Quantitative assessment of the Antarctic fur seal IUCN Red List category in 2025

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Abstract

The IUCN Red List assessment of the Antarctic fur seal was last updated in 2016 and assigned a category of Least Concern. Here, I provide the quantitative basis of a new assessment, using the latest data available for all the distribution range, including a new analysis of the South Georgia subpopulation. This subpopulation comprises 96% of the global population and is therefore critical to assign a reliable Red List Category for the species. The results indicate an average annual change between 2007/09 and 2022 of -3.93% (SD=0.61) for South Georgia, and an estimated reduction over three generations of -0.57 (SD=0.05). With a mature population of 1,024,797 [95% CI: 873,500; 1,200,048] seals in 2022 and new adjustments for pre-breeders and pre-territorial individuals for 2022, the most recent total population at South Georgia would be 1,983,687 [1,606,408-2,411,876], approximately 1.5 million seals less than in 2007/9. This decline is well supported by an associated decline of temporary migrants largely from South Georgia to Signy Island, South Orkney Islands, evaluated over 49 consecutive survey years. Elsewhere in the South Atlantic region of the Southern Ocean, Bouvetøya which was the second largest subpopulation had an estimated 3-generation reduction of -0.65 (SD=0.03). But the South Shetland Islands is now the most affected subpopulation, with an estimated 3-generation reduction of -0.91 (SD=0.001), and can be considered Critically Endangered. In contrast, the East Antarctica subpopulation continues to be Least Concern, and with an estimated 2.62% (SD=0.09) annual increase is now the second largest subpopulation, although some of its breeding locations are still Data Deficient. With an overwhelming influence of South Georgia, the global reduction was estimated as -0.57 (SD=0.05). As the causes of the reduction are highly unlikely to be reversible, have not ceased, and some are not yet understood, the results support a Category of Endangered according to criterion A2 for the Antarctic fur seal. This important change, from Least Concern, is due entirely to newly obtained data, which supersedes previous insufficient and some incorrect data which supported the previous assessment.

# Contributions:

Data support and project management – All the Antarctic fur seal data from Bird Island, South Georgia, and Signy Island, South Orkney Islands used in this 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.

Genetic recapture data – Bird Island samples were analysed and contributed by the J. Hoffman lab at University of Bielefeld, Germany, especially by J. Hoffman and A. Paijmans in collaboration with BAS.

Additional data and project management – South Georgia mainland, South Sandwich Islands, and Signy Island: Bucktrout, P., Collins, M., Coleman, J., Dunn, M., Dickens, J., Fenney, N., Fox, A., Hollyman, P., and Ratcliffe, N., Wood, A. G.

Data support from other locations – de Bruyn, N., Delord, K., Guinet, C., Goldsworthy, S., Jordaan, R., Krause, D. J., Lea, M.-A., and Lowther, A. Below, section ‘Pup count data for other subpopulations’ lists additional references when data were obtained from the literature.

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**Keywords:** Antarctic fur seal, *Arctocephalus gazella*, abundance, assessment, decline, reduction, IUCN, Red List.

# 1 Introduction

The Antarctic fur seal (*Arctocephalus gazella*) is one of the smallest otariids (eared seals), and has a circumpolar distribution around Subantarctic and Antarctic islands of the Southern Ocean where it aggregates to breed. It has a four-month lactation, which is one of the shortest in its family, probably as an adaptation to the extreme seasonality of its nursing environment. Contrary to other Antarctic pinnipeds, which primarily rely on stored energy reserves during lactation, it requires constant foraging to rear the offspring, and heavily relies on a nearby productive and predictable foraging environment. Additionally, it is highly sexually dimorphic, with a polygynous breeding system that significantly determines longevity and lifetime breeding success. Despite being physiologically reproductive at ages three to five, mature males mostly hold breeding territories between ages nine and ten and have brief reproductive lives subsequently. Starting at age three and above, females normally produce a single pup nearly every year and can live up to 20 years or more. Due to its high fecundity and distribution in highly productive waters, the Antarctic fur seal is the second most abundant pinniped in the Southern Hemisphere, and the most abundant otariid globally ([Wickens and York 1997](#Xaa71d90870b046cb63037efa6453bd62bc360b3); [Costa, Weise, and Arnould 2007](#Xac115291acd5d7821a7f4ce934957fadbf23378); [Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)). As a numerically important predator of Antarctic krill (*Euphausia superba*), it is a main component of Southern Ocean ecosystems, particularly of the South Atlantic region ([Croxall and Prince 1979](#Xbfbe1e8e885e11c1ae9f7efc08f7e25e569b821); [Croxall et al. 1988](#ref-RN1899); [Agnew 1997](#ref-RN1960)), being a key indicator species of their state, function, and services.

According to Humble et al. ([2018](#ref-https://10.1534/g3.118.200171)) and Paijmans et al. ([2020](#Xb6935f476e50e679ddb786aa09c4a67d56b3808)), there are at least four distinct genetic groups or subpopulations, with the largest found in the South Atlantic sector of the Southern Ocean, including South Georgia, Bouvetøya, and the South Shetland Islands ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947); [Forcada and Staniland 2018](#Xc3f2e89d9e803be54eeddf525438cc95624fdb5)) (**Fig1**). Together, these three subpopulations comprise approximately 98% of the global abundance, but all have experienced rapid declines due to increasing external pressures ([Forcada 2021](#X18803383f3700fe6c7fd758315bce727fe89dbe); [Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947); [Forcada and Hoffman 2014](#ref-https://doi.org/10.1038/nature13542); [Krause et al. 2022](#ref-https://10.3389/fmars.2021.796488), [2024](#ref-https://doi.org/10.1111/mam.12327); [Hofmeyr 2016](#X71f83c25f5844e56179bf393f49eabea0997d1d)).

At Bird Island (NW South Georgia; **Fig.2b**), fur seal pup production declined from 60,500 to 27,900 between 2009 to 2017, or 9.2% per year, and the mature female population declined annually by 7.2% ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)). At Bouvetøya (**Fig1**; 5), the second largest subpopulation with approximately 66,000 seals by 2002 ([Hofmeyr et al. 2005](#X7454ecdc990e4f863ac1919f8121c3fd3669348)), pup counts declined annually by 5.6%, between 2001 and 2007 ([Hofmeyr 2016](#X71f83c25f5844e56179bf393f49eabea0997d1d)). And at the South Shetland Islands (**Fig1**, 4; **Fig2a**), with approximately 41,000 seals in 2002 ([Krause et al. 2022](#ref-https://10.3389/fmars.2021.796488)), annual pup counts at study areas in the southwest declined by 90.9% between 2008 and 2023 ([Krause et al. 2024](#ref-https://doi.org/10.1111/mam.12327)), or a 5.6% per year. At the entire archipelago, counts declined from 10,057 pups in 2002 to 7,602 in 2008 ([Krause et al. 2022](#ref-https://10.3389/fmars.2021.796488)), equivalent to an annual decline of 4.6%.

In the South Atlantic region, subpopulations are declining because of directional environmental effects, particularly at South Georgia ([Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f); [Forcada and Hoffman 2014](#ref-https://doi.org/10.1038/nature13542); [Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)). However, there are known competing effects such as local top-down control ([Schwarz et al. 2013](#ref-RN5194); [Krause et al. 2024](#ref-https://doi.org/10.1111/mam.12327)), and other potential effects which are difficult to quantify ([Forcada 2021](#X18803383f3700fe6c7fd758315bce727fe89dbe); [Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947); [Krause et al. 2024](#ref-https://doi.org/10.1111/mam.12327)). These include, for example, competitive exclusion from staple prey by increasing whale populations, e.g., Baines et al. ([2022](#X7decfbfbe61778782be622c59e3f11e1dc95986)), Biuw et al. ([2024](#ref-RN6224)), and Savoca et al. ([2024](#ref-RN6252)), and by locally increasing commercial fisheries ([Lowther et al. 2020](#X68fe48c47d2e03058dd08a74bfdc98fea8842d2); [Watters, Hinke, and Reiss 2020](#ref-RN6223)); emerging pollutants (e.g., [Aznar-Alemany et al. 2019](#X53d51a7cf4ff477eeb415d53a6a7d36280279c8)), including microplastics ([Garcia-Garin et al. 2020](#Xdda0bdf609d62cbd9c138f30cb1cb33de49dd1a)), with concerns over their persistence and toxicity (e.g., [Brault et al. 2013](#ref-RN6250)); and outbreaks of new epizootic diseases such as avian influenza (H5N1) ([Bennison et al. 2024](#ref-RN6219); [Brownell et al. 2024](#ref-RN6247)).

Other breeding locations, currently part of a single genetic group named here the ‘East Antarctica’ subpopulation, are distributed in subantarctic islands of the southern Indian and southwestern Pacific Oceans (**Fig1**; locations 6-10). Recently, pup counts at most locations, including Marion Island (Prince Edward Islands) ([Wege et al. 2016](#ref-https://doi.org/10.1111/mms.12306)), Possession Island (Crozet archipelago), Courbet Peninsula (Kerguelen archipelago) ([Guinet et al. 2025](#ref-RN6225)), Heard Island (Heard Island and McDonald Islands) ([Page et al. 2003](#X550e3cdbf2f36eac68c51272c4c188169afed79)), and Macquarie Island ([Goldsworthy et al. 2009](#X900c7297a62c11770e773a1d7a5b1f7c444134f)) (**Fig. 1**), have remained stable or slowly increasing annually, by approximately 1 to 4%.

The latest assessment of the species by the International Union for the Conservation of Nature (IUCN) ([Hofmeyr 2016](#X71f83c25f5844e56179bf393f49eabea0997d1d)) recognises that the global population is in decline, which is mostly driven by the rapid declines observed in the subpopulations of the South Atlantic region. However, the Red List category assigned is *Least Concern*, which is unlikely to reflect the real magnitude of recent population reductions. Here, I reanalyse the change of each subpopulation using the latest available data to provide an up-to-date assessment for the species. I first reanalyse data from Bird Island, South Georgia, as main source of correction factors and adjustments across the species range, because comparable data from other regions are mostly lacking. The results include adjustments to scale up pup production counts to total mature population; and estimates of generation time (generation length, hereafter), required to evaluate population reduction. The analysis also evaluates and projects the overall population change at South Georgia with the most recently collected survey data at selected locations. I also analyse count data from Signy Island, representative of the seasonal male migration from South Georgia to the South Orkney Islands, to track and confirm by proxy nearly five decades of population change at South Georgia. Next, I use the most recent population data available from all the other species breeding locations to evaluate conservation status according to IUCN categories and criteria ([IUCN 2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)).

# 2 Materials and methods

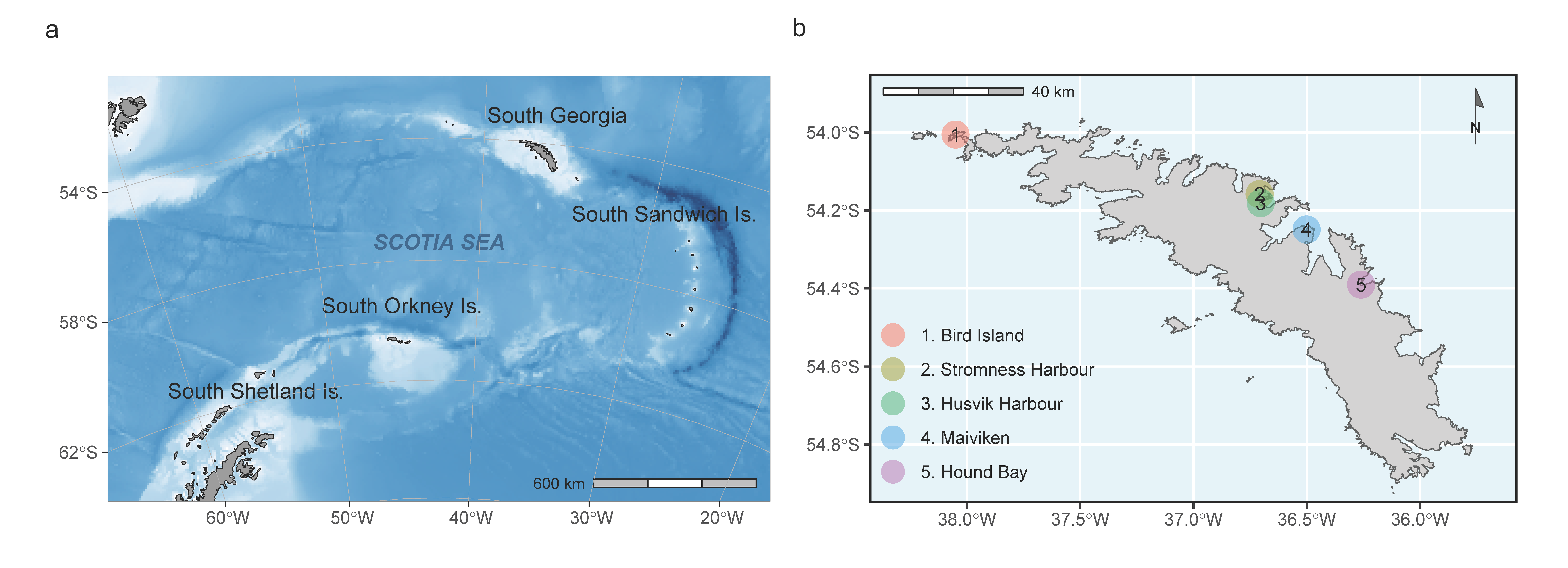
## 2.1 Study populations, distribution and abundance

South Georgia, in the Southwest Atlantic region of the Southern Ocean (**Fig1**), is by far the largest Antarctic fur seal subpopulation with an estimated 97-98% of the global pup production and 3.5 [3.1, 3.9] million seals in 2009 ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)). The subpopulation includes small numbers of breeders in the South Orkney and South Sandwich Islands archipelagos (**Fig.1**), also located in the Scotia Sea (**Fig.2a**), although the genetic identity of the South Sandwich seals has not been assessed. The South Orkney Island group (**Fig.2a**) has a population almost exclusively composed of non-resident juvenile and adult males in post-breeding temporary migration, largely from South Georgia ([Boyd et al. 1998](#ref-https://doi.org/10.1139/f97-314); [Kightley and Caldwell 1982](#X5cb60c4476d8fce32c2d59e0a2c1d0970791bf1); [K. A. Jones et al. 2021](#X9006c39b7700a0009ae080b4443d31b00440e5d); [Laws 1973](#Xa8b4a9a05b653b8343c79051227d0e705fff22f)), although there are small numbers of temporary migrants from the South Shetland Islands ([Lowther et al. 2020](#X68fe48c47d2e03058dd08a74bfdc98fea8842d2); [Ouled-Cheikh et al. 2024](#ref-https://doi.org/10.1111/gcb.17191)), given the relative proximity of both archipelagos. Males from South Georgia and South Shetland Islands typically migrate temporarily along the Weddell Sea and west Antarctic Peninsula, and as far South as the Bellingshausen Sea ([K. A. Jones et al. 2021](#X9006c39b7700a0009ae080b4443d31b00440e5d); [March et al. 2021](#Xc0a33997345731b45febe23c3f6de2c7a2480b8)). There are also incidental records of pups in the Antarctic Peninsula, e.g., near Palmer Station ([Larsen et al. 2025](#ref-https://doi.org/10.1002/ece3.70833); [Parmelee et al. 1977](#ref-RN6230)), but these are exceptional and extralimital within the species current breeding range.

