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Total Abundance and Harvest Impacts on Eastern Hudson Bay and James Bay Beluga 2015–2022

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Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

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ABSTRACT

Belugas from the James Bay population (JAM) and Belcher Islands-Eastern Hudson Bay (BEL-EHB) stock are harvested by hunters from all Nunavik communities and the Nunavut community of Sanikiluaq. In 2020–2021, a total of 366 belugas were reported harvested by Nunavik hunters, including 41 animals harvested in the Long Island area. From those, an estimated 139 BEL-EHB animals were harvested. Another 19 BEL-EHB animals were harvested in Sanikiluaq. A population model fitted to a time series of 8 aerial survey estimates using Bayesian methods and taking into account removals by harvesters provided a 2021 abundance estimate of 16,700 belugas in James Bay and a range of 2,900–3,200 belugas in eastern Hudson Bay, depending on model assumptions. The James Bay population has levelled off since the last assessment, whereas the BEL-EHB stock is currently declining at a rate of 2.5% per year. A harvest of 190 belugas per year in James Bay, would result in a 50% probability of decline in the JAM population after 5 years. The Potential Biological Removal (PBR) for this population is 296 belugas. If a Precautionary Approach framework was used to manage beluga in James Bay, a range of 170–173 belugas could be harvested annually. For the BEL-EHB stock, two model runs were completed and harvests were evaluated against two benchmarks or thresholds over time frames of 5 and 10 years. Depending on model assumptions, benchmarks and timeframes, harvests should not exceed levels of 0–70 BEL-EHB belugas annually for the stock to remain above the benchmark abundance estimate. The PBR for this stock is 5 animals. Over a 50-year time period, if the annual harvest of beluga from the BEL-EHB stocks stays within 20–25 animals annually, then there is a high probability of staying above the precautionary reference level.

Key words: Beluga, *Delphinapterus leucas*, abundance, genetics, Nunavik, harvest

INTRODUCTION

Nearshore beluga (*Delphinapterus leucas*) surveys flown in 1978 and 1980 indicated that beluga abundance in eastern Hudson Bay might be as low as 160–250 individuals, much reduced from the 6,000–7,000 or more whales thought to have occupied the area prior to the high commercial harvests (1854 to 1868; Breton-Provencher 1980; Finley et al. 1982). In Ungava Bay, summer coastal surveys indicated even fewer animals with perhaps less than 50 individuals concentrated around the Mucalic River Estuary (Figures 1, 2; Finley et al. 1982). Subsequent surveys identified larger numbers of around 1,400 animals (not corrected for diving) in eastern Hudson Bay, while no animals were seen on transects in surveys of Ungava Bay (Smith and Hammill 1986). These relatively low estimates combined with high harvests, led to DFO establishing harvest quotas for beluga, as well as seasonal and area closures in the mid-1980s.

Since the signing of the [Nunavik Inuit Land Claim Agreement](#) (NILCA) in 2006, the beluga harvest in northern Quebec waters has been co-managed by the Wildlife Management Boards and Fisheries and Oceans Canada (DFO); the relevant Boards are the Nunavik Marine Region Wildlife Board in the NILCA region and jointly with the Eeyou Marine Region Wildlife Board in the areas where the land claims overlap. A new management plan recently approved by the Minister of DFO for 2021–2026, balances harvesting rights with conservation objectives as identified within the land-claim agreements. The management plan conservation objective is to maintain the population at or above the 2015 abundance estimate of 3,400 animals and that the probability of a decline due to harvesting must not exceed 50% (Hammill et al. 2017a, 2021). This objective is to be met through a combination of harvest limits in the southeastern Hudson Bay coastal area (referred to as “the Arc”), and seasonal closures in Hudson Strait and Ungava Bay.

An understanding of abundance and spatial distribution is essential for sustainable harvest management. If a species is abundant with individuals showing no strong pattern of home-range use or sub-structuring within the wider distribution of the stock, then all members of the population within the area are likely exposed to any harvesting events. However, if there is evidence of stock sub-structuring and site-fidelity patterns, then harvesting (or other perturbations) concentrated on one area might have a disproportionate impact on that component of the population (DeFur et al. 2007; Bonnell et al. 2022).

