

Appendix S3: Time Series Reanalyses

Circumpolar analysis of the Adélie penguin reveals the importance of environmental variability in phenological mismatch

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Intro

Trends in penguin breeding phenology were previously analyzed at Admiralty Bay (1991-2006) and Humble Island (1991-2000) by Lynch et al. (2012) and at Point Géologie (1952-2005) by Barbraud and Weimerskirch (2006). Lynch et al. (2012) concluded that penguin breeding phenology was advancing (occurring earlier over time) over 16 years, from 1991-2006, at Admiralty Bay and over 10 years, from 1991-2000, at Humble Island. Barbraud and Weimerskirch (2006) concluded that penguin breeding phenology was becoming increasingly delayed (breeding occurring later over time) over 54 years, from 1952-2005. This suggests a dichotomy between phenological trends on the Western Antarctic Peninsula (Admiralty Bay and Humble Island) and Eastern Antarctic (Point Géologie).

We found no evidence to support the notion of a shift in Adélie penguin breeding phenology or a dichotomy between the Western Antarctic Peninsula and Eastern Antarctica. However, the length of the time series used in these previous studies differs from those used here. Lynch et al. (2012) also incorporated species other than the Adélie penguin in their previous analysis.

Table S1: Outline of time periods used in this study and previous ones at Point Géologie, Admiralty Bay, and Humble Island. Trends found are also included. +: delaying trend, 0: no trend, -: advancing trend.

Site	Study	Time Period	Trend Found
Admiralty Bay	Lynch et al. 2012	1991 - 2006	-
Admiralty Bay	This study	1986 - 2012	0
Humble Island	Lynch et al. 2012	1991 - 2000	-
Humble Island	This study	1991 - 2010	0
Point Géologie	Barbraud and Weimerskirch 2006	1952 - 2005	+
Point Géologie	This study	1979 - 2012	0

Methods

Time series reanalyses

To resolve this discrepancy in phenological trends, we reanalyzed these time series. Temporal trends for Adélie penguin clutch initiation dates (CIDs) were modeled individually using a Bayesian approach. Phenology was modeled as normally distributed with a mean μ_i that is a linear function of year (i). The coefficients of the linear model for μ_i were given uninformative normal priors. The precision ($1/\sigma^2$) was given an uninformative gamma prior.

$$\begin{aligned}
y_i &\sim N(\mu_i, \sigma^2) \\
\mu_i &= \alpha + \beta * Year_i \\
\alpha &\sim N(0, 0.001) \\
\beta &\sim N(0, 0.001) \\
1/\sigma_2 &\sim Gamma(0.01, 0.01)
\end{aligned}
\tag{S1}$$

Models were fitted using the R package ‘R2jags’ (Su and Yajima 2015), to interface with JAGS (Plummer 2003) in the R statistical environment (R Development Core Team 2016). Inferences were derived from 10,000 samples, following a ‘burn-in’ period of 40,000 draws using 3 chains. Model convergence was assessed through a visual analysis of posterior chains, in addition to the use of the Gelman-Rubin convergence diagnostic (Brooks and Gelman 1998). All models unambiguously converged.

CID data (x_{ij}) were normalized across years (i) for each distinct time period used in previous analyses (j), to create a standardized variable (S) that allows for more meaningful inter-site comparisons:

$$S_{ij} = \frac{x_{ij} - \bar{x}_j}{sd(x_j)}
\tag{S2}$$

Resampling of time series

To determine the effect on the length and the particular period used in these studies, we re-sampled each time series over various lengths of time, from 3 years to the entire length of the time series used in the primary analysis of this study. For each length of time, 1000 random segments (consisting of consecutive years) were sampled from the complete time series. A frequentist linear model was fitted to each sample to determine whether a phenological trend was apparent. The proportion of randomly sampled segments determined to be statistically significant at the $\alpha = 0.05$ level were then recorded for each length of time.

Results

Estimated trends in penguin breeding phenology at Admiralty Bay (Fig. S1, Table S2) were similar for both periods of time analyzed. Estimated slopes for both models were near zero (Table S2, Fig. S4).

