

A preliminary evaluation of the evidence supporting fishery-driven localised depletion effects on the performance and demographic trends of pygoscelid penguins in Subarea 48.1

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Abstract

Two independent lines of evidence have been presented to the working groups and SC-CAMLR that claim to demonstrate that fishery-driven localised depletion of krill around pygoscelid penguin colonies has had a deleterious effect on their performance traits and demographic trends, that are equivalent to the impacts of climate variation. One study utilises 30 years of penguin foraging and reproductive performance of penguins in relation to krill biomass using 30 years of data collected at two colonies in the South Shetland Islands, whereas the other uses demographic rate changes derived from a comprehensive dataset of penguin population count data across Subarea 48.1 matched against acoustic measurements of krill biomass and krill catches at the gSSMU scale (Watters et al., 2020). The second uses estimated population trajectories across a wide range of penguin breeding colonies in relation to krill catches within a 30km radius (Krüger et al., 2021). Both studies then explore the synergistic relationships to measurements of broad-scale climactic variation (El Niño-Southern Oscillation; ENSO, and the Southern Annular Mode; SAM). Herein we provide a preliminary assessment of the efficacy of both approaches in drawing conclusions, that are now being used at the Commission level, as representing sound scientific advice. We demonstrate that several underlying assumptions in Watters et al. 2020 are contrary to the published scientific literature, and when the model syntax is re-written to reflect these, predicted penguin performance against long term expected means are substantially different to those presented to CCAMLR. The evidence provided by Krüger et al. (2021) uses a different analytical approach, however given the details provided we were unable to recreate the initial results and could not test the sensitivity of the model to some of the assumptions made. We do, however, point to areas in which we have concerns, and would welcome collaboration in order to clarify and address these through a more in-depth future analysis. Overall while our preliminary assessment focuses on potential issues, future work will centre on considering competitive interactions both at appropriate time and space scales between the fishery as well as between a range of krill dependent predators beyond just pygoscelid penguins.

Introduction

Concerns over the potential impact of localised depletion of krill through concentrated fishing effort on krill-dependent predators has been a topic of debate within SC-CAMLR and its Working Groups for many years. Recently, two studies have been presented that suggest that local harvesting rates can impact predator performance to the same degree as poor environmental conditions (Watters et al., 2020) and when poor climactic conditions are coupled to locally high harvest rates the synergistic impacts on predators are evident (Krüger et al., 2021).

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While both studies attempt to tackle the same overall problem, they do so using very different methodologies. Watters et al. (2020) analysed various performance indices in relation to local krill biomass (LKB), local harvesting rates (LHR) and the Oceanic Niño Index (ONI) using a hierarchical bayesian model. The penguin performance indices (including those collected under CEMP) were collected at two sites (Cape Shireff on Livingstone Island and Copacabana on King George Island, South Shetland Islands; Figure 1) in the period 1982 - 2016 whereas krill abundance data, which cover the at-sea distributions of chinstrap, gentoo and Adélie penguins, were collected during summer (1996 - 2011) and winter (2012, 2014 and 2015). By drawing in monthly krill catches from the C1 Catch and Effort data and climate data (ONI), the authors use a hierarchical analysis of variance approach to estimate the variance in performance indices as a function of Local Krill Biomass (LKB), Local Harvesting Rates (LHR; the ratio of krill catch to LKB) and ONI. In contrast, Krüger et al. (2021) utilise a broader range of penguin colonies across chinstrap and gentoo penguins throughout the Antarctic Peninsula area, in combination with their respective abundance survey estimates (number of occupied nests) from an open-source database (www.penguinmap.org). The authors calculate population trends for appropriate sites, and using the CCAMLR C1 Catch and Effort data to extract annual catch values within a 30km radius of each colony. Finally, Krüger et al. (2021) use the sign of the difference in the number of nests between annual surveys as a response in a binomial generalised linear mixed effects model using the accumulated annual catch and the mean wintertime Southern Annular Mode (SAM) to determine the relative contributions of each predictor and their interactive effects on population abundance trends. Both studies draw similar conclusions; that local harvesting levels of krill impact predators, and the degree of impact can either be similar to that of poor environmental conditions or have a synergistic impact when high local harvesting coincides with poor conditions.

The conclusions of these papers have been propagated into Commission documentation supporting the reformulation of the D1MPA proposal (CCAMLR-39/BG/02) as well as into Commission discussions (CCAMLR-39, Para 5.48 & Para 5.51). However, while the two studies have moved from Working Papers of EMM into the realm of the peer-reviewed literature, there are some areas of concern regarding the structuring of these studies that we think deserve attention. Some of these concerns are unique to each study while others are common across both, and we structure our paper accordingly. Firstly, we review Watters et al. (2020) and Krüger et al. (2021) through the lens of some of the ecological assumptions made versus the available evidence pertaining to them. Within the constraints of the data and analytical methods that are available from the studies, we also quantify how rationalising these assumptions to the evidence available changes the model outputs and on the conclusions drawn. We then highlight some overarching concerns applicable to both papers.

Watters et al. (2020) / WG-EMM 2019/11

A key goal for the paper is to highlight the consequences of mismatching scales at which the Antarctic krill fishery is managed with the scales at which ecological interactions between fishing extractions and dependent predators occur. To do this, they create two strata aligned with groups of SSMU (gSSMU); gSSMU #1 including those SSMU inside the Bransfield Strait (APBSE and APBSW) and gSSMU #2 incorporating SSMU north of the South Shetlands, including Elephant Island (APDPE, APDPW and APEI) represented in Figure 1. These gSSMU cover $15,500\text{nm}^2$ and $20,600\text{nm}^2$, respectively, and are used to characterise both krill biomass and harvesting rates that are “local” to the penguin colonies for which performance data are used. The reasoning behind scaling to gSSMU are linked to the foraging behaviour of the penguins for which performance data area available i.e. breeding, adult pygoscelids. The authors cite Hinke et al. (2017) as the evidence supporting usage of the two gSSMU as appropriate strata.

Pygoscelid penguins exhibit staggered breeding, with Adélies commencing first, followed by chinstraps then gentoos (Black, 2016). Adélie penguins are the first to fledge their chicks and thus cease to be centrally foraging, typically departing mid-February for their moulting grounds on the sea ice. Chinstrap penguins depart for a pre-moult foraging trip towards the end of February and return to land in order to moult, before departing again for their overwinter trip (Hinke et al., 2015, 2019)(Figure

2). Conversely, gentoo penguins appear to remain near their breeding colonies overwinter (Korczak-Abshire et al., 2021).

We use the Argos-CLS PTT telemetry data provided by the supporting studies to characterise the actual at-sea habitat used, in the context of the relative stage of breeding for each species (though we also recommend Warwick-Evans et al. (2018) and Lowther et al. (this meeting) amongst other work, for further quantification of foraging behaviour of breeding penguins in this area). For each species, we refrain from undertaking extensive state-space modelling of location errors and merely exclude locations with a “Z” error class, accepting the remaining locations had varying degrees of uncertainty around them, then calculated the 99% Minimum Convex Polygon (home range) using the R package *adehabitatHR* and calculate their associated areas in nm^2 . For chinstrap penguins at Cape Shireff, this equated to a home range area of $\sim 4,782 nm^2$, or only 23% of the gSSMU to which their performance metrics are indexed against (Watters et al., 2020). For the same species at Copacabana the 99% MCP home range is $2,905 nm^2$, or $\sim 19\%$ of gSSMU #1 in the Bransfield Strait. Similarly for Adélie penguins, the breeding foraging range occupied $1,139 nm^2$ or only $\sim 7\%$ of the area of gSSMU #1. After breeding, available overwinter PTT telemetry and light geolocating data on chinstrap and Adélie penguins suggests a wide dispersal westwards into the Pacific sector of the Southern Ocean, and eastwards into the Weddell Sea and Atlantic sectors, with a relatively small proportion of chinstraps from the study sites remaining within 500km of their breeding colonies (Hinke et al., 2019). Yet despite the evidence supporting widespread post-breeding migration of both Adélie and chinstrap penguins, the model used by Watters et al. (2020) constrains both species from Copacabana to gSSMU #1 and chinstraps from Cape Shireff to gSSMU #2 over winter (Supplementary Material 1 & 2, code lines 258 to 279). This has the effect of constraining the variability in performance indices from these species to LHR, LKB and ONI over winter in areas where the species has a demonstrated tendency to migrate away from (Figure 2). This is particularly important given that the fishery can now be characterised with a late autumn/early winter start which places a seasonal element on LHR towards increased values in the winter (Figure 5).

Our preliminary review thus far raises two areas of concern. Firstly, that the scales at which “local” predictors are summarised are in some cases almost 15 times larger than the habitat exploited by the penguins monitored. Local Harvest Rate is a function of the catch and its distribution; we demonstrate catch distribution varies across breeding seasons within the original gSSMU, using available C1 Catch and Effort data during the austral summer period, relevant to the breeding season and thus centrally foraging Adélie and chinstrap penguins between 2009 and 2018 for Subarea 48.1 (Figure S1).

Secondly, that the known overwinter migratory behaviour of Adélie and chinstrap penguins are poorly reflected in the model formulation. To demonstrate the impact that these ecological assumptions have on the model output, we rerun the model of Watters et al. (2020) with modified code. To avoid an overly burdensome paper, we shortly summarise those code changes here, and if requested during the meeting we are happy to include the rmarkdown version of this paper with the modified code in place, or submit the modifications to the meeting in some other format.

We also note an additional coding error that may influence how the original, unmodified results are interpreted. In summarising the model outputs into boxplots, the text in the paper seemingly classifies the “Worst Case” with “neutral” ONI ($-0.5 ^\circ C < ONI < 0.5 ^\circ C$; LKB > 1 Mt; and LHR ≥ 0.1) and the code relating to developing the original manuscript Figure 2 (Supplementary Material 1, lines 661-663) uses Parameter set 36 from the output dataframe, which actually reflects a “warm” ONI component ($> 0.5 ^\circ C$; LKB > 1 Mt; and LHR ≥ 0.1). Yet the discussion in Watters et al. (2020) also suggests that the likelihood of their “Worst Case” includes future warming (see Figure 3 below)

We agree that any “Worst Case” should reflect ENSO conditions into the future under a warming climate. However, climate change is likely to increase ENSO in amplitude - both El Niño (ONI “warm”) and La Niña (ONI “cold”) (Capotondi et al., 2015). How this increasing amplitude can be integrated appropriately into the presented modelling framework to match with long-term predicted mean performance of predators has not been explored yet. As such, and for the sake of comparison with the original study, we maintain the authors designation of ONI “neutral” when rendering the “Worst Case” boxplots, though caution that this is unlikely to be a realistic assumption

Modifications

1. We scale the gSSMU LKB to the SSMU that the summer tracking data indicate penguins occupied. To do this, we calculate the area (nm^2) of the SSMU for which the predator occupies and the gSSMU to which it is assigned, then create a scaling ratio. For example, we scale LKB for Cape Shireff chinstrap penguins solely to ADPDW (Figure 1) by multiplying the gSSMU LKB by the areal ratio of ADPDW/gSSMU #2. We then select the corresponding SSMU catch values provided in Watters et al. (2020) (Supplementary Info) to estimate SSMU-scale LHR. We also caution that while considering the gSSMU scale of harvesting as inappropriate for “local” effects, even the SSMU-scale catch levels likely do not reflect pressures at scales relevant to breeding penguins (Supplementary Figure 1).
2. We remove Adélie and chinstrap penguins from the model formulation over winter; that is, we attribute each species as “NA” during winter (to account for dispersal after breeding), thus removing them from association with any gSSMU.
3. The authors place LKB/LHR values in March into the “summer” period. However fishing effort over the period that performance indices are available is not uniform over the thirty year period, with catch over the preceding decade tending towards a nonlinear increase from the middle of March and three years where catch rates increased rapidly from the beginning of the month (Figure 4). Given the highly variable rates of catch throughout the study period, we run scenarios that classify March as either summer or winter to reflect the linkage between March and the breeding state of penguins i.e. Adélie and chinstrap penguins have either migrated out of the area or have ceased to be centrally foraging species by March.

Thus we reformulate the underlying assumptions above into a new model construct, in which performance indices from gentoo, chinstrap and Adélie penguins during the summer are included, but Adélie and chinstrap penguins cease to be centrally foraging species after breeding and migrate out of the area. The performance indices are matched in space and time but using SSMU level estimates of LKB and LHR. We re-run the model that includes imputed values for LKB in years where survey data are missing. We further consider two alternatives for considering March, either in a) summer or b) winter.

We present the outputs both in the same boxplot format as Figure 2 in the original manuscript, and as individual cases grouped and colour-coded as ONI “warm” (≥ 0.5 ; red), ONI “neutral” ($-0.5 < ONI > +0.5$; white) and ONI “cold” (< -0.5 ; blue). We also recreate the original marginal probabilities in Table 1 of Watters et al. (2020), and two additional tables in the same format with the probabilities extracted from our reformulated model, the difference between the latter two tables reflecting whether March is in summer or winter.

Results

From the original Watters et al. (2020) model, the probability that the Worst Case would cause penguin performance indices to drop below their long-term mean was 77%, while relative to the Best Case there was a 93% probability that penguin performance would decline as a response to high LHR. Similarly, there was a 99% probability that high LHR and LKB under neutral ONI (“Worst Case”, though see above for comments on this) would drive penguin performance to fall below its long term mean (Table 1).

Our reformulation displays a rather different picture, and while we refrain from providing an exhaustive in-text comparison, we highlight a few examples here. Comparing the original model outputs with ours, relative to the “Best Case”, the probability of negative impacts to penguins due to high LHR dropped precipitously from $\geq 93\%$ to 37% (Table 3). In other words, when considering the migration of penguins in accordance with their known ecology (Figure 2), the relative probability of negative impact of LHR drops from a near-certainty to 1-in-3 (Table 2 and 3). Given the temporal separation between fishing and penguin breeding over the preceding decade, our results are unsurprising.

The probability that the effects of warm or neutral ONI would be more detrimental to penguin performance were greater than for the Worst Case (Table 2 and 3). When we consider the marginal effects of neutral ONI and high LHR, the probabilities that the former would negatively impact penguin performance below the long-term mean was 4 times greater than the impact of high LHR (Table 2 and 3). Looking at the case-by-case and selected plots in Figure 4 the overwhelming dominace of the ONI state can clearly be seen. La Niña (“cold” ONI) conditions resulted in predictive probabilities of performance that were equal to, or surpassing, those of the Best Case irrespective of increased LKB or LHR. Even more counterintuitively, an increase in LHR to even high levels has a lower probability of decreasing penguin performance than that of the Best Case (Table 2 and 3). However, it is important to note that overall our intention is not to suggest that increased fishing is beneficial; merely that when the model is reconditioned on ecological knowledge, the outputs in its current formulation should be treated with caution.

