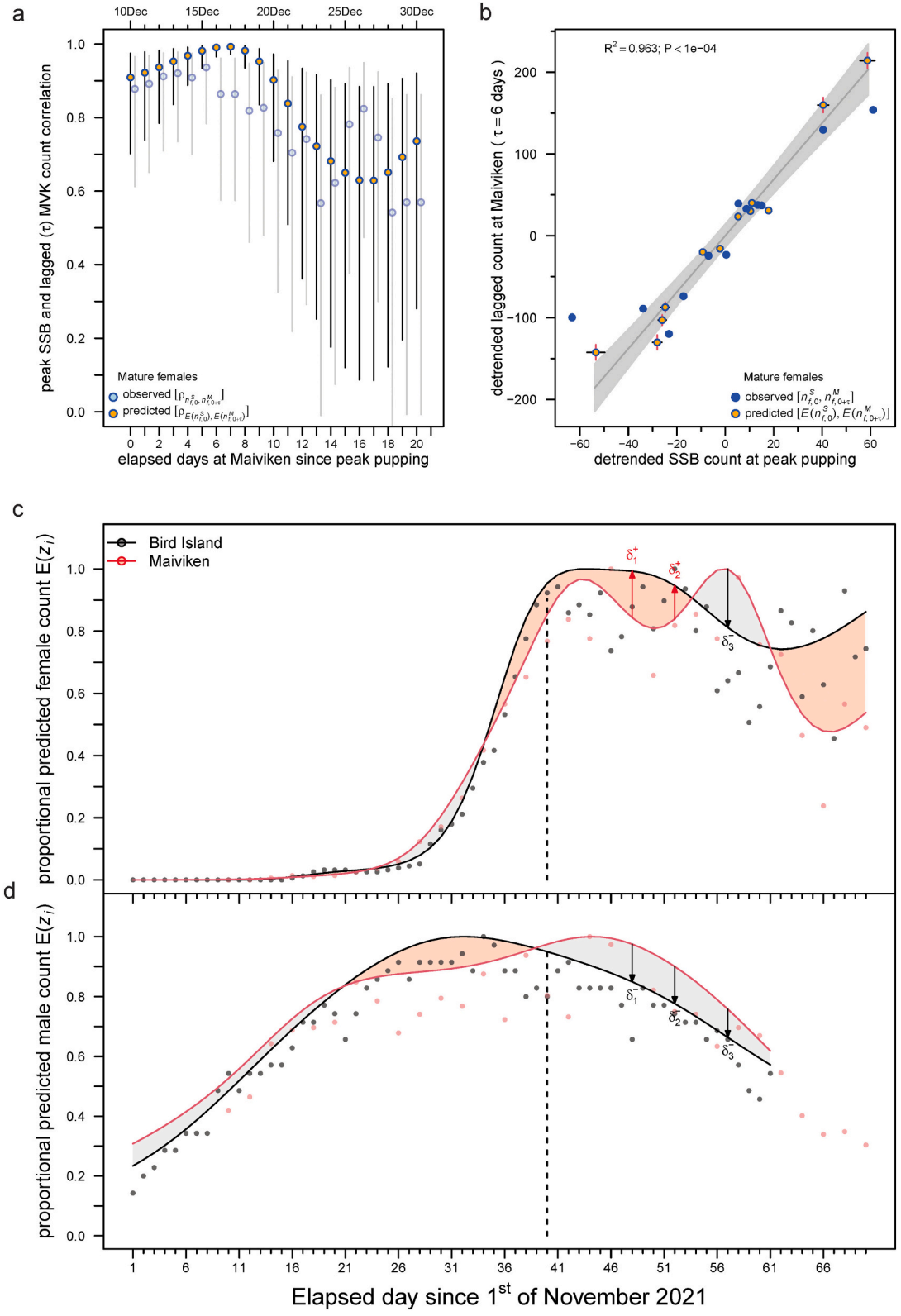


Fig. 3. Correlation of mature individual counts between Bird Island and Maiviken. a) Variation in the Pearson's correlation coefficient between predicted (GAM) and observed female counts at SSB peak pupping and MVK for 2014–2025, with MVK evaluated between zero to 20 days post-peak. b) Maximum correlation of detrended counts, with regression of MVK at day 6 post-peak against SSB at peak. c) Rescaled Poisson GAM fits to 2022 female counts, and d) male counts. Points are individual observations; dashed line is peak pupping day; red/grey shading indicates negative/positive differences in haul-out behaviour; with arrows showing predicted count differences (δ) between sites at the time of RPAS survey counts in 2022. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

2024). We thus assessed population reduction based on the mature population only, over the longer of 10 years or three generations.

According to IUCN guidelines, mature individuals are capable of reproduction, but "those who will never produce new recruits should not be counted" (IUCN, 2024). Due to major sex differences in life history, the mature population has more females than males, according to this definition. Despite sexual maturation at 3–5 (Payne, 1979), pre-territorial males begin holding breeding territories at around age 7 (mean age 9–11) and typically hold them for only 1–2 years. By contrast, female mean age at first breeding is 4–5 and they survive and continue breeding for much longer (Forcada, 2021; Forcada et al., 2023b).

