

FIGURE 6.3: Region-level Penguindex for Regions 1-5 for (a-e) Adélie, (f-i) Chinstrap, and (j-l) Gentoo penguin populations from 1980-2019. Each black line denotes the mean, the white lines the 95% credible intervals, and the gray lines each iteration. Each blue line denotes the null model index. Identified change points are reported in Appendix S2: Table S1.



FIGURE 6.4: Region-level Penguindex for Regions 6-8 for Adélie penguin populations from 1980-2019. (Chinstrap and Gentoo penguin populations were not present in Regions 6-8.) Each black line denotes the mean, the white lines the 95% credible intervals, and the gray lines each iteration. Each blue line denotes the null model index. Identified change points are reported in Appendix S2: Table S1.

initial period of growth. Most of this decline occurred between 1992-1995 (1992 index 0.985, 95% CI 0.662-1.413; 1995 index 0.598, 95% CI 0.409-0.853), while recent declines have been slower. The average Adélie population on the Central- and Northwest AP (14 populations; Region 1, Figure 6.3a) declined by 75.7% (95% CI = 67.3-82.3%) of

baseline by 2007 following a small amount of initial growth. In later years, Adélie populations on the Central- and Northwest AP were more stable on average (2019 index 0.235, 95% CI = 0.149-0.358; null model index 1.079).

For Adélie populations on the Southwestern AP (9 populations; Region 2, Figure 6.3b), two short periods of initial growth—first rapid until 1983 (1983 index 1.159, 95% CI 0.670-01.861) and then slow between 1983-1987 (1987 index 1.170, 95% CI 0.628-1.976)—were followed by three longer periods of slow decline—1987-1999 (1999 index 0.978, 95% CI 0.485-1.759), 1999-2003 (2003 index 0.822, 95% CI 0.455-1.320), and 2003-2019 (2019 index 0.570, 95% CI = 0.299-1.023; null model index 1.145). On the Northeastern AP (7 populations; Region 4, Figure 6.3d), Adélie populations increased steadily until 1998, by 74.4% (95% CI = 19.3% decrease - 254.2% increase) on average. Between 1998 and 2019, however, these Adélie penguin populations decreased just as steadily (2019 index 1.034, 95% CI = 0.382-2.219; null model index 1.064). The Bellingshausen Sea (Region 6, Figure 6.4a) had only one Adélie penguin population and contributed little to the global Adélie Penguindex.

#### **Regional Chinstrap trends**

The majority of Chinstrap breeding populations were located in Elephant Island, the South Orkney Islands, and the South Shetland Islands (60 populations; Region 3, Figure 6.3h). On average, these populations declined by 74.4% (95% CI = 81.0-66.7%) between 1980-2019. Prior to 1986, however, these populations increased on average by 31.5% (95% CI = 7.8-59.1%). After 1986, these populations declined at various rates until 2009 (2009 index 0.324, 95% CI = 0.256-0.411), after which populations remained relatively stable until 2019 (2019 index 0.256, 95% CI = 0.256-0.411). On average, Chinstrap populations on the Central- and Northwestern AP (31 populations; Region 1, Figure 6.3f) declined by only 30.9% (95% CI = 0.6-52.8%). Compared to Elephant Island, the South Orkney Islands, and the South Shetland Islands, Chinstrap populations on the Central- and Northwestern AP displayed a much steeper period of growth

prior to 1985, more than doubling the 1980 baseline on average (1985 index 2.12, 95% CI = 1.41-3.00). Chinstrap populations in this region declined after this initial period of growth, first quickly until 1991 (1991 index 0.768, 95% CI = 0.612-0.961) and then slowly from 1991-2005 (2005 index 1.193, 95% CI = 0.786-1.754). The Southwestern AP (Region 2, Figure 6.3g) and Ross Sea (Region 5, Figure 6.3i) each had two or fewer Chinstrap penguin populations and contributed little to the global Chinstrap Penguindex. Null models for all regional-level Chinstrap indices were stable at 1.0.

#### **Regional Gentoo trends**

Gentoo penguin populations on the Central- and Northwestern AP (39 populations; Region 1, Figure 6.3j) increased on average over 10-fold (2019 index 11.529, 95% CI = 8.362-15.482). Initial growth was slow until 2001 (2001 index 3.622, 95% CI = 2.584-4.983), then steeper between 2001 and 2015 (2015 index 12.343, 95% CI 9.090-16.094). The growth of these populations, however, stalled between 2015-2019. Growth was relatively steady for Gentoo breeding populations on Elephant, South Orkney, and South Shetland Islands (Region 3, Figure 6.3k), with the average population increasing by 287.6% (95% CI = 195.2-664.2%) by 2019. On the Northeastern AP (Region 4, Figure 6.3l), Gentoo penguin populations increased 17-fold on average (2019 index 17.050, 95% CI = 3.094-51.692). With only 4 Gentoo penguin populations, this region contributed relatively little to the global Gentoo Penguindex. Null models for all three regional-level Gentoo penguin indices were stable at 1.0.