A complete re-analysis of the available genetic material was conducted to assess the structure of the beluga populations occurring in the Hudson Bay-Strait Complex (Parent et al. 2023). Five genetically distinct populations of beluga were identified: Western Hudson Bay (WHB), James Bay (JAM), EHB, Belcher Islands (BEL), and Cumberland Sound (CSB). The definition of these populations have been further supported by lines of evidence that individuals belonging to each population also show strong intra- and inter-annual summer site fidelity based on: behavioural observations and genetics (Caron and Smith 1990; Colbeck et al. 2013); telemetry (Richard and Stewart 2009; Bailleul et al. 2012), passive acoustic monitoring (Booy et al. 2021); genetic, isotopic and contaminants (Brennin et al. 1997; Brown Gladden et al. 1997, 1999; de March et al. 2002, 2004; de March and Postma 2003; Postma et al. 2012; Rioux et al. 2012; Turgeon et al. 2012; Colbeck et al. 2013). A sixth population, Ungava Bay, is acknowledged based on historical abundance data and for conservation (COSEWIC 2014), although it has not been characterized genetically due to a lack of samples (Parent et al. 2023). There is concern that loss of some population components, particularly older animals, will result in loss of ecological knowledge within groups, thereby limiting the potential for population recovery, as has been seen in some areas of Hudson and Ungava Bays and in the St. Lawrence Estuary beluga (Caron and Smith 1990; Colbeck et al 2013; O’Corry-Crowe et al. 2018, 2020; Ouellet et al 2021; Bonnell et al. 2022).

Of the six populations, two, (EHB and BEL) show strong overlap in summer distribution. Moreover, they share some haplotypes that are part of the eastern haplogroup which can cause misassignments between BEL and EHB populations (Parent et al. 2023). Grouping BEL and EHB populations into one genetic reference group defined as the BEL-EHB stock continues to distinguish animals from this summering area, reduces classification errors and their distribution is consistent with the zone covered by the summer eastern Hudson Bay aerial surveys (Parent et al. 2023; St-Pierre et al. 2023).

For the most part, belugas belonging to the different populations or stocks in the Hudson Bay-Strait complex overwinter in Hudson Strait and Ungava Bay, where they are harvested during fall, winter, and spring. Skin samples provided by hunters from their catches provide information on the proportion of the catch taken in the fall, winter, and spring hunts that belong to the different populations considered (de March and Postma 2003; Turgeon et al. 2012; Mosnier et al. 2017), and in particular the BEL-EHB stock identified in Parent et al. (2023). Currently, animals harvested from the JAM and WHB populations are reported and recorded. Harvest levels do not exceed sustainable levels for these populations (Hammill et al 2017a; the present study).

Since 1985, summer beluga abundance in eastern Hudson Bay and in James Bay has been monitored using aerial surveys (Gosselin et al. 2002, 2009, 2013, 2017). The survey in eastern Hudson Bay is flown from the coast to west of the Belcher Islands, and therefore is considered to inventory both the BEL and EHB populations (i.e., the BEL-EHB stock). Similarly, the survey in James Bay is considered to inventory the JAM population. A population model incorporating information on catch levels and stock composition has been fitted to aerial survey estimates to provide insights into abundance and trend. The model has also been used to provide harvest advice (Hammill et al. 2005; Doniol-Valcroze et al. 2012, 2013, 2014; Hammill et al. 2017a, 2021).

A new aerial survey covering James Bay and the summering area of the BEL-EHB stock was flown in summer 2021 (St-Pierre et al. 2023). The Ungava Bay area was not included, but a survey there is planned for 2022.

Here we incorporate information from the new aerial survey and genetic analyses into the population model to provide insight into the current status of the BEL-EHB stock and for the first time the status of the James Bay population (St-Pierre et al. 2023; Parent et al. 2023). Harvest levels respecting the current management objective are provided for the BEL-EHB and James Bay beluga populations. Harvest advice based on other potential management frameworks is also provided.

METHODS

The population model is fitted to the corrected time series of aerial survey abundance estimates (1985–2021), while incorporating reported harvest data (1974–2021) from each of the 14 communities in Nunavik and the Nunavut community of Sanikiluaq (Figure 1). It takes into account the proportion of animals from the BEL-EHB stock in the harvest, as determined by a genetic mixture analysis of samples provided by hunters (Hammill et al. 2017a; Mosnier et al. 2017; Parent et al. 2023; St-Pierre et al. 2023).