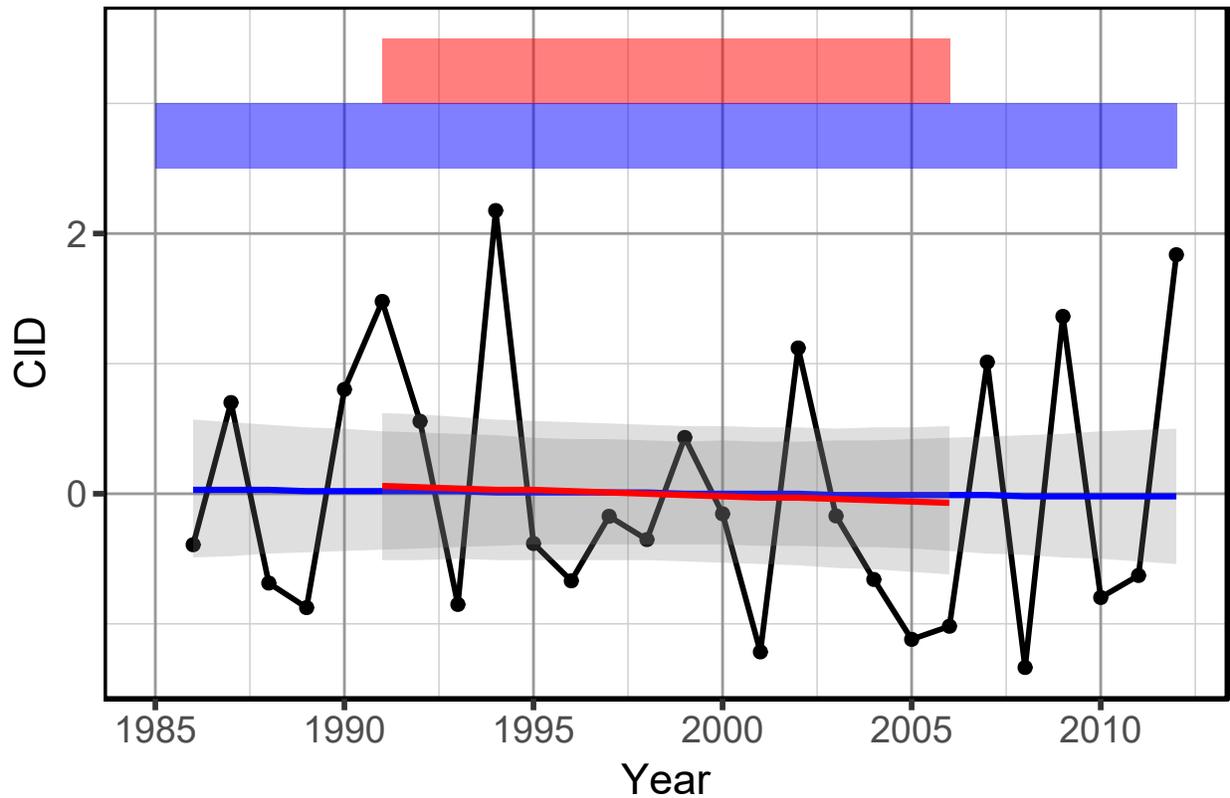


Figure S1: Adélie penguin breeding phenology over time at Admiralty Bay (Fig. 1). Standardized clutch initiation date (CID) is shown on the y-axis, year on the x-axis. The red bar represents the period of time analyzed by Lynch et al. (2012). The blue bar represents the period of time analyzed in this study. Red and blue lines represent model fits for 1991-2006 (used by Lynch et al. [2012]) and 1986-2012 (used by this study), respectively.

Estimated trends in penguin breeding phenology at Humble Island (Fig. S2, Table S2) were also similar for both periods of time analyzed. Estimated slopes for both models were near zero (Table S2, Fig. S4).