In summary, Watters et al. (2020) believe that penguins are responding to both the environment and fishing. We agree that penguins are responding to the environmental changes, however we believe that the fishery effect is flawed because the scales at which their model incorporates fishing bear no relevance to the scales at which penguins exploit (Figure S1). The penguin performance in the orginal model was also insensitive to marginal changes in LKB whichc corroborate previous failed attempts to parameterise functional responses of penguins. This insensitivity is in line with our results, but we propose that even the SSMU scale is inappropriate for matching food availability and harvesting pressure to predator performance (Figure S1).

In light of these findings, and the scales of management originally proposed by us in WG-EMM 2019/18, we support the direction of discussions during WG-ASAM this year to consider spatial scales of management to areas in which the fishery operates, rather than at the Subarea level.

Krüger et al. (2021) / WG-EMM 2019/10

The key objective of the paper by Krüger et al. (2021) is to examine the potential synergistic effects of climate change and increased fishing activity in recent decades on the breeding performance of chinstrap and gentoo penguins. The authors make the implicit assumption that there has been a general decrease in krill density in response to climate change, although this is still a topic of debate and is not supported by recent large-scale surveys in the Scotia Sea (SG-ASAM 2019/08 Rev.1).

To address this topic, the authors fit a Generalized Linear Mixed Effects model of the general form:

$$\lambda = \text{catch} * \text{SAM} + (1|\text{colony ID})$$

where λ is an index of change in penguin breeding performance, *catch* is annual krill catch, *SAM* is the Southern Annular Mode index, and the term in brackets indicate a random intercept term by colony. We would like to discuss some points regarding both the model formulation and the input data that we believe raise some potential concerns about the overall approach and the conclusions drawn. Based on the issues we raise here, we would welcome the opportunity to collaborate openly on a) recreating these analyses b) testing their sensitivity to the assumptions made and c) develop alternative approaches to alleviate these issues and provide a less biased result. Below we go through these issues in some detail. Unlike in the case of Watters et al. (2020), scripts are not provided for the analyses done by Krüger et al. (2021), and therefore we have not been able to recreate their analyses or test various aspects of data input, underlying assumptions and alternative model formulations. Additionally, there appear to be some discrepancies between the data provided in the supplementary material and what was actually used in the paper.

Response variable: Penguin breeding performance

As the basis for the index of change in breeding performance (λ), Krüger et al. (2021) use data on the number of occupied nests (breeding pairs) counted at a large number of sites throughout the Antarctic Peninsula collected between 1980 and 2017. These data are available from the Mapping Application

for Penguin Populations and Projected Dynamics (MAPPPD) data archive (www.penguinmap.com; Humphries et al. (2017)). Krüger et al. (2021) include count data on occupied nests based on surveys carried out in November or December, reflecting the early breeding season. They further subset the data to include only colonies for which at least 2 survey estimates are available throughout the 38-year period under consideration (i.e. 1980-2017). These data are provided in the supplementary materials for the paper. Based on the raw counts, they calculate an index of temporal variation in population growth rate using:

$$\lambda_{std} = ((n_b/n_a)/years_{b-a} - 1$$

where n is the number of breeding pairs counted in Nov-Dec of a given year, b and the number of breeding pairs counted in the nearest previous year, a , in which a Nov-Dec survey was conducted, divided by the interval between surveys (i.e. $b - a$). While this index may be a robust index of relative population change, the authors then convert λ_{std} into a binary index, $bin\lambda_{std}$ that takes the value 1 for negative growth and 0 for positive growth. The rationale is that this value can be interpreted as the probability of population decline in response to catch and environmental change. However by only taking the sign of the change and creating a binary response the authors completely ignore the magnitude of the absolute or relative change in population size; that is, a decline of 1% or 99% of the population size in year a is considered equivalent in the model.

Predictor variables: Krill catch and SAM

As in the case of Watters et al. (2020), Krüger et al. (2021) also use CCAMLR C1 Catch and Effort data from the krill fishery to estimate fishing pressure, but in this case only hauls within a 30km radius are considered for each specific colony. This selection is based on previous observations that foraging of pygoscelid penguins is more probable within 30 km of the colonies during the breeding season (Warwick-Evans et al., 2018). While they initially summarise these data within distinct time periods (reflecting different important stages of the penguin annual cycle), these are only used for illustrative purposes (Fig 3 in Krüger et al., 2021). When modelling the effect of fisheries on population response, the authors instead use accumulated annual catches within these 30km areas, making the assumption that the number of breeding penguins counted in a given survey is affected by local resource availability, also during the non-breeding period in winter. While this might be valid for gentoo penguins which appear to remain close to the breeding colonies also outside the breeding season (Korcak-Abshire et al., 2021), it is questionable how appropriate this is for chinstraps that have displayed tendencies to disperse much more widely during winter (see above section and references therein). An additional issue with the spatial restriction of catch data is that a high proportion of surveys are associated with accumulated annual catch rates = 0. While this may not pose a serious problem for chinstraps (79% of colonies have had some level of catch within their 30km radius) the problem may be quite serious for gentoos (51% of colonies had catch within a 30km radius).

The authors use monthly data on the Southern Annular Mode (SAM) index to represent environmental variability (Doddridge and Marshall, 2017; Kwok and Comiso, 2002). Based on an observed 0-3 month lagged correlation between SAM and relevant local climate variables (fractional sea ice cover, open water sensible heat flux and sea level air pressure), the authors exclude SAM values for months coinciding with the breeding season. As discussed in the review of Watters et al. (2020) above, the climactic conditions over the WAP are a function primarily of the Amundsen Sea Low and its interactions with both ENSO and SAM, as well as the bathymetry of the local areas. There is a rich scientific literature addressing climate-driven hydrographic variability in the WAP , none of which is considered in this paper.

Spatio-temporal mismatch

While the above sections describe some of our specific concerns with the various input data to the GLME, our main concern relates to issues of mismatch between these various data in space and time. Given the different data selections and transformations, the specific model specification presented in Krüger et al. (2021) is:

$$bin\lambda_{std} = catch_y * SAM + (1|colony ID)$$

where the subscript y denotes the accumulated krill catch within 30km of each colony over the year last survey in a survey interval (i.e. year b using the notation in the performance equation above). Similarly, the SAM index is the mean SAM index over almost the same period, but excluding the three months of the breeding season itself. To clarify this, we change the subscripts in the model equation:

$$bin\lambda_{std_I} = \sum_{i=0}^{i=12} catch_i * \frac{\sum_{i=0}^{i=8} SAM_i}{9} + (1|colony ID)$$

Here, I represents the survey interval, expressed in months rather than years, while i represents the number of months prior to the start of the survey carried out in the last year of the interval I . While i is always ≤ 12 , I is always ≥ 12 . In fact, based on the Krüger et al. (2021) supplementary dataset, $I > 12$ in $\sim 26\%$ and 47% of all intervals for Chinstraps and Gentoos respectively (Figure 5). This illustrates the substantial and increasing issue of temporal mismatch between the response variable and the explanatory variables with increasing I . As I increases, the difference in the number of breeding pairs between the first and last year of an interval will increasingly be a function of the catch rates and environmental conditions in ALL years in the interval, not just the final year. In the extreme case, it is highly unlikely that an overall decrease in breeding population size of Chinstraps at Penguin Island between 1980 and 2000 is in large part a response of local catch rates and SAM index in the single year preceding the 2000 breeding season survey. In addition, with increasing I , the probability that a change in number of breeding pairs has been monotonous and linear throughout the entire interval becomes less likely, and the probability decreases that $bin\lambda_{std_I}$ has the same sign as the actual (unobserved) change between the last two breeding seasons in the interval.

Possible tests and alternative modelling approaches

To address the issues raised above, the analyses of Krüger et al. (2021) should be re-run with e.g. random subsets of the data or with data substitutions/permutations of the survey estimates. For instance, additional simulated surveys could be inserted into intervals $I > 12$, specifically such that it changes the monotonous trend over the interval to change the sign of the associated $bin\lambda_{std_I}$. Additionally, the 30km radius for catch rates could be relaxed, at least for months outside of the breeding period, when especially chinstraps are known to disperse widely throughout the wider West Antarctic shelf regions (see Fig. 2).

In general, we strongly argue that the spatio-temporal mismatch between the various input data must be explicitly accounted for in some way. One relatively simple approach would be to relax the temporal restriction of covariate data, such that catch rates and SAM values for all years/months within an interval between surveys are combined, rather than only using values from within the last year before the next survey. However, the most appropriate general strategy would be to include an approach for estimating spatio-temporal autocorrelation structures in the data, and exploiting these structures explicitly in the modelling. For instance, colonies closer could “borrow strength” from each-other in cases of long intervals between consecutive surveys at some colonies, especially for survey estimates of breeding population size. Additional consideration of lagged recruitment (fledging to reproductive age) is also needed, alongside the ability to detect it given irregular surveying effort and methods for longitudinal detection (such as banding or other permanent marking). We would very much welcome the opportunity to discuss various options for such approaches directly with the authors.

Discussion

Our preliminary review of the evidence supporting localised effects of fishing coupled with broad-scale climactic phenomena having an impact on the vital statistics of pygoscelid penguins (performance and abundance trends) are based on assumptions that potentially do not reflect current knowledge of penguin breeding phenology and movement.

Of greatest concern, however, is that the interpretation of model outputs from both approaches (either from both the original studies or the modified parameters we describe) are under boundary conditions that we feel are not appropriate. Both approaches consider only the fishery and broad-scale climate phenomena as the only two causes of krill abundance variability at geographic scales relevant to penguins. Neither study considers, for example, the impact of rebounding baleen whale populations or migratory male Antarctic fur seals beyond brief mentioning. Humpback whales have increased in abundance throughout the life of the krill fishery, and there are sufficient telemetry and distance sampling studies in the scientific literature to demonstrate the degree and significance of spatiotemporal overlap with breeding penguin populations (see Santora and Veit (2013), Lowther et al. (2020), Oosthuizen et al., Johannessen et al., Lowther et al. submitted to this meeting, and Figure S2 as examples). Importantly, the distribution of these and numerous other unconsidered competitors is not uniform in either space or time, and their impact on local availability of krill is likely to be considerable. It is also worth noting that neither study considers the impact of climate on the terrestrial breeding grounds, such as chick mortality through “wetting down” by increased rainfall (Chapman et al., 2011).

Similarly, the utilisation of broad-scale climatological phenomena to characterise impacts at scales that predators are dependent upon is problematic. The Amundsen Sea Low (ASL) is the dominant climate feature for the western Antarctic Peninsula. The El Niño-Southern Oscillation modulates the ASL, with El Niño (La Niña) shallowing (deepening) its pressure, causing more northwesterly (southeasterly) winds and upwelling (restricted influx) of Circumpolar Deep Water onto the shelf. The Southern Annular Mode also influences the pressure of the ASL, with the current trend of negative SAM constructively (destructively) interfering with ASL when in phase with El Niño (La Niña) events (e.g. Clem et al. (2016)). The result is a set of above-surface climate conditions that drive changes in water mass intrusion that is in turn dependent on *interactions* between two climate processes. The bathymetry of the Antarctic Peninsula which also influences the hydrographic conditions is complex (particularly at scales that are important to centrally-foraging predators such as penguins) and the structuring of krill aggregations in time and space in the WAP have been linked to mesoscale circulation processes (Santora et al., 2012), which are unlikely to be uniformly affected by macroscale processes.

Our work into the future will progress along three lines, and we welcome any and all offers of collaboration into this work. Firstly, we will progress this debate into the scientific literature in order to ensure a balanced discussion occurs in that forum. Secondly, we will be examining in further detail some of the additional predictors used and their efficacy, the modelling frameworks into which they are brought, and how their incorporation influences the interpretation of the responses. Finally, we shall also be exploring alternative modelling approaches that reflect more of the physical and biological complexity of the system in question. In all cases, our goal is to ensure that the best available objective scientific evidence is presented to our environmental managers and, where appropriate, flag that disagreement exists. Our paper is intended to be viewed in this light to generate constructive dialogue that addresses our common concern of the potential for localised fishing to impact dependent aspects of the ecosystem.

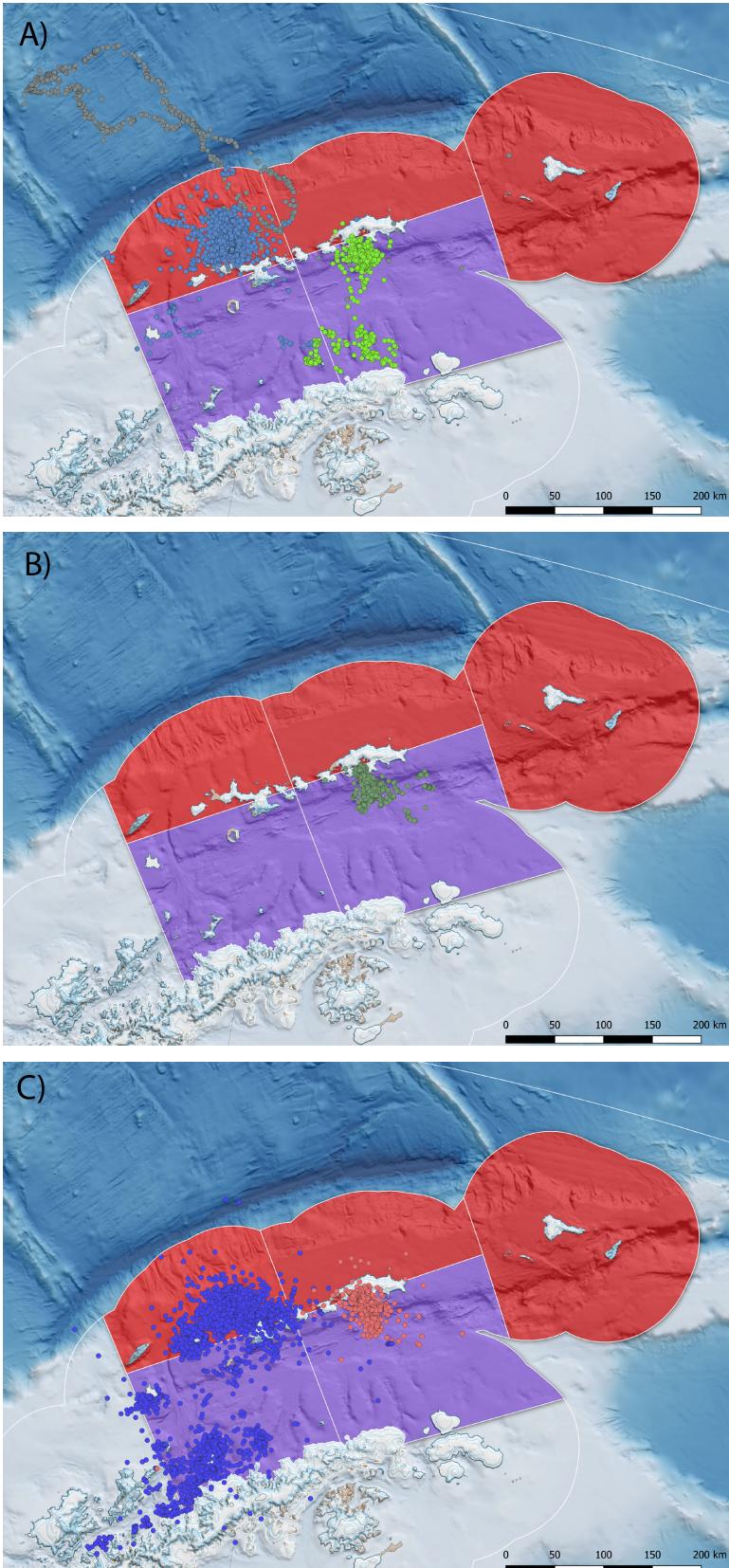


Figure 1: Penguin foraging behaviour during summer breeding, derived from available ARGOS-CLS PTT data presented in Hinke et al. 2017. A) Chinstrap penguins from Cape Shirreff (blue) and Copacabana (green) truncated at 10th March in line with known phenology (Black 2016; Lowther et al. (this meeting)). Elongated grey track represents a single animal) B) Adélie penguins truncated to the end of January and C) gentoo penguins until ~August, representing all available PTT data provided. The SSMU are combined and coloured according to gSSMU (red; gSSMU 2, purple; gSSMU 1) with chinstrap and Adélie penguin 99% MCP home ranges occupying between 7-19% of the gSSMU to which they were assigned.