## 6.4 Discussion

To our knowledge, this is the first comprehensive examination of genus-wide trends for *Pygoscelis* penguins across the whole of the Antarctic. Our results identify key eras of global change for the average pygoscelid breeding population. While the dominant approach to Antarctic monitoring strategies has been to model overall population abundance [39, 53], the LPI framework used here instead aims to measure average trends in populations. Since region-level Penguindex calculations equally weight all populations within a region regardless of their size, our index is different from one calculated by aggregating populations at larger scales. Thus the trends described here by a region-level Penguindex are not commensurate with the trends observed for the total abundance of that species across the region (i.e., as in [39], Fig 2). For example, a region-level Penguindex for a species can be interpreted as describing the average percentage increase or decrease in any given population's abundance within that region, enabling trends in all populations to be reflected in the index rather than being dominated by the largest population. We see the Penguindex and the LPI framework as a complement to ongoing efforts to model aggregated abundance across the Antarctic.

#### 6.4.1 Stark differences in individual species trends

Over the last four decades, our time series suggest an average decline of 21% within Chinstrap penguin populations across the Antarctic. While data is sparse, studies up to the 1990s found many Chinstrap populations to be increasing [73, 106, 185], with evidence of this growth dating back to the mid 1950s [52]. For example, [52] note a five-fold increase at North Point (S. Orkney Islands) between 1958 and 1978. However, more recent studies have established global declines in Chinstrap populations [143, 169, 194, 210]. Our global Chinstrap Penguindex quantifies both this initial period of Chinstrap population growth and its subsequent crash.

In stark contrast to the grim global trend of Chinstrap populations, however, Gentoo penguin populations have skyrocketed, with our global Gentoo Penguindex suggesting that the average population more than doubled between 1980 and 2019. In fact, an analysis of the public LPR database [139] reveals that the growth observed for Gentoo penguins is in the top 89th percentile for species undergoing population growth (see Appendix S1: Section S3). The regional trends observed here also align with previous studies showing that Gentoo populations along the Western AP have experienced the most rapid growth [95].

Compared to the overwhelming decline of Chinstrap populations and staggering growth of Gentoo populations, Adélie penguin populations across the Antarctic have experienced little change on average over the 40 years considered here. Even within an initial era of growth identified between 1980-1986, the average Adélie population never grew to more than 5.8% of the 1980 baseline, and went on to decline back to this baseline by 2019. Regional Adélie trends differ markedly, with declines in Adélie populations across the AP and sub-Antarctic islands being offset by increases in populations in the Ross Sea and Eastern Antarctica. These trends are similar to those identified by the first (and only) global Adélie penguin census, conducted in 2014 [141].

#### 6.4.2 Notable eras of population change may be linked to warming

While Adélie populations on the Western AP and sub-Antarctic islands (Elephant, South Orkney, and South Shetland Islands) decreased drastically between 1980-2019, each constituent region was identified as having a recent distinct era of change in which declines slowed significantly. These eras each started roughly between 2003-2006 and extended until the end of our study period (2019). This recent leveling of decline among Adélie populations is perhaps related to the shift between a long period of steady warming to a recent period of cooling (beginning circa 1999) identified by Turner et al. [226, 229], with a lag roughly consistent with the time necessary for a shift in either reproductive success or juvenile survival to affect breeding abundance [218]. Adélie penguins have a tight-knit coupling to Antarctic sea ice [16, 73, 237] that has been the subject of considerable research over the last 40 years, though the relative roles of climate and Antarctic krill fishing as drivers of Adélie trends on the Peninsula remain subject to debate. Our findings are consistent with, though not conclusive of, climatically-driven forcings playing a key role in the observed and much discussed declines of Adélie penguins in this region.

While, on average, the 2019 abundance of Adélie populations on the Northeastern AP was nearly identical to the 1980 abundance, our data suggest that these populations were not stable over the 40 year time series considered here [27]. We identified a clear era of growth between 1980-1998 followed by an era of decline (1998-2019). Thus the period of warming across the AP prior to 1999 [226, 229] was correlated with growth of Adélie populations on the Northeastern AP, in contrast to the decline seen on the Western AP and sub-Antarctic islands. Additionally, the period of cooling observed across the AP after 1999 was met with declines in these Northeastern AP populations. These trends may indicate that the sea ice concentration in the Weddell Sea was unfavorably high at the start of our time series in 1980, and that the warming period prior to 1999 benefited Adélies until the region began to cool again.

Our species-level index for Gentoo penguins also suggests a recent period of relative stagnation in the growth of the average population, with a distinct period of stability identified between 2015-2019. While we have been unable to identify any promising potential environmental drivers for this halt in growth of Gentoo populations, it is clear that recent years have marked a new era for this species.

# 6.4.3 Global *Pygoscelis* trends are dominated by different species over time

Species-level pygoscelid penguin trends were equally weighted to obtain the global *Pygoscelis* Penguindex. Four distinct eras of global pygoscelid trends were identified, beginning with a period of growth across Antarctica for all species (1980-1986). Between 1986 and 1996, growth in the average Gentoo population was balanced with the

decline in the average Adélie and Chinstrap populations, resulting in virtually complete stagnation in the global *Pygoscelis* Penguindex across this era. For the next two decades, from 1996-2015, growth in Gentoo populations outweighed the declines in Adélie and Chinstrap populations, as illustrated by a steadily rising global *Pygoscelis* Penguindex. As discussed above, recent years have seen a halt of growth in Gentoo penguin populations. This change point was identified in the global pygoscelid index as well, with the recent era between 2015-2019 demonstrating a global decline in the Penguindex as stable Gentoo populations were eclipsed by continuing, albeit gradual, declines in Adélie and Chinstrap populations.