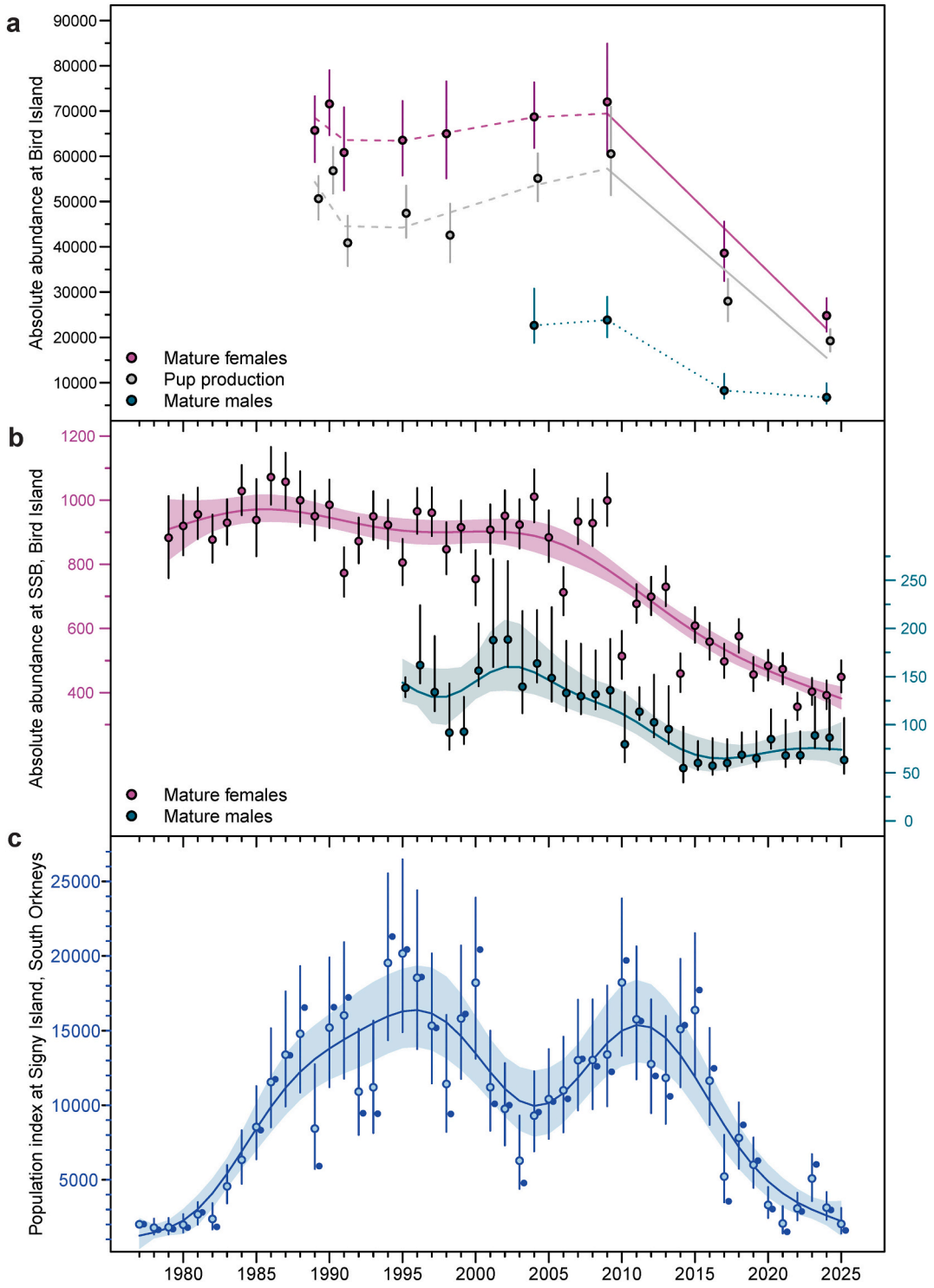


Fig. 4. Absolute abundance of mature Antarctic fur seals and pup production at Bird Island, South Georgia, and abundance index at Signy Island, South Orkney Islands. a) BI abundance estimates in seasons with total island counts. Straight lines are fitted segmented regression models, with continuous-line segments depicting significant declines. Dotted lines connect mature male abundance estimates. b) Absolute abundance of mature males and females at BI-SSB. Smoothed lines are nonlinear trends based on GAMs. c) Population index at SI, with fitted smooth trends, including 95% credible intervals in vertical bars and shaded areas for model estimates and trends, respectively.

2.3.2.1. Generation length. This was the average age of parents in the population (Coale et al., 1972; IUCN, 2024),

$G = \sum_x x l_x m_x) / \sum_x l_x m_x)$, where x is age and summations are from age zero to the last observed age, 24 for females and 18 for males; m_x is the fecundity at age x; and l_x is survivorship up to age x. We used posterior simulations of pre-disturbance (pre-2009; Forcada et al. (2023b)) vital rate estimates from the IPMs to build matrix population models, generate sex-specific life table simulations using age-from-stage decomposition methods (Caswell, 2001) as implemented in *R* package *Rage* (Jones et al., 2022), and derive estimates of G. These were weighted by the relative abundance of mature seals of each sex, as required (IUCN, 2024).

2.3.2.2. Population change and reduction. Based on the observed population trajectories at Bird Island (Fig. 4), we assumed an exponential decline to calculate population reduction. We considered two population sizes: N_1, in the first year (t_1), and N_T in the last year (t_T) of data. The observed period was $T - 1 = t_T - t_1$, and the observed change, N_T/N_1, expressed as % annual change was $\%AC = 100(AC - 1)$, where $AC = (N_T/N_1)^{\frac{1}{T-1}}$.

To evaluate population reduction, the assessment year (AY) was 2025, and the assessment period was 26 years (over 3G, where G=8.6; see Results), starting in 1999. As this preceded and outlasted the interval between the first and last available population estimates, population size three generations before AY (N_{3G}) was N_1/AC^t, where AC was the annual change over the number of years (t) between 1999 and the t_1. Here, AC was the geometric mean estimate of $ln\lambda$ derived from the IPMs for period 1999 to t_1. The current population (N_C) was $N_T AC^t$, where AC was evaluated between t_T and AY, and reduction was estimated as

$$R = 1 - \left(\frac{N_T}{N_1}\right)^{\frac{3G}{T-1}}.$$

2.3.2.2.1. South Georgia. The total mature population size of South Georgia (N_1^M) was obtained from comprehensive helicopter surveys in 2007/09 (t_1) (data repository in Forcada et al. (2023a)). As the population size in 2022 (t_T) was only available for a few representative locations (Fig. 2b) we derived a population total using a projection model. This assumed that abundance of each colony c surveyed in t_1 changed at mean annual rate $\overline{AC}_c$, which was an average of the AC_s of the colonies surveyed (s) in 2007/9 and 2022, weighted by the geodesic distance (d) from c to each colony s;

$$\overline{AC}_c = \frac{\sum_s d_{cs} AC_s}{\sum_s d_{cs}}.$$

This allowed a colony c to change at an annual rate which was nearer to a rate observed among s locations which were geographically closer. Total mature abundance was obtained as

$$\widehat{N}_T^M = \sum_c \widehat{N}_{1,c}^M \widehat{\overline{AC}}_c^{(T-1)},$$

where the uncertainty of $\widehat{\overline{AC}}_c$ reflected the uncertainty of the IPM simulations used to obtain the AC_s, and was carried over when combined with simulations used to obtain $\widehat{N}_{1,c}^M$.

2.3.2.2.2. South Sandwich Islands. Pup surveys in 1998 and 2011 provided minimum counts after the pupping season (Convey et al., 1999; Lynch et al., 2016) and were corrected for pre-count mortality as observed at the corresponding counting dates at BI-SSB in each year. A survey of Zavodovski Island was completed halfway through the 2024 pupping season (15 December 2023) and the $\widehat{N}^M$ adult population was

$$\widehat{N}^M = \left[n_i^p \left(1 + \widehat{q}_i^p\right) / \widehat{p}_i\right] \widehat{\pi}_M,$$

where for day i, n_i^p was the observed pup count, q_i^p was cumulative pup mortality up to i, $\widehat{\pi}_M$ was the adjustment of pup count to mature abundance, described in the next section, and $\widehat{p}_i$ was the proportion of total pup production that was n_i^p. This was obtained with a logistic model of cumulative daily pup counts at SSB (P_i) (Forcada et al., 2005). For 2024 and day i, this was

$$P_i = \frac{\theta_1}{1 + e^{(\theta_2 - j)/\theta_3}} + \varepsilon_i$$

where j was day since November 1st, θ_1 the horizontal asymptote of the accumulative births, θ_2 the expected mean birth date, and θ_3 was a scale parameter.

Given the observed net increase in pup counts between 1998 and 2011, and also to 2024 for Zavodovski Island, we assumed that the remaining islands had a similar annual change to Zavodovski Island since 2011 to produce estimates of current mature population and annual change. Although differences in population dynamics between islands, particularly at Visokoi which is the most populated, could slightly change the projected estimates.

2.3.2.2.3. Adjustment of pup counts, and total population size. Estimates of mature individuals were obtained from local pup production values (n^p) and the ratio of pup production and mature individual abundance estimates from the fitted IPMs. This was $\widehat{N}^M = n^P \widehat{\pi}_M$,

where

$$\widehat{\pi}_M = \frac{\sum_{t=1}^{T} \left(\frac{N_t^{BI} + N_t^{NB} + N_t^T + N_t^{NT}}{N_t^{BI}}\right)}{T}.$$

In year t, N^{BI} was abundance of breeding females including breeding immigrants, N^{NB} of mature females skipping breeding, $N^T$of territorial males, and N^{NT} of mature non-territorial males. Averaged over time, $\widehat{\pi}$ reflects temporal variation incorporated in adjusted pup counts.