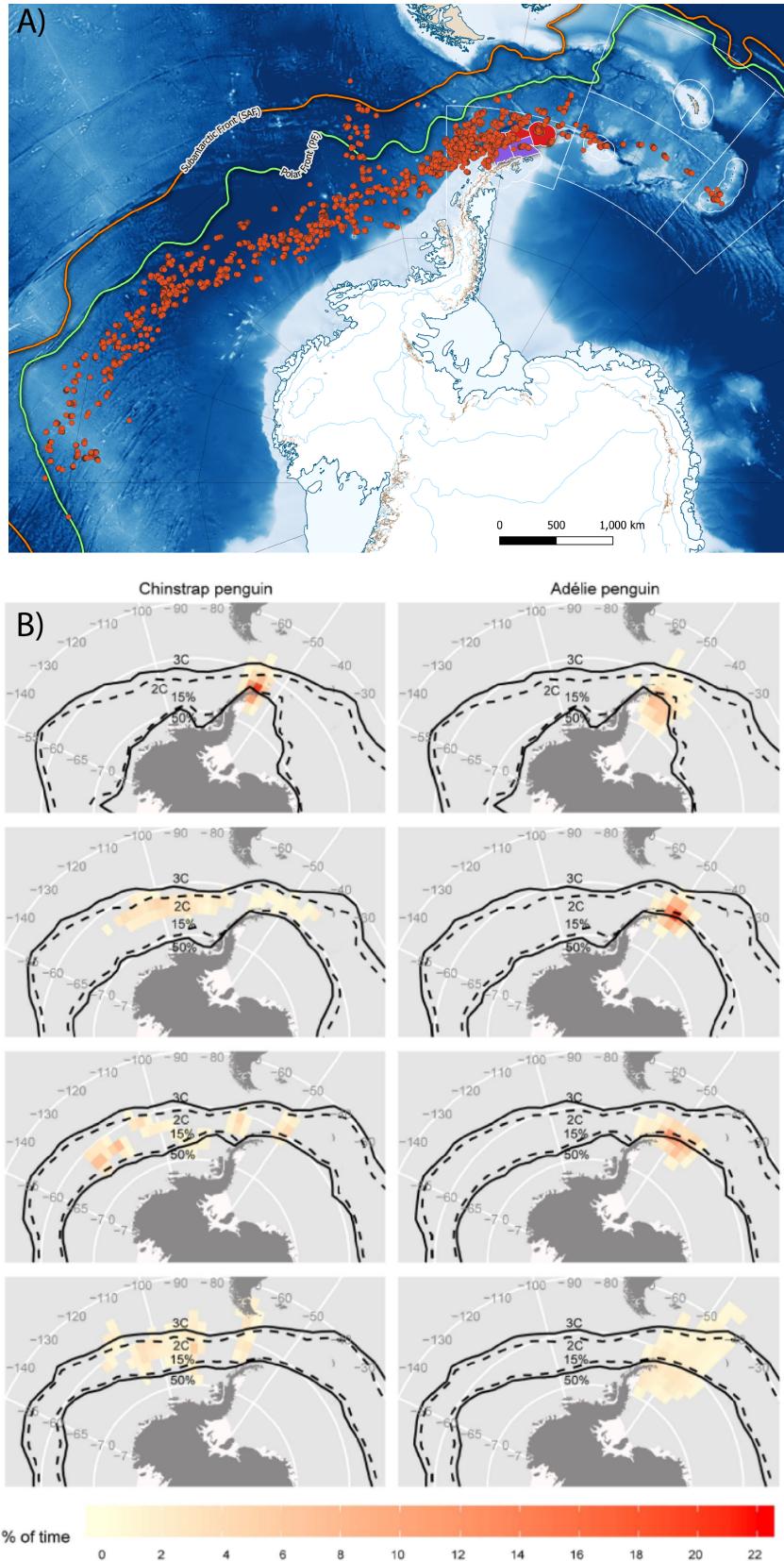


Figure 2: A) Distribution of overwinter movement for chinstrap penguins, relative to the gSSMU's to which they were attributed, created from telemetry data available in Hinke et al. 2019. B) Adélie and chinstrap penguin movement recorded by light geolocators, highlighting the large longitudinal range both species disperse through at the end of breeding (taken from Hinke et al. 2015). In the original model formulation by Watters et al. 2020, the winter performance indices for both species are matched to macroscale levels of ONI variability but gSSMU-scale estimates of LKB and LHR.

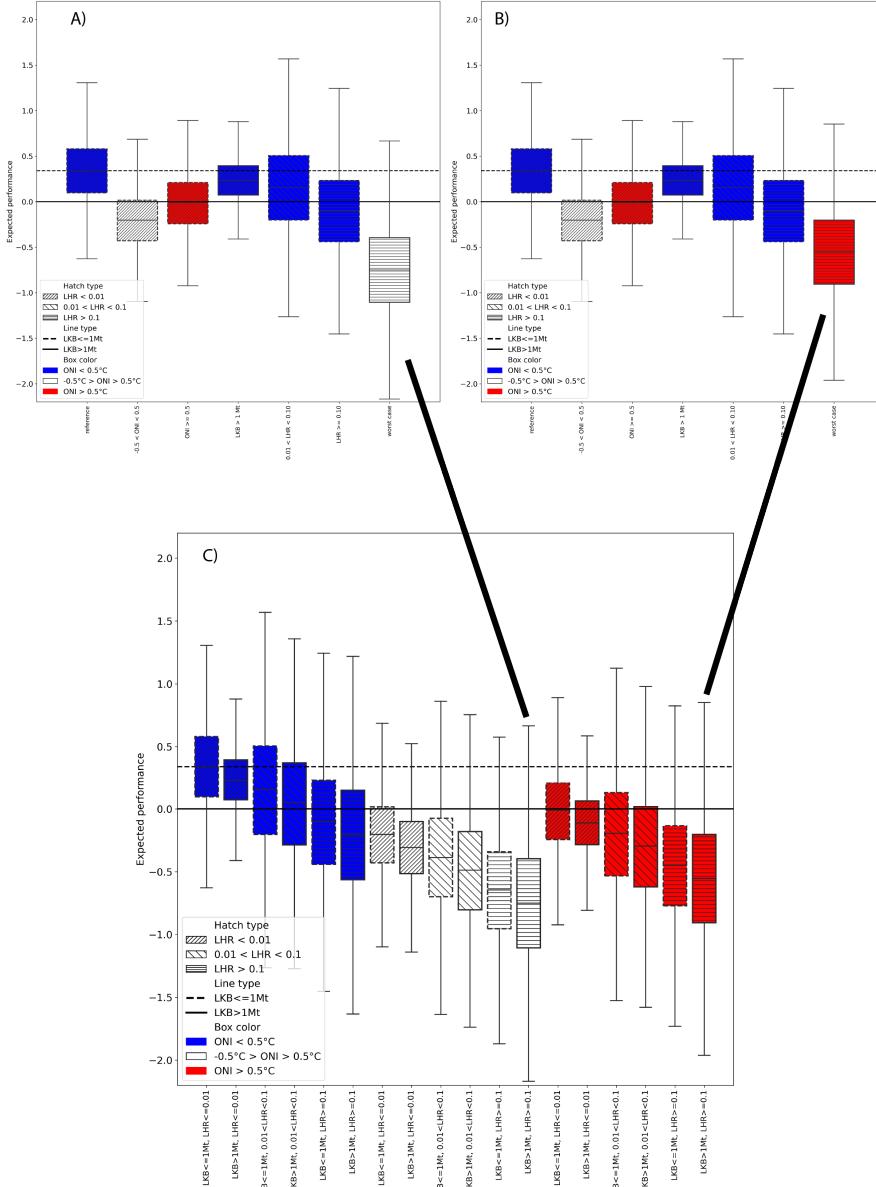
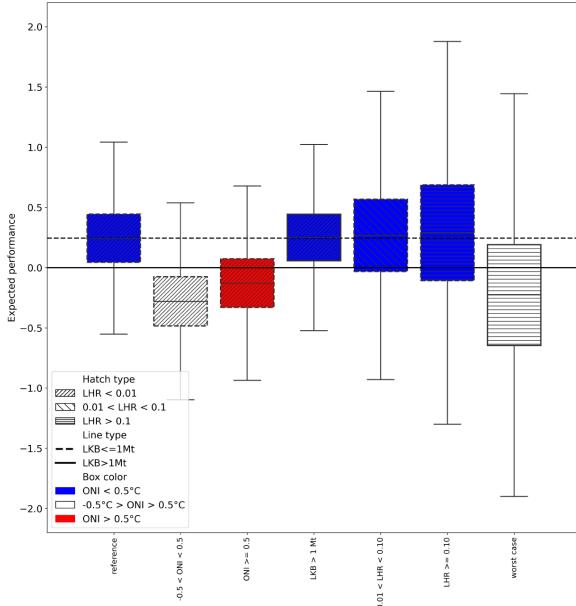


Figure 3: Original Figure 1 plot from Watters et al. 2020 with A) Neutral ONI and B) Warm ONI constituting the Worst Case selected. C) Displays the original case-by-case plots recreated from the paper, with Case 12 representing the intention while data from Case 18 was selected for rendering the boxplot. Note that the expected performance under neutral ONI Worst Case is poorer than under the warm ONI that was presented in the original paper. Henceforth, to facilitate comparison, we refer to the ONI Neutral plot however we consider this unrealistic if the intention is to portray a Worst Case of a continuing warming climate.

A) March (Summer)



B) March (Winter)

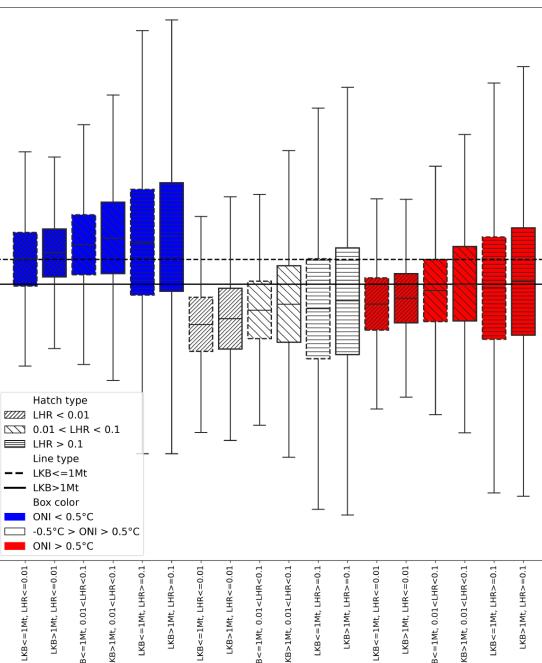
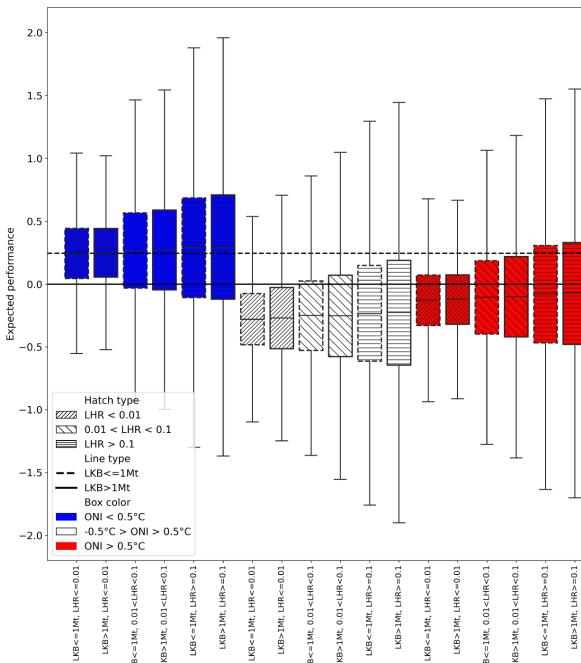
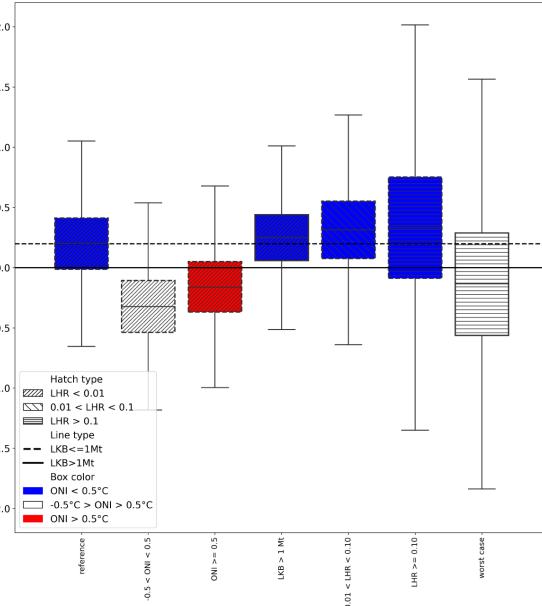


Figure 4: Model output for the alternative Watters et al. 2020 scenario outlined above (all species initially present, Adélie and chinstrap penguins migrate out of the area after breeding, LKB and LHR rescaled to SSMU and March included in summer or winter). Selected cases as per Watters et al. 2020 for March in A) Summer and B) Winter are provided, with the corresponding case-by-case boxplots presented beneath. Boxplots are colour-coded by ONI state (red=warm, white=neutral, blue=cold). In all cases, the marginal effect of ONI dominated the expected performance of penguins against their long-term mean, irrespective of LKB or LHR.