While changes in the global Penguindex are driven by different species through time, it is important to note that both Adélie and Chinstrap penguins outnumber Gentoo penguins almost ten-fold across the Antarctic [95, 141, 210]. Thus the Penguindex provides information that is complementary, but not equivalent, to changes in overall penguin abundance. Instead, the Penguindex reflects average population change on a percentage basis by treating species trends equally regardless of the species population size, as described above.

#### 6.4.4 Benefits of state-space models and the Penguindex approach

State-space models (SSMs) similar to the one employed here are valuable in their ability to synthesize data collected by different methods or with different precision by incorporating observation error into their estimation of trends [39, 114, 129, 174]. Here, the use of our hierarchical Bayesian SSMs also allowed for a more informed modeling approach than is provided by a generalized additive model (GAM) like the one employed by the LPI for interpolation [47, 159]. In the traditional LPI framework, a GAM not only interpolates missing data but also smooths time series, reducing interannual variation and affecting the resulting index. As *Pygoscelis* penguin time series display considerable interannual fluctuations [39, 218, 240], preserving this variability is important to understanding their dynamics and producing an accurate index of pygoscelid biodiversity. As an aggregation of species population trends, the traditional LPI can mask variation in the underlying data. By maintaining empirical interannual variation with the use of our SSMs and including species-specific indices to aid interpretation, the reflection of different species trends in the Penguindex can help to illustrate underlying environmental changes happening in the Antarctic. SSMs also allow for the incorporation of covariates or spatial autocorrelation to improve interpolation of missing data, which stand as future improvements to the Penguindex and the underlying SSMs.

The traditional LPI framework has several other shortcomings that we mitigate in the formulation of the Penguindex. First, the LPI is sensitive to random fluctuations in underlying population time series [32], leading to shifting a counterfactual rather than a fixed baseline set at 1980. The null models utilized in the Penguindex address this issue by allowing for a null expectation of the index that is robust to large population fluctuations. While most null model indices are fairly static, some (particularly for Adélies in Regions 1-3, see Figure 6.3) demonstrate an increasing counterfactual rather than a constant standard equal to the 1980 index. Additionally, the use of the geometric mean in the standard LPI means it is often sensitive to extremes. While the aggregation of the Penguindex does not weight population time series based on their size, and thus may still be sensitive to the influence of small populations, our region-level indices, showing underlying regional trends, and use of credible intervals, illustrating the variation in each index, aid in the determination of global and species-wide trends.

#### 6.4.5 Updating the LPI for Antarctica and expanding the Penguindex

*Pygoscelis* penguins and the Southern Ocean ecosystem are extremely underrepresented in the database underlying the LPI and the biennial LPR. Though MAPPPD has identified 271 Adélie, 358 Chinstrap, and 109 Gentoo penguin breeding populations across the Antarctic, the Living Planet database currently includes only 76 Adélie, 18 Chinstrap, and 66 Gentoo time series. Through our analysis we have aggregated and adapted all MAPPPD pygoscelid penguin abundance observations into the format required for integration into the LPI [159] (see Appendix S1: Section S4). The inclusion of all MAPPPD *Pygoscelis* time series will drastically increase the data coverage for these Antarctic sentinels and our work provides a starting point for more comprehensive Antarctic coverage in the LPI.

Here we have started with the three Antarctic penguin species with the greatest data coverage. Ongoing efforts to track Emperor penguins using satellite imagery will greatly expand data availability for this species of conservation concern, and we consider the incorporation of these data into the Penguindex—and, further, the LPI—as a top priority. In addition, King and Macaroni penguins were recently added to MAPPPD. While these two species have relatively few populations in this region and the time series are particularly short and/or sparse, we expect that the Penguindex can be expanded to include them in the near future. Finally, penguins are only one small component of Antarctic biodiversity. As time series are collated for other species of long-standing research interest (e.g., pack-ice seals, petrels, fur seals, whales; [26, 28, 82, 195]), their full incorporation into the LPI will allow for a straight-forward assessment of biodiversity trends by a wide range of stakeholders.

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# Appendix A

# Difficulties in summing log-normal distributions for abundance and potential solutions

# A.1 Supplementary Methods



FIGURE A.1: Parameter values used in the simulation study and global bird abundance study. Log-normal parameter values  $\mu$  and  $\sigma$  used in both the simulation study and the re-analysis of Callaghan et al.'s global bird abundance data.



FIGURE A.2: Reconstructed global species abundance distribution for global bird abundance. The global species abundance distribution, calculated using the median of each species' simulated abundance distribution (each a log-normal distribution) for the re-analysis of the global bird abundance data. A constant 1 is added for species predicted to have zero abundance. Reproduction of Fig 2A in Callaghan et al. (shown on the same scale,  $\log_{10}$ ).



FIGURE A.3: Examples of reconstructed species' simulated abundance distributions for global bird abundance study. Species shown, from top to bottom: Ring-billed Gull; Green Heron; Northern Wheatear; Ashy Prinia; Osprey; Acorn Woodpecker; Yellow-tailed Black-Cockatoo; and Midget Flowerpecker. Reproduction of Fig 2B in Callaghan et al. (shown on the same scale,  $\log_{10}$ , in millions).

# A.2 Derivation of linearity of difference in global abundance estimates

Consider  $n = \{10, 100, 1000\}$  i.i.d. log-normally distributed populations  $N_1, N_2, ..., N_n$  each satisfying  $\log(N_{i_t}) \sim N(\mu, \sigma^2)$ . Let the *D* be equal to the logged-difference between the median of the posterior for the aggregate sum of populations and the sum of the individual population medians. Then

$$D = \log(M - S), \tag{A.1}$$

where *M* is the median of the posterior for  $N = N_1 + N_2 + ... + N_n$ , the aggregate sum of populations and *S* is the sum of the individual medians of each population.