We used IPM simulations of these parameters together with log-normal deviates of pup counts/production based on their mean and variance, $\widehat{Var}(n_P)$, when available. Otherwise, we only used the mean ($\overline{n}_P$). An adjustment from pup counts to total population was

$$\widehat{\pi}_T = \frac{\sum_{t=1}^{T} \left(\frac{N_t^{BI} + N_t^{NB} + N_t^{PB} + N_t^T + N_t^{NT} + N_t^{PT}}{N_t^{BI}}\right)}{T},$$

where N^{PB} was the abundance of female pre-breeders and N^{PT} the abundance of pre-territorial males.

2.3.3. South Orkney Islands

2.3.3.1. Population dynamics. We evaluated population trends at Signy Island (SI) using a log-linear model with a discrete-time stochastic Gompertz formulation (Dennis and Taper, 1994; Lebreton and Gimenez, 2013) of the observed fur seal count y_t for year t, in response to a year-lagged count, y_{t-1}, with coefficient ν. The time series length was 49 years, from 1977 to 2025. To accommodate positive skewness from numerous low counts, we used a negative binomial error distribution (e.g., Davis and Wu (2009)), with $y_t \sim NB(r, p_t)$, where r and p_t were the dispersion and success rate parameters respectively, so that $p_t = \frac{r}{\left(r + E[y_t]\right)}$. Expressed in natural log scale, $x_t = lnE[y_t]$, the Gompertz Negative Binomial Model (*GNBM*) was formulated as

$$ln\left(\frac{x_t}{x_{t-1}}\right) = \upsilon + (1 + \nu) y_{t-1}^T + \varepsilon$$

where intercept υ measures intrinsic growth rate, equivalent to $ln(\lambda)$ when $E[y] = 1$, ν is a density-dependence coefficient, and ε and error term.

2.3.3.2. Synchrony between the south Orkneys and South Georgia. We assessed temporal population fluctuation similarity using SI counts and BI-SSB mature female abundance (Fig. 4), the longest time-series for South Georgia (47 years; 1979 to 2025). We used a mixed-effects formulation (*GNBMM*) with two independent random effects (Grosbois et al., 2009; Lahoz-Monfort et al., 2011; Santin-Janin et al., 2014). A time-specific random effect $\delta_t \sim N(0, \sigma_\delta^2)$ modelled common synchronous variation across sites; and a separate time-specific random effect for each site s, $\epsilon_{t,s} \sim N(0, \sigma_\epsilon^2)$, accounted for additional, asynchronous variation. The effects were incorporated as

$$ln\left(\frac{x_{s,t}}{x_{s,t-1}}\right) = \upsilon_s + (1+\nu_{s,0})y^T_{s,t-1} + \delta_t + \epsilon_{t,s}$$

and $\sigma_\delta^2 + \sigma_{\epsilon_s}^2$ is between-year variance unexplained by density-dependence. The variances are equally partitioned between sites in the shared term (σ_δ^2), but not between unshared components ($\sigma_{\epsilon_s}^2$).

The fraction of between-year variance accounted by the shared component is the intra-class correlation, $ICC_s = \sigma_\delta^2 / \left(\sigma_\delta^2 + \sigma_{\epsilon_s}^2\right)$, which measures the synchrony of SI with BI, and BI with SI. ICC_s approaches 1 when the shared (synchrony) component is large relative to the unshared component and tends to zero otherwise.

2.3.3.3. Association between Signy Island and South Georgia. We investigated the population effects of BI on temporary immigration at SI at appropriate time-lags (τ), which were examined with a cross-correlation function $R_{y_{BI},y_{SI}}(\tau) = E\left[y_{BI,t-\tau}, \overline{y}_{SI,t}\right]$, where τ is difference in years. We then augmented the *GNBM* as

$$ln\left(\frac{x_t}{x_{t-1}}\right) = \upsilon + (1+\nu_0)y^T_{SI,t-1} + \nu_1 y^T_{BI,t-\tau} + \varepsilon,$$

where ν_0 is a density-dependence coefficient, and ν_1 is a fixed-effect of the BI-SSB mature female abundance series at time-lag τ.

The implementation of the population dynamics models (GNBM and GNBMM), and description of model fitting, selection, and assessment is detailed in Appendix 2 (Supplementary Material).

2.3.3.4. Scales and patterns of fluctuation in population time-series. Discriminating between short-term fluctuations and long-term trends in Antarctic fur seal abundance is essential to assess population changes at South Georgia, and is a requirement for a formal assessment (IUCN, 2024). We used wavelet decomposition to analyse mature female abundance at BI-SSB and the SI population index, revealing transient dynamics at each site, and temporal synchrony patterns across sites. Wavelet power ($W_x(f,\tau)$, at each location x) and cross-wavelet analyses ($W_{x_1,x_2}(f,\tau)$), obtained with *R* package *biwavelet* [v0.20.22; Gouhier et al., 2024], identified cyclical and gradual changes in both time series (Cazelles et al., 2008), distinguishing these from long-term declines.

3. Results

Hereafter, inference from Bayesian posterior distribution simulations is presented as standard errors (SE) in parentheses, and credible intervals [CI] in squared brackets, typically of 95% unless indicated otherwise. The implementation, assessment, and selection of IPMs is detailed in Appendix 1 (Supplementary Material), including capture-recapture and GAMM model selection.

Selection of female IPMs supported the fit of a best model which included correlated temporal random effects in ϕ^B, ϕ^N, ψ^{BN} and $\psi^{NB}$and uncorrelated effects in survival and breeding probabilities of immature seals. Density-dependent vital rate models had substantially lower support (ΔWA*IC* from 31 to 80; Appendix 1, Table A1.1), with the best option being density-dependent slopes (d^-) for each vital rate. Models that included both a density slope and a temporal random effect had parameter identifiability problems and uninformative confidence intervals.

Without extra-temporal variation, density-dependent formulations indicated significant negative effects on ϕ^B and ψ^{NB} and positive density effects on ϕ^N and ψ^{BN} (Appendix 1, Table A1.2). Thus, models with temporal random effects, correlated or uncorrelated, better captured total inter-annual variation, but confounded potential density dependence with unexplained variation.

A sensitivity analysis comparing estimates between models with and without density-dependence of geometric mean population growth rate ($\bar{\lambda}$), abundance of breeders at SSB $\left(N_B^{Ssb}\right)$, and population correction of peak female counts $\left(N_B^{Ssb}/E\left(n_j^{SSB}\right)\right)$, suggested very marginal differences in $\bar{\lambda}$ (0.25 to 0.30%) and up to 2% in population corrections (Appendix 1, Table A1.2). These very marginal differences supported the use of an overall more robust model for inference which accounted better for inter-annual variation through temporal random effects, as it had a much better fit according to its WAIC score.

3.1. Matrix models, life tables, and generation length

Given sex-specific differences in recapture data types and periods, pre-perturbation vital rates were averaged between 2001 and 2008 for females and between 1995 and 2007 for males, and the corresponding population projection matrices and derived life tables are in Appendix 3.

Matrix models were slightly modified with respect to the IPM formulation; recruitment ages were from three to seven and older in females, allowing for 7+ females never observed recruiting (absorbing state); and from seven to 11 and older in males, where the age group 11+ included males never observed in territories. The male matrix model also included a reproductive component (first row), parameterised with genetic parentage data from Hoffman et al. (2003), which is required to obtain a life table and generation length based on the cohort method.

Generation length estimates were 8.21 (SE = 0.28) for females and 9.90 (SE = 0.58) for males. Using Bird Island mean absolute abundance estimates for 2007/09 (72,068 [60,914; 84,953] for mature females and 24,290 [20,411; 29,364] for mature males), the weighted mean generation length was 8.63 (SE = 0.26; [8.17; 9.18]).