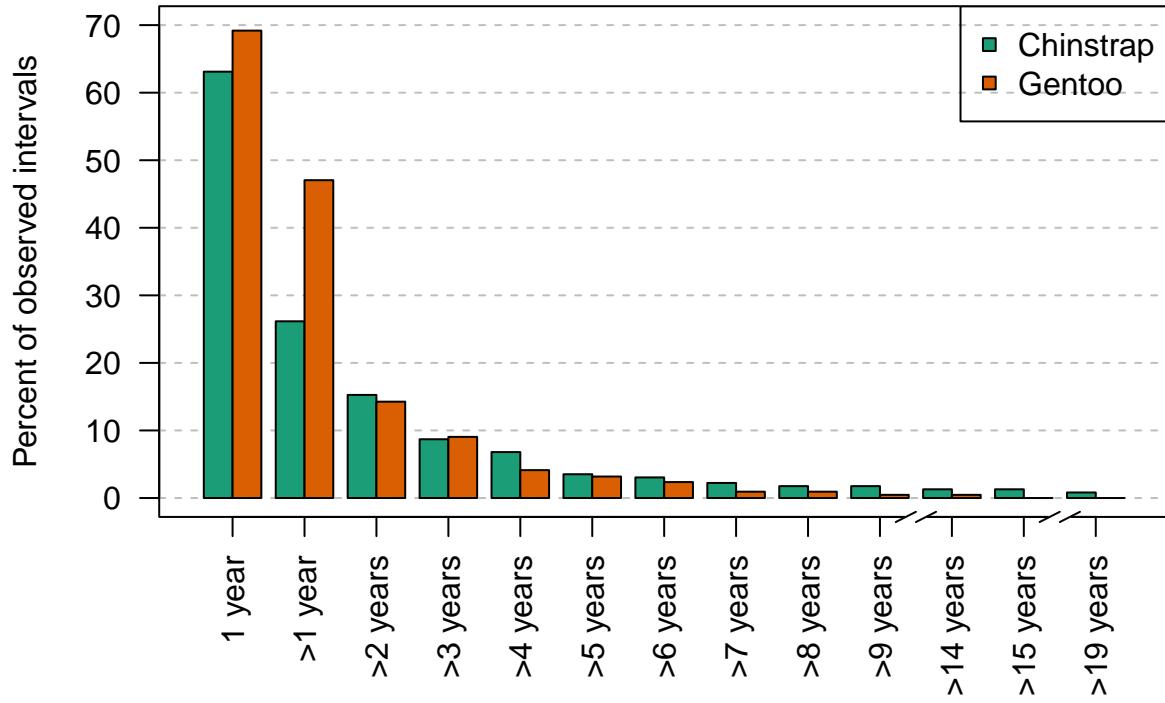


Figure 5: Frequency distribution (percent) of intervals between consecutive breeding surveys for chinstrap and gentoo penguins, taken from the supplementary data for Kruger et al 2021.

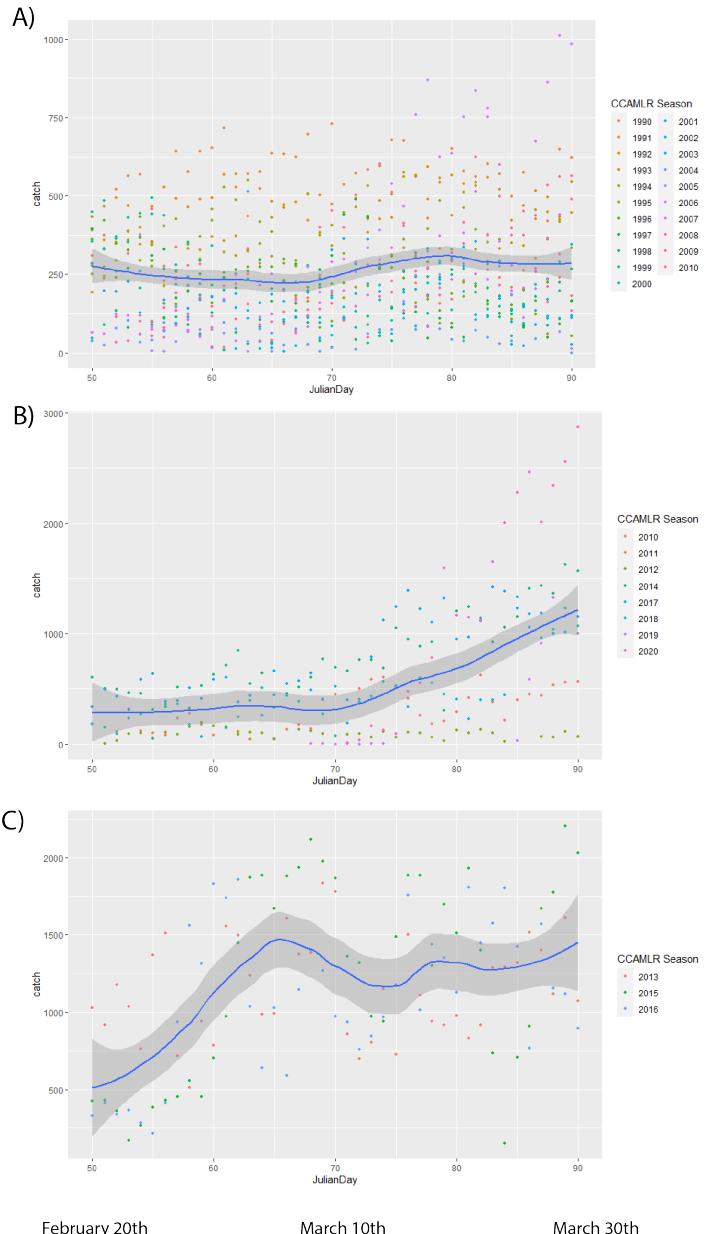


Figure 6: Daily accumulated catch (and fitted LOESS smooth curves) in Subarea 48.1 between 20th February and March 31st between A) 1990-2010 and B) 2010 to 2020. Catch in the Subarea was relatively consistent during the latter stages of penguin breeding at approximately 250tonnes/d (NOTE: different scaling of catch on y-axis between plots). However, since 2010 there has been a tendency for the fishery to increase its effort in the Subarea, starting around the middle of March. C) During this latter period, the fishery increased effort earlier on three occasions (2013, 2015 and 2016), starting before the beginning of March.

Table 1: Original table in Watters et al. 2020. In this and all subsequent tables below, the posterior and posterior predictive probabilities that the expected performance of penguins given the effects in the left hand column are less than the expected performance given the drivers in the column headings are provided. Worst Case is represented by neutral ONI; LHR ≥ 0.1 ; and LKB $\geq 1\text{Mt}$. The Best Case is represented by La Niña conditions, low LKB and low LHR.

Effects	Best Case	$-0.5^\circ\text{C} < \text{ONI} < +0.5^\circ\text{C}$	$\text{ONI} \geq +0.5$	Long-term μ	Long-term predicted μ
Best case				0.04	0.36
ONI Neutral	1.00			0.89	0.59
ONI warm	0.99			0.52	0.51
LKB High	0.71	0.02	0.12	0.01	0.41
LHR medium	0.75	0.16	0.31	0.32	0.44
LHR high	0.93	0.39	0.60	0.64	0.54
Worst case	0.99			0.99	0.78

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Table 2: Posterior and posterior predictive probabilities extracted from the model output for alternative Watters et al. 2020 scenario outlined above with March attributed to winter (Adélie and chinstrap penguins migrate out of the area after breeding, LKB and LHR rescaled to SSMU). Under this scenario, performance against the long term mean is worst for neutral and warm ONI conditions.

Effects	Best Case	$-0.5^\circ\text{C} < \text{ONI} < +0.5^\circ\text{C}$	$\text{ONI} \geq +0.5$	Long-term μ	Long-term predicted μ
Best case				0.04	0.40
ONI Neutral	1.00			0.97	0.62
ONI warm	0.99			0.81	0.56
LKB High	0.49	0.01	0.05	0.03	0.40
LHR medium	0.46	0.04	0.09	0.14	0.39
LHR high	0.45	0.10	0.16	0.23	0.39
Worst case	0.84			0.71	0.59

Table 3: Posterior and posterior predictive probabilities extracted from the model output for alternative Watters et al. 2020 scenario outlined above with March attributed to summer (Adélie and chinstrap penguins migrate out of the area after breeding, LKB and LHR rescaled to SSMU). Under this scenario performance against the long term mean is also worst for neutral and warm ONI conditions.

Effects	Best Case	$-0.5^{\circ}\text{C} < \text{ONI} < +0.5^{\circ}\text{C}$	$\text{ONI} \geq +0.5$	Long-term μ	Long-term predicted μ
Best case				0.10	0.42
ONI Neutral	1.00			0.98	0.63
ONI warm	0.99			0.86	0.56
LKB High	0.40	0.00	0.04	0.03	0.40
LHR medium	0.27	0.01	0.02	0.04	0.37
LHR high	0.37	0.08	0.13	0.21	0.38
Worst case	0.76			0.63	0.55

Supplementary material

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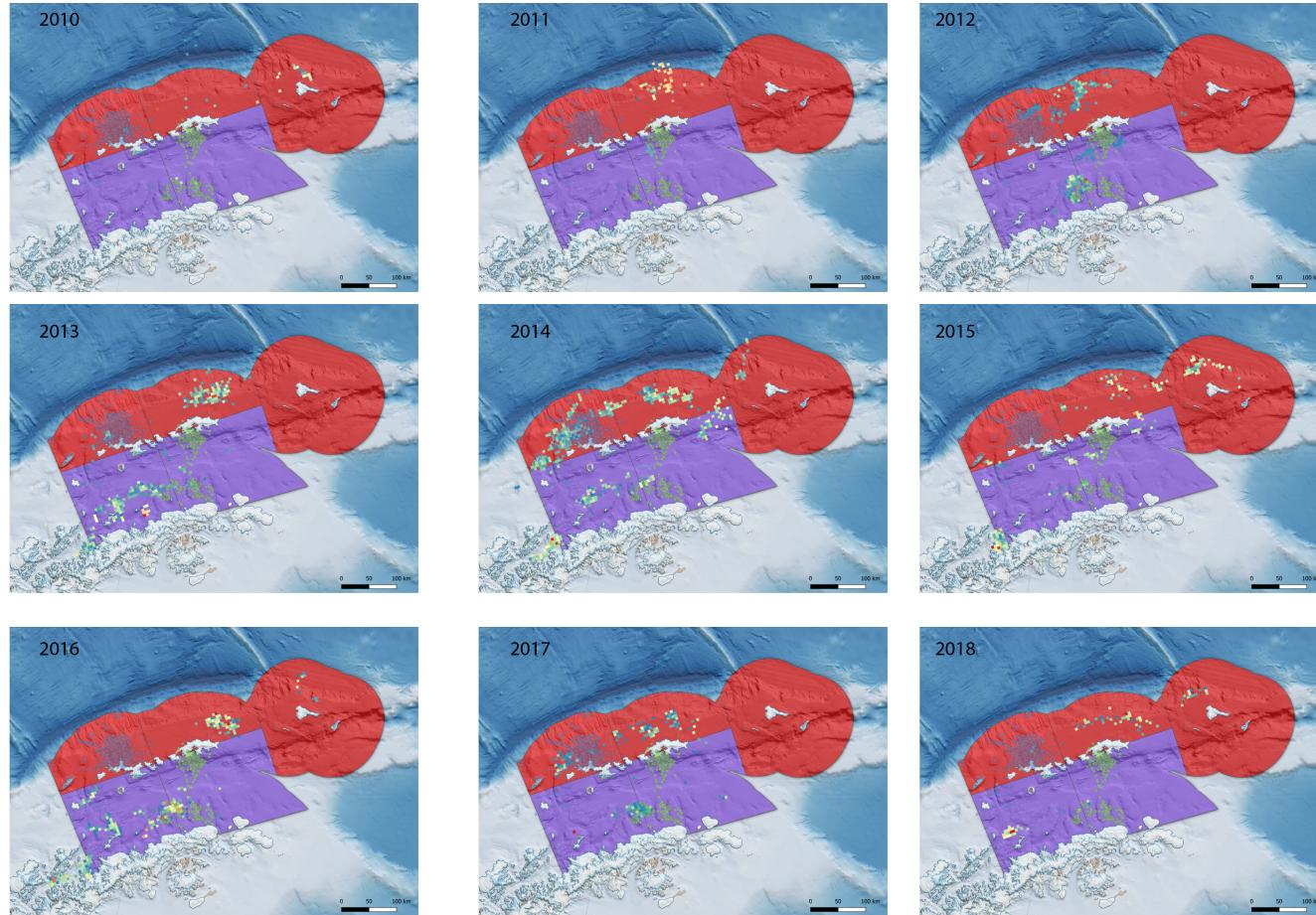


Figure S1: C1 Catch and Effort data for 2010 - 2018, for all catches during the period of the austral summer relating to Adélie and chinstrap penguins in Subarea 48.1 (i.e. up to 10th March). The telemetry data presented in Hinke et al. 2017 for chinstrap penguins at both Cape Shireff and Copacabana and the gSSMU used in the Watters et al. 2020 paper are superimposed to highlight the extreme variability in actual catch, relative to the scale of LHR used to reflect interactions with penguins. Our reanalysis re-scaled LHR to the SSMU level, though we contend that for the purposes of matching predator data at appropriate spatial scales even this is too coarse a resolution.