The sum of *n* i.i.d. log-normal random variables *N* has no closed form probability density function. However, the Fenton-Wilkinson (FW) approximation produces a commonly used estimate for the PDF of *N* [67]. According to the FW approximation [46], *N* can be approximated by a log-normal PDF with parameters  $\mu_N$  and  $\sigma_N^2$  such that

$$\sigma_N^2 = \frac{\log(e^{\sigma^2 - 1})}{n} + 1,$$
(A.2)

$$\mu_N = \log(ne^{\mu}) + \frac{1}{2}(\sigma^2 - \sigma_N^2).$$
(A.3)

Thus the median of *N* is given approximated by

$$M = \text{med}(N) \approx \frac{\log(ne^{\mu}) + \frac{1}{2}(\sigma^2 - \sigma_N^2)}{e^{\sigma_N^2/2}}$$
(A.4)

$$=\frac{\log(ne^{\mu}) + \frac{1}{2}(\sigma^2 - (\frac{1}{n}\log(e^{\sigma^2 - 1}) + 1))}{e^{(\frac{1}{n}\log(e^{\sigma^2} - 1) + 1)/2}}$$
(A.5)

$$=\frac{\log(n) + \log(e^{\mu}) + \frac{1}{2}(\sigma^2 - (\frac{1}{n}\log(e^{\sigma^2 - 1}) + 1))}{e^{(\frac{1}{n}\log(e^{\sigma^2} - 1) + 1)/2}}$$
(A.6)

$$=\frac{\log(n)+\mu+\frac{1}{2}(\sigma^2-(\frac{1}{n}\log(e^{\sigma^2-1})+1))}{e^{(\frac{1}{n}\log(e^{\sigma^2}-1)+1)/2}}$$
(A.7)

$$= \frac{\mu}{e^{(\frac{1}{n}\log(e^{\sigma^2}-1)+1)/2}} + \frac{\log(n) + \frac{1}{2}(\sigma^2 - (\frac{1}{n}\log(e^{\sigma^2}-1)+1))}{e^{(\frac{1}{n}\log(e^{\sigma^2}-1)+1)/2}}.$$
 (A.8)

Setting  $a = \log(n) + \frac{1}{2}(\sigma^2 - (\frac{1}{n}\log(e^{\sigma^2-1}) + 1))$  and  $b = e^{(\frac{1}{n}\log(e^{\sigma^2}-1)+1)/2}$ , A.8 reduces to

$$M \approx \frac{1}{b}\mu + \frac{a}{b}.$$
 (A.9)

Since the median of each log-normally distributed population  $N_i$  is equal to  $e^{\mu}$ , the value of *S* can be found easily:

$$S = \sum_{i=1}^{n} \operatorname{med}(N_i)$$
  
=  $\sum_{i=1}^{n} e^{\mu}$   
=  $ne^{\mu}$ . (A.10)

Thus A.1 becomes

$$D = \log\left(\frac{1}{b}\mu + \frac{a}{b} - ne^{\mu}\right).$$
(A.11)

Differentiating with respect to  $\mu$  yields

$$\frac{dD}{d\mu} = \frac{\frac{1}{b} - ne^{\mu}}{\frac{\mu}{b} + \frac{a}{b} - ne^{\mu}} \tag{A.12}$$

$$\approx 1,$$
 (A.13)

since the  $e^{\mu}$  terms dominate all others in A.12 for sufficiently large values of  $\mu$ .

# A.3 How Bayesians interpret the tail of the skewed distributions

For simplicity, we limited our manuscript's discussion on the mechanics of summing distributions for population abundance. However, it is also worth reflecting on our interpretation of the posterior distribution and, specifically, on the interpretation of the log-normal distribution's long right tail. One interpretation of this long right tail is that such abundances are infrequent and thus including them in the aggregate sum (at the appropriately small probability) is appropriate. A more Bayesian interpretation would be that such tail events are not infrequent but are instead *unlikely to be true* (in the "degree-of-belief" sense), in which case they should not be included in the aggregate total. While extreme outcomes (i.e. those in the right tail of the distribution) are by nature rare, the probability of drawing at least one extremely large abundance when summing across posteriors can be quite high, and eventually inevitable (as illustrated in Fig 1C in the main text), meaning the aggregate abundance will almost certainly include at least one very large draw, and thus will be larger than anticipated by the central tendencies of the individual populations. The interpretation of the Bayesian posterior in this context deserves discussion but falls outside the scope of our manuscript, which was written for an audience of conservation practitioners.

## A.4 Summing negative binomial distributions

Consider a collection of  $n = \{10, 100, 1000\}$  independent and identically negative binomially-distributed populations of animals, each with an abundance that is modeled as  $N_{i,t} \sim NB(\mu, k)$  where  $\mu$  is the mean of abundance, varying between 2,000 and 160,000, and k is the overdispersion ("size") parameter, fixed at 4. (The overdispersion parameter measures the amount of clustering, or aggregation, or heterogeneity in the data: a smaller k means more heterogeneity; when k = 0, the NB distribution is equivalent to the Possion distribution.) Each population consists of m = 1000negative binomially-distributed draws. If an estimate for the total abundance across all of these populations (the "regional" abundance) is sought, then the distribution of interest, that of the regional abundance, is thus the sum of many log-normal distributions. We first consider the choice of summary statistic for a single negative binomial distribution, and then consider the differences between methods of summing across multiple distributions. Similar to that of the log-normal distribution, the mean of a negative binomial random variable is pulled toward the extreme values of the distribution's long right tail and, as a result, the mean is always larger than the median (Fig A.4).