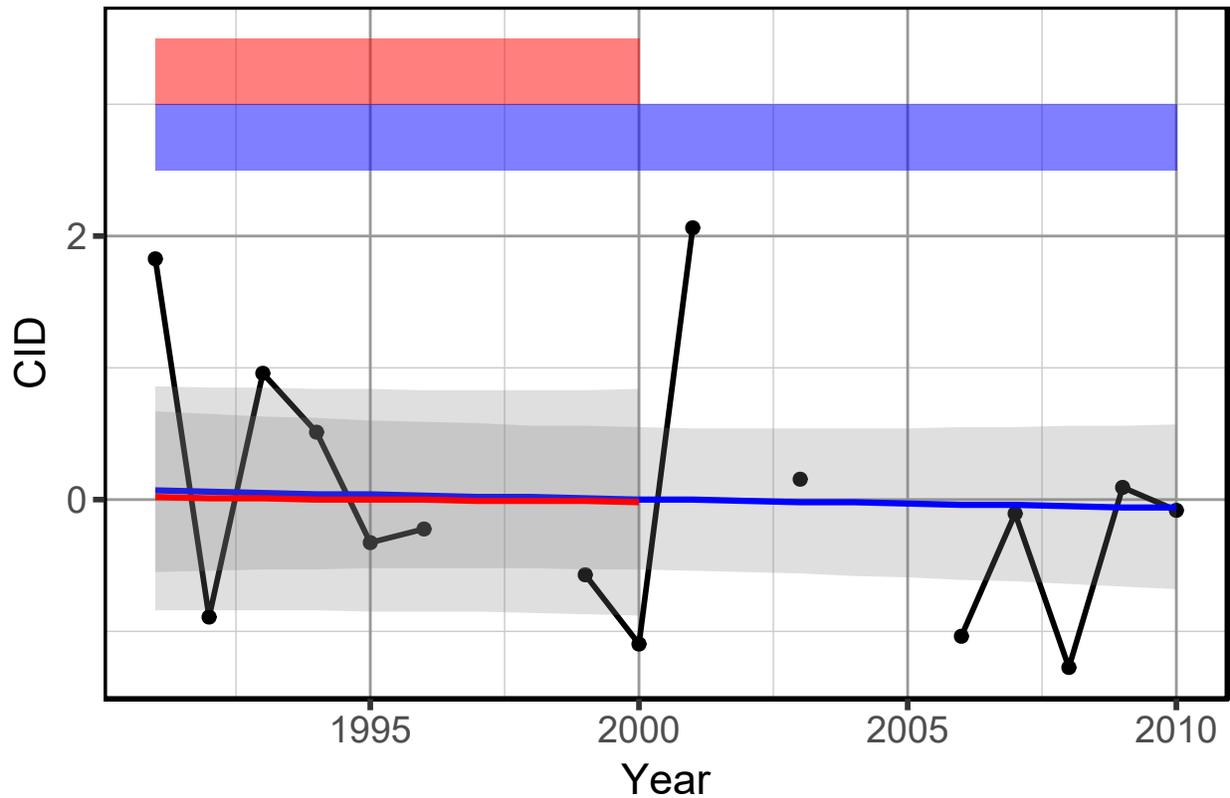


Figure S2: Adélie penguin breeding phenology over time at Humble Island (Fig. 1). Standardized clutch initiation date (CID) is shown on the y-axis, year on the x-axis. The red bar represents the period of time analyzed by Lynch et al. (2012). The blue bar represents the period of time analyzed in this study. Red and blue lines represent model fits for 1991-2000 (used by Lynch et al. [2012]) and 1991-2010 (used by this study), respectively.

Estimated trends in penguin breeding phenology at Point Géologie (Fig. S3, Table S2) were different between the two periods of time analyzed. The time period 1952-2005, used by Barbraud and Weimerskirch (2006), showed a stronger trend than did the time period 1979-2012, used in this study (Table S2, Fig. S4).