DATA INPUTS

Census data consist of eight visual systematic aerial surveys estimates flown in 1985, 1993, 2001, 2004, 2008, 2011, 2015 and 2021 (St-Pierre et al 2023). Belugas detected in estuaries were assumed to represent total counts and were added to the availability and perception bias-corrected estimates (Table 1). All surveys were flown along similar parallel line designs, but over time data collection and analyses have changed between surveys. Details on survey

methods and analyses are available in Smith and Hammill (1986), Kingsley (2000), Hammill et al. (2004), Gosselin et al. (2009, 2013, 2017) and St-Pierre et al. (2023).

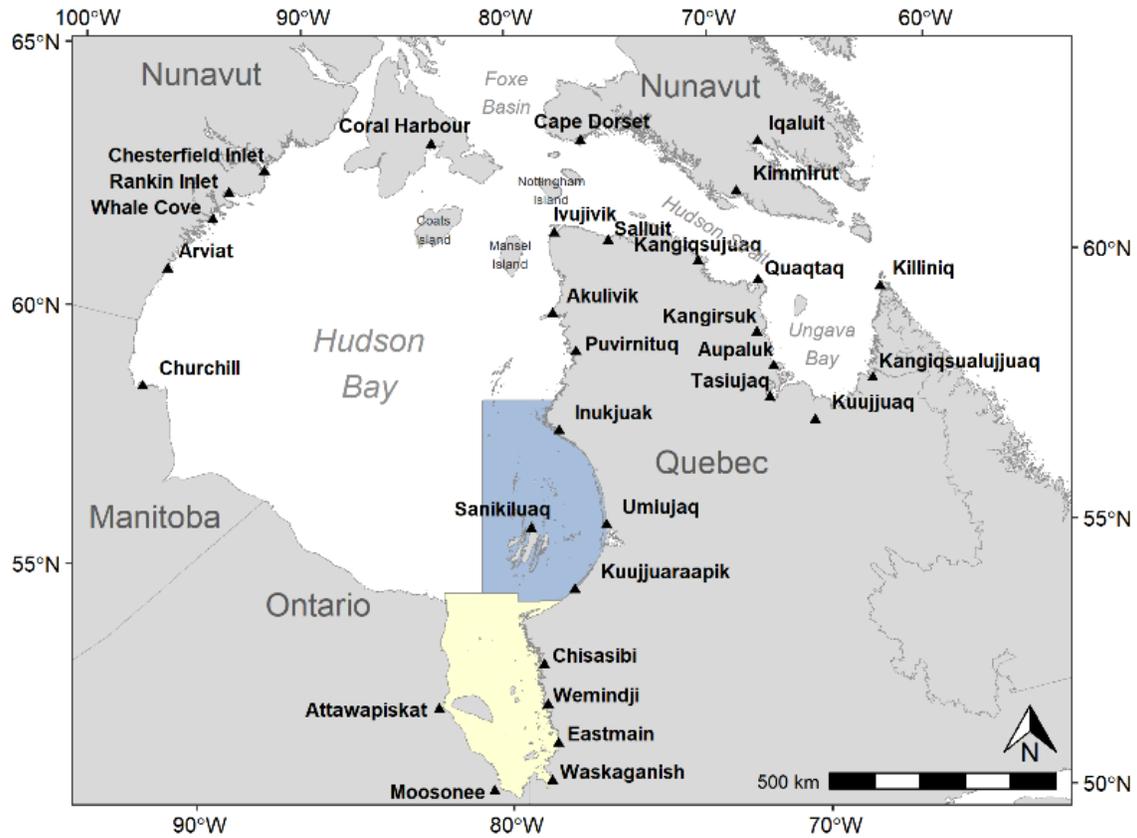


Figure 1. Map of the area of interest showing the summer area distribution of the BEL-EHB stock (blue) and James Bay population (yellow).