FIGURE A.4: Negative binomial distribution for abundance with  $\mu = 20,000$  and k = 2.

We now consider summing across multiple populations whose abundances are described each by a negative binomial distribution. Unlike the case of the log-normal distribution, the probability generating function of the sum of *n* negative binomial random variables is known in closed form. The sum  $S = X_1 + X_2 + ... + X_n$  where each  $X_i$  follows the negative binomial distribution has been shown to be a mixture binomial random variable [41, 74]. However, we show in Fig A.5 that sums of negative



FIGURE A.5: The distribution of m = 1000 sums of NB-distributed abundance samples across n = 1000 independent populations. Each NB-distributed population has mean abundance  $\mu = 4000$  and overdispersion parameter k = 2. The values of the sum of the medians, median of sums, and mean of sums (which is equal to the sum of the means) are shown.

binomial random variables behave similarly to those of log-normal random variables when the median is used as the measure of central tendency. If the median is used as a point estimate of abundance, it follows that either the median of the sums or the sum of the medians represents the best estimate of the aggregate abundance. However, since the median of sums is not the sum of medians, these two methods give different estimates for total abundance across the region, with the latter approach (sum-thensummarize, giving the median of the sums) yielding a significantly larger estimate of total abundance than former (summarize-then-sum, giving the sum of the medians), as shown in Fig A.6. This phenomenon is similar to that described for the log-normal distribution.



FIGURE A.6: The logged difference in global abundance estimates for  $n = \{10, 100, 1000\}$  i.i.d. negative binomial-distributed populations is plotted against the mean abundance  $\mu$ . Solid lines represent the mean of each set of 10 ensembles. For each simulation, we draw m = 1000 samples for each population and calculate the difference between the median of the sample-wise aggregated regional population and the sum of the empirical population medians.

# Appendix B

# Heavy-tailed distributions in animal population modeling

**B.1** Heavy-tailed distributions for Adélie penguin abundance



FIGURE B.1: Skewness-kurtosis plot for empirical Adélie abundance data on the linear scale  $(\frac{N_{t+1}}{N_t})$ , including values for 1000 bootstrap samples. Values are also given for several common distributions.

Distribution	Parameter	Estimate	Standard error	
Normal	mean	0.015	0.020	
INOIIIIdi	sd	0.309	0.014	
	mu	-0.001	0.011	
Student's $t$ <sup>+</sup>	sigma	0.175	0.012	
	df	2.542	0.401	
Logistic	location	0.002	0.013	
	scale	0.154	0.007	
Cauchy	location	-0.001	0.010	
	scale	0.126	0.009	
Gumbel *	mu	-0.120	0.015	
	sigma	0.278	0.010	

TABLE B.1: Estimates and standard errors for each parameter for the distributions in Table 3.2 fitted to empirical Adélie penguin abundance between 1970-2019  $(\log(\frac{N_{t+1}}{N_t}))$ . <sup>†</sup>The nonstandard Student's *t* distribution, with mean  $\mu$ , standard deviation  $\sigma$ , and degrees of freedom  $\nu$ , is fit here (it is defined for use in R by the ggdist package [112]). \*The Gumbel distribution is defined for use in R by the VGAM package [238]. All other distributions are defined in Base R.

Distribution	Parameter	Estimate	Standard error
Log-pormal	meanlog	0.012	0.018
Log-normai	sdlog	0.289	0.013
Camma	shape	10.192	0.897
Gamma	rate	9.580	0.864
Weibull	shape	2.276	0.082
Weibuli	scale	1.189	0.035
Log-logistic **	shape	6.514	0.288
Log-logistic	scale	1.002	0.013
	shape1	0.560	0.071
Burr **	shape2	8.376	0.603
	rate	1.113	0.027

TABLE B.2: Estimates and standard errors for each parameter for the distributions in Table 3.1 fitted to empirical Adélie penguin abundance between 1970-2019 ( $\frac{N_{t+1}}{N_t}$ ). \*\*The log-logistic and Burr distributions are defined for use in R by the actuar package [66]. All other distributions are defined in Base R.

# **B.2** Fitting heavy-tailed distributions in JAGS

Distribution	Parameter	MLE Estimate	MLE Standard Error	
Logistic	$\mu = 1$	0.99	0.99	
	s = 2	1.96	0.77	
Student's t	<i>u</i> _ 5	5.08	515	
(Standard)	$\nu = 0$	5.08	5.15	
Student's t	$\mu = 1$	0.98	0.98	
	$\sigma = 0.5$	0.51	0.51	
	$\nu = 5$	5.07	5.24	
Gamma	$\alpha = 5$	4.92	4.92	
	$\beta = 2$	1.93	1.93	
Weibull	k = 1.5	1.52	1.52	
	$\lambda = 1$	0.99	1.00	

## **B.2.1** Table 3.4 Supplementary Results

TABLE B.3: Estimates and standard errors for each parameter using MLE (using the fitdistrplus package in R [61]), as compared to true parameter values, for the distributions in Table 3.4.