3.2. Abundance, trends, and connection between South Georgia and South Orkney Islands

The GAMM components of the IPMs revealed better support for temporal random effects without autocorrelation (AR1), and the estimated overdispersion (σ_ε) was 0.207 [0.128; 0.319] for females and 0.025 [0.001; 0.069] for males.

From the fit of quasi-Poisson GAM models of the daily haulout counts at SSB and MVK (Fig. 3), variance inflation was 2.07 for SSB, with estimated degrees of freedom (d. f.) of 6.8, with approximately 97.7% of the deviance explained. For MVK, these values were 4.79, 6.1 and 96.9%, respectively. For SSB males, vales were 0.11, 7.4 d. f., and 96.3%, whereas for MVK males these were 0.81, 5.6 d. f., and 89.2%.

Estimates of K_j, the adjustment to accommodate differences in haulout counts between SSB and MVK, were 1.17 (SE = 0.06) on 18th December, 1.12 (SE = 0.06) on 22nd December, and 0.81 (SE = 0.04) on 27th December of 2021 for the females; and for the males, these were 0.83(0.09), 0.83 (0.011), and 0.88 (0.18), respectively. The estimates of $N_M^S/E\left(n_j^S\right)$ for the same survey days were 3.49 (0.68), 3.77 (0.73), and 4.52 (0.90) for males; and 2.58 (0.24), 2.41 (0.22), and 3.39 (0.33) for females, respectively.

As expected, differences in predicted haulout counts between SSB and other locations increased as a function of day since peak pupping, proximity to Maiviken, and distance from Bird Island. For days away from peak, and proximity to MVK, biases in mature female abundance

varied between 5.3 and 19.5%, and between 13 and 16.5% in males, when only the SSB haulout counts were used in population corrections. The total mature population estimates for survey locations in 2022 are summarised in Table 1, and an assessment of potential biases associated with differences in hauling out dynamics between geographic locations is presented in Table A.4.1, Appendix 4 (Supplementary material).

For Bird Island (BI), South Georgia, the female IPM geometric mean population growth rate, $ln(\bar{\lambda})$, was 0.951 [0.943; 0.958] between 2010 and 2025; and 0.970 [0.962; 0.978] between 2001 and 2025. Based on full island estimates, the mature female population at BI declined annually by 11.5% [12.7;15.7] between 2009 and 2024, and the decline was nearly-half, 5.9% [3.0; 8.7] between 2017 and 2024, in agreement with the trends at SSB. Pup production declined annually by 11.4% [9.8; 12.9] between 2009 and 2024, and by 5.2% [2.3; 8.0] between 2017 and 2024. The number of mature males declined annually by 7.97% [5.36; 9.79] between 2009 and 2024, and the shape of this decline, as in mature females since 2009, was consistent with an exponential model. Estimates of total abundance and trends, including SSB, are shown in Fig. 4.

Mature female abundance at Maiviken study areas declined annually by 2.45% [0.94; 3.95] between 2010 and 2025; and the decline of mature individuals for the area surveyed in 2022, which includes most study colonies, was 4.03% [2.12; 5.93] between 2007 and 2022. Here, mature female population estimates were 6493 [5929; 7135], 5743 [4859; 6769], and 3365 [2745; 4111] in 2007, 2009, and 2022 respectively.

Modelled seal counts at Signy Island (SI) (Fig. 4) showed a similar trend to BI since 2010, also consistent with an exponential decline. The annual decline was 13.7% [9.19; 16.80] between 2010 and 2025, and values in 2024–25 were similar to values from the early 1980s. As discussed in Dunn et al. (2025), the large count variation between the early 2000s and 2015 likely reflects a temporary pause in regional warming, which expanded seasonal sea ice and reduced haul-out opportunities.

After accounting for density-dependence and despite large sub-decadal variation, the inter-annual change in numbers was synchronised between BI and SI. Parameter estimates for fitted models (*GNBMM*) suggested maximum synchrony between BI and SI at lags of 3 to 7 years (Fig. 5b; Table A2.1, Appendix 2, Supplementary Material); which was also supported by the detrended cross-correlation analysis (Fig. 5a). BI-SSB abundance, lagged by 3 and 6 years, was positively associated with SI seal numbers (Fig. 5c, d). A 6-year lag yielded lower dispersion in predicted values, especially at higher densities, suggesting a possible cohort maturation effect in migrant males at SI, in synchrony with pup production and population fluctuations at South Georgia.

The wavelet analysis illustrates fluctuation in population cycles at both locations. The power spectrum of BI-SSB (Fig. 6a) shows a change on the scale of 5–6 years initially (2000), to 3–4 years after the 2009 population collapse. There were changing cycles of 3–4 years in the late 1980s to 5–6 years by early 2000s at SI (Fig. 6b). The main difference between these locations is observed from the early 2000s to the early 2010s and is likely to respond to mid-term changes in sea ice around SI.

The covariation of cycles between both time-series and the phase analysis (Fig. 6c) show how the 2009 decline at BI led to a similar 3–5-year cycle at SI between 2010 and 2015, although slightly lagged. The analysis also shows how the three-generation decline, between 2000 and 2025, outlasted several population cycles, characterised by differences in periodicity and duration of short to mid-term fluctuations.

Table 1
Antarctic fur seal population change at South Georgia. Adjusted mature population estimates in year ($\boldsymbol{N_t^M}$) are provided for assessment years t_1 and t_T to estimate annual change estimates over the maximum observed period (T). In parentheses are standard deviations of posterior distribution simulations. Estimates at t_T and of annual change for South Georgia are from the entire archipelago's projected population.

Location	t_1	$N^M_{t_1}$	t_T	$N^M_{t_T}$	% Annual change
South Georgia	2007/9	1,721,200 (71,700)	2022	1,024,800 (83,300)	−3.93 (0.61)
Bird Island	2004	91,400 (4860)	2024	31,550 (2200)	−5.19 (0.41)
Stromness harb.	2007/9	10,720 (870)	2022	6790 (630)	−3.00 (0.79)
Husvik harbour	2007/9	13,125 (1070)	2022	9500 (885)	−2.46 (0.92)
Maiviken	2007/9	6515 (305)	2022	3364 (345)	−4.34 (0.71)
Hound Bay	2007/9	5775 (491)	2022	3345 (308)	−4.12 (0.91)

3.3. Antarctic fur seal population projection and assessment for South Georgia

Survey data indicated a decline across all monitored locations (Table 1), consistent with the population collapse observed at Bird Island in 2009 and its subsequent downward trend. At Maiviken, located in the centre-east of South Georgia and distant from Bird Island (Figs. 2b, 4), the annual change was slightly lower than at Bird Island (Table 1). Counts at Maiviken over 16-years (Fig. 7) corroborate this trend, and the patterns in mature female abundance at BI-SSB (Fig. 4) and Maiviken (Fig. 7) were comparable, with synchronised interannual variability even when long-term trends were removed. Spearman's rank correlations ($\rho = 0.463$ [0.200–0.711]; non-detrended $\rho = 0.64$ [0.495–0.768]) support this similarity, despite the relatively short time series.

Based on the projection of the 2007–09 data to 2022, the average annual change at South Georgia was −3.93% (SE = 0.61; [−2.73; −5.13]), with a mature population of 1,024,797 [873,500; 1,200,048] seals in 2022 (Table 1), including 834,319 [709,490; 979,666] females and 190,478 [152,610; 237,723] males. Applying adjustments for female pre-breeders and pre-territorial males for 2022, the most recent population estimate is 1,983,687 [1,606,408; 2,411,876], which is approximately 1.5 million seals fewer than in 2007/9.