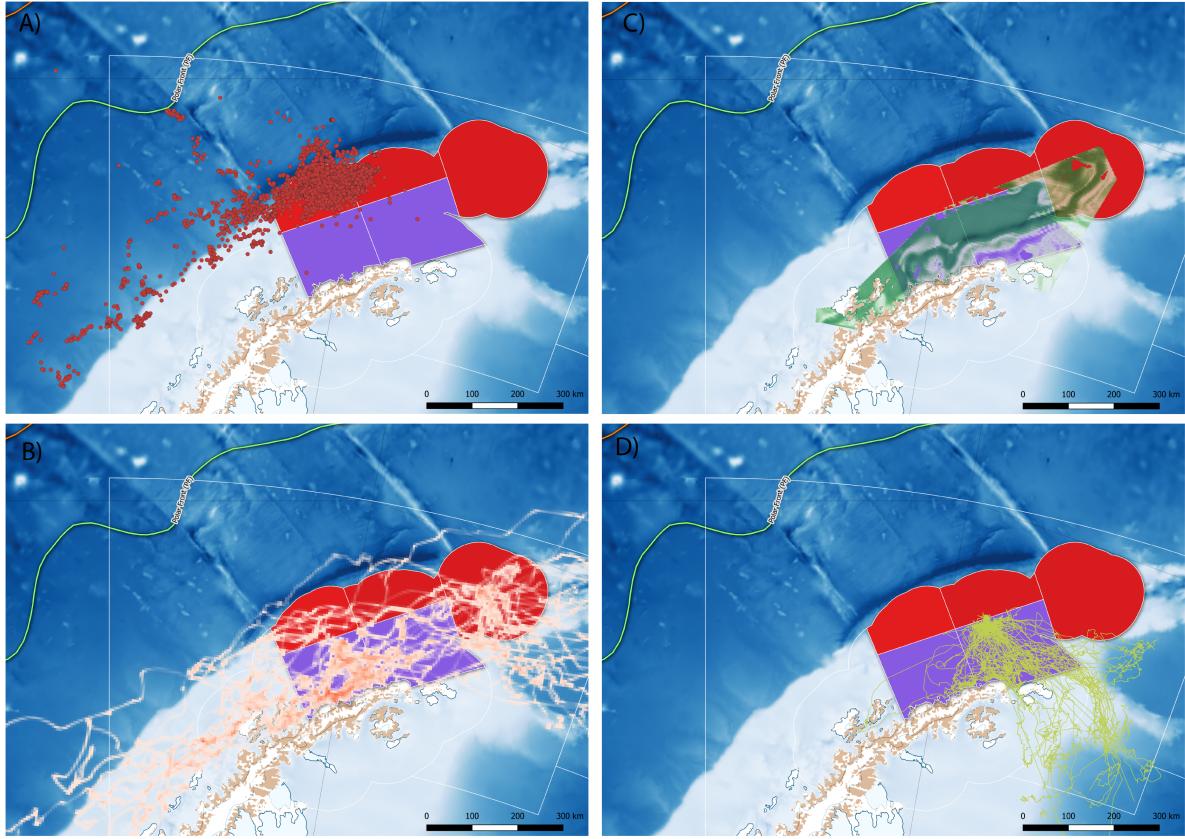


Figure S2: The summer distribution of foraging effort by A) adult female Antarctic fur seals (adapted from telemetry data available in Hinke et al. 2017), B) migratory adult male Antarctic fur seals (adapted from Lowther et al. 2020) C) humpback whales throughout December (adapted from Johannessen et al., this meeting) and D) nonbreeding adult Adélie penguins during the breeding season (adapted from data in Oosthuizen et al., this meeting). Potential effects of competitive overlap between pygoscelid penguins and other krill dependent predators, particularly those who have increased their abundance dramatically over the preceding 40 years, are excluded from both approaches, creating an unrealistic set of boundary conditions for interpreting the variance in penguin vital rates.

```

1 #####DATA PREP AND MODEL CODE (IMPUTATION OF BIOMASS = TRUE)----
2 #original paper here:
3 https://doi.org/10.1038/s41598-020-59223-9
4 #requirements - raw Supplementary Files from original Watters et al. (2020) publication available here:
5 https://www.nature.com/articles/s41598-020-59223-9#Sec8
6 # the analyses with imputation takes several hours - the scenarios outlined in the paper are provided as .csv
7 # files in the Zenodo repository provided which is open access via the DOI here (https://doi.org/10.5281/zenodo.5040114)
8 # and provided in the manuscript.
9 # the raw files to conduct the analyses from first principles are also available from the Watters et al.2020 manuscript
10 #SCRIPT MODIFICATIONS:
11 #L. 225 - 233. These changes modify the Acoustic biomass estimates by the ratio of SSMU / gSSMU
12 #L. 253. Alter March to either Summer or Winter. Currently set to Winter.
13 #L. 255 - 258. Modify the gSSMU configurations to reflect only SSMU
14 #L. 284, 286 & 290. Set CHPE and ADPE in WINTER to NA - removing from model / migration out of area
15 #L. 666. Incorrect parameter set selection for "Worst Case" Fig 2 / "Selected Cases" plot.
16 library(tidyverse)
17 make.localhr.data<-function(trim=1,plot.winter=FALSE){
18   # fledge weight (fwt)
19   # bigger indicates better summer
20   fwt<read.csv("fweight.csv",header=TRUE,stringsAsFactors = FALSE)
21   fwt<-tapply(fwt$WT,list(fwt$YEAR,fwt$PROJECT,fwt$SPECIES),mean)
22   fwt<-data.frame(YEAR=rep(dimnames(fwt)[1]),dim(fwt)[2]*dim(fwt)[3]),
23     PROJECT=rep(rep(dimnames(fwt)[2]),each=dim(fwt)[1],dim(fwt)[3]),
24     SPECIES=rep(dimnames(fwt)[3],each=dim(fwt)[1]*dim(fwt)[2]),
25     fwt=c(fwt),stringsAsFactors = FALSE)
26   fwt$matchme<-paste(fwt$PROJECT,fwt$SPECIES,sep="|")
27   tt<-tapply(fwt$fwt,list(fwt$matchme),mean,na.rm=TRUE)
28   ttt<-tapply(fwt$fwt,list(fwt$matchme),sd,na.rm=TRUE)
29   mean.fwt<-tt[match(fwt$matchme,names(tt))]
30   sd.fwt<-ttt[match(fwt$matchme,names(ttt))]
31   fwt$std.mean.fwt<-(fwt$fwt-mean.fwt)/sd.fwt
32   fwt<-fwt[,c(4:5)]
33   #omits<-(fwt$SPECIES=="ADPE"&fwt$PROJECT=="CS")/(fwt$SPECIES=="CHPE"&fwt$PROJECT=="COPA")
34   #fwt<-fwt[!omits,]
35   names(fwt)[4]<"index"
36   fwt$param=rep("FWT",dim(fwt)[1])
37   fwt$season=rep("S",dim(fwt)[1])
38   # make stuff reference the correct "calendar year" for matching up with krill survey and catch data
39   # summer indices are relevant to the second year in the split-season designation
40   fwt$cal.yr<as.numeric(substr(fwt$YEAR,1,4))+1
41   #print(str(fwt))
42   #
43   # post-hatch success (phs) (numbers of chicks creched/numbers of chicks hatched)
44   # bigger indicates better summer
45   phs<read.csv("success.csv",header=TRUE,stringsAsFactors = FALSE)
46   phs$phs<-phs$N_CRECHE/phs$N_CHICKS
47   phs$phs<-log(phs$phs/(1-phs$phs))
48   phs$matchme<-paste(phs$PROJECT,phs$SPECIES,sep="|")
49   tt<-tapply(phs$phs,list(phs$matchme),mean,na.rm=TRUE)
50   ttt<-tapply(phs$phs,list(phs$matchme),sd,na.rm=TRUE)
51   mean.phs<-tt[match(phs$matchme,names(tt))]
52   sd.phs<-ttt[match(phs$matchme,names(ttt))]
53   phs$std.logit.phs<-(phs$phs-mean.phs)/sd.phs
54   phs<-phs[,c(4:9)]
55   names(phs)[4]<"index"
56   phs$param=rep("PHS",dim(phs)[1])
57   phs$season=rep("S",dim(phs)[1])
58   # summer indices are relevant to the second year in the split-season designation
59   phs$cal.yr<as.numeric(substr(phs$YEAR,1,4))+1
60   #print(str(phs))
61   #
62   # trip duration (td)
63   # smaller indicates better summer (thus need to switch direction of index)
64   td<read.csv("tripduration.csv",header=TRUE,stringsAsFactors = FALSE)
65   td<-td[,c(1:3,8)]
66   # next line is to make trip duration point in same direction as fwt and phs (max td is 59.95 for all trips)
67   # call this "revtd" for "reversed" trip duration
68   td[,4]<-60-td[,4]
69   names(td)[4]<-"revtd"
70   td<-tapply(td$revtd,list(td$YEAR,td$PROJECT,td$SPECIES),mean)
71   td<-data.frame(YEAR=rep(dimnames(td)[1]),dim(td)[2]*dim(td)[3]),
72     PROJECT=rep(rep(dimnames(td)[2]),each=dim(td)[1],dim(td)[3]),
73     SPECIES=rep(dimnames(td)[3],each=dim(td)[1]*dim(td)[2]),
74     revtd=c(td),stringsAsFactors = FALSE)
75   td$matchme<-paste(td$PROJECT,td$SPECIES,sep="|")
76   tt<-tapply(td$revtd,list(td$matchme),mean,na.rm=TRUE)
77   ttt<-tapply(td$revtd,list(td$matchme),sd,na.rm=TRUE)

```

```

78 mean.revtd<-tt[match(td$matchme,names(ttt))]
79 sd.revtd<-ttt[match(td$matchme,names(ttt))]
80 td$std.revtd<-(td$revtd-mean.revtd)/sd.revtd
81 td<-td[, -c(4:5)]
82 names(td)[4]<-"index"
83 #omits<-(td$SPECIES=="ADPE"&td$PROJECT=="CS")/(td$SPECIES=="CHPE"&td$PROJECT=="COPA")
84 #td<-td[!omits,]
85 td$param=rep("REVTD",dim(td)[1])
86 td$season=rep("S",dim(td)[1])
87 # summer indices are relevant to the second year in the split-season designation
88 td$cal.yr<-as.numeric(substr(td$YEAR,1,4))+1
89 #print(str(td))
90 #
91 # generate the winter indices
92 #
93 # adult male mass at E1 lay (mml)
94 # bigger indicates better winter
95 ade1<-read.csv("massatlay.csv",header=TRUE,stringsAsFactors = FALSE)
96 mml<-ade1[,c(1:3,5)]
97 mml<-tapply(mml$WT_MALE,list(mml$YEAR,mml$PROJECT,mml$SPECIES),mean,na.rm=TRUE)
98 mml<-data.frame(YEAR=rep(dimnames(mml)[1]),dim(mml)[2]*dim(mml)[3]),
99 PROJECT=rep(rep(dimnames(mml)[2]),each=dim(mml)[1]),dim(mml)[3]),
100 SPECIES=rep(dimnames(mml)[3]),each=dim(mml)[1]*dim(mml)[2]),
101 mml=c(mml),stringsAsFactors = FALSE)
102 mml$matchme<-paste(mml$PROJECT,mml$SPECIES,sep="|")
103 tt<-tapply(mml$mml,list(mml$matchme),mean,na.rm=TRUE)
104 mean.mml<-tt[match(mml$matchme,names(tt))]
105 sd.mml<-tt[match(mml$matchme,names(ttt))]
106 mml$std.mean.mml<-(mml$mml-mean.mml)/sd.mml
107 mml<-mml[, -c(4:5)]
108 names(mml)[4]<-"index"
109 #omits<-(mml$SPECIES=="ADPE"&mml$PROJECT=="CS")/(mml$SPECIES=="CHPE"&mml$PROJECT=="COPA")
110 #mml<-mml[!omits,]
111 mml$param=rep("MML",dim(mml)[1])
112 mml$season=rep("W",dim(mml)[1])
113 # most winter indices (except rec) are relevant to the first year in the split-season designation
114 mml$cal.yr<-as.numeric(substr(mml$YEAR,1,4))
115 #print(str(mml))
116 #
117 #
118 # adult female mass at E1 lay (fml)
119 # bigger indicates better winter
120 fml<-ade1[,c(1:3,6)]
121 fml<-tapply(fml$WT_FEMALE,list(fml$YEAR,fml$PROJECT,fml$SPECIES),mean,na.rm=TRUE)
122 fml<-data.frame(YEAR=rep(dimnames(fml)[1]),dim(fml)[2]*dim(fml)[3]),
123 PROJECT=rep(rep(dimnames(fml)[2]),each=dim(fml)[1]),dim(fml)[3]),
124 SPECIES=rep(dimnames(fml)[3]),each=dim(fml)[1]*dim(fml)[2]),
125 fml=c(fml),stringsAsFactors = FALSE)
126 fml$matchme<-paste(fml$PROJECT,fml$SPECIES,sep="|")
127 tt<-tapply(fml$fml,list(fml$matchme),mean,na.rm=TRUE)
128 ttt<-tapply(fml$fml,list(fml$matchme),sd,na.rm=TRUE)
129 mean.fml<-tt[match(fml$matchme,names(tt))]
130 sd.fml<-tt[match(fml$matchme,names(ttt))]
131 fml$std.mean.fml<-(fml$fml-mean.fml)/sd.fml
132 fml<-fml[, -c(4:5)]
133 names(fml)[4]<-"index"
134 #omits<-(fml$SPECIES=="ADPE"&fml$PROJECT=="CS")/(fml$SPECIES=="CHPE"&fml$PROJECT=="COPA")
135 #fml<-fml[!omits,]
136 fml$param=rep("FML",dim(fml)[1])
137 fml$season=rep("W",dim(fml)[1])
138 # most winter indices (except rec) are relevant to the first year in the split-season designation
139 fml$cal.yr<-as.numeric(substr(fml$YEAR,1,4))
140 #print(str(fml))
141 #
142 #
143 #
144 # avg egg density using both eggs (egg)
145 # bigger indicates better winter
146 e1e2<-read.csv("egg.csv",header=TRUE,stringsAsFactors = FALSE)
147 egg<-e1e2[,c(1:3)]
148 egg$egg<-(e1e2[,5]+e1e2[,7])/(e1e2[,6]+e1e2[,8])
149 egg<-tapply(egg$egg,list(egg$YEAR,egg$PROJECT,egg$SPECIES),mean,na.rm=TRUE)
150 egg<-data.frame(YEAR=rep(dimnames(egg)[1]),dim(egg)[2]*dim(egg)[3]),
151 PROJECT=rep(rep(dimnames(egg)[2]),each=dim(egg)[1]),dim(egg)[3]),
152 SPECIES=rep(dimnames(egg)[3]),each=dim(egg)[1]*dim(egg)[2]),
153 egg=c(egg),stringsAsFactors = FALSE)
154 egg$matchme<-paste(egg$PROJECT,egg$SPECIES,sep="|")