The numbers of breeding females and pups at the South Orkney Islands are extremely low, and counted as less than 70 in the entire archipelago in the early 1970s. At Signy Island, which has been monitored annually since 1977 ([Kightley and Caldwell 1982](#X5cb60c4476d8fce32c2d59e0a2c1d0970791bf1)), despite several annual counts of more than 20,000 individuals between 1994 to 2000, only a maximum of five pups were recorded in any year of the same period, and pup numbers have declined to near zero since 2000 ([Waluda, Gregory, and Dunn 2010](#Xf718da9b414ff6758587e2ce5e3e4dfc1b5d9bf)). Similarly, 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](#Xa92e542fabc51663fbb13764d3e5e4f00790b0e)). At the South Sandwich Islands, breeders and pups have rarely been counted due to difficult access to locations, but since the early 1960s ([Holdgate 1963](#Xc0e8050be998954443ece7d4713097962a9f9b5)) and after the regional recovery from sealing, pup numbers increased to at least 1,750 by 1997/98, of which 500 were attributed to Zavodovski Island ([Convey, Morton, and Poncet 1999](#Xa202934fdec7762213b6c529a608dd8c5d6b312)), which was counted again in 2023/24 (**Table 1**). Published records with more recent data for other islands, including Visokoi which had a count of 900 in 1997/98, are lacking.



**Figure 1**: Distribution of breeding populations of Antarctic fur seals with detail on genetic subpopulations. The table shows estimated pup production up to 2010 or before, for remote locations not recently surveyed. Colours corresponds to identified genetic subpopulations



**Figure 2**: **a** Scotia Sea, with breeding locations of the putative genetic subpopulation of South Georgia, including South Sandwich and South Orkney Islands, and the subpopulation of the South Shetland Islands. **b**, Locations of South Geogia 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**)

## 2.2 Data

### 2.2.1 South Georgia

Antarctic fur seal demographic, genetic, and count data representative of South Georgia were collected at a long-term monitoring location of Bird Island named Special Study Beach (SSB) (54.0116S, 38.0507W; location 1, **Fig.2b**), from 1979 to 2025 ([Croxall and Prince 1979](#Xbfbe1e8e885e11c1ae9f7efc08f7e25e569b821); [Doidge, Croxall, and Baker 1984](#Xc0330eec81292c180fd0e3922fccc7da467dfa9); [Duck 1990](#X23e4bef500422800e910360c7394b16019ef1b7); [Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f); [Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)). Additional data were obtained from Maiviken (54.2435S, 36.5033W; location 4, **Fig. 2b**), where a set of colonies named Burnet 1-3, Little, Poa 1-3 and Tortula are counted annually during the breeding season. Maiviken is situated on South Georgia mainland approximately 105 km to the east of Bird Island.

#### 2.2.1.1 Bird Island capture-recapture and productivity data

Capture-mark-recapture of individuals, monitoring of pup production, and collection of individual count data at Bird Island used in this analysis started in 1979 ([Doidge, Croxall, and Baker 1984](#Xc0330eec81292c180fd0e3922fccc7da467dfa9)) and have been consistently collected since 1984 onwards ([Duck 1990](#X23e4bef500422800e910360c7394b16019ef1b7); [Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f)). Annually at SSB, from November 1st to mid-January, daily numbers of new and total females, newborn pups and territorial males are consistently recorded during twice-daily surveys. Within a season, female breeding status and performance is monitored through tags, and territory tenure by males is monitored through individual temporary paint marks. For between-year recaptures, a variable sample of females has been captured since 1984 every season, reliably aged from sectioned post-canine teeth, marked with plastic tags on the fore flippers, and subcutaneous electronic chips (Passive Integrated Transponder tags, PIT-tags) fitted since 1997. Flipper tags have been given to each cohort of newborn pups since 1984 and PIT-tags implanted since 2001; and genetic samples from pups and breeding females are collected upon capture. For each territorial male, genetic tagging is obtained each season with a small biopsy remotely acquired using a low-power crossbow bolt with a modified sampling syringe. Females and males are highly philopatric and return ashore to breed almost every year ([Lunn and Boyd 1991](#ref-https://doi.org/10.2307/1381999); [Hoffman and Forcada 2012](#X6014e6f5551ad154b3843f16b9125097a6c0ed9); [Hoffman, Trathan, and Amos 2006](#X8e0a2e29f9369516889c12b0123f2df678c9dee)), once established as breeders and territorials respectively. Early pup mortality is estimated from the recovery of dead pups, prior to flipper-tagging approximately 1.5 months after birth.

#### 2.2.1.2 Count data

Count data were collected as close as possible to the peak pupping day. The pupping season, from mid-November to mid-January, peaks with high spatial synchrony between the 6th to 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 later dates ([Duck 1990](#X23e4bef500422800e910360c7394b16019ef1b7); [Forcada et al. 2005](#ref-https://doi.org/10.1890/04-1153); [Hofmeyr et al. 2007](#Xe8a173ee12d54ef39940b83dee14ac2b58b5d9b); [Goebel et al. 2009](#X74871d8e082465d59429593f1672abee02367db)).

Apart from the daily counts at SSB during the breeding season, complete counts of the entire Bird Island were obtained in nine seasons, including visual counts in December 1988, 1989, 1990, 1994, and 1997, and photographic counts in December of 2003, 2008, 2016, and 2023. (Hereafter, a breeding season is referred to by the second year of the split-year austral summer, e.g., 2023-24 is 2024.). Counts were conducted from elevated vantage points in all the breeding beaches by trained biologists.

Comprehensive aerial photographic data of South Georgia mainland were obtained during two helicopter surveys of all the fur seal breeding beaches conducted in December 2006 and 2008. For this analysis I use the count data available at the repository Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947)), with emphasis on counts corresponding to locations 2 to 5 in **Fig.2b** to reassess the population at South Georgia. Surveys of these locations were repeated in December 2021 using RPAS (Remotely Piloted Aerial Systems). In these and other image-based surveys, two observers working independently using consistent training and methodology produced counts from digital images, classifying seals in four categories: pups, females, territorial males and non-territorial males.

From 2009 to 2025, colonies at Maiviken were visited every second day during the summer breeding season (November-February) to count numbers of fur seal males, females, pups and juveniles ([Hollyman 2021](#X481d90a8c47f53e0fd82e48bd0360471c588b9c)). The data record is from 2009 to date (2025), although counts from 2009 were sparse and likely to be inconsistent in methodology compared with subsequent records. Therefore, for this analysis I only retain the data for 2010 to 2025.

Altogether, and with a maximum straight-line distance between any two counting or monitoring locations of 125km, the data obtained for 2021/22 provide a representative sample of geographic population variation over space and time at South Georgia.

### 2.2.2 South Orkney Islands

#### 2.2.2.1 Count data

At Signy Island, South Orkney Islands (60.3385S, 45.0037W; **Fig.2**a), count data were collected around the entire island as part of a long-term monitoring programme which started in 1977 ([Kightley and Caldwell 1982](#X5cb60c4476d8fce32c2d59e0a2c1d0970791bf1)), and continued to date with only a few interruptions due to weather or logistic constraints ([Waluda, Gregory, and Dunn 2010](#Xf718da9b414ff6758587e2ce5e3e4dfc1b5d9bf); [Dunn et al. 2025](#ref-https://doi.org/10.1111/gcb.70290)). Counts by two trained observers using consistent methodology took place between mid-February and early March every year, when fur seals numbers peak.

### 2.2.3 Pup count data for other subpopulations

Available pup production and abundance data up to 2004 for all the species range are summarised in SCAR ([2006](#ref-RN5984)); although some of the numbers reported are known to be unreliable because are only guesses, due to lack of proper counting efforts, and use biased adjustments, all of which needs revision and reassessment, as is the case of the subpopulation of South Georgia. For other regions, many reported records are total pup counts at breeding locations, from which extrapolations to total population size were also produced in some occasions. As discussed in the **Population-reduction** section below, earlier extrapolations are based on inaccurate scaling factors, and, also, do not separate mature population from pre-breeders, which is a requirement in Red List assessments. Here, I only provide total pup production counts or estimates, summarised in **Table 1**, which I used in subsequent calculations together with the new mature population estimates for South Georgia.

| Breeding location | season | count | method | source | Notes |
| --- | --- | --- | --- | --- | --- |
| South Sandwich Islands | 1997/98 | 1,750 | Visual | Ref. 1 | Late February; UC |
| Zavodovski Island, SSI | 1997/98 | 500 | Visual | Ref. 1 | Late February; UC |
| 2023/24 | 1,265 | RPAS | Dickens (pc) | Peak pupping |
| South Shetland Islands | 1995/96 | 9,530 | Visual | Ref. 2 | Late January; UC |
| 2001/02 | 10,057 | Visual | Ref. 3 | Late January; UC |
| 2007/08 | 7,602 | Visual | Ref. 4 | Late December; UC |
| 2024/25 | 901 | Visual | Ref. 5 | Late December; UC |
| Nyrøysa, Bouvetøya | 1996/72 | 15,489 (754) | Visual | Ref. 6 | Early January |
| 1998/99 | 15,448 (370) | Visual | Ref. 6 | Early January |
| 2000/01 | 15,215 (353) | Visual | Ref. 6 | Early January |
| 2001/02 | 15,523 (480) | Visual | Ref. 6 | Early January |
| 2007/08 | 11,000 | ? | Ref. 7 | Extrapolation? |
| 2014/15 | 8,080 (310) | Visual | Lowther (pc) | Early January |
| Marion Island | 1999/00 | 343 | Visual | Ref. 8 | February; UC |
| 2000/01 | 464 | Visual | Ref. 8 | February; UC |
| 2003/04 | 744 (5) | Visual | Ref. 8 | February; UC |
| 2006/07 | 1,105 (9) | Visual | Ref. 9 | January; UC |
| 2009/10 | 1,379 (27) | Visual | Ref. 9 | January; UC |
| 2012/13 | 1,553 (64) | Visual | Ref. 9 | January; UC |
| 2015/16 | 2,052 (107) | Visual | de Bruyn (pc) | January |
| 2018/19 | 2,434 (169) | Visual | de Bruyn (pc) | January |
| 2021/22 | 2,528 (134) | Visual | Jordaan (pc) | January |
| 2024/25 | 3,172 (156) | Visual | Jordaan (pc) | January |
| Prince Edward Island | 2000/01 | 404 | Visual | Ref. 9 | Late December; UC |
| Crozet, Possession Is | 1999/00 | 234 | Visual | Ref. 10 |  |
| 2003/04 | 295 | Visual | Ref. 10 |  |
| 2020/21 | 504 | Visual | Ref. 11 |  |
| 2023/24 | 530 | Visual | Ref. 11 |  |
| Kerguelen, Nuageuses Is. | 2000/01 | 3,600 | Visual | Ref. 12 | December; UC |
| Kerguelen, Courbet Peninsula | 2000/01 | 1,600 | Visual | Ref. 12 | December; UC |
| 2009/10 | 4,287 | Visual | Ref. 11 | December; UC |
| 2023/24 | 4,793 | Visual | Ref. 11 | December; UC |
| Heard Island | 2000/01 | 1,012 | Visual | Ref. 13 | November - March |
| 2003/04 | 1,278 | Visual | Goldsworthy (pc) |  |
| McDonald Island | 1979/80 | 100 | Visual | Ref. 10 |  |
| Macquarie Island | 1999/00 | 152 | Visual | Ref. 10 | November - March |
| 2003/04 | 165 | Visual | Ref. 10 | November - March |
| 2011/12 | 189 | genetic | Goldsworthy (pc) | November - March |

**Table 1**. Antarctic fur seal pup counts obtained at breeding locations other than South Georgia and South Orkney Islands. Parentheses in *count* are estimated standard errors, normally obtained from mark-recapture estimates of pup production. *method* is either visual, RPAS (Remotely Piloted Air System), or both. *source* is either literature cited, or personal communications (pc) from various contributors, including those listed in next section. References cited are as listed here; Ref. 1: Convey, Morton, and Poncet ([1999](#Xa202934fdec7762213b6c529a608dd8c5d6b312)); Ref. 2: Meyer, Walker, and Holt ([1996](#ref-RN6244)); Ref. 3: Goebel et al. ([2003](#ref-RN5389)); Ref. 4: Goebel et al. ([2009](#X74871d8e082465d59429593f1672abee02367db)); Ref. 5: Krause, Woodman, and Goebel ([2025](#ref-RN6246)); Ref. 6: Hofmeyr et al. ([2005](#X7454ecdc990e4f863ac1919f8121c3fd3669348)); Ref. 7: Hofmeyr ([2016](#X71f83c25f5844e56179bf393f49eabea0997d1d)); Ref. 8: Hofmeyr et al. ([2006](#X3c880abc80a690b880856d0a6eda3322eff3c1d)); Ref. 9: Bester, Ryan, and M. ([2003](#X062aae40a7355b0f2fa83537e4d470cfbc50e7a)); Ref. 10: SCAR ([2006](#ref-RN5984)); Ref. 11: Guinet et al. ([2025](#ref-RN6225)); Ref. 12: Lea et al. ([2008](#ref-https://doi.org/10.3354/meps07305)); Ref. 13: Page et al. ([2003](#X550e3cdbf2f36eac68c51272c4c188169afed79)). In *Notes*, UC stands for undercount.

## 2.3 Analysis

### 2.3.1 Population modelling

#### 2.3.1.1 South Georgia

I obtained an up-to-date assessment for Bird Island and other locations at South Georgia with the latest available data and using population analysis methods of Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947)). The analysis used integrated population models (IPMs) to evaluate population numbers, vital rates and other demographic parameters, and corrections for seal survey counts. It combined different data sources including individual recapture histories of fur seal pups and adults, pup production, and individual daily count data. To evaluate abundance change and trends at locations away from SSB, I assumed that the dynamics of their daily counts are highly correlated to those at SSB. This is accurate within Bird Island and with Maiviken (MVK), another study site located 105km East of Bird island as the crow flies ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)), which is closer to the additional survey locations in 2022 (**Fig.2**b). However, I relaxed this assumption by also incorporating daily counts at Maiviken in the analysis. This accounted for differences in haul out patterns between this study location and SSB, and corrected counts at other locations based on their proximity to either study site.

##### 2.3.1.1.1 Integrated population models (IPMs)

###### 2.3.1.1.1.1 Females

I used the same models as described in Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947)) with different formulations for females and males. For females, the expected number of individuals in year +1 is described with the following age-stage-structured population projection model, which assumes a birth pulse and a pre-breeding census:

where for year ,

* is the number of pre-breeders for ages =1,…,7
* is the number of pre-breeders aged 7 or above never observed breeding
* is the number of mature non-breeders
* is the number of mature breeders
* is pup survival from birth to tagging at 1.5 months of age
* is apparent survival from tagging to the end of the first census year
* is apparent survival of seals aged =2,…,7 between and +1
* is apparent survival of pre-breeders never observed breeding between and +1
* is apparent survival of mature non-breeders between and +1
* is apparent survival of mature non-breeders between and +1
* is the probability that a pre-breeder of age starts breeding at that age between and +1
* is the probabilities of being in and or in +1, conditional on surviving
* is the probabilities of being in and or in +1, conditional on surviving
* is the proportion of females at birth
* is the number of breeding immigrants at +1 per mature female at .