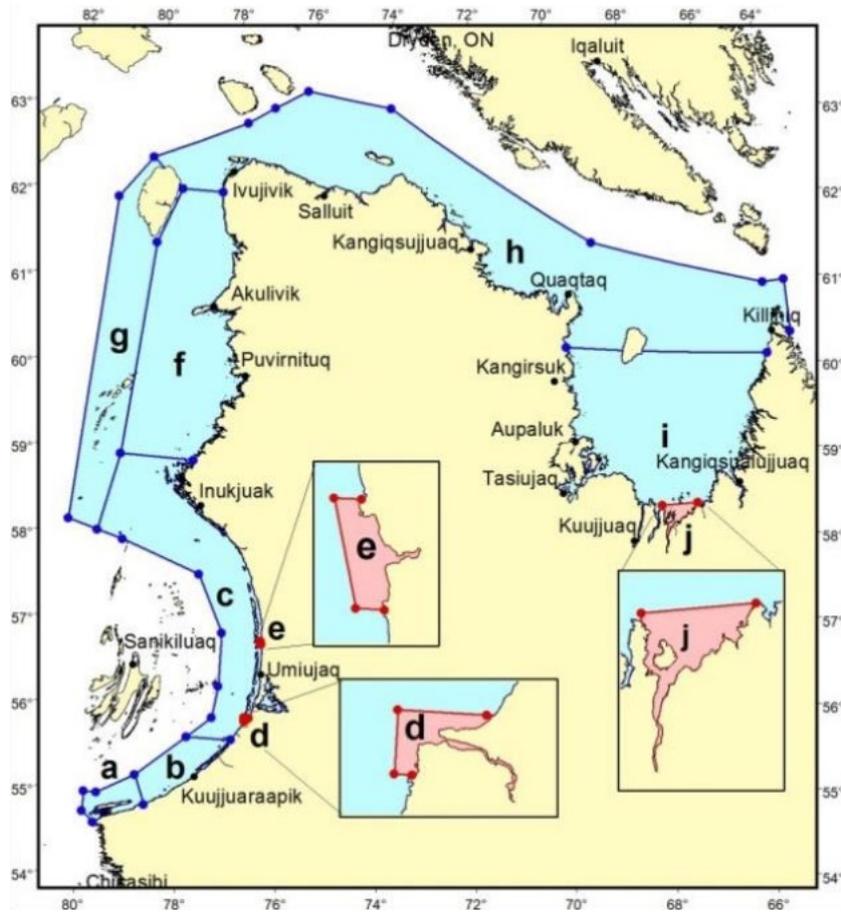


Figure 2. Map of hunt management areas in Nunavik. a: Long Island; b, c: Eastern Hudson Bay (BEL-EHB stock distribution), includes the offshore waters west of the Belcher Islands (Nunavut) which are not managed under the current management plan; Nunavut (this area is not managed under the current management plan; f, g: Northeastern Hudson Bay; h: Hudson Strait; i: Ungava Bay. Areas d, e and j (Little Whale, Nastapoka and Mucalic River Estuaries) are closed areas.

Table 1. Abundance estimates from aerial surveys for the BEL-EHB stock, Western Hudson Bay (WHB), James Bay (JAM) and Ungava Bay (UNG) beluga populations. Indices were corrected for availability and perception bias (Matthews et al. 2017; St-Pierre et al 2023). Belugas were seen in Ungava Bay, but none on transect. The estimated abundance is 32 (95% CI=0-94) (Doniol-Valcroze and Hammill 2012). "NF" represents no survey flown.

Year	BEL-EHB (SE)	WHB (SE)	JAM (SE)	UNG
1985	6,711 (1,936)	NF	6,511 (1,842)	*
1987	NF	31,124 (6,967)	NF	NF
1993	4,163 (1,760)	NF	12,811 (3,569)	*
2001	4,570 (2,265)	NF	28,242 (7,971)	*
2004	7,368 (2,899)	51,761 (15,875)	14,021 (4,667)	NF
2008	4,764 (1,404)	NF	39,152 (27,296)	*
2011	5,001 (2,350)	NF	23,324 (7768)	NF
2015	7,841 (3,687)	54,473 (5,329)	21,860 (6,126)	NF
2021	2,501 (719)	-	14,213 (3,187)	NF

In Nunavik, harvest information is collected weekly from each community via the network of wardens (1974–2021) and from Sanikiluaq (1977–2022) at the end of the season and grouped according to season and management area where harvesting occurs (Lesage et al. 2009; Figure 2; Appendix A, Table A1). The estimated harvests of animals belonging to the BEL-EHB stock were determined using a genetic mixture analysis (Table 2; Parent et al. 2023). The proportion of animals from the BEL-EHB stock in the Hudson Strait harvests was similar or slightly higher than levels reported in previous assessments. However, the proportion of the BEL-EHB stock harvested in the Sanikiluaq area (Table 2) was much higher than in previous assessments (see Appendix A, Table A2). The harvests from the James Bay population were comprised of animals harvested in the Long Island area. All belugas harvested directly in the Arc area (outlined in Figures 1 and 2) during the summer belonged to the BEL-EHB stock. Estimated removals of animals from the BEL-EHB stock based on the proportions used in the last meeting are found in Appendix A (Tables A1, A2).