```

```

155 tt<-tapply(egg$egg,list(egg$matchme),mean,na.rm=TRUE)
156 ttt<-tapply(egg$egg,list(egg$matchme),sd,na.rm=TRUE)
157 mean.egg<-tt[match(egg$matchme,names(tt))]
158 sd.egg<-ttt[match(egg$matchme,names(ttt))]
159 egg$std.mean.egg<-(egg$egg-mean.egg)/sd.egg
160 egg<-egg[,c(4:5)]
161 names(egg)[4]<-"index"
162 #omits<-(egg$SPECIES=="ADPE"&egg$PROJECT=="CS") | (egg$SPECIES=="CHPE"&egg$PROJECT=="COPA")
163 #egg<-egg[!omits,]
164 egg$param=rep("EGG",dim(egg)[1])
165 egg$season=rep("W",dim(egg)[1])
166 # most winter indices (except rec) are relevant to the first year in the split-season designation
167 egg$cal.yr<-as.numeric(substr(egg$YEAR,1,4))
168 #print(str(egg))
169 #
170 #
171 # clutch initiation date (cid)
172 # earlier indicates better winter
173 cid<-read.csv("cid.csv",header=TRUE,stringsAsFactors = FALSE)[,1:4]
174 # next line is to make CID point in same direction as other
175 #indices where bigger indicates better conditions (take diff from Dec 31)
176 # call this "revcid" for "reversed" CID
177 cid[,4]<-as.vector(as.POSIXlt(paste(substr(cid$YEAR,1,4),"12-31",sep=""))-strptime(cid[,4],"%m/%e/%Y"))
178 names(cid)[4]<-"revcid"
179 cid$matchme<-paste(cid$PROJECT,cid$SPECIES,sep="|")
180 tt<-tapply(cid$revcid,list(cid$matchme),mean,na.rm=TRUE)
181 mean.cid<-tt[match(cid$matchme,names(tt))]
182 sd.cid<-ttt[match(cid$matchme,names(ttt))]
183 cid$std.revcid<-(cid$revcid-mean.cid)/sd.cid
184 cid<-cid[,c(4:5)]
185 names(cid)[4]<-"index"
186 cid$param=rep("REVCID",dim(cid)[1])
187 cid$season=rep("W",dim(cid)[1])
188 # most winter indices (except rec) are relevant to the first year in the split-season designation
189 cid$cal.yr<-as.numeric(substr(cid$YEAR,1,4))
190 #uncomment next line if decide to remove gentoos because of their more plastic breeding phenology
191 #cid<-cid[cid$SPECIES!="GEPE",]
192 #print(str(cid))
193 #
194 # cohort recruitment (rec)
195 # bigger indicates better winter
196 rec<-read.csv("recruitment.csv",header=TRUE,stringsAsFactors = FALSE)[,1:4]
197 names(rec)[4]<-"rec"
198 rec$rec<-log(rec$rec/(1-rec$rec))
199 rec$matchme<-paste(rec$PROJECT,rec$SPECIES,sep="|")
200 tt<-tapply(rec$rec,list(rec$matchme),mean,na.rm=TRUE)
201 ttt<-tapply(rec$rec,list(rec$matchme),sd,na.rm=TRUE)
202 mean.rec<-tt[match(rec$matchme,names(tt))]
203 sd.rec<-ttt[match(rec$matchme,names(ttt))]
204 rec$std.logit.rec<-(rec$rec-mean.rec)/sd.rec
205 rec<-rec[,c(4:5)]
206 names(rec)[4]<-"index"
207 rec$param=rep("REC",dim(rec)[1])
208 rec$season=rep("W",dim(rec)[1])
209 # recruitment is relevant to the second year in the split-season designation (the winter of first independence)
210 rec$cal.yr<-as.numeric(substr(rec$YEAR,1,4))+1
211 #print(str(rec))
212 #
213 # read in the krill survey and fishery data
214 #
215 # krill survey biomass
216 survey<-read.csv("krillsurveywithJoinville.csv",header=TRUE,stringsAsFactors = FALSE)
217 # use next line if want to filter acoustic data to have minimum number of miles (comment out if not desired)
218 # as per CSR, 80 nmi would be about equivalent of 2 tracklines in the Bransfield
219 #survey<-survey[survey$nmi.count>=80,]
220 # could try changing "biomass" in following line to "mean.density.gm2" or "median.density.gm2" but haven't done that
221 # change here
222 survey.mod = as_tibble(survey) %>%
223   group_split(gSSMU)
224   # 28.7/(28.7+22) #fraction of nmi area # change here
225 survey.mod[[1]]$biomass = survey.mod[[1]]$biomass * 0.566075
226   # 15.8/(15.8+16.4+36.2)fraction of nmi area # change here
227 survey.mod[[2]]$biomass = survey.mod[[2]]$biomass * 0.230994
228   # 22.0/(28.7+22.0) change here
229 survey.mod[[3]]$biomass = survey.mod[[3]]$biomass * 0.433925
230   # change here
231 
```

```

232 survey.mod[[4]]$biomass = survey.mod[[4]]$biomass * 1
233 # change here
234 survey = data.frame(bind_rows(survey.mod[[1]],survey.mod[[2]],survey.mod[[3]],survey.mod[[4]]))
235
236 # use next line if want to filter acoustic data to have minimum number of miles (comment out if not desired)
237 # as per CSR, 80 nmi would be about equivalent of 2 tracklines in the Bransfield
238 #survey<-survey[survey$nm.count>=80,]
239 # could try changing "biomass" in following line to "mean.density.gm2" or "median.density.gm2" but haven't done that
240 survey<-tapply(survey$biomass,list(survey$Year,survey$gSSMU),mean,na.rm=TRUE)
241 survey<-data.frame(cal.yr=rep(dimnames(survey)[[1]],dim(survey)[2]),
242 gSSMU=rep(dimnames(survey)[[2]],each=dim(survey)[1]),
243 survey=c(survey),stringsAsFactors = FALSE)
244 survey$season<-ifelse(survey$cal.yr<2012,"S","W")
245 # use next line if want to remove winter survey data altogether (comment out if not desired)
246 #survey<-survey[survey$season=="S",]
247 survey$matchme<-paste(survey$cal.yr,survey$season,survey$gSSMU,sep="|")
248 #print(str(survey))
249 #
250 #
251 # krill fishery catches
252 fishery<-read.csv("c1.csv",header=TRUE,stringsAsFactors = FALSE)
253 # change here - current modification for March in Winter permutation
254 fishery$season<-ifelse(is.element(fishery$Month,c(10:12,1:2)),"S","W") #1:3 if March in Summer
255 gSSMU1<-c("APBSE") # change here
256 gSSMU2<-c("APDPW") # change here
257 gSSMU3<-"APBSW" # change here
258 gSSMU4<-c("APW","APE") # change here
259 fishery$gSSMU<-rep(NA,dim(fishery)[1])
260 fishery$gSSMU<-ifelse(is.element(fishery$AssignedSSMU,gSSMU1),1,fishery$gSSMU)
261 fishery$gSSMU<-ifelse(is.element(fishery$AssignedSSMU,gSSMU2),2,fishery$gSSMU)
262 fishery$gSSMU<-ifelse(is.element(fishery$AssignedSSMU,gSSMU3),3,fishery$gSSMU)
263 fishery$gSSMU<-ifelse(is.element(fishery$AssignedSSMU,gSSMU4),4,fishery$gSSMU)
264 fishery<-fishery[!is.na(fishery$gSSMU),]
265 fishery<-tapply(fishery$TotalCatch,list(fishery$CalendarYear,fishery$gSSMU,fishery$season),sum)
266 fishery<-data.frame(cal.yr=rep(dimnames(fishery)[[1]],dim(fishery)[2]*dim(fishery)[3]),
267 gSSMU=rep(rep(dimnames(fishery)[[2]],each=dim(fishery)[1]),dim(fishery)[3]),
268 season=rep(dimnames(fishery)[[3]],each=dim(fishery)[1]*dim(fishery)[2]),
269 catch=c(fishery),stringsAsFactors = FALSE)
270 fishery$cal.yr<-as.numeric(as.character(fishery$cal.yr))
271 fishery$gSSMU<-as.numeric(as.character(fishery$gSSMU))
272 fishery$matchme<-paste(fishery$cal.yr,fishery$season,fishery$gSSMU,sep="|")
273 #print(str(fishery))
274 # now match predator data with krill data
275 out<-rbind(fwt,phs,td,mml,fml,egg,cid,rec,make.row.names=FALSE)
276 # all birds from Copa always forage in gSSMU 1 (Bransfield SSMUs)
277 # CHPE from Cape Shirreff always forage in gSSMU 2 (Drake Passage SSMUs)
278 # GEPE from Cape Shirreff forage in gSSMU 2 during summer and gSSMU 1 during winter
279 #out$gSSMU<-ifelse(out$PROJECT=="COPA",1,
280 # ifelse(out$SPECIES=="CHPE",2,
281 # ifelse(out$SPECIES=="GEPE"&out$PROJECT=="CS"&out$season=="S",2,1)))
282 out$gSSMU<-rep(NA,dim(out)[1])
283 out$gSSMU<-ifelse(out$SPECIES=="ADPE"&out$PROJECT=="COPA"&out$season=="S",1,out$gSSMU)
284 out$gSSMU<-ifelse(out$SPECIES=="ADPE"&out$PROJECT=="COPA"&out$season=="W",NA,out$gSSMU)
285 out$gSSMU<-ifelse(out$SPECIES=="CHPE"&out$PROJECT=="COPA"&out$season=="S",1,out$gSSMU)
286 out$gSSMU<-ifelse(out$SPECIES=="CHPE"&out$PROJECT=="COPA"&out$season=="W",NA,out$gSSMU)
287 out$gSSMU<-ifelse(out$SPECIES=="GEPE"&out$PROJECT=="COPA"&out$season=="S",1,out$gSSMU)
288 out$gSSMU<-ifelse(out$SPECIES=="GEPE"&out$PROJECT=="COPA"&out$season=="W",1,out$gSSMU)
289 out$gSSMU<-ifelse(out$SPECIES=="CHPE"&out$PROJECT=="CS"&out$season=="S",2,out$gSSMU)
290 out$gSSMU<-ifelse(out$SPECIES=="CHPE"&out$PROJECT=="CS"&out$season=="W",NA,out$gSSMU)
291 out$gSSMU<-ifelse(out$SPECIES=="GEPE"&out$PROJECT=="CS"&out$season=="S",2,out$gSSMU)
292 # use following line if GEPE at CS forage in gSSMU 2 during winter
293 #out$gSSMU<-ifelse(out$SPECIES=="GEPE"&out$PROJECT=="CS"&out$season=="W",2,out$gSSMU)
294 # use following line if GEPE at CS forage in gSSMU 1 during winter
295 out$gSSMU<-ifelse(out$SPECIES=="GEPE"&out$PROJECT=="CS"&out$season=="W",3,out$gSSMU)
296 #
297 out$matchme<-paste(out$cal.yr,out$season,out$gSSMU,sep="|")
298 out$Survey<-Survey$Survey[match(out$matchme,Survey$matchme)]
299 out$catch<-fishery$catch[match(out$matchme,fishery$matchme)]
300 #
301 out<-out[!is.na(out$gSSMU),]
302
303 # pull in the environmental indices
304 #
305 # SOUTHERN ANNULAR MODE
306 sam<-read.csv("sam.csv")
307 names(sam)<-c("yr","mo","sam")
308 sam$season<-ifelse(is.element(sam$mo,c(10:12,1:3)),"S","W")

```

```

309 sam$YEAR<-ifelse(is.element(sam$mo,10:12),sam$yr+1,sam$yr)
310 sam<-tapply(sam$sam,list(sam$YEAR,sam$season),mean)
311 sam<-data.frame(YEAR=rep(dimnames(sam)[[1]],2),season=rep(dimnames(sam)[[2]],each=dim(sam)[1]),sam=c(sam))
312 out$sam<-sam$sam[match(paste(out$cal.yr,out$season,sep="|"),paste(sam$YEAR,sam$season,sep="|"))]
313 out$sam.sign<-ifelse(out$sam<0,"Neg","Pos")
314 #
315 # OCEANIC NINO INDEX
316 oni<-read.csv("oni.csv",stringsAsFactors = FALSE)
317 oni$yr<-ifelse(is.element(oni$SEAS,c("OND","NDJ")),oni$YR+1,oni$YR)
318 oni$season<-ifelse(is.element(oni$SEAS,c("OND","NDJ","DJF","JFM")),"S",NA)
319 oni$season<-ifelse(is.element(oni$SEAS,c("AMJ","MJJ","JJA","JAS")),"W",oni$season)
320 oni<-na.omit(oni)
321 oni<-tapply(oni$ANOM,list(oni$yr,oni$season),mean)
322 oni<-data.frame(yr=rep(dimnames(oni)[[1]],2),season=rep(dimnames(oni)[[2]],each=dim(oni)[1]),oni=c(oni))
323 out$oni<-oni$oni[match(paste(out$cal.yr,out$season,sep="|"),paste(oni$yr,oni$season,sep="|"))]
324 out$oni.class<-ifelse(out$oni <= -0.5, "Cool","Neutral")
325 out$oni.class<-ifelse(out$oni >=0.5, "Warm",out$oni.class)
326 #
327 #
328 # some clean up
329 #
330 out$catch[is.na(out$catch)]<-0
331 out<-out[!is.na(out$sam),]
332 out<-out[!is.nan(out$index),]
333 out<-out[!is.na(out$index),]
334
335 write.csv(out, file = "out.csv")
336 # will not try to impute missing winter surveys
337 # but will keep winter performance indices if want to plot them
338 if(!plot.winter){out<-out[!(is.na(out$survey)&out$season=="W"),]}
339 #
340 # if require minimum number of data points per study
341 if(!is.null(trim)){
342   study<-as.numeric(factor(paste(out$PROJECT,out$SPECIES,out$param,sep="|")))
343   study.n<-table(study)
344   keepers<-as.numeric(as.vector(dimnames(study.n[study.n>trim])[1]))
345   out<-out[is.element(study,keepers),]
346 }
347 out
348 }
349 junk<-make.localhr.data()
350 # write out data
351 write.csv(junk, file = "junk.csv")
352 modelstring<-
353
354   model{
355     for(i in 1:nsummerobs){
356       lower[i]<-max(10000,catch[i])
357       summer[i]~dlnorm(mu.logsummer[gssmu[i],samclass[i]],tau.logsummer) T(lower[i],100000000)
358     }
359
360     for(i in 1:2){ # two gSSMUs #change here
361       for(j in 1:2){ # two SAM classes
362         mu.logsummer[i,j]~dunif(0.1*mean.logsummer[i,j],10*mean.logsummer[i,j])
363       }
364     }
365     tau.logsummer<-pow(sigmalogsummer,-2)
366     sigmalogsummer~dunif(0.1*sd.logsummer,10*sd.logsummer)
367     for(i in 1:nsummerobs){
368       hr.summer[i]<-ifelse(impute.me[i]==1,catch[i]/summer[i],1)
369       bmass.summer[i]<-ifelse(impute.me[i]==1,summer[i],1)
370     }
371     for(i in (nsummerobs+1):nobs){
372       hr.summer[i]<-0
373       bmass.summer[i]<-0
374     }
375
376     for(i in 1:nobs){
377       hr[i]<-ifelse(impute.me[i]==1,hr.summer[i],catch[i]/survey[i])
378       hrclass[i]<-ifelse(hr[i]<=0.01,1,ifelse(hr[i]>=0.1,3,2))
379       bmass[i]<-ifelse(impute.me[i]==1,bmass.summer[i],survey[i])
380       bclass[i]<-ifelse(bmass[i]<=1000000,1,2)
381     }
382
383     for(i in 1:nobs){
384       X[i,1]<-1.0      # intercept