The IPM’s likelihood is , and includes a multi-state Cormack-Jolly-Seber capture-mark-recapture model formulated as a Bayesian state-space model ([Gimenez et al. 2007](#Xaba4c64f3266160a4c6fc1e86c7de650be208e5); [Kéry and Schaub 2012b](#Xb9139cb6202d0cccee7ea863c385dad6efd7320)) with a state process and an observation process, denoted together as . The model includes 12 states and represents survival and accession to breeding for pre-breeders () of ages 3 to 7, survival and transition of mature breeders () and for skippers or non-breeders (), and two absorbing states, one for pre-bredeers older than 7 which are never seen breeding, and on for dead () or permanently emigrated females. The main data are the female encounter histories () as defined by categories specified in the observation process. The state process for marked individual , age , and year is

where rows and columns are departure and arrival states between years and +1, including an absorbing state, , for pre-breeders which are never observed breeding. The observation process is conditional on the true individual states, , in season and comprises five types of female observations:

* - observed as newborn, subsequently tagged and released as a pup
* - observed as pre-breeder of ages 1 to 7 or above (7+)
* - observed as breeder
* - observed as non-breeder

and an unobserved category, , which is dead or permanently emigrated. The observation process relates to the true states through the probabilities of detecting individuals observed as at time , , and is formulated as

where rows are states , for , , , and , and columns are observation types in year . Note that detection probabilities are combined for ages 1 to 3 (), which are less likely to be encountered, and for ages 4 to 7+ (), to avoid parameter identifiability problems due to lack of data when fitting the models.

The matrix population model, with a system process and an observation process, , contributes to estimate population sizes and demographic rates, including immigration (). Pup production data (), which is observed with little error at SSB ([Forcada et al. 2005](#ref-https://doi.org/10.1890/04-1153)), is equivalent to the observed breeding female population, and defines the observation process. For model fitting, I selected Poisson distributions to introduce demographic stochasticity, as follows.

Note that the observed pup production () results from the number of breeders, which includes new recruits from SSB, breeders already at SSB, and breeding immigrants from elsewhere. The distinction between and allows for estimates of the fecundity (or pregnancy) rate, , which is the number of mature females () in year which survive and breed in year +1, excluding recruits and immigrants in year +1, divided by the number of mature females surviving to year +1; and importantly, estimates of number of immigrants, . This is achieved through the observation process as

The last component of the likelihood, , evaluates the proportion of the estimated SSB population, , that represents a total daily female count at the SSB (denoted with superscript ). For this, daily counts obtained between November 1st and December 31st ( for day ) are modelled with a generalised additive mixed model (GAMM) with a Poisson-log-normal structure ([Gelman and Hill 2006](#X8f27e0392f3022422033ceaffc661bd8d9fd199)), which takes into account overdispersion. The more general model also considered autocorrelation of first order in female counts:

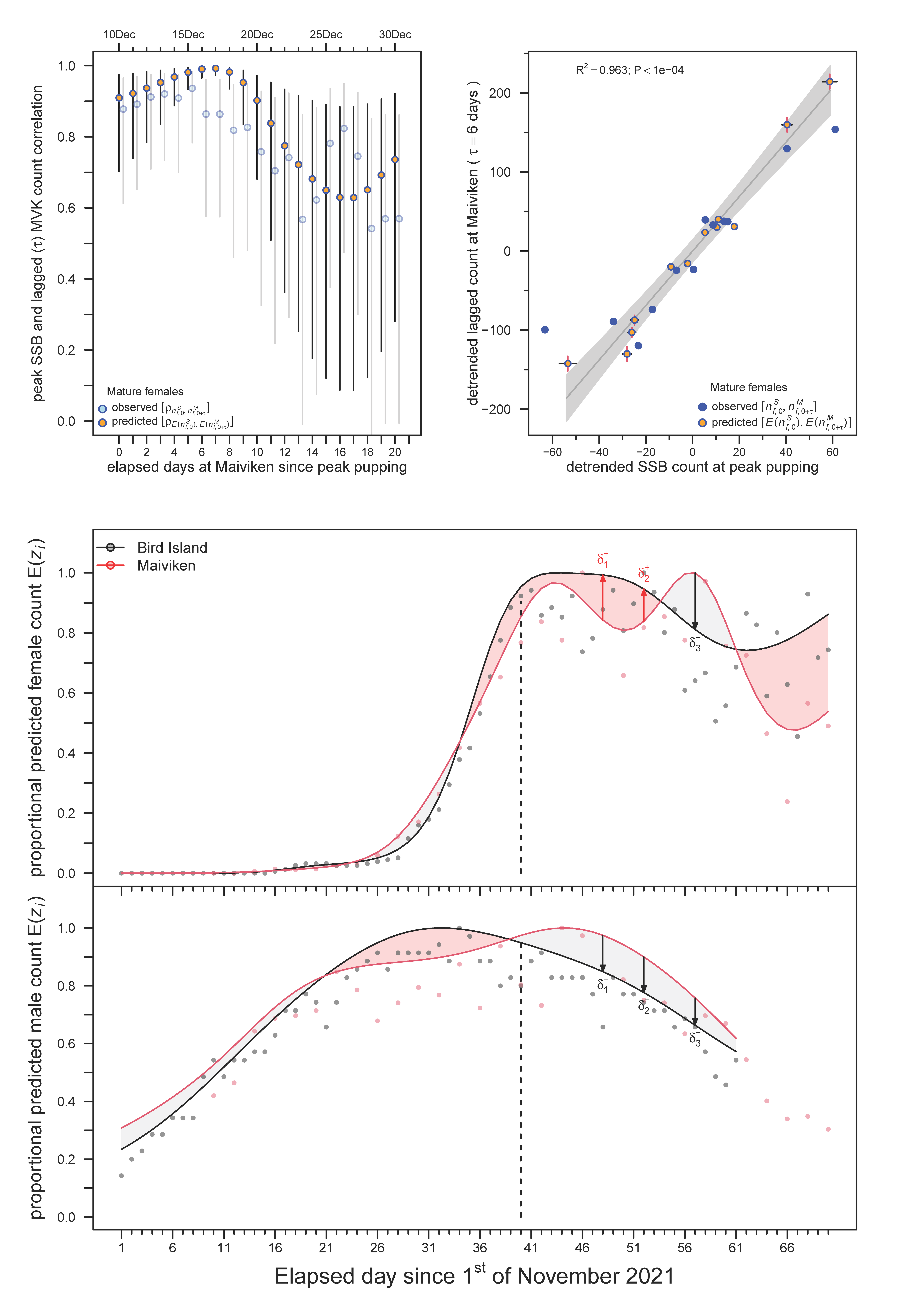
where is the th day of the survey season, are unknown parameters (penalties), is a vector of spline basis functions, is an autocorrelation parameter with values between -1 and 1, is the residual associated with observation at day t-1, and an overdispersion parameter. The likelihood is , where are smoothing parameters.

The combined likelihood produces derived quantities and , where , are mature non-breeding and mature breeding females respectively; and is the predicted female count at SSB on the day. These multipliers of observed counts scale up estimates to total number of mature

and breeding females

at other locations, where is the female count at colony on day . Note that the second quantity is equivalent to pup production, and the first quantity is the parameter of interest for the Red List assessment.

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 other locations, as previously shown ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)). However, correlation between locations decays fast after the first six days following peak pupping, largely due to differences in haul out behaviour. This is shown in **Fig.3** for female counts during season 2022.



**Figure 3**: Correlation of female counts at SSB and Maiviken (MVK; 105km E of SSB). Top left panel is the Pearson’s correlation coefficient of predicted (from GAMM model) and observed counts at SSB during peak pupping, and at Maiviken from 0 to 20 days after peak, for 2014 to 2025. The top right panel shows in detail the maximum correlation of observed counts, with the regression of predicted counts at MVK on day 6 after peak against SSB at peak; counts at both locations were detrended to remove observed long-term trends. The bottom panels show the fit of Poisson GAM models with predictions rescaled to provide proportional predicted counts (with values between 0 and 1) for breeding females and territorial males during season 2022, when RPAS flights were conducted. Dots are observed counts, the black dashed vertical line is the estimated day of peak pupping, red and grey shaded areas correspond to negative and positive differences in counts between locations due to differences in seal haulout behaviour, and coefficients are predicted differences between SSB and MVK on days when RPAS counts were obtained.

As seasonal count data were also available for Maiviken (MVK), I incorporated differences in haul out patterns between SSB and MVK to make observed counts at or near MVK scalable and comparable according to the ratios or , which relate specifically to SSB counts. For this, I obtained predicted counts at both locations from Poisson GAMs fited to daily data, and predictions were rescaled to range between 0 and 1; .

To obtain a corrected MVK count on day , I assume a difference of size in between locations. At the transformed scale,

, where is , when , and is when . See for example lower panels of **Fig. 3**. Thus, a rescaled MVK count with respect to SSB, is , where

, if

, if

, if .

This adds prediction uncertainty to counts away from SSB, more likely to follow a MVK haul out pattern, and for counts closer to SSB, some of the uncertainty can be reduced by obtaining and average corrected count at colony , , weighted by the inverse of the distance in km from to SSB and to MVK. This is obtained as

,

where and , with as distance in km. Thus, a count closer to SSB will assume a more similar daily haul out pattern to this location, with , whereas a count closer to MVK will have a stronger influence of , with .

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

and to account for pre-breeders and obtain an estimate of total number of females at a survey area I use ,

where is the estimated number of pre-breeders of age , for , at SSB.

###### 2.3.1.1.1.2 Males

The male IPM has a combined age-stage matrix model with pre-territorial males () of ages 1 to 11+ (ages 11 or older), and mature states including Territorial () and mature non-territorial (). The lowest observed age at first territory tenure is 7, and first-time territorials older than 11 are seldom observed. The expected number of individuals in year +1 is

where for year ,

* is the number of pre-territorial males for ages =1,…,11
* is the number of territorial males skipping a breeding season
* is the number of territorial males
* is pup survival from birth to tagging at 1.5 months of age
* is apparent survival from tagging to the end of the first census year
* is apparent survival of seals aged =2,…,11, between and +1
* is apparent survival of territorial males skipping a breeding season between and +1
* is apparent survival of territorial males between and +1
* is the probability that a male of age starts holding territory at that age between and +1
* is the probabilities of being in and or in +1, conditional on surviving
* is the probabilities of being in and or in +1, conditional on surviving
* is the proportion of females at birth
* is the the proportion of immigrants among territorial males at +1.

The male IPM’s likelihood is . It is similar to the female IPM likelihood, but the capture-mark-recapture component is split into separate likelihoods given the different data types (PIT-tag vs genetic recaptures), sample size, and short temporal overlap of two data sets. Pups with implanted PIT-tags at birth represent largely pre-territorial component, and are used to model survival and accession to territories, and , with likelihood ; and territorial males captured and recaptured through genetic sampling contribute to estimate their survival (), territory tenure () and temporary emigration rates (), with likelihood .

In the MSCJS model the state process equation for marked pre-territorial individual of age in year , is formulated as

where rows and columns are departure and arrival states between years and +1, assuming that at age 11 all males which survive are territorial. The observation process conditional on true individual states () comprises three types of observations:

* - observed as newborn, subsequently tagged and released as a pup
* - observed as pre-territorial of ages 1 to 11
* - observed as territorial.

and an unobserved category, , which is dead or permanently emigrated. The observation process includes the probabilities of detecting individuals observed as at time , , and is formulated as

where rows are states (pup), , for , , and , and columns are observation types in year .

As the elapsed time between birth and accession to territory can be 10 years or more, observations of pre-territorials becoming territorials over 25 years of study were only a small fraction of the total number of PIT-tagged male pups. This limited parameter estimability, statistical power and model selection, making IPM fitting inefficient. As a valid alternative ([Besbeas et al. 2002](#X3ec0215d86f31207d9dbdaa0b4af35f9ea4aa09)), I used informative priors for and in the IPMs, obtained from a simplified MSCJS recruitment model ([Pradel and Lebreton 1999](#X609734269c752d9b7fedbeff6c473e2aec7ad1c)) fitted independently to the PIT-tag data set. For this, I combined detection probabilities for pre-territorial of ages 1 to 11 (), which are mostly unobservable, and set , constant for the th age.

The MSJS likelihood, , is based on a multi-state Jolly-Seber model with hierarchical state-space formulation and parameter-expanded data augmentation ([Royle and Dorazio 2009](#X08738e5edda4671c75edff062a42010c5975e17); [Kéry and Schaub 2012a](#Xb5d32850daacebb23c959079c35c0385896685c)). The model considers only territorial males. The total number of individuals alive during the study is , and is the probability that a new territorial male enters the population in year , so that the number of new territorial males in a year is

.

For data augmentation ([Kéry and Schaub 2012a](#Xb5d32850daacebb23c959079c35c0385896685c)), I consider individuals, of which is a subset, and is derived as a restricted dynamic occupancy model ([Royle, Dorazio, and Link 2007](#X360a7745cf5ae67e5af6dd6d176a894f50b5ec4)). This relies on , which is the probability that a male from holds territory for the first time in year , so that

,

and

.

The state process equation for male and year , and state is formulated as

where the states in rows and columns are (not yet territorial in the population), , , and (Dead or permanently emigrated), between years and +1. The observation process is

where is the recapture probability of territorial males and non-territorial males are unobserved, as in a temporary emigration model ([Schaub et al. 2004](#ref-https://doi.org/10.1890/03-3110)).

The number of new territorial males each year () confounds males born at SSB starting to hold territory with immigrants that never held a territory at SSB before, and the two components are separated with the demographic part of the IPM (below), which combines both male capture-recapture data sets.

The matrix population model, , with data on male pup production, , which defines the observation process, contributes to estimate population sizes and demographic rates, including immigration (). For model fitting, I select Poisson distributions which introduce demographic stochasticity. For the pre-territorial component, the equations are

For the territorial data set, the MSJS model directly produces estimates of , , and , which allows for an estimate of immigrants as

The fraction of the estimated representative study population, , that is a territorial male count () obtained between November 1st and December 31st, is modelled with a Poisson GAMM, exactly as in the female IPM. It is the last component of the male IPM likelihood, and results in derived quantities and , where and are mature () and territorial () males respectively; and which is the predicted male count at SSB on the th day.

These are Used as multipliers of observed counts at other locations to obtain estimates of total number of mature males

and territorial males

,

where is the male count at colony on day .

The estimate of mature males at a study area adjusting for differences in haul out between SSB and MVK is

,

and an absolute estimate of total number of males at a study area is obtained adjusting for pre-territorial males,

,

where is the estimated number of pre-territorials of age , for , at SSB. (See female section for the derivation of .

##### 2.3.1.1.2 IPMs implementation, assessment, and selection

I closely follow methods of Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947)) and make the assumption of independence between data sets. As in many IPMs, this is not met when for example, I use the encounter histories of individuals which are also counted. However, based on recent experimental evidence ([Abadi et al. 2010](#ref-https://doi.org/10.1890/08-2235.1); [McDonald et al. 2016](#ref-https://doi.org/10.1111/ele.12578); [Weegman et al. 2021](#ref-https://doi.org/10.1002/eap.2258)), this is unlikely to be a source of bias and affect model estimation and performance, provided that model assumptions are met (see [Riecke et al. 2019](#Xb91ad7e398c3bc33d93293f3c05c12b5661a029)). These assumptions have already been evaluated for earlier versions of the the same data sets in model components of our IPMs which have been used independently elsewhere ([Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f); [Forcada and Hoffman 2014](#ref-https://doi.org/10.1038/nature13542)). For example, the effects of tag-loss on survival. However, when fitting the models, I used predictive checks to assessed the ability of the models to generate data that were consistent with the observed data ([Gelman et al. 2002](#X0b481827a7f6f0fa99ff60bd01ffdc31999ee75)) (data not presented), and in particular in relation to variation between estimates of survival and emigration derived from the IPM.