Table 2. Proportion of BEL-EHB animals taken in the different management areas in the waters around northern Quebec and in Nunavut (Sanikiluaq) as shown in Figures 1 and 2 (Parent et al. 2023). N_{samp} : number of individual samples; N_{event} : number of different hunting dates. The Hudson Strait Pilot Project results were based on animals harvested in the Hudson Strait and collected after: Nov. 1 in Ivujivik, Nov. 5 in Salluit, Nov. 10 in Kangiqsujaq and Nov. 15 in Quaqtaq. 95CI = 95% Credibility interval. Nunavik Management areas

Season	N_{samp}	N_{event}	Mean proportion BEL-EHB	Lower 95CI	Higher 95CI
Spring					
Hudson Strait	824	364	0.12	0.086	0.165
NE Hudson Bay	2	1	-	-	-
Ungava Bay	143	87	0.05	0.008	0.118
Fall					
Hudson Strait	512	202	0.44	0.351	0.53
NE Hudson Bay	45	19	0.50	0.239	0.762
Ungava Bay	6	6	-	-	-
Hudson Strait Pilot Project	43	10	0.22	0.088	0.383
Sanikiluaq (Nunavut)					
Season	N_{samp}	N_{event}	Mean proportion BEL-EHB	Lower 95CI	Higher 95CI
Spring	229	99	0.63	0.515	0.734
Fall	49	35	0.61	0.351	0.839
Winter	76	11	0.40	0.130	0.7082

POPULATION MODEL

A stochastic stock-production model was fitted using Bayesian methods to estimate current abundance and evaluate the impact of different harvest levels on future population trend (Doniol-Valcroze et al. 2013; Hammill et al. 2017a). Observation error (associated with data collection and abundance estimation) was separated from the process error (arising from natural variability in population dynamics) using a hierarchical state-space model that considers survey data to be the outcome of two distinct stochastic processes: a state process and an observation process (de Valpine and Hastings 2002).

The state process describes the underlying population dynamics and the evolution of the true stock size over time, using a discrete formulation of the Pella-Tomlinson model (Pella and

Tomlinson 1969; Innes and Stewart 2002) modified to allow the process error to have either positive or negative impact on the growth rate:

$$N_t = N_{t-1} \cdot (1 + (\lambda_{max} - 1) \cdot [1 - (N_{t-1}/K)^\theta]) \cdot \varepsilon_{pt} - R_t$$

with $\varepsilon_{pt} \sim \log N(0, \tau_p)$

and $R_t = C_t \cdot (1 + SL)$

where N is the abundance at time t or $t-1$, λ_{max} is the maximum rate of increase, K is the environmental carrying capacity and theta (θ) defines the shape of the density-dependent function. The process error (ε_{pt}) was given a lognormal distribution, with a mean of 1, while the precision of the process error (τ_p), followed a gamma distribution. Removals (R_t) were calculated in adjusting reported catches (C_t) of whales for struck and loss (SL , i.e., the proportion of animals that were wounded or killed but not recovered), as well as non-reported catches.

The observation process describes the relationship between true population size (N_t) and observed data (Survey estimates, S_t). In our model, this relationship was assumed to follow a gamma distribution considering an error term ε_{St} corresponding to the precision of the survey estimate.