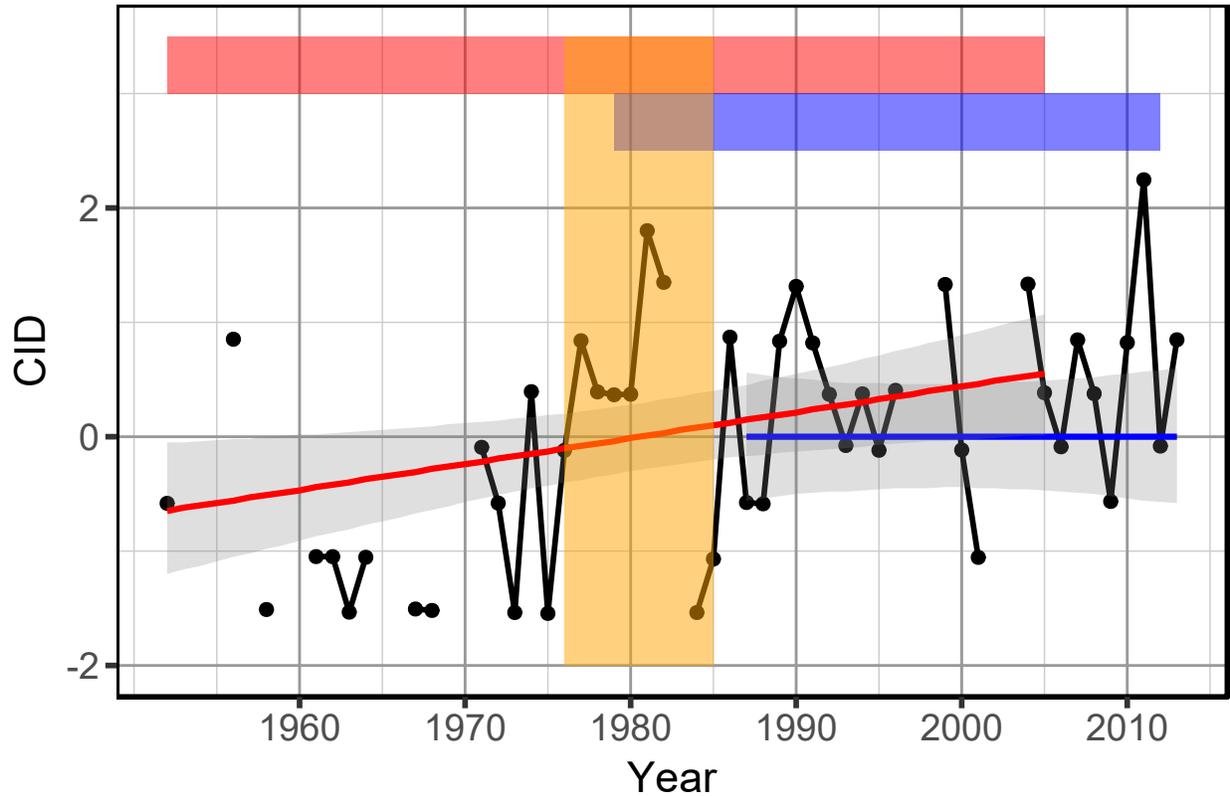


Figure S3: Adélie penguin breeding phenology over time at Point Géologie (Fig. 1). Standardized clutch initiation date (CID) is shown on the y-axis, year on the x-axis. The red bar represents the period of time analyzed by Barbraud and Weimerskirch (2006). The blue bar represents the period of time analyzed in this study. The orange bar denotes period of regime shift at this site (Jenouvrier et al. 2005). Red and blue lines represent model fits for 1952-2005 (used by Barbraud and Weimerskirch [2006]) and 1979-2012 (used by this study), respectively.

Table S2: Parameter estimates (posterior mean and 95% credible intervals) for penguin breeding phenology as a function of time. \hat{R} represents the Gelman-Rubin convergence diagnostic. Values near 1 signify convergence for that particular parameter. Letter codes represent breeding sites: AB = Admiralty Bay, HI = Humble Island, PG = Point Géologie. B & W = Barbraud and Weimerskirch 2006

Site	Study	Parameter	Mean	Lower 95% CI	Upper 95% CI	\hat{R}
AB	Lynch et al. 2012	α	16.99	-45.18	78.39	1
AB	Lynch et al. 2012	β	-0.01	-0.04	0.02	1
AB	This study	α	4.28	-48.05	56.04	1
AB	This study	β	0	-0.03	0.02	1
HI	Lynch et al. 2012	α	7.45	-54.18	70.06	1
HI	Lynch et al. 2012	β	0	-0.03	0.03	1
HI	This study	α	13.71	-43.54	71.64	1
HI	This study	β	-0.01	-0.04	0.02	1
PG	B & W 2006	α	-44.84	-78.74	-9.16	1
PG	B & W 2006	β	0.02	0	0.04	1
PG	This study	α	0.03	-54.84	54.43	1
PG	This study	β	0	-0.03	0.03	1