I use Markov Chain Monte Carlo (MCMC) methods in BUGS language and program JAGS ([Plummer 2003](#Xcbc5c418e20d358d32c963db63751198f93dc24)), run from (v4.5.0 [R\_Core\_Team 2024](#ref-R-base)) using packages ([Kellner 2024](#ref-jagsUI)) and ([Plummer 2024](#ref-rjags)) to fit the IPMs. To specify priors, I use Normal distributions with numbers of pre-breeders, breeders and mature non-breeders observed in the first year for the initial population sizes. For the capture-recapture part, model fit was initially assessed with frequentist multistate goodness-of-fit testing ([Pradel, Wintrebert, and Gimenez 2003](#X6fca6bfa840b2c61bf8f67a853a93d9cac97337)) using ([Gimenez et al. 2018](#X3b8711bd2d19319ba12faaabf5843e7c8767a40)). Selection of best models was subsequently based on WAIC ([Gelman, Hwang, and Vehtari 2014](#X4bc4f6a643c6c8ab30def4991b898c2d70584a2); [Watanabe 2010](#X5345a79620485ad24d00ab8f37476d1db77fe95)), and the IPMs were fitted with the best mark-recapture modelling options.

I selected temporal variation in parameters as much as possible to reflect the population state at the time of data collection and obtain accurate abundance estimates; but it was not always possible when data were sparse as in the male mark-recapture. For the female IPM, I used independent temporal random effects for and for ages 1 to 7 and 3 to 7 respectively, , , , , and (e.g.  , where , with diffuse Uniform priors for . I used correlated temporal random effects for , and, , where and is a temporal variance-covariance matrix describing the temporal variance of each parameter () and the temporal covariance among parameters ([Link and Barker 2005](#Xc639ede450fe85f7e90bc3af8c1d135f969f8de)). For I used priors from an inverse Wishart distribution ([Gelman and Hill 2006](#X8f27e0392f3022422033ceaffc661bd8d9fd199)) with scale matrix as identity matrix and for degrees of freedom. For the genetic mark-recapture part of the male IPM, I chose the best combination of , , and , either with temporal random effects, correlated temporal random effects, or constant values over time based on the lowest WAIC of a fitted set of models with different parameter combinations (data not presented). For juveniles and pre-territorials, and were selected as informative Beta priors with shape parameters obtained from an independent best fit of a multistate mark-recapture model of the PIT-tag data set. The priors incorporated temporal variation as observed in the data record, reflecting uncertainty due to environmental stochasticity at the time of the survey counts.

The GAMMs of daily counts in the IPMs were implemented using methods of Wood ([2016](#X2dbcf5361a0c715328c6da3865f68c75278ef2b)). Thus, I used multivariate Normal priors on the smooth coefficients in the JAGS models, and the smoothing parameters and smoothing penalty matrices directly specified the prior multivariate normal precision matrix as input data. I implemented preliminary model selection based on WAIC to test for overdispersion and autocorrelation in daily counts before incorporating the best Poisson models in the IPMs.

In all IPM analyses, I used 200,000 iterations of three Markov chains and discarded the first 50,000 samples of each chain as burn-in phase, thinning the remainder to every 10th sample. I assessed chain convergence visually using trace plots, through the mixing of the chains and sample autocorrelation plots, and using the potential scale reduction factor statistic of less than 1.05 to retain posterior distribution samples ([Gelman and Shirley 2011](#ref-https://doi.org/10.1201/b10905-7); [Vehtari et al. 2021](#ref-https://doi.org/10.1214/20-BA1221)).

#### 2.3.1.2 South Orkney Islands

##### 2.3.1.2.1 Population dynamics

I evaluated population trends at Signy Island using a log-linear model with a discrete-time stochastic Gompertz formulation ([Dennis and Taper 1994](#ref-https://doi.org/10.2307/2937041); [Lebreton and Gimenez 2013](#ref-https://doi.org/10.1002/jwmg.425)) of the observed fur seal count for year , in response to a year-lagged count, , with coefficient . To accommodate positive skewness from numerous low counts, I used a negative binomial error distribution (e.g., [Davis and Wu 2009](#X289b32d1c05187793f3e9054977bc7dbeff7085)), with , where and were the dispersion and success rate parameters respectively, so that .

Expressed in natural log scale, , the Gompertz Negative Binomial Model (*GNBM*) was formulated as

where intercept measures intrinsic growth rate, equivalent to when , is a density-dependence coefficient, and and error term.

##### 2.3.1.2.2 Synchrony between South Orkneys and South Georgia

To formally test for synchrony between locations, I use a mixed-effects formulation (*GNBMM*) with two independent random effects ([Grosbois et al. 2009](#ref-RN5896); [Lahoz-Monfort et al. 2011](#ref-RN6177); [Santin-Janin et al. 2014](#ref-RN5892)). A time-specific random effect which models common synchronous variation across sites; and a separate time-specific random effect for each site , which accounts for additional and asynchronous variation. The effects are incorporated as

,

Here, is between-year variance unexplained by density-dependence. The variances are equally partitioned between sites in the shared term (), but not between unshared components (). The fraction of between-year variance accounted by the shared component is the intra-class correlation,

,

which measures the synchrony of SI with BI, and BI with SI. When the shared (synchrony) component is large relative to the unshared component, approaches 1, and tends to zero otherwise.

##### 2.3.1.2.3 Connection between Signy Island and South Georgia

To further examine the association of the population abundance at Signy Island (SI) with the abundance at Bird Island (BI), I used a cross-correlation analysis function , where is a difference in years, to uncover lagged correlations between both time-series. Based on these, I then investigated the population effects of BI, proxy for South Georgia, on temporary immigration at SI at appropriate time-lags (). For that, I augmented the basic *GNBM* as

,

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

##### 2.3.1.2.4 Model fitting, selection, and assessment

I fitted Gompertz negative binomial models using a state-spece framework and with the same software and approach as the IPMs described in the previous section. To specify priors, I selected , where is for Uniform distribution, as dispersion parameter for each site (SI or BI). In single site GNBMs, for intrinsic growth rate I used , where is for Normal distribution; and in two-site GNBMs, for site I used and . In single-site GNBMs, priors for density-dependence effects were ; and for density-dependence and lagged () BI effects on SI, these were and . In single-site GNBMs, system process variation priors were (where is for Gamma distribution); and for two-site, synchrony GNBMMs, for each , and .

I used 350,000 iterations of four Markov chains and discarded the first 250,000 samples of each chain during the burn-in phase, thinning the remainder to every 25th sample, and thus producing 16,000 posterior simulations for inference. I assessed chain convergence visually using trace plots, through the mixing of the chains and sample autocorrelation plots, and using the potential scale reduction factor statistic of less than 1.05 to retain posterior distribution samples ([Gelman and Shirley 2011](#ref-https://doi.org/10.1201/b10905-7); [Vehtari et al. 2021](#ref-https://doi.org/10.1214/20-BA1221)). I assessed the ability of the models to generate data that were consistent with the observed data using posterior predictive checks ([Gelman et al. 2002](#X0b481827a7f6f0fa99ff60bd01ffdc31999ee75)).

##### 2.3.1.2.5 Scales and patterns of fluctuation in population time-series

To discriminate fluctuations from long-term trends, I investigated scales and patterns in population fluctuations across locations using a wavelet decomposition of the BI-SSB mature female abundance and SI population index. This highlighted short-lived (transient) dynamics, which combined led to mean synchrony across locations. I used wavelet power analyses for estimates at each location (), and a cross-wavelet of both locations , using R package [v0.20.22; Gouhier, Grinsted, and V. ([2024](#Xf4cdf3ecac51a649d762916c195aef32192c26e))]. The cross-wavelet helped identifying cyclical patterns in both time-series, how these varied across different time scales, and revealing common patterns of gradual change ([Cazelles et al. 2008](#ref-RN1858)), and how these patterns differed from long-term declines.

### 2.3.2 IUCN Red List criteria selection and assessment

For assessments purposes, currently distinct genetic groups are considered subpopulations as defined by the IUCN; i.e., “geographically or otherwise distinct groups in the population between which there is little demographic or genetic exchange (typically one successful migrant individual or gamete per year or less)” ([IUCN 2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)). Here, I consider the four identified subpopulations under this definition, with the caveat that the genetic identity of the South Sandwich Islands remains to be ascertained.

Major observed subpopulation declines are environmentally driven and are ongoing, but the specific causes remain uncertain and exacerbated by other effects. Because the declines are likely to be irreversible in the near future, largely due to poor mitigation of climate change and other anthropogenic effects, my main focus was to evaluate status under IUCN Red List Criteria A1-A4, with special emphasis on criterion A2. This is defined as “population reduction observed, estimated, inferred, or suspected in the past where the causes of reduction may not have ceased or may not be understood or may not be reversible” ([IUCN 2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)). Other criteria were less likely, due to best evidence including the large size of the global population of the species, and absence of perceived significant change in range size or area of occupancy.

The assessment thus focused on population size reduction to assign Red List category. It was based on the mature population only, over the longer of 10 years or three generations. Due to major differences in life history between sexes, the mature population has a much higher proportion of females than males. According to IUCN guidelines, mature individuals are capable of reproduction, but “those who will never produce new recruits should not be counted” ([IUCN 2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)). Pre-territorial males, while physiologically able to reproduce from ages 3 to 4 ([Payne 1979](#ref-RN4179)), they only start holding breeding territories when they are at least 7, at near physical maturation, but the mean age at first territory is between 9 and 11, depending on densities of individuals ([Forcada 2021](#X18803383f3700fe6c7fd758315bce727fe89dbe)).

#### 2.3.2.1 Generation length

This metric was evaluated as the average age of parents in the population ([Coale 1972](#ref-RN6237); [IUCN 2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)),

,

where is age and summations are from age 0 to the last observed age of reproduction, which is 24 for females and 18 for males; is the fecundity at age; and is survivorship up to age .

For this analysis, I used the posterior simulations of vital rates from the fitted IPMs to generate simulations of their core matrix population models. I then used age-from-stage decomposition methods ([Caswell 2001](#ref-RN312)) as implemented in package ([O. R. Jones et al. 2022](#X558d43adb4b830041675aabeda4f36efaa4df56)) to generate life table simulations for each sex, and derived generation length estimates.

As there is significant generation length variation in response to the environment (e.g., [Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)), I used pre-disturbance vital rate values, corresponding to the period immediately prior to the population collapse of Bird Island in 2009. Additionally, because generation length varies between sexes, was weighted by the relative frequency (abundance) of mature seals of each sex, obtained directly from the fitted IPMs.

#### 2.3.2.2 Population change and reduction

Based on the observed population trajectories at Bird Island ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)) and at the study areas of the South Shetland Islands (e.g., Figure3 in Krause et al. ([2022](#ref-https://10.3389/fmars.2021.796488))), I assumed an exponential decline model to calculate reduction of the subpopulations in the South Atlantic region, and of the total population. For this, I considered two populations, which was population size in the first year (), and which was the size in the last year (), and the observed period was the number of years between the first and last observation, . The observed change, was expressed as annual change as

,

or as a percent annual change, as . Population reduction was evaluated for an interval equivalent to three times the generation length (), and was estimated as

.

I based calculations of population reduction under IUCN Red List Criteria A1-A4 on the *Criterion A tool* (<https://www.iucnredlist.org/resources/criterion-a>). However, I did it separately to include uncertainty in population estimates, generation times, and pre-assessment annual change rates (see below), which is not possible with the tool.

Because a length interval could precede and/or outlast the interval between the first and last population estimates available for the assessment, I selected the years of data from each breeding location which more closely matched the assessment period. When this was not possible but there were two separate population estimates, I obtained the population three generations ago as

,

where was the annual change over the number of years () between the beginning of the assessment period and the year when was obtained. This was not always the same as the estimated between and (above), and it was therefore obtained from the best additional data available for each breeding location. For example, at South Georgia it was obtained from the geometric mean estimates of derived from the IPMs. For other locations in **Table 1**, pup production values preceding, or soon after, the start of the assessment period were available, and this was less of an issue.

The current population (), if the assessment year was later than , was obtained as

,

where was evaluated over the period between and the assessment year ().

For this analysis, the assessment year was 2025, which gave an assessment period of nearly 26 years, starting in 1999, and was equivalent to three times the estimated generation length of 8.6 years (see Results section, below). For South Georgia, reduction was evaluated with data derived from this analysis and the published record. For other breeding locations, I used pup production/count data available in the published and unpublished records (**Table 1**).

##### 2.3.2.2.1 Adjustment of pup counts to mature, and total population size

Only pup counts, representative of total pup production, were available from one or more breeding locations of South Shetland Islands, Bouvetøya, and East Antarctica (**Table 1**). Estimates of mature individuals were thus obtained from local pup production values () and the ratio of pup production and mature individual abundance estimates from the fitted IPMs. This was obtained as

where the multiplier was

where in year , are breeding females including immigrants (see the female IPM formulation), are mature females skipping breeding, are territorial males, and are mature non-territorial males. Averaged over a number of years, the estimate of reflects temporal variation, which was incorporated in extrapolations of pup counts. To incorporate further uncertainty, I used the IPM simulations of these parameters together with log-normal deviates of pup production based on their mean and variance, , when the variance was available. Otherwise, I only used the mean ().

An adjustment from pup counts to total population was obtained as

where was the abundance of female pre-breeders and the abundance of pre-territorial males.

Previously, extrapolations from pup counts to total population (e.g., [Hofmeyr et al. 2005](#X7454ecdc990e4f863ac1919f8121c3fd3669348); [Krause et al. 2022](#ref-https://10.3389/fmars.2021.796488)) were based on adjustments derived by Payne ([1979](#ref-RN4179)) from unrepresentative and incomplete data, and grossly overestimated total population size ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)), especially of males. Additionally, these multipliers adjusted for total population, as opposed to mature population only, which was the objective of the assessment. Here, such old adjustments are deemed unreliable, as discussed below, and I derived robust adjustments from the IPMs, relevant to the assessment period.

##### 2.3.2.2.2 South Georgia population projection

The total mature population size of South Georgia () was obtained from two comprehensive helicopter surveys of all the breeding locations conducted in 2007/09 (), and the data are available at ([Forcada et al. 2023a](#X498390a9858d250345ef1f2b3f98eb9714fa780)). The population size in 2022 () was only available for a few representative locations (**Fig. 2a**) and, therefore, I derived a population total using a projection model. The model assumed that abundance of each colony surveyed in changed at an annual rate , which was an average of the of the five colonies surveyed in 2007/9 and 2022, weighted by the distance () from to each colony ;

.

This ensured that regional differences in annual change where taken into account, and a colony would change at an annual rate which was more similar to a rate observed at the locations which were geographically closer.

Total mature abundance was obtained as

.

where the uncertainty of the estimated reflected the uncertainty of the IPM simulations used to obtain the , and was carried over when combined with the simulations used to obtain .

# 3 Results and discussion

## 3.1 IPM assessment

The formulation of the capture-recapture part of the female and male IPMs was supported by the frequentist goodness-of-fit tests, which did not indicate lack of fit of Arnason-Schwarz multi-state model structures. Included in the IPM likelihoods, convergence in the MCMC chains was successfully achieved, with test values under 1.1. All the posterior estimates of demographic rates had a maximum proportion of the posterior distribution with the same sign as the mean (≥ 0.95). When fitted as independent capture-recapture likelihoods, the posterior distribution of survival and transition probability estimates showed maximum overlap compared to their distributions as part of the IPMs, which suggest very little discrepancy in their posterior distributions.