```

```

386     X[i,2]<-equals(bclass[i],2)-equals(bclass[i],1) # b2
387     X[i,3]<-equals(hrclass[i],2)-equals(hrclass[i],1) # hr2
388     X[i,4]<-equals(hrclass[i],3)-equals(hrclass[i],1) # hr3
389     X[i,5]<-equals(oniclass[i],2)-equals(oniclass[i],1) # o2
390     X[i,6]<-equals(oniclass[i],3)-equals(oniclass[i],1) # o3
391   }
392
393
394   for(i in 1:nobs){
395     index[i]~dnorm(mu[i],tau.index)
396     mu[i] <- inprod(X[i,],beta[])
397   }
398
399   beta[1]~dnorm(0, 0.0001)
400
401   beta[2]~dnorm(0, 0.0001)
402
403   beta[3]~dnorm(0, 0.0001)
404   beta[4]~dnorm(0, 0.0001)
405
406   beta[5]~dnorm(0, 0.0001)
407   beta[6]~dnorm(0, 0.0001)
408
409
410   # half-cauchy for variation among indices
411   tau.index<-pow(sd.index,-2)
412   #sd.index~dunif(0,10)
413   sd.index~dt(0,t.tau.index,1)T(0,)
414   t.tau.index<-pow(t.sd.index,-2)
415   # hyperprior for half-cauchy scale
416   t.sd.index~dunif(0,2)
417
418   # derived quantities
419   # first the design matrix for easily interpreting effects
420   # row 1 -- ONI=cool, LKB<=1Mt, LHR<=0.01 (reference or best case)
421   # row 2 -- ONI=cool, LKB>1Mt, 0.01<LHR<0.1
422   # row 3 -- ONI=cool, LKB<=1Mt, LHR>=0.1
423   # row 4 -- ONI=cool, LKB>1Mt, LHR<=0.01
424   # row 5 -- ONI=cool, LKB<=1Mt, 0.01<LHR<0.1
425   # row 6 -- ONI=cool, LKB>1Mt, LHR>=0.1
426   # row 7 -- ONI=neutral, LKB<=1Mt, LHR<=0.01
427   # row 8 -- ONI=neutral, LKB>1Mt, 0.01<LHR<0.1
428   # row 9 -- ONI=neutral, LKB<=1Mt, LHR>=0.1
429   # row 10 -- ONI=neutral, LKB>1Mt, LHR<=0.01
430   # row 11 -- ONI=neutral, LKB<=1Mt, 0.01<LHR<0.1
431   # row 12 -- ONI=neutral, LKB>1Mt, LHR>=0.1 (worst case)
432   # row 13 -- ONI=warm, LKB<=1Mt, LHR<=0.01
433   # row 14 -- ONI=warm, LKB>1Mt, 0.01<LHR<0.1
434   # row 15 -- ONI=warm, LKB<=1Mt, LHR>=0.1
435   # row 16 -- ONI=warm, LKB>1Mt, LHR<=0.01
436   # row 17 -- ONI=warm, LKB<=1Mt, 0.01<LHR<0.1
437   # row 18 -- ONI=warm, LKB>1Mt, LHR>=0.1
438   for(i in 1:18){
439     mu.new[i]<-inprod(predX[i,],beta[]) # posterior expectation at new data points
440     index.new[i]~dnorm(mu.new[i],tau.index) # posterior predictive
441   }
442
443   # some interesting probabilities
444
445   # that effects change expected performance relative to the reference case
446   # high biomass
447   prob[1]<-ifelse(mu.new[2]<mu.new[1],1,0)
448   prob.new[1]<-ifelse(index.new[2]<index.new[1],1,0)
449   # med hr
450   prob[2]<-ifelse(mu.new[3]<mu.new[1],1,0)
451   prob.new[2]<-ifelse(index.new[3]<index.new[1],1,0)
452   # high hr
453   prob[3]<-ifelse(mu.new[5]<mu.new[1],1,0)
454   prob.new[3]<-ifelse(index.new[5]<index.new[1],1,0)
455   # neutral ONI
456   prob[4]<-ifelse(mu.new[7]<mu.new[1],1,0)
457   prob.new[4]<-ifelse(index.new[7]<index.new[1],1,0)
458   # warm ONI
459   prob[5]<-ifelse(mu.new[13]<mu.new[1],1,0)
460   prob.new[5]<-ifelse(index.new[13]<index.new[1],1,0)
461   # worst case
462   prob[6]<-ifelse(mu.new[12]<mu.new[1],1,0)

```

```

463 prob.new[6]<-ifelse(index.new[12]<index.new[1],1,0)
464
465 # that other effects are more extreme than environmental effects
466 # med hr has more negative effect than neutral ONI
467 prob[7]<-ifelse(mu.new[3]<mu.new[7],1,0)
468 prob.new[7]<-ifelse(index.new[3]<index.new[7],1,0)
469 # that high hr has more negative effect than neutral ONI
470 prob[8]<-ifelse(mu.new[5]<mu.new[7],1,0)
471 prob.new[8]<-ifelse(index.new[5]<index.new[7],1,0)
472 # that high krill biomass has more negative effect than neutral ONI
473 prob[9]<-ifelse(mu.new[2]<mu.new[7],1,0)
474 prob.new[9]<-ifelse(index.new[2]<index.new[7],1,0)
475 # that med hr has more negative effect than warm ONI
476 prob[10]<-ifelse(mu.new[3]<mu.new[13],1,0)
477 prob.new[10]<-ifelse(index.new[3]<index.new[13],1,0)
478 # that high hr has more negative effect than warm ONI
479 prob[11]<-ifelse(mu.new[5]<mu.new[13],1,0)
480 prob.new[11]<-ifelse(index.new[5]<index.new[13],1,0)
481 # that high krill biomass has more negative effect than warm ONI
482 prob[12]<-ifelse(mu.new[2]<mu.new[13],1,0)
483 prob.new[12]<-ifelse(index.new[2]<index.new[13],1,0)
484
485
486 # that effects change expected performance relative to long-term mean
487 # reference case
488 prob[13]<-ifelse(mu.new[1]<0,1,0)
489 prob.new[13]<-ifelse(index.new[1]<0,1,0)
490 # high biomass
491 prob[14]<-ifelse(mu.new[2]<0,1,0)
492 prob.new[14]<-ifelse(index.new[2]<0,1,0)
493 # med hr
494 prob[15]<-ifelse(mu.new[3]<0,1,0)
495 prob.new[15]<-ifelse(index.new[3]<0,1,0)
496 # high hr
497 prob[16]<-ifelse(mu.new[5]<0,1,0)
498 prob.new[16]<-ifelse(index.new[5]<0,1,0)
499 # neutral ONI
500 prob[17]<-ifelse(mu.new[7]<0,1,0)
501 prob.new[17]<-ifelse(index.new[7]<0,1,0)
502 # warm ONI
503 prob[18]<-ifelse(mu.new[13]<0,1,0)
504 prob.new[18]<-ifelse(index.new[13]<0,1,0)
505 # worst case
506 prob[19]<-ifelse(mu.new[12]<0,1,0)
507 prob.new[19]<-ifelse(index.new[12]<0,1,0)
508
509 }
510 "
511 # objects needed to fit the model and monitor variables of interest
512 # there's a trick here -- if is.na(survey) then make survey a big number to prevent
513 # division by zero during imputation procedure these will either be replaced
514 # by imputed values (summer surveys) or not used (winter surveys)
515 #
516
517 pred.matrix<-matrix(c(1,-1,-1,-1,-1,-1,
518 1,1,-1,-1,-1,-1,
519 1,-1,1,0,1,-1,
520 1,1,1,0,-1,-1,
521 1,-1,0,1,-1,-1,
522 1,1,0,1,-1,-1,
523 1,-1,-1,-1,1,0,
524 1,1,-1,-1,1,0,
525 1,-1,1,0,1,0,
526 1,1,1,0,1,0,
527 1,-1,0,1,1,0,
528 1,1,0,1,1,0,
529 1,-1,-1,-1,0,1,
530 1,1,-1,-1,0,1,
531 1,-1,1,0,0,1,
532 1,1,1,0,0,1,
533 1,-1,0,1,0,1,
534 1,1,0,1,0,1),nrow=18,ncol=6,byrow=TRUE)
535 hr.data<-list(index=as.vector(junk$index),
536 survey;ifelse(is.na(junk$survey),1E12,junk$survey),
537 catch=junk$catch,
538 gssmu=junk$gSSMU,
539 oniclass=as.numeric(factor(junk$oni.class)),
```

```

540 samclass=as.numeric(factor(junk$sam.sign)),
541 summer=junk$survey[junk$season=="S"],
542 impute.me=ifelse(is.na(junk$survey)&junk$season=="S",1,0),
543 meanlogsummer=tapply(log(junk$survey[junk$season=="S"]),
544 list(junk$gSSMU[junk$season=="S"],junk$sam.sign[junk$season=="S"])),
545 mean,na.rm=TRUE),
546 sdlogsummer=sd(log(junk$survey[junk$season=="S"]),na.rm=TRUE),
547 nobs=dim(junk)[1],
548 nsummerobs=as.vector(table(junk$season)[1]),
549 predX=pred.matrix)
550
551 #Plot the input
552
553 plot(as.vector(junk$index))
554 plot(ifelse(is.na(junk$survey),1E12,junk$survey))
555 plot(junk$catch)
556 plot(junk$gSSMU)
557 plot(as.numeric(factor(junk$oni.class)))
558 plot(as.numeric(factor(junk$sam.sign)))
559 plot(junk$survey[junk$season=="S"])
560 plot(ifelse(is.na(junk$survey)&junk$season=="S",1,0))
561 plot(tapply(log(junk$survey[junk$season=="S"]),list(junk$gSSMU[junk$season=="S"],
562 junk$sam.sign[junk$season=="S"]),
563 mean,na.rm=TRUE))
564 plot(sd(log(junk$survey[junk$season=="S"]),na.rm=TRUE))
565 plot(dim(junk)[1])
566 plot(as.vector(table(junk$season)[1]))
567
568 hr.params<-c("beta","milogsummer","sigmalogsummer","sd.index","t.sd.index")
569
570 beta.init1<-rep(-1,6)
571 beta.init2<-rep(0,6)
572 beta.init3<-rep(1,6)
573
574
575 hr.inits<-list(list(beta=beta.init1,t.sd.index=0.1,.RNG.seed=123,
576 .RNG.name="base::Super-Duper"),
577 list(beta=beta.init2,t.sd.index=1.0,.RNG.seed=456,
578 .RNG.name="base::Super-Duper"),
579 list(beta=beta.init3,t.sd.index=1.9,.RNG.seed=789,
580 .RNG.name="base::Super-Duper"))
581
582 hr.derived<-c("index.new","mu.new","prob","prob.new")
583
584 hr.imputed<-"hr"
585
586 # write out the input (to check how we are doing)
587 write.csv(hr.data$index, file = "index.csv")
588 write.csv(hr.data$survey, file = "survey.csv")
589 write.csv(hr.data$catch, file = "catch.csv")
590 write.csv(hr.data$gssmu, file = "gssmu.csv")
591 write.csv(hr.data$oniclass, file = "oniclass.csv")
592 write.csv(hr.data$samclass, file = "samclass.csv")
593 write.csv(hr.data$summer, file = "summer.csv")
594 write.csv(hr.data$impute.me, file = "imputeme.csv")
595
596 write.csv(hr.data$meanlogsummer, file = "meanlogsummer.csv")
597 write.csv(hr.data$sdlogsummer, file = "sdlogsummer.csv")
598 write.csv(hr.data$nobs, file = "nobs.csv")
599 write.csv(hr.data$nsummerobs, file = "nsummerobs.csv")
600 write.csv(hr.data$predX, file = "predX.csv")
601
602
603 # now do the analysis
604
605 library(coda)
606 library(rjags)
607
608 hr.jags<-jags.model(textConnection(modelstring),hr.data,hr.inits,n.chains=3,
609 n.adapt=250000)
610 # burn in for 150000 iterations
611 update(hr.jags, n.iter=500000)
612 hr.params.post<-coda.samples(hr.jags,hr.params,n.iter=125000,thin=25)
613 hr.derived.post<-coda.samples(hr.jags,hr.derived,n.iter=125000,thin=25)
614 hr.imputed.post<-coda.samples(hr.jags,hr.imputed,n.iter=125000,thin=25)
615 hr.params.summ<-summary(hr.params.post)
616 hr.derived.summ<-summary(hr.derived.post)