FIGURE B.2: Trace plots and posterior distributions for the JAGS built-in logistic distribution model (see Table 3.4).



FIGURE B.3: Trace plots and posterior distributions for the JAGS logistic distribution model using the zeros trick (see Table 3.4).



FIGURE B.4: Trace plots and posterior distributions for the JAGS logistic distribution model using the ones trick (see Table 3.4).



FIGURE B.5: Trace plots and posterior distributions for the JAGS builtin Student's *t* distribution model (see Table 3.4). Data simulated using a standard Student's *t* distribution (defined in Base R).



FIGURE B.6: Trace plots and posterior distributions for the JAGS Student's *t* distribution model using the zeros trick (see Table 3.4). Data simulated using a standard Student's *t* distribution (defined in Base R).



FIGURE B.7: Trace plots and posterior distributions for the JAGS Student's *t* distribution model using the ones trick (see Table 3.4). Data simulated using a standard Student's *t* distribution (defined in Base R).



FIGURE B.8: Trace plots and posterior distributions for the JAGS builtin Student's t distribution model (see Table 3.4). Data simulated using a nonstandard Student's t distribution (defined in the R package ggdist [112]).



FIGURE B.9: Trace plots and posterior distributions for the JAGS built-in Gamma distribution model (see Table 3.4).



FIGURE B.10: Trace plots and posterior distributions for the JAGS Gamma distribution model using the zeros trick (see Table 3.4).



FIGURE B.11: Trace plots and posterior distributions for the JAGS Gamma distribution model using the ones trick (see Table 3.4).



FIGURE B.12: Trace plots and posterior distributions for the JAGS built-in Weibull distribution model (see Table 3.4).



FIGURE B.13: Trace plots and posterior distributions for the JAGS Weibull distribution model using the zeros trick (see Table 3.4).



FIGURE B.14: Trace plots and posterior distributions for the JAGS Weibull distribution model using the ones trick (see Table 3.4).

Ν	Parameter	MLE Estimate	MLE Standard Error
1000	k = 1.5	1.52	0.037
	$\lambda = 1$	0.99	0.022
500	k = 1.5	1.53	0.053
	$\lambda = 1$	0.98	0.030
100	k = 1.5	1.41	0.111
	$\lambda = 1$	0.92	0.069
50	k = 1.5	1.60	0.169
	$\lambda = 1$	0.98	0.092

**B.2.2** Table 3.5 Supplementary Results

TABLE B.4: Estimates and standard errors for each parameter using MLE (using the fitdistrplus package in R [61]), as compared to true parameter values, for the fitted Weibull distributions in Table 3.5.



FIGURE B.15: Trace plots and posterior distributions for the JAGS built-in Weibull distribution model, fitting a dataset of size N = 500 (see Table 3.5).



FIGURE B.16: Trace plots and posterior distributions for the JAGS Weibull distribution model using the zeros trick, fitting a dataset of size N = 500 (see Table 3.5).



FIGURE B.17: Trace plots and posterior distributions for the JAGS Weibull distribution model using the ones trick, fitting a dataset of size N = 500 (see Table 3.5).



FIGURE B.18: Trace plots and posterior distributions for the JAGS built-in Weibull distribution model, fitting a dataset of size N = 100 (see Table 3.5).



FIGURE B.19: Trace plots and posterior distributions for the JAGS Weibull distribution model using the zeros trick, fitting a dataset of size N = 100 (see Table 3.5).



FIGURE B.20: Trace plots and posterior distributions for the JAGS Weibull distribution model using the ones trick, fitting a dataset of size N = 100 (see Table 3.5).



FIGURE B.21: Trace plots and posterior distributions for the JAGS built-in Weibull distribution model, fitting a dataset of size N = 50 (see Table 3.5).



FIGURE B.22: Trace plots and posterior distributions for the JAGS Weibull distribution model using the zeros trick, fitting a dataset of size N = 50 (see Table 3.5).



FIGURE B.23: Trace plots and posterior distributions for the JAGS Weibull distribution model using the ones trick, fitting a dataset of size N = 50 (see Table 3.5).

# Appendix C

# Variability, skipped breeding, and heavy-tailed dynamics in an Antarctic seabird

# C.1 Approximate Bayesian computation



FIGURE C.1: ABC-simulated time series shown with the observed time series for Cape Crozier from 1985 to 2018. Simulated time series are accepted (shown in blue) or rejected (shown in faint gray) based on mean absolute percentage error from observed time series.



FIGURE C.2: Histograms of accepted values for demographic parameters in the ABC parameter estimation, shown with their priors (blue).

# C.2 Bayesian population model

### C.2.1 Model description

We used a Bayesian state-space model to estimate annual Adélie nest abundances for all 271 known Adélie breeding sites from 1970 – 2020. We model the intrinsic rate of growth  $r_i$  for the  $i_{\text{th}}$  site as only the region-specific mean  $\gamma_{R[i]}$ . Regions are dictated by the Antarctic Conservation Biogeographic Regions, as determined by [219]. We purposefully avoided additional covariates as to create a simplistic default model whose predictive ability could be compared to that of more biologically nuanced process models.