Model selection of female IPMs improved with correlated temporal random effects in , and , independent temporal random effects in survival and breeding probabilities (recruitment) of immature seals, and recapture probabilities modelled as invariant over time. Models without temporal effects on survival and breeding had much lower support. Due to limited sample size, the best male IPM had a simplified parameter structure, with temporal random effects for and time-invariant options for the rest of the parameters. This structure was identical to the recent analyses of a reduce version of this data set and additional detail can be found in Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947)).

The fit of GAMM likelihoods within the IPMs showed comparable support for models with temporal random effects and temporal autocorrelation (AR1), with marginal differences in WAIC. Estimated autocorrelation parameters were non-significantly different from 0, and thus a simplified Poisson-log-normal was selected throughout. When fitted independently, the GAMM likelihoods provided almost identical posterior distributions for parameters of interest as those obtained when fitted in the IPMs. This suggests that with a good choice of prior distribution and initial parameter estimates, fitting them independently was acceptable, with the advantage of saving computing time and fitting problems due to model complexity.

## 3.2 Life tables and generation length

The population projection matrix for females was slightly modified to include recruitment ages from three to seven, allowing for an absorbing state of seals aged seven or older never observed recruiting; this was a slightly different formulation than in the IPM, to derive life table and generation length estimates. The matrix models comprised averaged vital rates from 2001 to 2008, which is a pre-perturbation period before the major 2009 decline, as required by IUCN guidelines ([IUCN 2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)). The mean estimate and standard deviation are

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The age structured models included a maximum observed age of 25, and the corresponding mean and standard deviation of the female life table is:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 0 | 0.4237 (0.0357) | 1 (0) | 0 (0) | 0 (0) | 0 (0) |
| 1 | 0.9744 (0.0312) | 0.4237 (0.0357) | 0 (0) | 0 (0) | 0 (0) |
| 2 | 0.9369 (0.0527) | 0.4125 (0.0329) | 0.0206 (0.0091) | 0.0085 (0.0037) | 0.0169 (0.0075) |
| 3 | 0.6396 (0.0601) | 0.3860 (0.0328) | 0.0871 (0.0127) | 0.0335 (0.0050) | 0.1005 (0.0149) |
| 4 | 0.8007 (0.0480) | 0.2462 (0.0257) | 0.1759 (0.0170) | 0.0432 (0.0054) | 0.1728 (0.0214) |
| 5 | 0.7693 (0.0400) | 0.1969 (0.0213) | 0.1950 (0.0163) | 0.0383 (0.0046) | 0.1916 (0.0230) |
| 6 | 0.7917 (0.0328) | 0.1512 (0.0162) | 0.2130 (0.0158) | 0.0322 (0.0039) | 0.1931 (0.0235) |
| 7 | 0.8023 (0.0183) | 0.1197 (0.0131) | 0.2234 (0.0157) | 0.0267 (0.0033) | 0.1870 (0.0234) |
| 8 | 0.8073 (0.0129) | 0.0961 (0.0113) | 0.2295 (0.0157) | 0.0220 (0.0028) | 0.1762 (0.0228) |
| 9 | 0.8097 (0.0107) | 0.0776 (0.0097) | 0.2332 (0.0156) | 0.0181 (0.0024) | 0.1627 (0.0218) |
| 10 | 0.8108 (0.0097) | 0.0629 (0.0083) | 0.2355 (0.0153) | 0.0148 (0.0021) | 0.1479 (0.0206) |
| 11 | 0.8113 (0.0092) | 0.0510 (0.0071) | 0.2370 (0.0151) | 0.0121 (0.0017) | 0.1329 (0.0192) |
| 12 | 0.8116 (0.0089) | 0.0414 (0.0061) | 0.2380 (0.0149) | 0.0099 (0.0015) | 0.1183 (0.0179) |
| 13 | 0.8117 (0.0088) | 0.0337 (0.0052) | 0.2388 (0.0148) | 0.0080 (0.0013) | 0.1044 (0.0165) |
| 14 | 0.8117 (0.0087) | 0.0274 (0.0044) | 0.2393 (0.0146) | 0.0065 (0.0011) | 0.0916 (0.0151) |
| 15 | 0.8117 (0.0086) | 0.0222 (0.0037) | 0.2397 (0.0145) | 0.0053 (0.0009) | 0.0798 (0.0138) |
| 16 | 0.8117 (0.0086) | 0.0181 (0.0032) | 0.2400 (0.0144) | 0.0043 (0.0008) | 0.0693 (0.0125) |
| 17 | 0.8116 (0.0085) | 0.0147 (0.0027) | 0.2402 (0.0144) | 0.0035 (0.0007) | 0.0599 (0.0113) |
| 18 | 0.8116 (0.0085) | 0.0119 (0.0023) | 0.2404 (0.0143) | 0.0029 (0.0006) | 0.0516 (0.0101) |
| 19 | 0.8116 (0.0085) | 0.0097 (0.0020) | 0.2406 (0.0142) | 0.0023 (0.0005) | 0.0443 (0.0091) |
| 20 | 0.8115 (0.0085) | 0.0079 (0.0017) | 0.2407 (0.0142) | 0.0019 (0.0004) | 0.0379 (0.0081) |
| 21 | 0.8115 (0.0085) | 0.0064 (0.0014) | 0.2408 (0.0142) | 0.0015 (0.0003) | 0.0324 (0.0072) |
| 22 | 0.8115 (0.0085) | 0.0052 (0.0012) | 0.2409 (0.0141) | 0.0013 (0.0003) | 0.0276 (0.0064) |
| 23 | 0.8114 (0.0085) | 0.0042 (0.0010) | 0.2410 (0.0141) | 0.0010 (0.0002) | 0.0235 (0.0056) |
| 24 | 0.8114 (0.0084) | 0.0034 (0.0009) | 0.2410 (0.0141) | 0.0008 (0.0002) | 0.0199 (0.0050) |

**Table 2**. Antarctic fur seal female life table for pre-disturbance (pre-decline) years based on derived vital rate estimates from the fitted female IPM model. Column parameters are referred to interval , where is the age at the start of the age interval. These are , or probability of survival for seals entering the interval; , or survivorship, which is the proportion of initial cohort surviving to the start of age interval; , or per-capita rate of reproduction during interval; , or expected number of offspring per cohort member produced during interval; and . Standard errors are in parentheses.

The population projection matrix for males was slightly modified to include recruitment ages from seven to eleven, allowing for an absorbing state of animals eleven or older never observed recruiting. It comprised averaged vital rates from 1995 to 2007, which is the pre-perturbation period before the major 2009 decline. For this period the male population growth was near stable ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)). The mean estimate and standard deviation of the matrix model are

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This model includes a reproductive component (first row), which is required to obtain a life table for estimating generation length based on the “cohort” method of Coale ([1972](#ref-RN6237)). The mean and standard deviation of the derived life table, including a maximum observed age of 18, is

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 0 | 0.7193 (0.0145) | 1 (0) | 0 (0) | 0 (0) | 0 (0) |
| 1 | 0.8129 (0.0131) | 0.7193 (0.0145) | 0 (0) | 0 (0) | 0 (0) |
| 2 | 0.8401 (0.0099) | 0.5849 (0.0210) | 0 (0) | 0 (0) | 0 (0) |
| 3 | 0.8299 (0.0106) | 0.4915 (0.0226) | 0 (0) | 0 (0) | 0 (0) |
| 4 | 0.7890 (0.0167) | 0.4080 (0.0210) | 0 (0) | 0 (0) | 0 (0) |
| 5 | 0.7190 (0.0243) | 0.3219 (0.0180) | 0 (0) | 0 (0) | 0 (0) |
| 6 | 0.6271 (0.0312) | 0.2315 (0.0158) | 0.0033 (0.0021) | 0.0008 (0.0005) | 0.0045 (0.0029) |
| 7 | 0.5353 (0.0501) | 0.1453 (0.0141) | 0.0192 (0.0048) | 0.0028 (0.0008) | 0.0196 (0.0056) |
| 8 | 0.4859 (0.0870) | 0.0781 (0.0121) | 0.0528 (0.0107) | 0.0042 (0.0012) | 0.0333 (0.0099) |
| 9 | 0.5201 (0.1058) | 0.0385 (0.0113) | 0.0962 (0.0160) | 0.0038 (0.0015) | 0.0341 (0.0138) |
| 10 | 0.6042 (0.0813) | 0.0210 (0.0099) | 0.1498 (0.0215) | 0.0032 (0.0018) | 0.0323 (0.0183) |
| 11 | 0.6377 (0.0358) | 0.0133 (0.0081) | 0.1665 (0.0199) | 0.0022 (0.0014) | 0.0246 (0.0158) |
| 12 | 0.6409 (0.0252) | 0.0087 (0.0059) | 0.1702 (0.0202) | 0.0015 (0.0010) | 0.0179 (0.0124) |
| 13 | 0.6384 (0.0414) | 0.0057 (0.0041) | 0.1713 (0.0204) | 0.0010 (0.0007) | 0.0127 (0.0093) |
| 14 | 0.6143 (0.1273) | 0.0037 (0.0028) | 0.1718 (0.0205) | 0.0006 (0.0005) | 0.0089 (0.0068) |
| 15 | 0.5454 (0.2295) | 0.0025 (0.0019) | 0.1721 (0.0207) | 0.0004 (0.0003) | 0.0064 (0.0049) |
| 16 | 0.4597 (0.2909) | 0.0018 (0.0013) | 0.1731 (0.0207) | 0.0003 (0.0002) | 0.0049 (0.0036) |
| 17 | 0.3759 (0.3189) | 0.0014 (0.0009) | 0.1742 (0.0212) | 0.0002 (0.0002) | 0.0042 (0.0026) |
| 18 | 0 (0) | 0.0012 (0.0006) | 0.1759 (0.0214) | 0.0002 (0.0001) | 0.0037 (0.0020) |

**Table 3**. Antarctic fur seal male life table for pre-disturbance (pre-decline) years based on derived vital rate estimates from the fitted female IPM model. Column parameters are referred to interval , where is the age at the start of the age interval. These are , or probability of survival for seals entering the interval; , or survivorship, which is the proportion of initial cohort surviving to the start of age interval; , or per-capita rate of reproduction during interval; , or expected number of offspring per cohort member produced during interval; and . Standard errors are in parentheses.

From the sex-specific life tables, the cohort-method generation length estimate is 8.21 (SD=0.28) for females and 9.90 (SD=0.58) for males. Using mean absolute abundance estimates for mature females and mature males between 2007-2009, when the population of South Georgia was estimated to be at its maximum, the mean generation length weighted by the abundance of mature seals of each sex is 8.63 (SD=0.26). This value is used subsequently for the population reduction assessment.

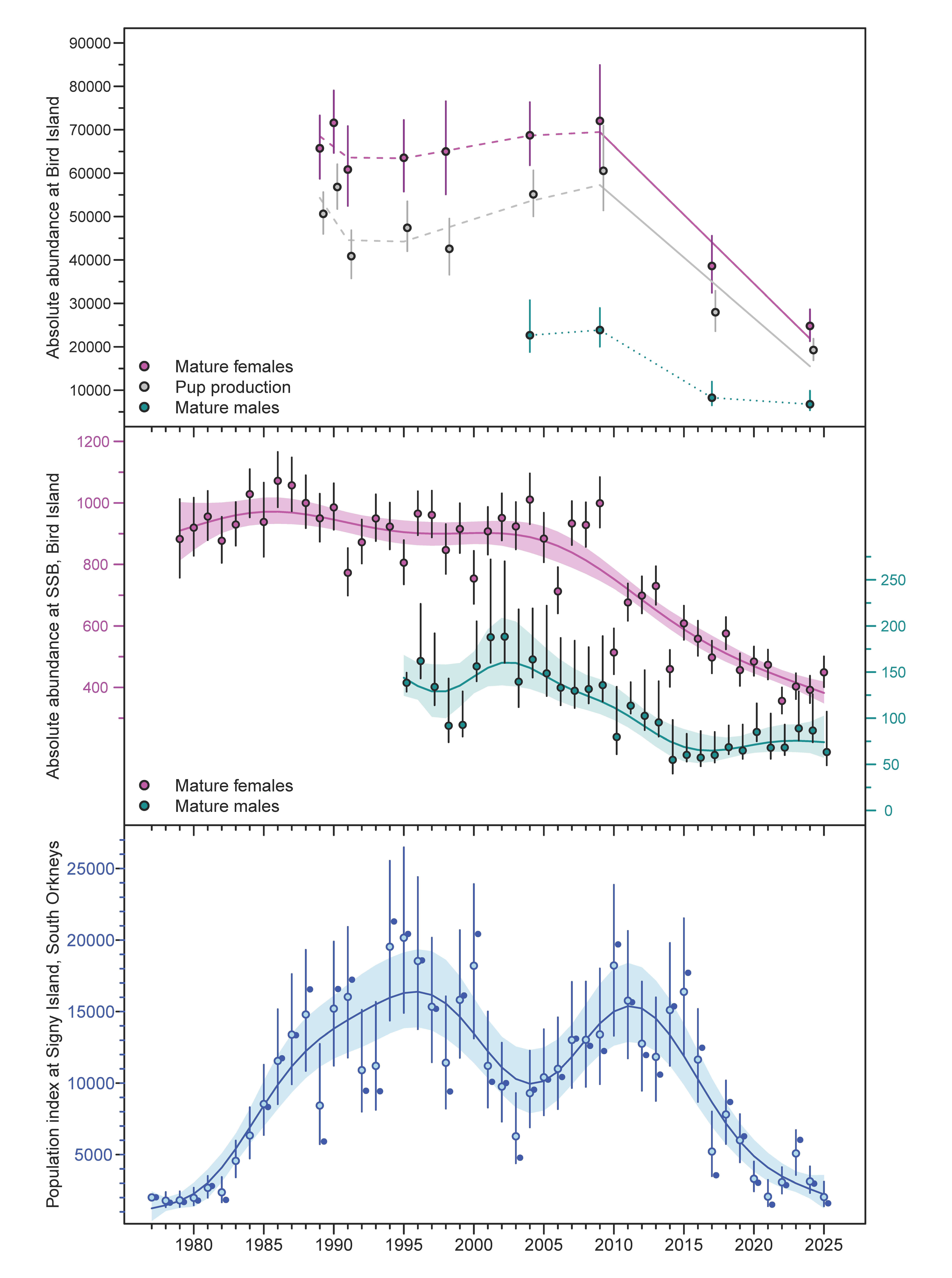
## 3.3 Adjustments to scale-up pup production to mature and total population

Using the IPM estimates of absolute abundance, an estimate of the ratio of mature individuals to pup production for the interval 2001 and 2005 was 1.482 [95% CI: 1.392, 1.582], and was used as the mean adjustment from a pup count to mature population. The ratio of total population, including mature, pre-breeders and pre-territorials, to pup production, equivalent to a mean adjustment to total population, was 3.026 [2.767, 3.303].