Site	Study	Parameter	Mean	Lower 95% CI	Upper 95% CI	\hat{R}
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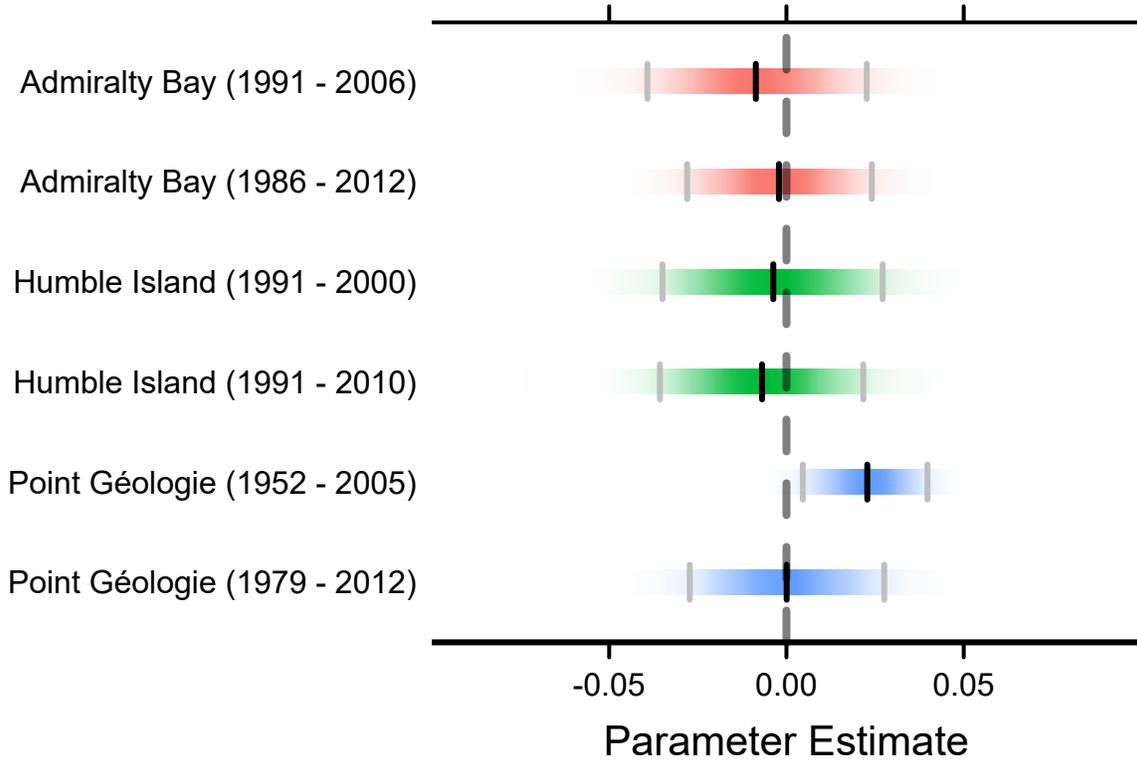


Figure S4: Posterior estimates for slope (β) parameters at Admiralty Bay, Humble Island, and Point Géologie. Time periods correspond to those used in previous studies by Lynch et al. (2012) and Barbraud and Weimerskirch (2006), as well as this study.

Time series reanalyses

Time series reanalyses using subsets of the time series showed that 'statistically significant' trends in Adélie penguin breeding phenology may be found when using particular subsets (Fig. S5).