The mean annual change between 1996 and 2006 from the IPMs was 0.979 (0.005), which is consistent with previous stochastic $ln\lambda$ estimates (Forcada et al., 2008). We used this value to back-project the population of South Georgia from 2007/9 (t_1) to 1999 (t_{3G}) and obtain a three-generation (3G) mature population, N^M_{3G}= 2,136,953 [1,854,114; 2,461,876]. The annual change for the observed period (t_1 to t_T) was 0.883 (0.017) and was used to obtain the current population, N^M_C= 910,114 (89,753). Over three generations, annual population change was −3.24% (0.44), and population reduction was −0.57 (0.05; [−0.65; −0.48]), with a probability of 0.92 of being lower than or equal to −0.50. This supports a greater than 50% reduction, and hence we argue that 'Endangered' is the most appropriate Red List Category based on criterion A2.

3.4. Antarctic fur seal population assessment for the South Sandwich Islands

For Zavodovski Island, early pup-mortality estimates (q^p_t) for 1998 and 2011 were 0.392 [0.352; 0.433] and 0.162 [0.133; 0.194], and for the 15th of December 2024 was 0.035 [0.016; 0.061]. The proportion ($\widehat{p}_i$) of the total pup production that was a count on December 15th after correction for mortality was 0.845 [0.801–0.883]. This produced an adjusted pup count of 1551 [1476; 1641] pups, and a mature population ($\widehat{N}^M$) of 2299 [2120; 2502]. Here, $\widehat{\pi}_M$was 1.482 (0.049; [1.392; 1.582]) (see also Appendix 4 for adjustment estimates).

Table 2 shows data by island when available, including annual change estimates between seasons and locations. Over three generations, mature fur seals at Zavodovski Island increased annually by 3.13% [2.70; 3.57], which is similar to the assumed increase for the entire archipelago (3.12% [2.59; 3.66]), even though Zavodovski increased

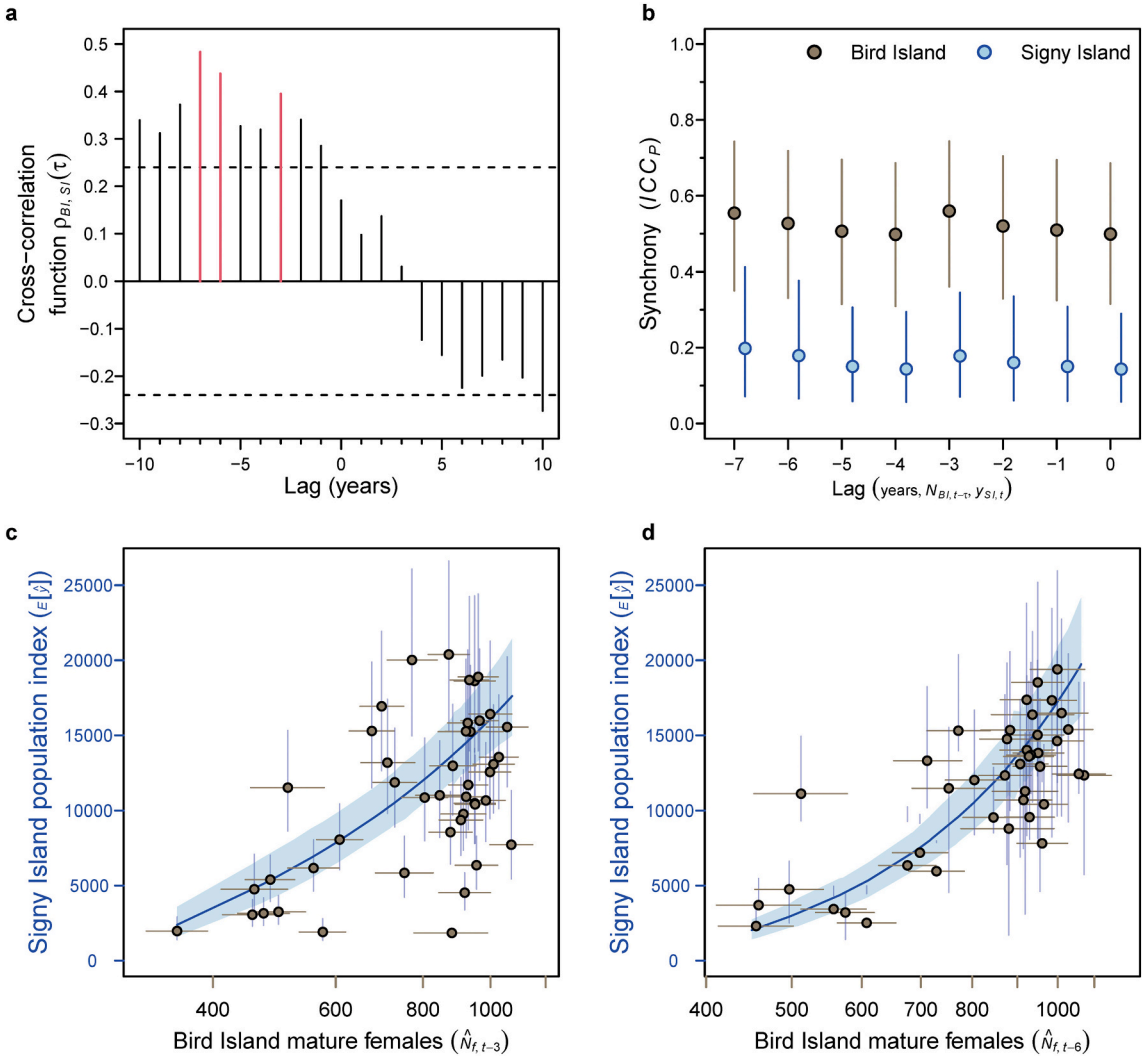


Fig. 5. a) Similarity between Signy Island (SI) fur seal population index counts and Bird Island-SSB (BI) mature female absolute abundance as a function of time delay (lag) applied to Bird Island, when the trend of both time-series is removed. b) Synchrony of BI abundance with SI population index, and of SI with BI, at different lags in years, based on *GNBMMs*. c) Fixed-effect of BI mature female abundance with negative 3-year lag on SI population index. d) Fixed-effect of BI mature female abundance with a negative 6-year lag on SI population index. Vertical and horizontal bars are 95% credible intervals, and solid blue lines and light blue areas are the mean and 95% credible intervals of the fitted *GNBM*. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

more rapidly since 2011 (5.32% [4.47; 6.21]). With an estimated three-generation increase of 4430 [3575; 5371] (123% [95; 155]) mature individuals, the classification of the Antarctic fur seal population of the South Sandwich Islands would be Least Concern, and it is currently the only known increasing breeding group in the South Atlantic region.

4. Discussion

Population projections combining helicopter and drone survey data indicate a highly probable reduction exceeding 50% over the last three generations in Antarctic fur seals at South Georgia. As this subpopulation represents approximately 96% of the total global abundance, this reduction has a disproportionately large influence on the species' overall decline. When considered alongside declines in the South Shetland Islands and Bouvetøya (Hofmeyr, 2016; Krause et al., 2024), our findings strongly suggest that the current classification of 'Least Concern' is no longer appropriate for South Georgia, and most likely for the species at large, which warrants the need for a global reassessment.