Previously, Payne ([1979](#ref-RN4179)) indicated that the total population size at the end of the breeding season was 4.1 times the number of pups born. However, to account for unobservable population components, including, for example, the majority of the pre-territorial males which is nearly 80% of the total male population ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)), he could only use limited data. His adjustment was obtained from calculations of body mass at age from a small sample of known age seals from Bird Island, with the remark: “Nothing is known of the structure of the male herd other than the mean age of a small sample of breeding bulls” ([Payne 1979](#ref-RN4179)). He also used for his adjustment a population growth rate calculated from pup production values obtained over a decade apart, between late 1950s and mid 1970s, with substantially different and hardly comparable methods ([Croxall and Prince 1979](#Xbfbe1e8e885e11c1ae9f7efc08f7e25e569b821)). Additionally, he assumed survival rates at age, for a population age structure obtained with little data that was largely affected by unquantified loss of plastic tags, which were the main individual marking method at the time. As a result, his highly biased multiplier is not even within the confidence limits of the recently and robustly estimated factor of 2.96 [2.64, 3.33] for South Georgia ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)); although it has been repeatedly used until recently (e.g., [Boyd 1993](#Xcc7f7bc0df5c21c90a9a4ab37d2501c8efec44c); [Hofmeyr et al. 2005](#X7454ecdc990e4f863ac1919f8121c3fd3669348); [Krause et al. 2022](#ref-https://10.3389/fmars.2021.796488)). For this analysis, I updated pup count adjustments with the IPM models that use the most up-to-date recapture data of known females (n=4,029) and males (n=6,108), and all of them were reliably tagged with electronic chips and/or genetic markers, which are permanent marking methods.

## 3.4 Bird Island abundance and trends, and connection with the South Orkney Islands

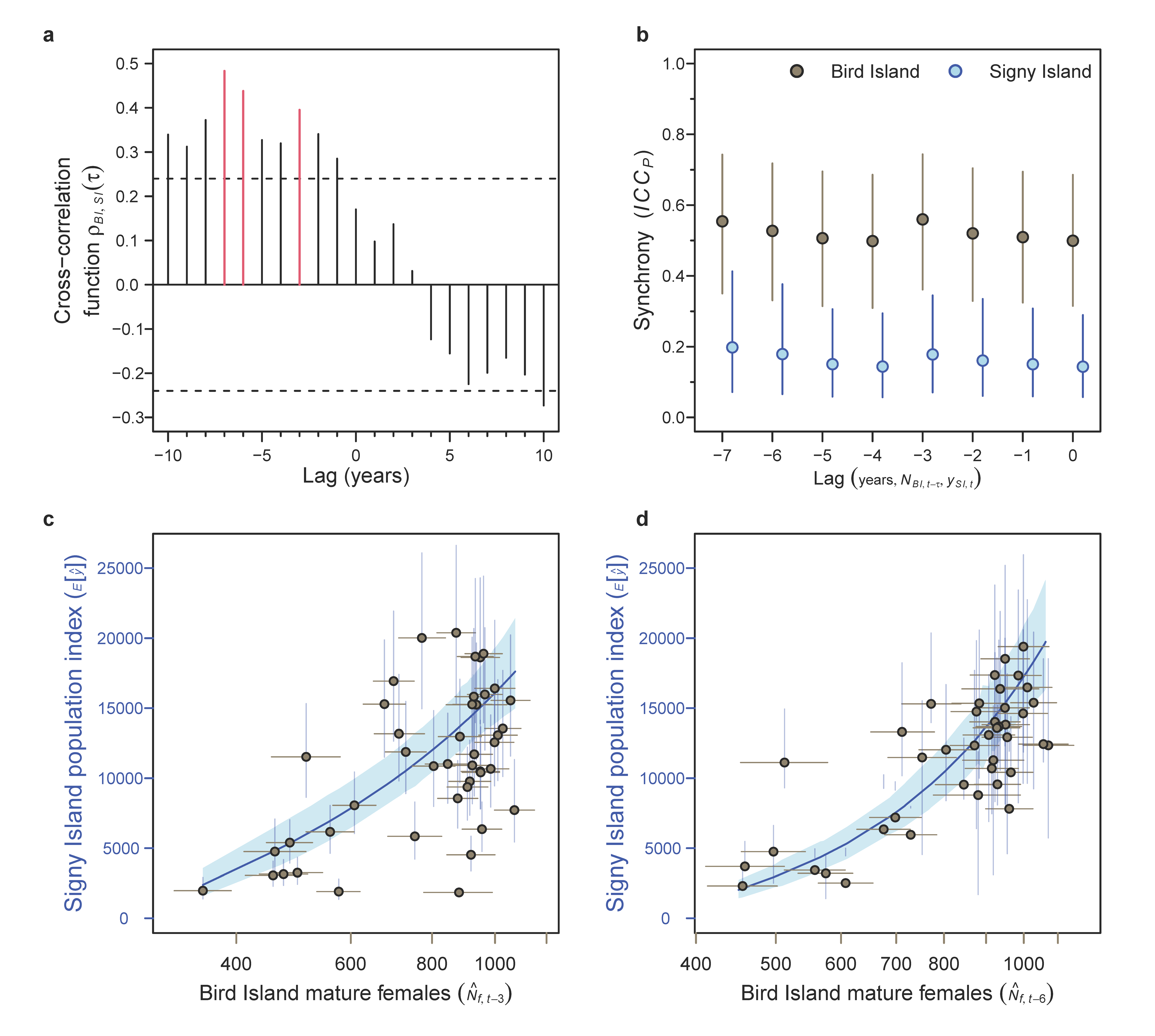
The current female IPM extends previous results in Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947)) with more recent estimates of total abundance and trends at Bird Island and at SSB. The results suggest a geometric mean population growth rate, , of 0.951 [95% CI: 0.943, 0.958] for period 2010 to 2025; and of 0.970 [0.962, 0.978] for period 2001 to 2025. Based on full island estimates, pup production at Bird Island declined annually by 11.4% [9.8, 12.9] from 2009 to 2024, and for the period 2017 to 2024 it declined by 5.2% [2.3, 8.0]. 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 the decline of mature females since 2009, is consistent with an exponential model.



**Figure 4**: Absolute abundance of mature Antarctic fur seals and pup production at Bird Island, South Georgia; and abundance index based on seal counts at Signy Island, South Orkney Islands. The top panel shows abundance estimates for mature males, mature females, and breeding females (equivalent to pup production) during seasons when total island counts were produced. The straight lines show the fit of segmented regression models, with continuous-line segments depicting significant declines. The dotted lines simply connect mature male abundance estimates. The centre panel shows the absolute abundance of mature males and females at the Special Study Beach of Bird Island, which is the reference study population for South Georgia. Smoothed lines show nonlinear trends based on GAMs, with shaded areas as 95% credible intervals. The bottom panel show the population index at Signy Island, South Orkney Islands, with fitted smooth trends, including 95% credible intervals. Vertical bars are 95% credible intervals from model estimates.

Seal counts at Signy Island (**Fig. 4**, bottom panel) showed a similar decline as Bird Island since 2010, which is also consistent with an exponential decline. Large variation in counts between the early 2000s and 2015 is discussed elsewhere ([Dunn et al. 2025](#ref-https://doi.org/10.1111/gcb.70290)), but mostly responded to a temporary absence of warming in the Antarctic Peninsula and Western Weddell Sea, which increased the seasonal sea ice extent and decreased the numbers of seals hauled out during counts; Antarctic fur seals are more ice intolerant than other Antarctic phocids and prefer more ice-free haul-outs ([Siniff et al. 2008](#ref-RN138)).

Despite this large subdecadal (mid-term) variation, the inter-annual change in numbers at BI and SI was synchronised, even after accounting for density-dependence. Parameter estimates for fitted population dynamics models (*GNBMM*) suggested maximum synchrony between BI, at lags of between 3 and 7 years, with SI (**Table 4**; **Fig. 5b**); which was also supported by the detrended cross-correlation analysis (**Fig. 5a**). Modelled as a fixed-effect, BI abundance lagged 3, and 6 years respectively, explained significantly the numbers at SI (**Fig. 5c, d**). Although for a 6 year lag, the dispersion of observed values around the fitted model was lower, particularly for higher densities of seals at both locations. This could be a potential cohort maturation effect in the temporary migrant male population observed at SI, which would propagate in time as the pup production and maturing population of South Georgia fluctuated.

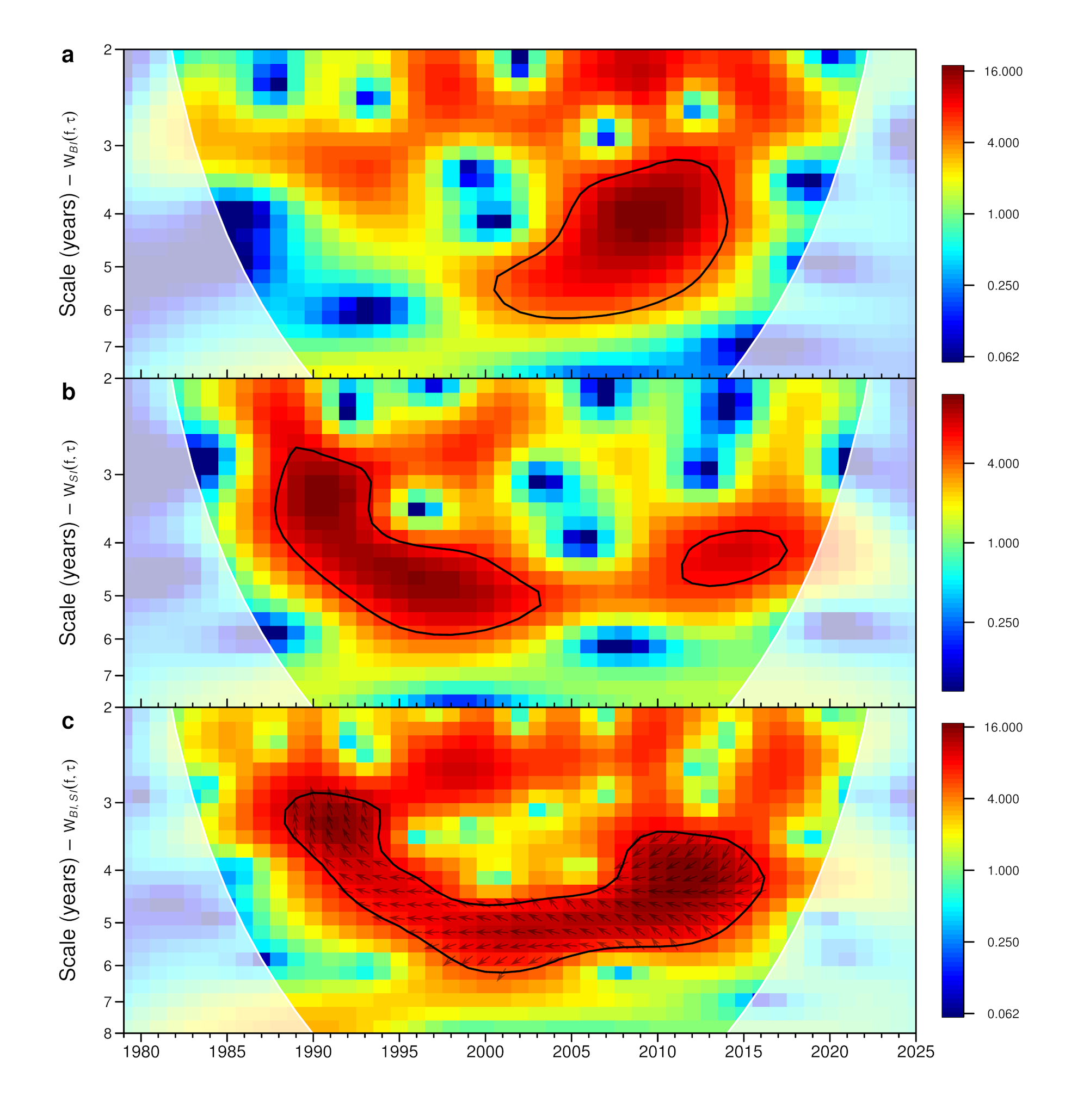


**Figure 5**: **a** Similarity between Signy Island (SI) fur seal population index counts and Bird Island-SSB (BI) mature female absolute abundance as a function of time delay (lag) applied to Bird Island, when the trend of both time-series is removed. **b** Synchrony of BI abundance with SI population index, and of SI with BI, at different lags in years; synchrony is based on random effects in modified . **c** Fixed-effect of BI mature female abundance with a negative lag of 3 years on SI population index. **d** Fixed-effect of BI mature female abundance with a negative lag of 6 years 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 .

| Parameter | =0 | =0-1 | =0-2 | =0-3 | =0-4 | =0-5 | =0-6 | =0-7 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 43.82 (5.19) | 43.61 (5.34) | 43.54 (5.38) | 43.77 (5.26) | 43.08 (5.67) | 42.86 (5.91) | 43.01 (5.82) | 43.32 (5.57) |
|  | 25.77 (12.15) | 25.84 (12.24) | 25.52 (12.28) | 30.97 (11.51) | 27.36 (12.34) | 27.67 (12.39) | 26.9 (12.43) | 28.27 (12.08) |
|  | 1.23 (1.02) | 1.39 (1.04) | 1.52 (1.16) | 2.29 (1.21) | 1.96 (1.24) | 2.14 (1.42) | 2.25 (1.49) | 2.11 (1.34) |
|  | 1.06 (0.83) | 1.16 (0.82) | 1.34 (1.00) | 1.99 (1.07) | 1.83 (1.07) | 2.13 (1.35) | 2.34 (1.47) | 2.10 (1.25) |
|  | 1.42 (0.82) | 1.64 (0.89) | 1.72 (1.00) | 2.60 (1.03) | 2.12 (1.15) | 2.17 (1.28) | 2.21 (1.32) | 2.13 (1.21) |
|  | -0.16 (0.12) | -0.18 (0.12) | -0.20 (0.15) | -0.30 (0.16) | -0.27 (0.16) | -0.32 (0.20) | -0.35 (0.22) | -0.31 (0.18) |
|  | -0.15 (0.09) | -0.18 (0.10) | -0.19 (0.11) | -0.28 (0.11) | -0.23 (0.12) | -0.24 (0.14) | -0.24 (0.14) | -0.23 (0.13) |
|  | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) |
|  | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) | 0.03 (0.01) |
|  | 0.15 (0.06) | 0.15 (0.06) | 0.15 (0.06) | 0.15 (0.05) | 0.16 (0.06) | 0.16 (0.07) | 0.15 (0.07) | 0.14 (0.06) |
|  | 0.50 (0.11) | 0.51 (0.11) | 0.52 (0.12) | 0.56 (0.12) | 0.50 (0.12) | 0.51 (0.12) | 0.53 (0.12) | 0.57 (0.12) |
|  | 0.17 (0.09) | 0.17 (0.09) | 0.19 (0.10) | 0.20 (0.09) | 0.16 (0.08) | 0.17 (0.09) | 0.19 (0.10) | 0.22 (0.11) |

**Table 4**. Parameter estimates for fitted Gompertz Negative Binomial Mixed-Models () to Signy Island Antarctic fur self population counts and Bird Island mature female abundance estimates, including density dependence and effects of Bird Island mature female fur seal population at different time lags (), in years. Parameters are described in the methods section of the main text.

A wavelet analysis further illustrates the connection between Signy Island with Bird Island, showing the comparative fluctuation and association between trends at both locations. The wavelet power spectrum of the SSB-Bird Island mature female abundance **Figure 6a** showed a significant change in fluctuations, from a scale of 5-6 years initially (2000), to 3-4 years after the major population collapse in 2009. **Figure 6b** shows the change in cycles of 3-4 years in the late 1980s to 5-6 years by early 2000s. The covariation of cycles between both time-series (**Figure 6c**) shows how the 2009 decline at BI led to a similar 3-5 year cycle at SI between 2010-2015, although slightly lagged. This analysis thus confirms the periodicity and duration of short to mid-term fluctuations over the study period, and how the long-term decline for 2000-2025 outlasted several population cycles.