## C.2.2 Antarctic Conservation Biogeographic Regions

Adélie penguin colony sites were grouped into the following ACBRs [219] (listed here with the number of sites and number of total site/year observations in each):

- 1. North-east Antarctic Peninsula (6 sites, 12 total observations)
- 2. South Orkney Islands (22 sites, 73 total observations)
- 3. Northwest Antarctic Peninsula (80 sites, 481 total observations)
- 4. Central South Antarctic Peninsula (2 sites, 4 total observations)
- 5. Enderby Land (27 sites, 192 total observations)
- 6. Dronning Maud Land (0 sites)
- 7. East Antarctica (32 sites, 58 total observations)

- 8. North Victoria Land (28 sites, 217 total observations)
- 9. South Victoria Land (10 sites, 199 total observations)
- 10. Transantarctic Mountains (0 sites)
- 11. Ellsworth Mountains (0 sites)
- 12. Marie Byrd Land (7 sites, 10 total observations)
- 13. Adélie Land (13 sites, 40 total observations)
- 14. Ellsworth Land (7 sites, 9 total observations)
- 15. South Antarctic Peninsula (1 site, 1 observation)
- 16. Prince Charles Mountains (26 sites, 55 total observations)

#### **Observation errors**

Counts were provided by the observer(s) as the nest or chick count y along with an associated accuracy score (which we convert to measurement error) such that y represented a draw from a distribution:

$$[y|lz,\sigma_o^2],\tag{C.1}$$

centered on the "true", or latent, count lz whose dispersion was controlled by  $\sigma_o^2$ , which represented the uncertainty in the count due to measurement imprecision. The accuracy scores were selected from a 4 point scale that penguin census counters traditionally use to represent count precision [52]. The precision for the 5th category was determined from highly uncertain nest abundance estimates derived from satellite imagery [141]. Table C.1 shows the reported accuracy categories and their confidence intervals.

 Reported accuracy
 Reported 95% confidence interval

 1
 (95, 105)

 2
 (90, 110)

 3
 (75, 125)

 4
 (50, 150)

 5
 (20, 500)

TABLE C.1: Reported accuracy categories and their confidence intervals. For each category, if 100 nests was the true count then the 95% confidence intervals for each accuracy category's distribution was defined as described here.

We used the log-normal distribution to model the observation process, as all counts must be positive. However, the confidence intervals (with the exception of category 5) were symmetric around the true count and did not correspond to the skewed credible intervals generated by the log-normal distribution. To compute the appropriate scale parameters for each accuracy category, we defined a function that output the squared

deviations between the upper and lower confidence interval (Table C.1) and the 0.975 and 0.025 quantiles from the cumulative density function for a log-normal distribution whose median was 100. We then used the optim function to select the scale parameter  $\sigma_o$  that minimized the sums of squares for each accuracy category.

#### Abundance process models

#### Nest abundance

For the purpose of clarity we build our nest abundance model in a series of steps, first modeling abundance on the arithmetic scale using the log-normal distribution. We then introduce a term to shift these distributions to the left as a corrective for biases that result when summing log-normal distributions, a step we explain more fully below. Finally, we re-express this model using logged abundance modeled normally and briefly discuss its equivalence to modeling abundance log-normally. Adopting the bracket notation from [78] for assigning group membership (for example, R[35] = 2 means that the  $35^{\text{th}}$  unit in the data (i = 35) is from region 2), we start by modeling "true" (hereafter latent) nest abundance  $z_{i,t}$  at the  $i_{\text{th}}$  breeding site located in region R[i] in the  $t_{\text{th}}$  season as:

$$\log(z_{i,t}) \sim \text{student-t}(\mu_{i,t} = \log(z_{i,t-1}e^{r_i}), \sigma_{R[i]}^2, \nu_{R[i]}),$$
 (C.2)

where the mean of the Student's *t* distribution,  $\mu_{i,t}$ , is a deterministic model for discrete exponential growth, such that nest abundance  $z_{i,t}$  is the product of nest abundance in the previous season  $z_{i,t-1}$  at the site and the intrinsic rate of growth,  $r_i$ . We model the intrinsic growth rate as just the regional mean  $\gamma_{R[i]}$  (without site effects or seasonal effects):

$$r_i = \gamma_{R[i]},\tag{C.3}$$

where gamma is modeled hierarchically as:

$$\gamma_{R[i]} \sim \operatorname{normal}(0, \sigma_{region}^2)$$
 (C.4)

In Equation C.2,  $\sigma_{R[i]}^2$  represents process error, or the variation in logged latent nest abundance due to unmodeled biotic or abiotic processes not captured by the simple growth model embedded as the distribution's median.

#### Chick abundance

We modeled the latent chick abundance  $zc_{i,t}$  at the  $i_{th}$  breeding site in the  $t_{th}$  season as:

$$zc_{i,t} \sim \text{binomial}(N_{i,t}, \alpha_{i,t})$$
 (C.5)

$$N_{i,t} = 2 \times \operatorname{round}(e^{lz_{i,t}}) \tag{C.6}$$

$$\alpha_{i,t} \sim \text{beta}(a = 1.875, b = 1.125).$$
 (C.7)

Pygoscelid penguins typically produce one chick per nest (the maximum number of chicks per nest is two), although breeding success can fluctuate considerably between sites and seasons. We use the well-informed priors  $\mu = 0.5$ ,  $\sigma^2 = 0.0625$  for  $\alpha_{i,t}$ ,

the proportion of chicks produced at the  $i_{th}$  site in the  $t_{th}$  season, to reflect observed variation in breeding success due to environmental and demographic stochasticity. Note that, when moment-matched, these priors result in a and b in Equation C.7.