The decline observed at South Georgia followed nearly a century of recovery after commercial sealing (Forcada et al., 2023b). By the mid-2000s, when the subpopulation likely peaked, environmental deterioration was probably reducing carrying capacity. In agreement, our analysis indicated possible density-dependent effects on female survival and breeding (Appendix 1, Table A1.2), but these occurred alongside substantial unexplained temporal variation which could not be modelled simultaneously. This was due to the need of detailed age structure in the IPMs, essential to estimate numerically important unobservable components of the population, which increased the total parameter count and limited overall parameter estimability. However, sensitivity analyses indicated minimal effects between models with and without density dependence on the estimated 47-year population decline, with differences under 0.3% in mean λ, and under 2% in population corrections (Appendix 1, Table A1.2). Thus, we retained the model with best fit for inference as it accounted better for overall temporal variation. Future assessments could incorporate additional data and consider alternative model structures to improve parameter identifiability and explicitly represent density-dependent processes.

Population reductions under criteria A1–4 for long-lived species are evaluated over three generations to avoid conflating long-term trends with short-term fluctuations, although data from shorter time series and

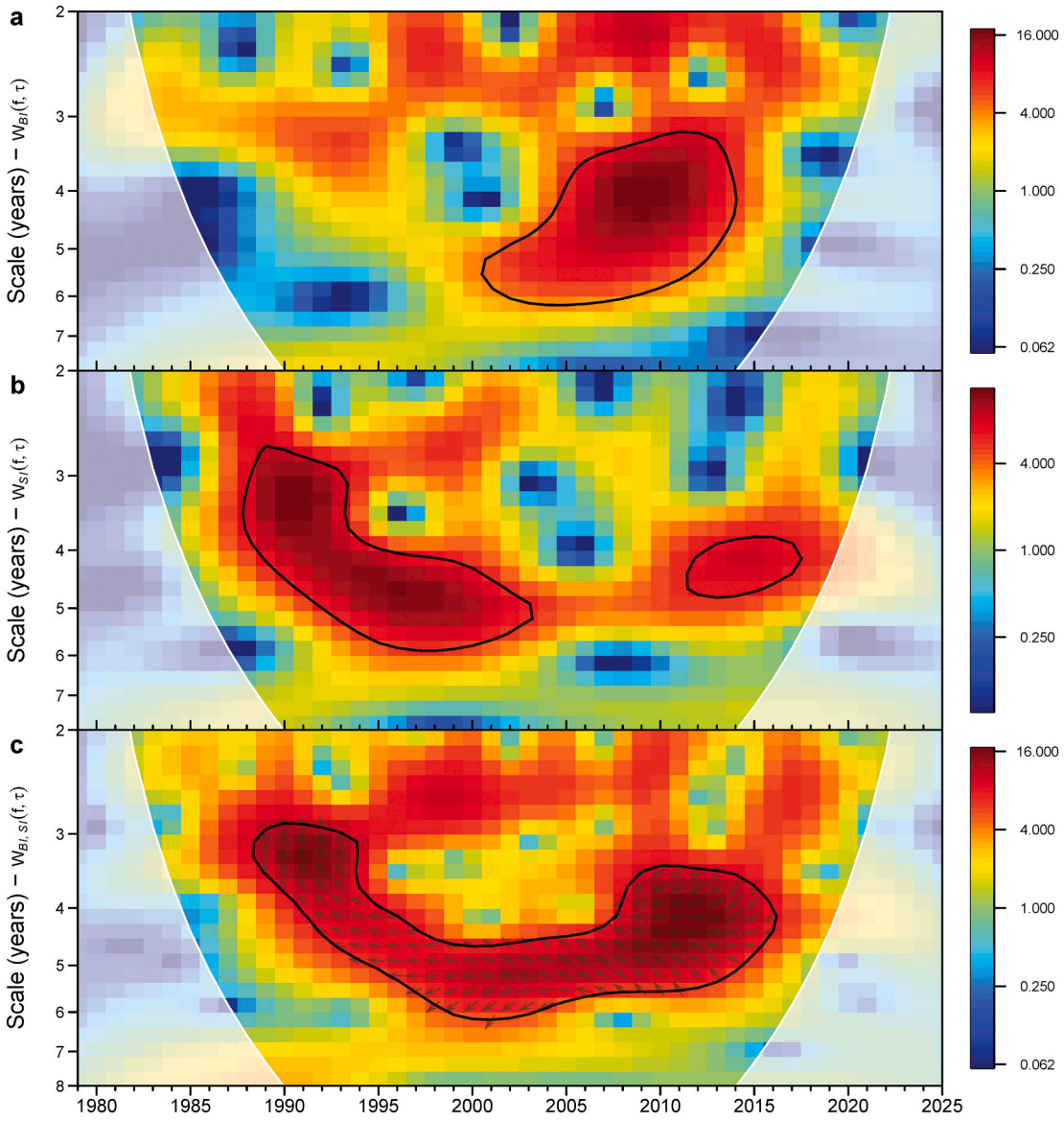


Fig. 6. a) Wavelet power spectrum of BI-SSB (South Georgia) mature female abundance. b) Wavelet spectrum of Signy Island population index. c) Cross-wavelet transform showing shared power and phase relationships between BI and SI, indicating covariation across time scales. Arrows denote phase: right = in phase, left = anti-phase, up = SI leads by $\pi/2$, down = BI leads by $\pi/2$. Black contours mark significant variation (compared to null model; i.e., red noise). Pale areas show less reliable values due to edge effects. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

population projections can also be used (IUCN, 2024). The population assessment for South Georgia spanned two generations, but in addition to the three-generation projection, there was strong empirical support for a three-generation decline at South Georgia. As the wavelet analysis, IPM results, and Signy Island population dynamics show, the decline outlasted several short-term fluctuations, and it was detected region-wide.

In north-western South Georgia, Bird Island was long considered an epicentre of Antarctic fur seal recovery following the end of commercial sealing in the 20th century (Bonner, 1968; Payne, 1977). Recolonisation of South Georgia likely peaked by 2009 with breeding habitat saturation (Forcada et al., 2023b), although Bird Island was already declining due to environmental pressures, worsened by a major population collapse in the winter of 2009 (Forcada and Hoffman, 2014). From January 2009 through to mid-2010, the krill biomass around South Georgia was very limited. Monitored colonies of Gentoo penguins (*Pygoscelis papua*) at Bird Island and Maiviken had catastrophic breeding failures and increased adult mortality, and the icefish (*Champsocephalus gunnari*) diet was very low in krill during 2009 (Jones et al., 2026) compared to other years. No krill were caught at South Georgia in 2009, and fishing was still limited in 2010.

At that time, it was unclear whether this decline extended across the entire archipelago, but recent data reveal consistent declines at Maiviken and at the other representative sites surveyed in 2022, and also at Signy Island, in the South Orkneys. There, numbers of temporary migrants, largely from South Georgia, rose in the mid-1980s, peaking in the 1990s with increasing subadult and adult male presence. However, pup counts have remained very low, and total counts have dropped sharply since 2010 (Carlini et al., 2006; Dunn et al., 2025), mirroring the decline at Bird Island and supporting a broader regional downturn.