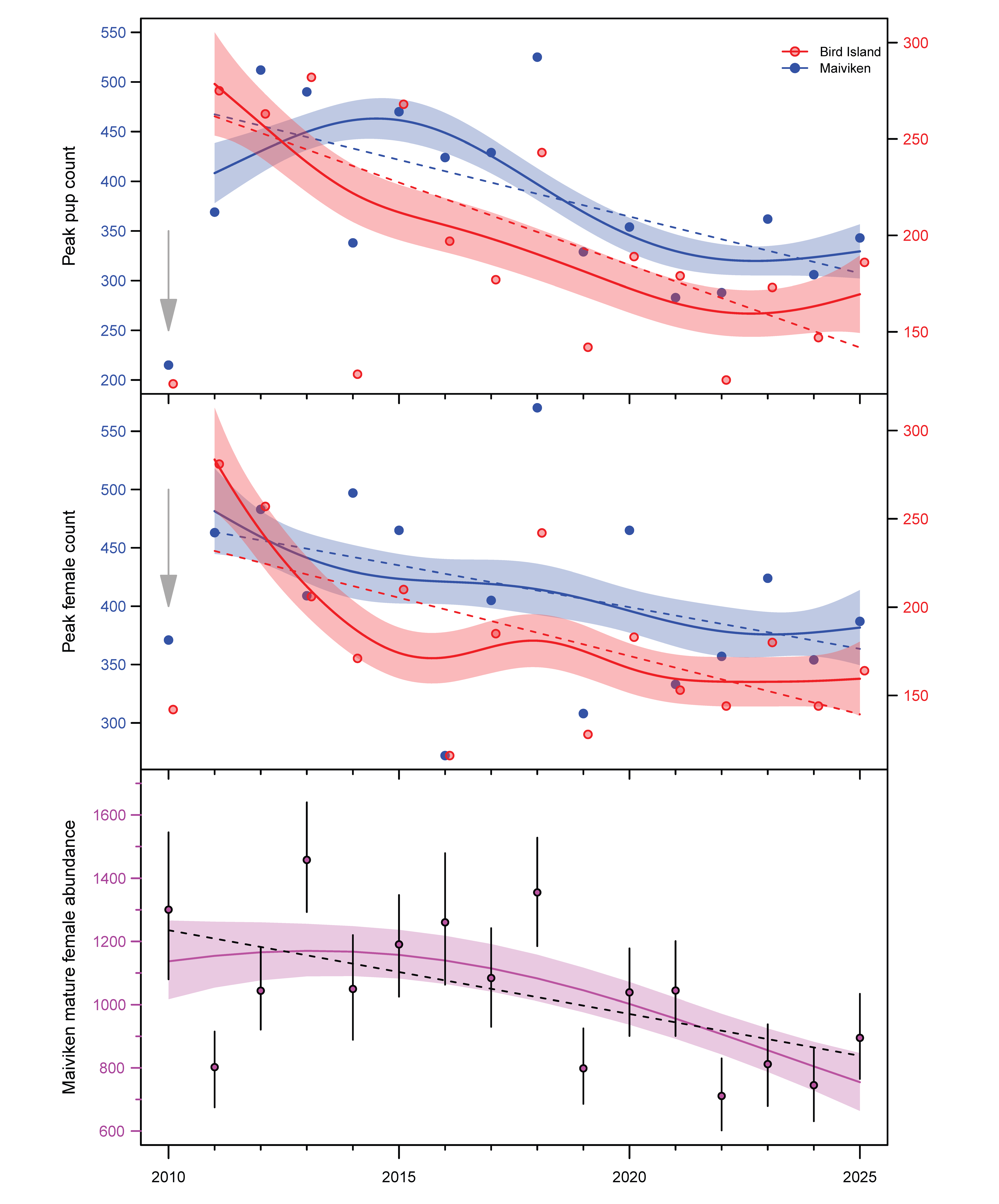


**Figure 6**: **a** Wavelet power spectrum of the SSB-Bird Island (BI), South Georgia, time-series of mature female abundance. **b** Wavelet for Signy Island population index. The different time-frequency components reveal patterns at various time scales, from short-term fluctuations to long-term trends. **c** Cross-wavelet transform showing shared power and phase relationship (arrows) between BI and SI in the time-frequency domain, indicating areas of high correlation. This shows how both locations vary together over time and across different time scales. Small arrows show phase differences between BI and SI. With right pointing arrows BI and SI are in phase; to the left, BI and SI are in anti-phase; pointing up, SI leads BI by π/2; and pointing down, BI leads SI by π/2. Warm and cool colours represent high and low power. Regions of significantly high temporal variation compared to a null model (red noise) are designated with black contours, and paler areas delimit the cone of influence, with outside values being less reliable due to edge effects.

Numbers of Antarctic fur seal temporary immigrants at the South Orkney Islands increased rapidly in the mid-1980s, with the recovery of the breeding population of South Georgia. The numbers at Signy Island peaked in the 1990s, with an increasing population of fur seal males, the majority of which were juvenile or pre-territorial (nearly 80% of the total male population). In contrast, pup counts at the main study locations, Signy and Laurie Islands, have been 0 since the mid-2010s ([Waluda, Gregory, and Dunn 2010](#Xf718da9b414ff6758587e2ce5e3e4dfc1b5d9bf); [Carlini et al. 2006](#Xa92e542fabc51663fbb13764d3e5e4f00790b0e)), suggesting that breeding at the South Orkney Islands continues to be marginal. Because fur seals at Signy Island are largely seasonal visitors from the entire South Georgia archipelago, after variation in sea-ice dynamics is taken into account ([Dunn et al. 2025](#ref-https://doi.org/10.1111/gcb.70290)), the results support that the large decline observed at Signy Island in the recent decades follows a similarly large decline at South Georgia.

## 3.5 Re-evaluation of fur seal population size and trends at South Georgia

Bird Island is thought to be the at the centre of the Antarctic fur seal population recovery at South Georgia, after the species became nearly extinct by commercial sealing ([Bonner 1968](#ref-RN5382); [Payne 1977](#ref-RN2643)). The recolonisation of South Georgia probably reached a peak by 2009, due to a maximum occupancy of suitable breeding habitat ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)); although by then Bird Island was already declining slowly due to increasing environmental pressures ([Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f)). This decline was exacerbated by a major population collapse in winter of 2009 ([Forcada and Hoffman 2014](#ref-https://doi.org/10.1038/nature13542)) (**Fig. 4**), but at the time it was unclear if this had affected South Georgia in its entirety. Individual aerial surveys in 2007, 2009, and 2022 support a decline at Maiviken (**Fig. 2b**, 4), that is only slightly slower than at Bird Island (**Table 5**), and supports declines at other locations also surveyed in 2007/9 and 2022 (**Table 5**). The time-series of fur seal counts at Maivken, at the center-east of South Georgia and far away from Bird Island and over 17 years of consistent monitoring (**Fig.7**), provides additional corroboration of this major population change and subsequent decline. Mature female abundance trends at BI-SSB (**Fig.4**, centre panel) and Maiviken study area are comparable, and both time series are synchronised when long-term trends are removed, showing similar interannual variation (see also **Fig.3**, top panels).



**Figure 7**: The top two panels show counts of pups and mature females at Maiviken and Bird Island during peak pupping (mean birthdate), between 2010 and 2025. Dots are observed counts; continuous blue and red lines and shaded areas show the fit of Poisson GAMs; and dashed lines are significant linear trends as estimated with robust-resistant regression models which account for outlying counts. Grey arrows point to the first counts after the 2009 population collapse, which were abnormally low due to a substantial breeding deferral triggered by a significant environmental anomaly. The lower panel shows mature female absolute abundance for the counting area, including those females which did not breed. Vertical bars are 95% credible intervals, and a gaussian low pass filter shows smoothed trends, together with the significant regression (dashed) line

Without a complete survey in 2022, to reevaluate population size and change at South Georgia I obtained a separate annual change estimate for each breeding location surveyed in 2007/9 and also in 2022, and obtained a population projection for South Georgia over the assessment period (**Table 5**). Based on this projection, the average annual change at South Georgia was -3.93% (SD=0.61), with a mature population of 1,024,797 [95%CI:873,500; 1,200,048] seals in 2022, including 834,319 [709,490; 979,666] females and 190,478 [152,610; 237,723] males. Applying adjustments for pre-breeders and pre-territorial individuals for 2022, the most recent total population at South Georgia would be 1,983,687 [1,606,408-2,411,876], approximately 1.5 million seals less than in 2007/9.

The large difference in numbers between sexes were due to the high polygyny of the species, which entails delayed access to reproduction and short reproductive lives in males. Fur seal males are physiologically capable to reproduce much earlier than the age when they reach physical maturity and are able to compete for breeding territories. But only at this point they effectively contribute to reproduction. For assessment purposes, mature individuals “is the number of individuals known, estimated or inferred to be capable of reproduction”; but “Mature individuals that will never produce new recruits should not be counted”; and “In the case of populations with biased adult or breeding sex ratios, it is appropriate to use lower estimates for the number of mature individuals, which take this into account” [IUCN ([2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)); 4.3). The mature male estimates I use here adhere to these guidelines.

| Location |  |  |  |  | % 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 (4,860) | 2024 | 31,550 (2,200) | -5.19 (0.41) |
| *Stromness harb.* | 2007/9 | 10,720 (870) | 2022 | 6,790 (630) | -3.00 (0.79) |
| *Husvik harbour.* | 2007/9 | 13,125 (1,070) | 2022 | 9,500 (885) | -2.46 (0.92) |
| *Maiviken* | 2007/9 | 6,515 (305) | 2022 | 3,364 (345) | -4.34 (0.71) |
| *Hound Bay* | 2007/9 | 5,775 (491) | 2022 | 3,345 (308) | -4.12 (0.91) |

**Table 5**. Population assessment and IUCN Red List Criteria for Antarctic fur seal subpopulation of South Georgia and breeding locations surveyed in 2022. Columns and are years when mature population estimates ( and ) were available to estimate reduction with an assumed exponential model, a generation length of 8.63 (SD=0.26), and an assessment year of 2025.

## 3.6 Global and subpopulation assessment using Red List category and criteria

### 3.6.1 South Georgia and South Orkney Islands

Using the IPM simulations, I derived an estimated mean annual change from 1996 to 2006, which was 0.98 (SD=0.01). It was consistent with a previously estimated stochastic for the same period at Bird Island ([Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f)), and therefore, I used it to project the population of South Georgia from 1999 () to 2007/9 (). For the observed period, to (2022), the annual rate of decline was faster, -3.93% [CI: -2.73; -5.13], and the estimated reduction over three generations was -0.57 [-0.65; -0.48], with a probability of 0.92 of being lower than or equal to -0.50. This supported a higher than 50% reduction, and the Red List Category **Endangered** as the most likely, based on the A2 criterion assessment, as discussed above.

At the South Orkney Islands, pup counts over the last three decades have been zero or near zero at the long-term studies of Laurie Island and Signy Island ([Carlini et al. 2006](#Xa92e542fabc51663fbb13764d3e5e4f00790b0e); [Waluda, Gregory, and Dunn 2010](#Xf718da9b414ff6758587e2ce5e3e4dfc1b5d9bf)); and have been zero at Signy Island since 2010. Surveys of Gosling, Monroe, Powell, and Michelsen Islands in 1974 produced a total count of 65 pups ([Laws 1981](#ref-RN6197)), but data for these areas are lacking because they are seldom visited for seal surveys. Based on the current absence of pupping at study sites, my assumption is that fur seal pupping at the South Orkney Island group continues to be marginal, as discussed in Dunn et al. ([2025](#ref-https://doi.org/10.1111/gcb.70290)).

### 3.6.2 South Sandwich Islands

Data from surveys of the South Sandwich Islands archipelago conducted in January and February 1997, and completed during February of 1998 ([Convey, Morton, and Poncet 1999](#Xa202934fdec7762213b6c529a608dd8c5d6b312)), provide the best baseline for total pup counts at this difficult to access location. The counts did not account for mortality and were grossly rounded; but better, or any subsequent data for that matter, are unavailable for most of the islands. Most of the pups in 1997/8 were found in Zavodovski (n=500), Visokoi (n=900), and Candlemas Islands (n=346), at the northwest of the Archipelago. In December 2023, a fur seal survey of Zavodovski Island only was completed, with an estimated RPAS count of 1,265 pups.

To assess the status of this breeding location, and given the observed increase at Zavodovski Island, I assumed no change at other unsurveyed locations. Thus, the mature population in from a total count of 1,750 pups in 1997/8 was 2,535 (SD=93); and in 2025 was estimated as 3,782 (SD=124). This implies a category of **Least concern**, on the basis of the population increase at Zavodovski Island only, but with two major caveats. First, 1997/1998 saw the second strongest El Niño event on record, which brought about significant breeding deferral and low pup production at South Georgia ([Forcada et al. 2005](#ref-https://doi.org/10.1890/04-1153); [Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f)). This was likely due to direct climatic effects on the marine environment around nearby South Georgia and adjacent areas ([Murphy et al. 2007](#ref-RN1961)). In all certainty, it would also be associated with a lower-than-average pup count at the South Sandwich Islands ([Forcada et al. 2005](#ref-https://doi.org/10.1890/04-1153)). And second, the assessment is questionable due to lack of data of at least Visokoi Island, where pups were most abundant in 1998. So for the South Sandwich Islands, the most realistic category is **Data Deficient**.

### 3.6.3 South Shetland Islands

Using a total pup count of 9,530 (SD=135) of the South Shetland Islands archipelago obtained in 1995/6 ([Meyer, Walker, and Holt 1996](#ref-RN6244)), and a total count of 10,057 (SD=142) from 2001/2 () (**Table 1**), I estimated an annual growth rate of 1.009 (SD=0.003) for the period 1996-2002. I then used this rate to back-project the population from to , and obtained a mature population size in (1999) of 14,531 (SD=556). In (2002), the mature population size was estimated as 14,913 (SD=531), and as 1,336 (SD=44) in (2025). The annual rate of change for the observed period (2002 to 2025) was -9.96% [-9.85; -10.06], and the estimated reduction over three generations was -0.908 [-0.911; -0.904], with maximum probability of being higher than 80%, and equal or higher than 90%. This corresponds to a category of **Critically Endangered** under Criterion A2, and also under Criterion A1, as the reduction was higher than 90%; although the causes of the decline are only partially known and have not ceased and are unlikely to be reversible, so Criterion A2 applies.

### 3.6.4 Bouvetøya

The pup count at Nyrøysa (Bouvetøya) for 1999, which is both and , was 15,448 (SD=370) ([Hofmeyr et al. 2005](#X7454ecdc990e4f863ac1919f8121c3fd3669348)), and corresponded to a mature population size of 22,832 (SD=1,141). A pup production estimate of 8,080 (SD=310) during season 2015 () was the latest data available, as research teams have not returned to the island since (A. Lowther, personal communication). This corresponds to a mature population size of 11,990 (SD=610), and an annual rate of change of -3.98% [CI:3.44; 4.52] between 1999 and 2015. Assuming a similar rate of decline until the assessment year (=2025), the reduction over three generations is -0.65 [-0.70; -0.60], which corresponds with maximum probability to a category of **Endangered** under criterion A2.

### 3.6.5 East Antarctica

#### 3.6.5.1 Marion Island and Prince Edward Island

For Marion Island, the closest available pup count to 1999 () was obtained in 2000 () and was 343 ([Wege et al. 2016](#ref-https://doi.org/10.1111/mms.12306)), which is equivalent to an estimated mature population of 509 (SD=17), and a mature population in of 470 (SD=36). The latest pup production estimate is for 2025 (), of 3,172 (SD=156) pups (**Table 1**), and corresponds to a mature population of 4,704 (SD=278). The estimated annual increase is 9.30% [8.88; 9.72], which supports a Red List Category of **Least Concern**.