```

```

617 hr.imputed.summ<-summary(hr.imputed.post)
618
619 # write input/output
620 # cat(capture.output(print(hr.params.post), file="hr_params_post.txt"))
621 sink("hr_params.txt")
622 print(hr.params.post)
623 sink()
624 sink("hr_derived.txt")
625 print(hr.derived.summ)
626 sink()
627 sink("hr_imputed.txt")
628 print(hr.imputed.summ)
629 sink()
630
631
632 require(ggmc)
633 hr.params.s<-ggs(hr.params.post)
634 hr.derived.s<-ggs(hr.derived.post)
635 #load in pre-processed mcmc objects to save time
636 # just want to copy hr.params.s to work with it for plotting diagnostics without screwing up the original object
637 # also get rid of chains for t.sd.index since this is not really a parameter of interest
638 HR.labels<-data.frame(Parameter=dimnames(hr.params.post[[1]])[[2]],
639   Label=c("alpha","beta[3]","beta[4]","beta[5]","beta[1]",
640         "beta[2]","K[B,-]","K[D,-]","K[B,+]","K[D,+]",
641         "sigma","phi","exclude"))
642
643 hr.params2.s<-ggs(hr.params.post,par_labels = HR.labels)
644 hr.params2.s<-hr.params2.s[hr.params2.s$ParameterOriginal!="t.sd.index",]
645
646 ggmc(hr.params.s,file="diagnostics_hr_params_final.pdf")
647 ggmc(hr.derived.s,file="diagnostics_hr_derived_final.pdf")
648
649 # plot posterior expectations of marginal effects
650
651 # Figure 2
652
653 # reference (best case)
654 boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(as.numeric(hr.derived.s$Parameter)==19),
655   range=0,ylim=c(-2,2),xaxt="n",xlim=c(0.5,7.5),ylab="expected performance",whisklty=1,boxwex=1,at=1)
656 # ONI
657 boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(is.element(as.numeric(hr.derived.s$Parameter),c(25,31))),
658   range=0,xaxt="n",yaxt="n",whisklty=1,boxwex=0.5,add=TRUE,at=2:3,col="gray80")
659 # biomass
660 boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(as.numeric(hr.derived.s$Parameter)==20),
661   range=0,xaxt="n",yaxt="n",whisklty=1,boxwex=1,add=TRUE,at=4,col="gray40",medcol="white")
662 # harvest rate
663 boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(is.element(as.numeric(hr.derived.s$Parameter),c(21,23))),
664   range=0,yaxt="n",xaxt="n",whisklty=1,boxwex=0.5,add=TRUE,at=5:6,col="black",medcol="white")
665 # worst case with PARAMETER 36 chosen - so with "warm" ONI. Should be (hr.derived.s$Parameter)==12
666 boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(as.numeric(hr.derived.s$Parameter)==36),
667   range=0,xaxt="n",yaxt="n",whisklty=1,boxwex=1,add=TRUE,at=7)
668 axis(1,at=1:7,labels=c("reference","-0.5 < ONI < 0.5","ONI >= 0.5","LKB > 1 Mt","0.01 < LHR < 0.10","LHR >= 0.10","worst case"))
669 abline(h=mean(hr.derived.s$value[as.numeric(hr.derived.s$Parameter)==19]),lty=2)
670 abline(h=0)
671
672 write.csv(hr.derived.s, file = "hr_derived_s.csv")
673 # # Added by me - plot all cases*
674 # # reference (best case)
675 boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(as.numeric(hr.derived.s$Parameter)==19),
676   range=0,ylim=c(-2,2),xaxt="n",xlim=c(0.5,18.5),ylab="expected performance",whisklty=1,boxwex=1,at=1)
677
678 boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(is.element(as.numeric(hr.derived.s$Parameter),c(20:36))),
679   range=0,xaxt="n",yaxt="n",whisklty=1,boxwex=0.5,add=TRUE,at=2:18,col="gray80")
680
681 axis(1,at=1:18,labels=c("1","2","3","4","5","6","7","8","9","10","11","12","13","14","15","16","17","18"))
682 abline(h=mean(hr.derived.s$value[as.numeric(hr.derived.s$Parameter)==19]),lty=2)
683 abline(h=0)
684
685 # Supplementary Figures
686
687 # S1 -- trace plots of main model parameters
688 ggs_traceplot(hr.params2.s) + facet_wrap(~ Parameter, ncol = 3, scales="free")
689
690 # S2 -- scale-reduction factors
691 ggs_Rhat(hr.params2.s)
692
693 # S3 -- Geweke Z-scores

```

```

694 ggs_geweke(hr.params2.s,shadow_limit = 1.96)
695
696 # S4 -- autocorrelation plots
697 ggs_autocorrelation(hr.params2.s)
698
699 # S5 -- crosscorrelations
700 ggs_crosscorrelation(hr.params2.s)
701 #hr.params2.s<-ggs(hr.params.post)
702 #hr.params2.s<-hr.params2.s[hr.params2.s$Parameter!="t.sd.index",]
703 #ggs_pairs(hr.params2.s,lower=list(continuous="density"))
704
705 # S6 -- posterior distributions
706 ggs_histogram(hr.params2.s) + facet_wrap(~ Parameter, ncol = 3, scales="free")
707 #ggs_density(hr.params2.s) + facet_wrap(~ Parameter, ncol = 3, scales="free")
708
709 # S7 -- plot posterior predictive distributions over data for visual posterior predictive check
710 xx<-junk
711 xx$impute.me<-ifelse(is.na(xx$survey) & xx$season=="S",1,0)
712 xx$imputed.hr<-hr.imputed.summ$statistics[,1]
713 xx$survey<-xx$impute.me==1<-xx$catch[xx$impute.me==1]/xx$imputed.hr[xx$impute.me==1]
714 xx$hr.class<-ifelse(xx$catch/xx$survey<=0.01,1,ifelse(xx$catch/xx$survey>=0.1,3,2))
715 xx$kb.class<-ifelse(xx$survey<=1000000,1,2)
716 xx$oni.class<-as.numeric(factor(xx$oni.class))
717 xx$case<-ifelse(xx$oni.class==1 & xx$kb.class==1 & xx$hr.class==1,1,
718 ifelse(xx$oni.class==1 & xx$kb.class==2 & xx$hr.class==1,2,
719 ifelse(xx$oni.class==1 & xx$kb.class==1 & xx$hr.class==2,3,
720 ifelse(xx$oni.class==1 & xx$kb.class==2 & xx$hr.class==2,4,
721 ifelse(xx$oni.class==1 & xx$kb.class==1 & xx$hr.class==3,5,
722 ifelse(xx$oni.class==1 & xx$kb.class==2 & xx$hr.class==3,6,
723 ifelse(xx$oni.class==2 & xx$kb.class==1 & xx$hr.class==1,7,
724 ifelse(xx$oni.class==2 & xx$kb.class==2 & xx$hr.class==1,8,
725 ifelse(xx$oni.class==2 & xx$kb.class==1 & xx$hr.class==2,9,
726 ifelse(xx$oni.class==2 & xx$kb.class==2 & xx$hr.class==2,10,
727 ifelse(xx$oni.class==2 & xx$kb.class==1 & xx$hr.class==3,11,
728 ifelse(xx$oni.class==2 & xx$kb.class==2 & xx$hr.class==3,12,
729 ifelse(xx$oni.class==3 & xx$kb.class==1 & xx$hr.class==1,13,
730 ifelse(xx$oni.class==3 & xx$kb.class==2 & xx$hr.class==1,14,
731 ifelse(xx$oni.class==3 & xx$kb.class==1 & xx$hr.class==2,15,
732 ifelse(xx$oni.class==3 & xx$kb.class==2 & xx$hr.class==2,16,
733 ifelse(xx$oni.class==3 & xx$kb.class==3 & xx$hr.class==1,17,
734 # plot the data
735 plot(jitter(xx$case[xx$impute.me==0],amount=0.25),xx$index[xx$impute.me==0],type="n",xlim=c(0.65,18.35),
736 ylim=c(-3.5,3.5),
737 xlab="case",xaxt="n",ylab="std performance index",pch=16)
738 # add posterior predictive distributions as box plots
739 for(i in 1:18){
740   boxplot(value~I(as.numeric(Parameter)),data=hr.derived.s,subset=(as.numeric(hr.derived.s$Parameter)==i),
741   range=1.5,outline=FALSE,xaxt="n",whisklty=1,boxwex=1,at=i,add=TRUE)
742 }
743 # plot the data
744 points(jitter(xx$case[xx$impute.me==0&xx$season=="S"],amount=0.2),xx$index[xx$impute.me==0&xx$season=="S"],
745 cex=0.5,col="red",pch=16)
746 points(jitter(xx$case[xx$impute.me==0&xx$season=="W"],amount=0.2),xx$index[xx$impute.me==0&xx$season=="W"],
747 cex=0.5,col="blue",pch=16)
748 points(jitter(xx$case[xx$impute.me==1],amount=0.2),xx$index[xx$impute.me==1],cex=0.5,col="red")
749 axis(1,at=1:18)
750 abline(h=0)
751
752 # misc stuff
753
754 junk2<-make.localhr.data(plot.winter=TRUE)
755 junk2$impute.me<-ifelse(is.na(junk2$survey)&junk2$season=="S",1,0)
756 junk2$imputed<-exp(ifelse(junk2$impute.me==0,NA,ifelse(junk2$gSSMU==1&junk2$sam.sign=="Neg",
757 hr.params.summ$statistics[7,1],
758 ifelse(junk2$gSSMU==2&junk2$sam.sign=="Neg",hr.params.summ$statistics[8,1],
759 ifelse(junk2$gSSMU==1&junk2$sam.sign=="Pos",hr.params.summ$statistics[9,1],
760 hr.params.summ$statistics[10,1]))))
761
762 library(lattice)
763 # plot the time series
764 xyplot(index~cal.yr|season,data=junk2,horizontal=FALSE,aspect=0.25,panel=function(x,y,subscripts,...,Z=junk2$survey,IMP=junk2$imputed){
765 z<-(Z[subscripts]-mean(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE))/sd(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE)
766 imp<-(IMP[subscripts]-mean(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE))/sd(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE)
767 panel.xyplot(x,y,...,pch=16,col="black")
768 panel.points(as.numeric(x),z,col="red",pch=16,cex=1.25)
769 panel.points(as.numeric(x),imp,col="red",pch=1,cex=1.25)
770 panel.abline(h=0,lty=2)},
```

```

771 ylim=c(-3.5,4.5),layout=c(1,2),xlab="year",ylab="std monitoring index")
772
773 # plot the time series with env indices (panel for Fig 1)
774 xyplot(index~cal.yr|season+PROJECT,data=junk2,horizontal=FALSE,aspect=0.5,panel=function(x,y,subscripts,...,Z=junk2$survey,
775 IMP=junk2$imputed,ONI=junk2$oni,SAM=junk2$sam){
776 z<-(Z[subscripts]-mean(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE))/sd(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE)
777 imp<-(IMP[subscripts]-mean(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE))/sd(c(Z[subscripts],IMP[subscripts]),na.rm=TRUE)
778 panel.xyplot(x,y,...,pch=16,col="black")
779 panel.points(as.numeric(x),z,col="red",pch=16,cex=1.25)
780 panel.points(as.numeric(x),imp,col="red",pch=1,cex=1.25)
781 tt.oni<-data.frame(as.numeric(x),ONI[subscripts])
782 tt.oni<-tt.oni[order(tt.oni[,1]),]
783 panel.lines(tt.oni[,1],tt.oni[,2],col="blue")
784 tt.sam<-data.frame(as.numeric(x),SAM[subscripts])
785 tt.sam<-tt.sam[order(tt.sam[,1]),]
786 panel.lines(tt.sam[,1],tt.sam[,2],col="dark green")
787 panel.abline(h=0,lyt=2),
788 ylim=c(-3.5,4.5),layout=c(2,2),xlab="year",ylab="index")
789
790
791 # some stuff to tablulate local harvest rates by year (including imputed estimates)
792
793 junk$impute.me<-ifelse(is.na(junk$survey)&junk$season=="S",1,0)
794 junk$survey<-ifelse(junk$impute.me==0,junk$survey,exp(ifelse(junk$gSSMU==1&junk$sam.sign=="Neg",
795 hr.params.summ$statistics[7,1],
796 ifelse(junk$gSSMU==2&junk$sam.sign=="Neg",hr.params.summ$statistics[8,1],
797 ifelse(junk$gSSMU==1&junk$sam.sign=="Pos",hr.params.summ$statistics[9,1],
798 hr.params.summ$statistics[10,1]))))
799 junk$hr<-junk$catch/junk$survey
800 junk$hihr<-(junk$hr>=0.10)
801
802 # table for supplementary info
803 jj<-unique(junk[,c(7,8,6,11,17,16)])
804 names(jj)<-c("calendar.year","stratum","season","catch","LHR","imputed")
805 jj$stratum<-ifelse(jj$stratum==1,"Bransfield","Drake")
806 jj$season<-ifelse(jj$season=="S","Summer","Winter")
807 jj$imputed<-ifelse(jj$imputed==1,"Yes","No")
808 # no catch data for 2016
809 jj<-jj[jj$calendar.year!=2016,]
810 write.csv(jj[order(jj[,1],jj[,2],jj[,3]),],file="hr.csv",row.names = FALSE)
811
812 # variation in catch by season and decade (panel for Fig 3)
813 tt<read.csv("c1.csv",header=TRUE,stringsAsFactors = FALSE)
814 tt<-tt[is.element(tt$AssignedSMU,c("APBSE","APBSW","APDPE","APDPW","APE","APEI","APPA","APW")),]
815 tt$FishingSeason<-ifelse(tt$Month==12,tt$CalendarYear+1,tt$CalendarYear)
816 tt$season<-ifelse(is.element(tt$Month,c(10:12,1:3)),"S","W")
817 tt$decade<-ifelse(tt$FishingSeason<1990,"before 1990",
818 ifelse(tt$FishingSeason>1989&tt$FishingSeason<2000,"1990-1999",
819 ifelse(tt$FishingSeason>1999&tt$FishingSeason<2010,"2000-2009","after 2009")))
820 tt$decade<-ordered(tt$decade,levels=c("before 1990","1990-1999","2000-2009","after 2009"))
821 tt<-tapply(tt$TotalCatch,list(tt$decade,tt$season),sum)
822 tt<-data.frame(catch=as.numeric(tt),decade=rep(dimnames(tt)[[1]],dim(tt)[2]),season=rep(dimnames(tt)[[2]],
823 each=dim(tt)[1]))
824 tt$decade<-ordered(tt$decade,levels=c("before 1990","1990-1999","2000-2009","after 2009"))
825 #
826 barchart(I(catch/1000)-season|decade,data=tt,layout=c(4,1),aspect=1,xlab="Season",ylab="Total catch (1000 t)")
```

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