Based on the estimated reduction and ongoing decline, this assessment supports a Red List category of 'Endangered' under criterion A2 for South Georgia, because the causes of the reduction have not ceased, are not fully understood (see section on "Threats"), and in great measure are

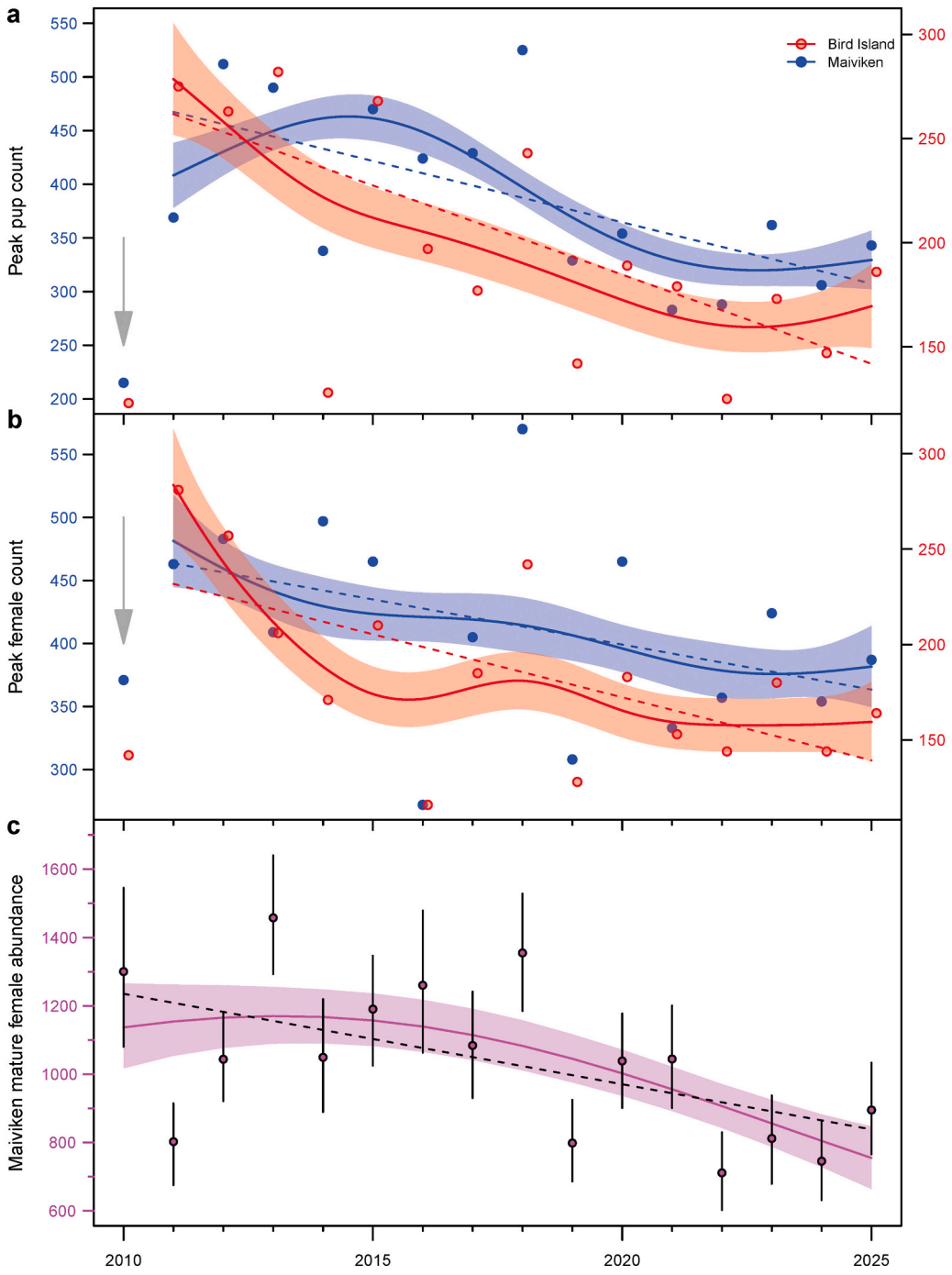


Fig. 7. *a)* Counts of pups and *b)* mature females at Maiviken and Bird Island during peak pupping (2010–2025). Points show observations; solid lines and shaded areas are Poisson GAM fits; dashed lines indicate significant linear trends from robust linear regression models. Grey arrows mark first post-collapse counts (2009), reflecting breeding deferral due to an extreme environmental anomaly. *c) Absolute m*ature female abundance at Maiviken (including non-breeders). Vertical bars are 95% credible intervals; trends are shown with low-pass filter (smoothed curve) and linear regression line (dashed line).

unlikely to be reversible without mitigation of greenhouse warming and other anthropogenic pressures. Compared to the previous assessment (Hofmeyr, 2016), this is a "nongenuine change", according to IUCN definitions (pg. 13; IUCN, 2024): "the change in category is the result of better knowledge about the taxon, e.g. owing to new or newly synthesized information about the status of the taxon (e.g., better estimates for population size, range size or rate of decline)". In this case, insufficient data led to incorrect assumptions about population size and growth for South Georgia (Appendix 5, Supplementary material), and a 'Least Concern' classification, even though a population decline was already mentioned.

In contrast, the South Sandwich Islands may represent the only increasing breeding aggregation of Antarctic fur seals in the South Atlantic region. With its current projected size and empirical growth rates recently observed at Zavodovski Island, this population could be comparable to or even larger than the current population at the South Shetland Islands. This requires further investigation, especially given the unknown genetic identity of breeders and pups, which could potentially make it a distinct subpopulation.

Table 2
Antarctic fur seal population change at the South Sandwich Islands. The first three columns are uncorrected pup counts (n^p), adjusted mature population estimates in year t ($\boldsymbol{N_t^M}$), and annual change with respect to previous estimate ($\boldsymbol{AC}$), with standard error in parentheses. The last two columns show the percentage of annual change and net mature population change over three generations. (*) Underestimated pup count. (‡) Projected values using average annual change.

Location		Season			% Annual change (3*G*)	Population change (3*G*)
		1997/98	2011	2024		
South Sandwich	n_t^p	1752	2914		3.12 (0.27) ‡	4430 (458)‡
	$\boldsymbol{N_t^M}$	3616 (130)	5019 (177)	8045 (406) ‡		
	$\boldsymbol{AC}$		1.026 (0.004)	1.037 (0.005)‡		
Zavodovski Is.	n_t^p	500	680	1265	3.13 (0.22)	
	$\boldsymbol{N_t^M}$	1032 (37)	1171 (41)	2299 (98)		1267 (105)
	$\boldsymbol{AC}$		1.010 (0.004)	1.053 (0.004)		
Visokoi Island	n_t^p	900	2040			
	$\boldsymbol{N_t^M}$	1858 (67)	3514 (124)			
	$\boldsymbol{AC}$		1.053 (0.004)			
Candlemas Is.	n_t^p	346	191*			
	$\boldsymbol{N_t^M}$	714 (26)	329 (12)			
Saunders Island	n_t^p	3				
	$\boldsymbol{N_t^M}$	6 (0.3)				
Thule Island	n_t^p	3	3			
	$\boldsymbol{N_t^M}$	6 (0.3)	5 (0.2)			

4.1. Threats

Greenhouse warming poses major threats to Antarctic fur seals and their ecosystems, affecting food availability, habitat, life history, and population dynamics (Forcada and Hoffman, 2014; Forcada et al., 2023b; Forcada et al., 2008; Krause et al., 2024; Ouled-Cheikh et al., 2024; Schwarz et al., 2013). Of particular concern are impacts on Antarctic krill (*Euphausia superba*), the primary prey of fur seal populations in the South Atlantic region. Sea ice contraction and warming disrupt krill biomass, distribution, physiology, and behaviour (Atkinson et al., 2019; Hill et al., 2013; Kawaguchi et al., 2024; McBride et al., 2021); whereas optimal sea ice conditions support strong krill cohorts, which enhance maternal foraging efficiency and pup growth in fur seals (Hiruki-Raring et al., 2012; Osman et al., 2004; Reid et al., 1999). Krill recruitment failures, linked to warming and low sea ice concentration, drive fur seal population declines at South Georgia (Croxall et al., 1988; Croxall et al., 1999; Forcada and Hoffman, 2014; Forcada et al., 2023b; Forcada et al., 2008). Here, krill biomass depends on advection from the Antarctic Peninsula and Weddell Sea (Mackintosh, 1972; Marr, 1962), leading to a highly variable availability to predators (Murphy et al., 2017; Murphy et al., 2007a; Murphy et al., 2007b). Sustained food shortages reduce fur seal breeding success and first-year survival, increase adult mortality and generation time (Forcada et al., 2023b; Forcada et al., 2008), and select for fitter individuals at the cost of overall population declines (Forcada and Hoffman, 2014).