There are no data for Prince Edward Island since 2001, when a pup count of 404 was reported ([Bester, Ryan, and M. 2003](#X062aae40a7355b0f2fa83537e4d470cfbc50e7a)). This corresponded to an estimated mature population of 599 [CL: 563; 639]. Without any data to evaluate , I used a conservative approach to contribute to the evaluation of the mature population of the East Antarctica subpopulation, and assumed no population change at this breeding location. I used this approach for other data deficient locations (see below).

#### 3.6.5.2 Crozet Islands

The main breeding location at Crozet Islands archipelago is in Possession Island, and has been surveyed repeatedly ([Guinet et al. 2025](#ref-RN6225)). The pup count in 2000 was 234, which corresponds to a mature population of 347 (SD=11), and a back-projected mature population of 337 (SD=15) in . The latest pup count was in 2024, of 530 pups, and corresponded to a mature population of 786 (SD=26). The projected population in is 813 (SD=27), assuming the same estimated annual growth of 3.47% obtained for the observed period. This supports a Red List Category of **Least Concern**.

#### 3.6.5.3 Kerguelen Islands

There are several breeding locations in the Kerguelen Islands archipelago, but only the Courbet Peninsula has been regularly counted ([Guinet et al. 2025](#ref-RN6225)). The closest assessment to 1999 () was in 2000, of 1,600 pups. There is another rounded pup count of 3,600 pups in 2000 at Nuageuses Islands ([Guinet et al. 2025](#ref-RN6225)), where the numbers are likely to have remained stable (C. Guinet, personal communication); but there are no more recent counts. Assuming that the population at Nuageuses Islands has remained constant, I added the pup count of 3,600 to both of two pup counts obtained at Courbet Peninsula to facilitate the assessment of the entire East Antarctica subpopulation. The mature population in would then be equivalent to 7,616 (SD=267), and with the latest pup count at Possession Islands of 4,793, it would be 12,698 (SD=415) in . The resulting estimated annual increase is 2.02%, which supports a Red List Category of **Least Concern**.

#### 3.6.5.4 Heard Island and McDonald Islands

Due to its remoteness and difficult access, the Heard Island and McDonald Islands group have been seldom visited, let alone counted the fur seal pups being born on them. In March 1980, “up to a 100 pups and 200 other” (*ditto*, Johnstone ([1982](#ref-RN6253))) were counted at McDonald Islands, being the last available data for this assessment ([Johnstone 1982](#ref-RN6253)); although the population was thought to be increasing ([SCAR 2006](#ref-RN5984)). As a result, this breeding location continues to be **Data Deficient**, and because the data preceds by far, it is not considered numerically in the assessment of East Antarctica.

In contrast, Heard Island was visited on several occasions, the more relevant being 2001, when 1,012 pups were counted, and the last one in 2004, with a count of 1,278 pups (S. Goldsworthy, personal communication). This would correspond to a mature population of 1,501 (SD=49) in 2001, and 1,895 (SD=62) in 2004, with a possible population in of 1,296 (SD=90). For the observed period, the annual increase was 8.089%. However, these data alone cannot warrant a new assessment, and I used the same approach as MacDonald and Kerguelen Islands, keeping the last value (in this case for 2004) stable until . The Red List category for Heard Island is therefore **Data Deficient**.

#### 3.6.5.5 Macquarie Island

There are three species of fur seals that breed at Macquarie Island; Antarctic, subantarctic (*A. tropicalis*) and New Zealand (*A. forsteri*) fur seals, although there are no females of New Zealand fur seals. All species hybridise, and best attempts at discriminating pups to species level depend on genetic rather than phenotypic identification, which tends to overestimate *A. gazella* as species ([Goldsworthy et al. 2009](#X900c7297a62c11770e773a1d7a5b1f7c444134f)). Based on these early counts, the number of *A. gazella* pups were approximately 100-105 in 1999, which would give an of 156 (SD=498), and an of 280 (SD=9) in 2012, when long-term studies were terminated. Annual change between these estimates and observed period would be 4.65%. As with previous populations, this supports a **Data Deficient** category; and I used the assumption of stability after the last count to evaluate its contribution to the East Antarctica subpopulation.

| Breeding location |  |  |  |  | Annual change | Category |
| --- | --- | --- | --- | --- | --- | --- |
| *Marion Island* | 470 (36) |  |  | 4,704 (278) | 9.30% (0.002) | Least Concern |
| *Prince Edward Is.* |  | 2001; 599 (20) |  |  |  | Data Deficient |
| *Crozet Islands* | 337 (15) | 2001: 347 (11) | 2024: 786 (26) | 813 (27) | 3.46% | Least Concern |
| *Kerguelen Islands* | 7,616 (267) | 2000: 7,712 (252) | 2024: 12,448 (407) | 12,698 (415) | 2.02% | Least Concern |
| *Heard Island* | 1,296 (90) | 2001: 1,501 (49) | 2004: 1,895 (62) |  |  | Data Deficient |
| *Macquarie Island* | 156 (8) |  | 2012: 280 (9) |  |  | Data Deficient |

**Table 6**. Population assessment and IUCN Red List Category at breeding locations of the East Antarctica subpopulation. Column is population size in 1999, three times the generation length or 26 years; is the first available population size; is the second available population size; and is the current population size. Values in parentheses are standard deviations derived from Bayesian simulations. Cells in columns for and start with the year when the value was obtained.

#### 3.6.5.6 East Antarctica subpopulation

For the assessment of East Antarctica (**Table 6**), I used the sum of the estimates of for all breeding locations of this subpopulation except McDonald Islands. To obtain , I used the estimates from the most recent data, or their projection to if these two values were not the same; and for other cases, I maintained the value of the more recent of or to provide an , assuming stability in growth or no change until the assessment year. This was the case of Maquarie Island, Heard Island, part of Kerguelen Islands, and Prince Edward Islands.

As seen above, when data were available for and , population growth was positive; and all the locations which had two population estimates, including those which were **Data Deficient**, also showed positive growth. Locations that were **Data Deficient** contributed little to total pup production/mature population, except perhaps Heard Island. This suggests that keeping their estimates constant until was likely to have a minor effect in the assessment of the entire subpopulation, with the Red List category unchanged, i.e., **Least Concern**. The annual combined increase for East Antarctica was 2.62% [CI: 2.45; 2.80] (**Table 7**).

### 3.6.6 Global population and species

From the combined estimates of and of all subpopulations, including South Sandwich Islands, the annual change for the global population was estimated as -3.19% [95% CI: -4.015; -2.347]. The estimated reduction was -0.57 [-0.64; -0.48], with a probability of 0.9 of being equal or lower than -0.50 (50%); which corresponds to to a Red List Category of **Endangered** (**Table 7**). This implies a major change of the conservation status of the species, which was previously considered of **Least Concern** but now is in an extinction risk Category.

Currently, only the East Antarctica subpopulation continues to be **Least Concern**, with the caveat that some of the breeding locations, although not generally the most productive, can be considered **Data Deficient**. In contrast, the South Atlantic region has seen the most precipitous declines for the species in the last decades. Numerically, South Georgia has had an overwhelming influence both in the reduction of the global population and also the population of this region. This is because it comprises approximately 96% of the global population according to this new assessment (**Table 7**).

In terms of severity of the reduction, the South Shetland Islands is the most affected subpopulation, as it can now be considered **Critically Endangered**, and its size is now smaller than at some of the East Antarctica breeding locations, whereas before it was the third largest subpopulation. It is potentially smaller in size than the population at the South Sandwich Islands, but concerns on data availability there preclude a proper comparison. The genetic identity of the South Sandwich Islands remains to be examined in order to understand if it can be considered a different subpopulation; and a new complete population assessment is needed.

To put this into perspective, the South Shetland Islands subpopulation which has been considered a genetic reservoir ([Krause et al. 2024](#ref-https://doi.org/10.1111/mam.12327)), is more likely to be now at risk of disappearing, or even of introgression through mixing with other subpopulations, given a potential temporary migratory expansion southwards of males and females (see [Larsen et al. 2025](#ref-https://doi.org/10.1002/ece3.70833)) as the habitat changes ([Ouled-Cheikh et al. 2024](#ref-https://doi.org/10.1111/gcb.17191)). This will provide different options for dispersal, recolonisation, and potentially new breeding locations, although this may only occur if the appearance of new habitats further South with sea ice loss also brings about appropriate conditions to accommodate the stringent seasonal central place foraging demands of breeding females.

| Population |  | |  | % of global | Population change | | | Red List Category |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Annual change | Reduction (R) | P(R ≤ -0.5) |
| **South Georgia** | 2,136,953 (153,084) | | 910,114 (89,753) | 96.40 (0.37) | -3.24% (0.44) | -0.57 (0.05) | R ≤ -0.5: 0.92 | Endangered |
| *South Sandwich Islands* | 474 (34) | | 3,782 (124)\* | 0.40 (0.04) | 1.40% |  |  | Data Deficient |
| **South Shetland Islands** | 14,529 (551) | 1,336 (44) | | 0.14 (0.01) | -8.77% (0.07) | -0.908 (0.002) | R ≤ -0.5: 1 R ≤ -0.8: 1 | Critically Endangered |
| **Bouvetøya** | 22,832 (1,141) | | 8,009 (582) | 0.86 (0.11) | -3.95% (0.29) | -0.65 (0.03) | R ≤ -0.5: 1 | Endangered |
| **East Antarctica** | 10,474 (410) | | 20,514 (710) | 2.19 (0.22) | 2.62% (0.09) |  |  | Least Concern |
| **GLOBAL** | 2,187,424 (153,141) | | 943,756 (89,727) | 100 | -3.19% (0.43) | -0.57 (0.05) | R ≤ -0.5: 0.90 | Endangered |

**Table 7**. Population assessment and IUCN Red List Category for Antarctic fur seal global population and subpopulations. Columns and ) are population estimates for the assessment period (1999-2025), equivalent to three times the generation length (3G) which is 26 years for the assessment year of 2025. The **% of global** value is the percentage of the size of each subpopulation, or breeding location in the case of the South Sandwich Islands, with respect to the global population. The probability of a population size reduction higher than 50% (or 80%) is under **P(R ≤-0.5)**. Values in parentheses are standard deviations derived from Bayesian simulations. \*The value for South Sandwich Islands is based on insufficient data; and the genetic identity of the the South Sandwich Islands is unknown, and for this assessment is assumed to not be the same as the South Georgia population.

## 3.7 Justification of the change in status

The results of this new assessment support a status of **Endangered** according to criterion A2 for the Antarctic fur seal, which was previously listed as **least concern**. Based on current studies, the causes of the reduction are highly unlikely to be reversible (e.g., due to insufficient climate change mitigation), have not ceased, and some are not yet understood. As noted above, the ongoing declines largely respond to directional environmental effects, particularly at South Georgia ([Forcada et al. 2023b](#ref-https://doi.org/10.1111/gcb.16947)), where increasing temperature and cascading ecosystem-wide repercussions determines the staple food supply required to sustain such a vast fur seal population ([Atkinson et al. 2019](#ref-RN2608); [Hill, Phillips, and Atkinson 2013](#ref-RN6233); [Kawaguchi et al. 2024](#ref-RN6208); [McBride et al. 2021](#ref-RN6217)). But the detail of the mechansims and processes remains elusive. In addition, there are competing effects such as local top-down control at the South Shetland Islands ([Krause et al. 2022](#ref-https://10.3389/fmars.2021.796488)), and potential effects for which quantification is almost intractable due to lack of data (see *Introduction*).

The large population reduction estimated for South Georgia has an overwhelming effect on the species Category, due to the numerical importance of this subpopulation. For long-lived species, reductions for criterion A are calculated over 3 generations, to avoid confusion with fluctuations, but data from shorter time series can be used to calculate the 3-generation reduction ([IUCN 2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c)). Here, the time series data for the projection of South Georgia spans 2 generations (2007-2022), but there is very strong supporting evidence of the long-term decline at South Georgia. This is shown by data from Bird Island, which has been declining since 1990 ([Forcada, Trathan, and Murphy 2008](#X26882c7626f5ce00a74000b0a28b44efac98f6f)) (see also **Fig. 4**, central panel), a period of over 4 generations. The long-term decline at South Georgia is also supported by the population index trajectory of Signy Island (South Orkney Islands), which is driven by fur seals from South Georgia in its majority ([Boyd et al. 1998](#ref-https://doi.org/10.1139/f97-314)), and its variation is explained by population changes at Bird Island (**Fig. 5**). Signy Island follows the same trajectory as Bird Island when mid-term sea ice effects are taken into account ([Dunn et al. 2025](#ref-https://doi.org/10.1111/gcb.70290)). Here, the time-series illustrates well an example of fluctuation due to environmental effects (2000-2009), embedded in an ongoing long-term decline (1994-2025) (**Fig.4**, lower panel; **Fig. 6**).

This assessment supports an important change, due entirely to newly obtained data, which supersedes previously used insufficient and incorrect data. The newly proposed Red List status can be thus considered a *Nongenuine change*, according to the latest IUCN definition of change [page 13; IUCN ([2024](#Xae9ca122ff89502040a3f075e18551f2fdb969c))]. “*New information* - 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)”, which in this case is better estimates for population size, and rate of decline. And “*Incorrect data* - The previous category was applied in error because incorrect data were used”. In this case, previously made incorrect assumptions on population size and growth, particularly for South Georgia.

The previous assessment was based on incomplete data which precluded an investigation of population reduction. Survey data, particularly from South Georgia which comprises 96% of the global abundance, were unavailable at the time of the previous assessment. Instead, the assessment quoted old and non-validated abundance estimates for South Georgia for 1991 ([SCAR 2006](#ref-RN5984)), which were very different from those reported previously ([Boyd 1993](#Xcc7f7bc0df5c21c90a9a4ab37d2501c8efec44c)) (2.7 million compared to 1.5 million, respectively); and from which population values for 1999/00 were derived as 4.5 and 6.2 million seals ([SCAR 2006](#ref-RN5984)). These figures were allegedly obtained from female counts, but there are no records or any other evidence of any female counts or surveys of South Georgia in 1999/00, at the British Antarctic Survey or elsewhere. Recently, the population in 2007/9, at the maximum of its recovery at South Georgia, has been robustly estimated as less than 4 million (3.5 million [CI:3,1 - 3,9]). It is likely that the previous incorrect estimates were extrapolated from female counts in 1991, reevaluated with some adjustment factor, and assuming an implausible annual growth rate of 6% to 14% ([SCAR 2006](#ref-RN5984)) obtained at Bird Island, the only place were long-term data were available. As seen above, this growth rate is inconsistent with the much lower annual growth rates observed at Bird Island [see also this analysis; Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947))].

Therefore, without representative pup counts or other survey data, previously reported numbers were conjectural uneducated guesses, only supported by a personal communication in SCAR ([2006](#ref-RN5984)). This, as discussed in Forcada et al. ([2023b](#ref-https://doi.org/10.1111/gcb.16947)), led to a category of **Least Concern** in 2016 ([Hofmeyr 2016](#X71f83c25f5844e56179bf393f49eabea0997d1d)), where the mature female population was reported to be around 550,000, a value which was not in the references cited to obtain such estimate. Additionally, this population value was cited as questionable by a personal opinion from a blog which was, again, based on no data and pure speculative criticism, adding even more confusion. For this reason, the previous assessment is not based on reliable population data, and therefore, the new assessment reports a *Nongenuine* change, due to the use of new and robust assessments of the latest data.

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