#### Initial season abundance

We modeled the logged latent nest abundance at the  $i_{th}$  site (for the first season nest abundance was recorded,  $t = I_i$ ) as:

$$lz_{i,t-1} \sim \operatorname{normal}(lz_{i,t} - \gamma_{R[i]}, \sigma_{R[i]}^2)$$
(C.8)

This method of hindcasting was possible because the exponential growth function can be inverted, making hindcasting nest abundances functionally no different than forecasting nest abundances into the future or in seasons of missing data within a site's time series. For sites whose first season of data was 1970, hindcasting was unnecessary.

#### **Observation process models**

We modeled the logged observed nest counts  $y_{n_s}$  and chick counts  $y_{c_s}$  recorded at the  $i_{th}$  breeding site in the  $t_{th}$  season as:

$$y_{n_{i,t}} \sim \operatorname{normal}(lz_{i,t}, \sigma_{n_{i,t}}^2)$$
 (C.9)

$$y_{c_{i,t}} \sim \operatorname{normal}(lz_{i,t}, \sigma_{c_{i,t}}^2) \tag{C.10}$$

where  $\sigma_{n_{i,t}}^2$  and  $\sigma_{c_{i,t}}^2$  are the observation errors in the recorded nest and chick count, respectively. These errors are computed from the accuracy ratings reported by the observer, the details of which are outlined in Section C.2.1. Here we model observations being drawn from a log-normal distribution whose median is  $lz_{i,t}$ , as over- and undercounts are equally likely. Note that sites can have both nest and chick counts in the same season.

## C.2.3 Results

	mean	sd	95%_HPDL	95%_HPDU	Rhat	n.eff
damma[1]	-0.008	0.014	-0.037	0.021	1.01	4018
namma[2]	-0.018	0.010	-0.039	0.002	1.01	1134
gamma[3]	-0.028	0.005	-0.040	-0.017	1.00	3525
gamma[4]	-0.332	1.569	-4 574	2 754	1.37	2802
gamma[5]	0.034	0.013	0.008	0.061	1.00	6626
gamma[6]	0.005	2 763	-5 226	5.411	1.00	7681
gamma[7]	0.010	0.011	-0.011	0.031	1.00	1594
gamma[8]	0.014	0.008	-0.001	0.030	1.00	7196
gamma[9]	0.015	0.016	-0.016	0.047	1.00	7500
gamma[10]	0.024	2 770	-5.567	5,202	1.00	7715
gamma[11]	0.027	2 755	-5.080	5 593	1.00	7500
gamma[12]	-0.006	0.088	-0.179	0.174	1.00	6851
gamma[13]	0.026	0.013	-0.001	0.049	1.00	3393
gamma[14]	-0.109	0.149	-0.425	0.193	1.00	5065
gamma[15]	-0.040	2 762	-5 377	5 487	1.00	7500
gamma[16]	0.008	0.017	-0.027	0.039	1.01	663
sigma[1]	0.078	0.066	0.007	0.220	1.02	108
sigma[2]	0.099	0.071	0.010	0.253	1.03	53
sigma[3]	0.145	0.014	0.118	0.172	1.00	898
sigma[4]	0.380	0.285	0.000	0.916	1.30	752
sigma[5]	0.210	0.031	0.146	0.270	1.00	1318
sigmal61	0.504	0.288	0.054	1.000	1.00	7312
sigma[7]	0.181	0.057	0.064	0.293	1.01	152
sigma[8]	0.193	0.018	0.156	0.226	1.00	1748
sigma[9]	0.237	0.019	0.200	0.275	1.00	6001
sigma[10]	0.502	0.289	0.045	0.992	1.00	7781
sigma[11]	0.503	0.288	0.005	0.951	1.00	7500
sigma[12]	0.656	0.194	0.336	0.999	1.00	722
sigma[13]	0.176	0.050	0.083	0.279	1.04	271
sigma[14]	0.562	0.243	0.174	0.996	1.00	904
sigma[15]	0.500	0.292	0.034	0.984	1.00	7144
sigmal16	0.084	0.029	0.036	0.147	1.01	994
nu[1]	30,634	20.728	1.518	71.652	1.00	7236
nu[2]	4.954	8.763	0.685	26.178	1.02	67
nu[3]	3.096	0.542	2.152	4.173	1.00	1390
nu[4]	20.042	21.935	0.105	63.240	1.73	5755
nu[5]	25.314	20.557	1.661	66.455	1.00	3360
nu[6]	28.323	21.353	0.051	69.676	1.00	7500
nu[7]	28.549	20.993	1.507	68.679	1.00	2584
nu[8]	20.858	17.118	2.769	56.903	1.00	3138
nu[9]	26.468	18.856	2.904	64.523	1.00	6984
nu[10]	28.192	21.240	0.054	69.847	1.00	7846
nu[11]	27,446	21.208	0.052	68.200	1.00	7468
nu[12]	29.186	20,962	1.068	70.054	1.00	5258
nu[13]	30.226	20.671	1.499	69.973	1.00	4779
nu[14]	28.564	20.992	0.448	69.295	1.00	5379
nu[15]	28.093	21.008	0.051	68.991	1.00	7500
nu[16]	27.153	20.534	0.628	68.154	1.00	4563
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FIGURE C.3: Model summary tables for mean growth rate  $(\gamma_{R_i})$ , standard deviation  $(\sigma_{R_i})$ , and degrees of freedom  $(\nu_{R_i})$  of the Student's *t* distribution for abundance for ACBR  $R_i$ .