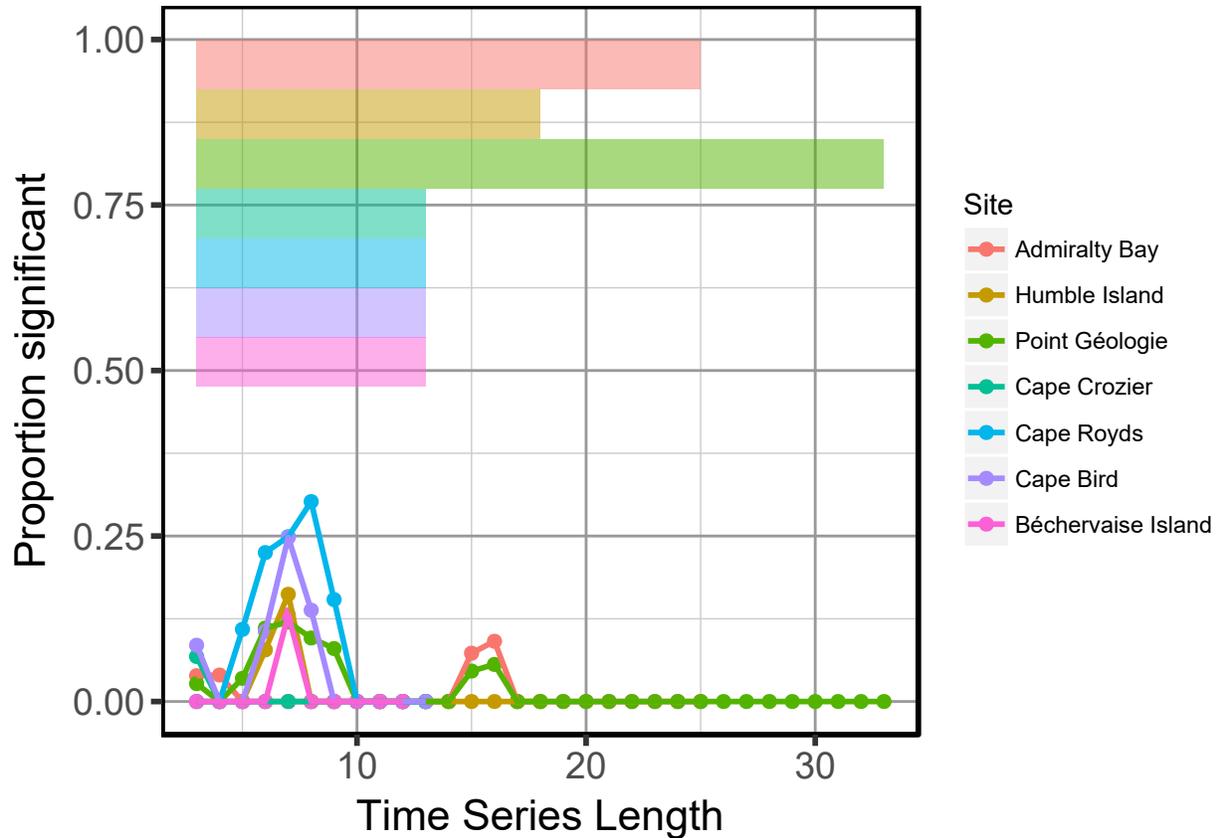


Figure S5: Proportion of time series subsets of a particular length that were found to have a ‘statistically significant’ trend in Adélie penguin breeding phenology (slope, β , parameter $p < 0.05$). Colored bars represent the length of time series at each site used in the primary analysis for this study.

Discussion

While our analysis of the time series suggested no trend in Adélie penguin breeding phenology at either Admiralty Bay or Humble Island, Lynch et al. (2012) suggested that a trend was apparent. This is surprising considering that we reanalyzed data over the same period of time used in this previous study. However, Lynch et al. (2012) used a hierarchical model, incorporating data from not only Adélie penguins, but also chinstrap penguins (*Pygoscelis antarctica*) and gentoo penguins (*Pygoscelis papua*). Lynch et al. (2012) also explicitly modeled individual nest breeding phenology, where we consider here mean population breeding phenology. As Hinke et al. (2012) point out, individual Adélie penguins exhibit some flexibility around a more rigid population mean. The inclusion of both individual level data and these other species likely resulted in the differing results between this study and Lynch et al. (2012).

Estimated trends at Point Géologie differ substantially. We attribute this difference to a regime shift at Point Géologie during the 1970s/1980s (Jenouvrier et al. 2005; Fig. S3). This discrete change in phenology is distinct from long-term trends in phenology and better explains the shift towards later breeding phenology between the 1950s and present at this site.

Evaluation of trends for random time series subsets at each site showed that ‘statistically significant’ trends can be found for some subsets of these time series, despite no trend being seen using the complete datasets. This is likely due to the low signal to noise ratio present in these time series. It should also be noted that a statistically significant trend does not equate to a biologically significant trend, particularly when large interannual variation persists in the system. Ultimately, we suggest that penguin breeding phenology is

not changing at a biologically significant rate. Any small trend that does exist is largely masked by large interannual variation.

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