Antarctic krill is a critical resource for millions of predators, including recovering whale populations that could now be dominant krill consumers (Baines et al., 2022; Biuw et al., 2024; Savoca et al., 2024; Zerbini et al., 2019). Antarctic fur seals, which rebounded from near extirpation in a whale-depleted ecosystem (Hoffman et al., 2022), now face renewed competition as whale populations recover, and krill distribution contracts southward due to climate change (Atkinson et al., 2019). Krill availability may be already limiting some recovering/recovered whale populations (Pallin et al., 2023), and similar implications for fur seals can be expected. However, without current and accurate estimates of krill demands by whales and other predators, the threat of competitive exclusion of krill to Antarctic fur seals remains difficult to quantify.

Simultaneously, a growing multinational krill fishery (CCAMLR, 2024) operates near important breeding aggregations of krill-dependent predators, including fur seals, seabirds and whales, with impacts that are difficult to quantify and manage (Lowther et al., 2020; McBride et al., 2021; Watters et al., 2020). Where there are locally high levels of competition between Antarctic fur seals and fisheries (e.g., Bamford et al., 2021; Owen et al., 2024), intensive krill extraction may lead to localized depletion of krill biomass for the predators (Cappell et al., 2022; Lowther et al., 2020; Watters et al., 2020), unless it is specifically avoided. Moreover, allocated krill extraction limits do not directly take climate change effects on krill into account, despite being identified as a potential risk to krill-dependent species in a fishery management context (Reiss et al., 2017). Consequently, the threat of competitive prey exclusion by fisheries is challenging to assess.

The role of pathogens, including those of anthropogenic origin, on Antarctic fur seal populations has not been considered significant until recently, while systematic sampling and epidemiological studies are lacking (Forcada, 2021). However, a highly pathogenic avian influenza (HPAI) H5 virus emerged in South American wildlife in 2022, rapidly spreading and causing mass mortality in birds and pinnipeds (Kuiken et al., 2026). It reached South Georgia in 2024, initially killing mostly brown skuas (*Stercorarius antarcticus*), elephant seals (*Mirounga leonina*), and Antarctic fur seals (Banyard et al., 2024; Bennison et al., 2024). Mortality in fur seals continued in 2025, although limited site access hampers robust impact assessments. HPAI H5's broad host range and virulence pose a significant, yet unevaluated conservation threat and, as with other aggressive pathogens, climate change is expected to intensify outbreak frequency, severity, and disease susceptibility (Gulland et al., 2022; Sanderson and Alexander, 2020).

Other potential threats include incidental mortality of Antarctic fur seals associated with fishing, and especially in mid-water trawls used by the Antarctic krill fishery (Hooper et al., 2005), although seal escape panels are now mandatory in the fishery, which significantly reduce mortality and is now very low. Indirectly, entanglement in plastic debris mostly from discarded or lost fishing gear is also a persistent problem for Antarctic fur seals at South Georgia (Waluda and Staniland, 2013). However, evaluation of the incidence of these impacts continues to be limited and very regional. Additionally, trace metals, particularly mercury and cadmium, are present in Antarctic fur seals breeding at South Georgia (Malcolm et al., 1994; Toro-Valdivieso et al., 2023), with concentrations that could be in the toxic range. The persistence and toxicity (Brault et al., 2013) of these and other emerging pollutants (e.g., Aznar-Alemany et al., 2019), including microplastics (Garcia-Garin et al., 2020), requires further assessment.

4.2. Protection

Antarctic fur seals were protected by the Antarctic Treaty Consultative Parties (ATCM) after adopting the Convention for the Conservation of Antarctic Seals (CCAS). This entered into force in 1978 and was

largely superseded by the Protocol on Environmental Protection of the Antarctic Treaty (Madrid, 1991; in force 1998), which explicitly prohibits commercial seal exploitation in Annex II. In 1999, the ATCM asked the Scientific Committee on Antarctic Research (SCAR) to review the status of Antarctic fur seals as a Specially Protected Species (SPS). Based on population trends, SCAR concluded they were neither threatened nor endangered under IUCN criteria (SCAR, 2006) (but see Appendix 5, Supplementary material). Consequently, the ATCM removed fur seals from the SPS list through Measure 4, although without implementing a monitoring or reassessment plan (Jabour, 2008).

Antarctic fur seals are protected under CITES Appendix II. South of 60°S, protection also falls under the Antarctic Treaty System and by designated areas such as Antarctic Specially Protected Areas (e.g., ASPA 149 in the South Shetland Islands) and marine protected areas such as the South Orkney Islands Southern Shelf Marine Protected Area (SOISS MPA) (CCAMLR, 2009). North of 60°S, they are mostly beyond-national-jurisdiction, but under national-jurisdiction areas in the CCAMLR convention area, which extends to the Polar Front. A major safeguard is the South Georgia and South Sandwich Islands MPA (1.24 million km^2), of which 470,000 km^2 are designated as no-take zones (GSGSSI, 2025), including the area within 30 km of the coast. Krill fishing is prohibited throughout the fur seal breeding season, and is only open for five months, although many fur seals, especially juveniles and breeding females, remain in the area during this time.

Additional effective conservation measures could be based on better knowledge of potential fishery impacts, natural sources of competitive prey exclusion, and the overarching role of greenhouse warming, including on Antarctic krill and the management of its commercial extraction. These measures would need to be effectively supported with regular assessments of the affected fur seal subpopulations.

Animal ethics

All animal handling procedures were evaluated and approved by the Animal Welfare and Ethics Review Body at the British Antarctic Survey, and this research was conducted under annual Regulated Activity Permits issued by the Government of South Georgia and the South Sandwich Islands (GSGSSI). Samples originating from South Georgia Islands were imported under permits from the Convention on International Trade in Endangered Species, and exported under permits issued by the GSGSSI and the UK Department for Environment, Food and Rural Affairs, under European Communities Act 1972.

CRediT authorship contribution statement

Jaume Forcada: Visualization, Validation, Supervision, Software, Resources, Methodology, Investigation, Formal analysis, Data curation, Conceptualization, Writing – original draft. **Pete Bucktrout:** Resources, Data curation. **Martin A. Collins:** Supervision, Project administration. **John Dickens:** Resources, Data curation. **Michael Dunn:** Supervision, Resources, Data curation. **Nathan Fenney:** Resources, Data curation. **Joseph I. Hoffman:** Resources, Formal analysis, Data curation, Writing – review & editing. **Philip R. Hollyman:** Supervision, Project administration. **Anneke J. Paijmans:** Resources, Formal analysis, Data curation. **Andrew G. Wood:** Supervision, Project administration, Data curation.

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Declaration of competing interest

All authors have nothing to declare.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.biocon.2026.112005.

Data availability

All the Antarctic fur seal data from Bird Island, South Georgia, and Signy Island, South Orkney Islands, used in the analysis are part of the British Antarctic Survey (BAS) core science programme. It was generated by zoological field assistants and scientists working for BAS since 1978 and is curated by the BAS Polar Data Centre. These and additional data and software required for reproducibility are available at https://github.com/JaumeForcada/Antarctic-fur-seal-IUCN-Assessment-2025/tree/main (Forcada, 2025) (doi:https://doi.org/10.5281/zenodo.15848682).

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