$$S_t \sim \Gamma(\alpha, \beta)$$

with $\alpha = N_t \cdot \beta$

and $\beta = N_t \cdot \varepsilon_{St}$

PRIORS

Existing information, traditional knowledge and expert opinions were used to formulate prior distributions for the random variables included in the model (Table 3). Beginning with the BEL-EHB stock, the initial population size was given a uniform prior between 2,000 and 15,000 individuals. The lower bound reflects observations of at least a few hundred belugas in the EHB estuaries, but recognizes that the population had been reduced considerably from pristine sizes (Smith and Hammill 1986; Reeves and Mitchell 1987). Doniol-Valcroze et al. (2012b), estimated a pristine population of around 8,000 (95% CI 7,200–8,700) assuming no losses during the commercial hunt. This estimate does not take into account the subsistence hunt. For K , a range of 5,000 to 20,000 was used. The upper bound encompassed the possible range of estimates of pristine population size, including if struck and loss rates were as high as 2, and would likely account for subsistence harvests at the time as well (Hammill et al. 2005; Doniol-Valcroze et al. 2012, 2013). The maximum rate of population increase is not known, but most studies have suggested a median estimate around 4%, with a range of 2–8% (Béland et al. 1988; Alvarez-Flores and Heide-Jørgensen 2004; Hobbs et al. 2006; Lowry et al. 2008; Doniol-Valcroze et al. 2012, 2013). We used a prior with a Beta distribution with a range of 0.02 to 0.06. Theta (θ) defines the point of maximum net productivity, which for marine mammals is generally considered to occur at 60% of carrying capacity, which results in a θ value of 2.39 (Taylor and DeMaster 1993; Butterworth et al. 2002; Hobbs et al. 2006).

Reported harvests underestimate the number of belugas killed because of animals wounded or killed but not recovered, as well as under-reporting. The struck and loss (SL) rates in Nunavik hunts are not known but studies from elsewhere indicate that they range from around 18 to 66%, the latter for deep-water hunting, e.g., along ice edges (Seaman and Burns 1981; Hobbs et al. 2006; Richard 2008). Heide-Jørgensen and Rosing-Asvid (2002) calculated a SL factor of 0.29 for Greenland, not including unreported catches. Innes and Stewart (2002) estimated a correction factor that accounted for SL and unreported whales in Baffin Bay at 0.41 whale per

whale landed. Richard (2008) estimated SL rates of 18% (CV = 6%). In previous assessments, a moderately informative prior following a Beta (3, 4) distribution with a median of 0.42 and quartile points at 0.29 and 0.55 was used (Doniol-Valcroze et al. 2013; Hammill et al. 2021). However, during public consultations, hunters felt that this rate was too high. Therefore, in this assessment SL was given a moderately informative prior following a Beta (1.135 / 2.763), which resulted in quantiles 0.025, 0.25, 0.5, 0.75 and 0.975, of 0.015, 0.123, 0.253, 0.426, and 0.753.

The stochastic process error terms (ε_{pt}) were given a log-normal distribution with a zero location parameter. The precision parameter for this log-normal distribution was assigned a moderately informative prior following a bounded gamma (1.5, 0.005) distribution. These parameters resulted in coefficients of variation (CV) with quantiles of .033, .049, .065, .091, and .218.

The proportions of animals from the BEL-EHB stock harvested in each management area (identified in Table 2) are incorporated into the model as probabilities (Table 3). Because the genetic mixing model assumes a multivariate Dirichlet distribution, the genetic priors for each stock proportion assumed a Beta distribution, with known mean and standard error, but for which the α and β parameters are not available. We solved the system of equations for the mean and variance of a Beta distribution to determine the values of α and β that describe the observed distributions. The Beta distributions were then used as priors for the proportions of animals from the BEL-EHB stock in the various hunts that vary spatially and temporally (Table 3). The model was run using 5 chains, with 60,000 runs, a burn-in phase of 25,000 iterations and a thinning of 50.

We obtained posterior estimates of all parameters using a Gibbs sampler algorithm implemented in JAGS (Plummer 2003). Results including mixing of the chains and convergence were also examined (Doniol-Valcroze et al. 2014; Hammill et al. 2017a). We tested for mixing of the chains using Geweke's test of similarity between different parts of each chain (Geweke 1996). The Brooks-Gelman-Rubin (BGR) diagnostic, which compares the width of the 80% credible interval of pooled chains with the mean of widths of the 80% credible interval of individual chains, was assessed for convergence between chains (Brooks and Gelman 1998).

Table 3a) Prior distributions, parameters, and hyper-parameters used in the Nunavik beluga population model BEL-EHB = Belcher-Eastern Hudson Bay stock, JAM = James Bay population. Prior median and 0.025 and 0.975 quantiles are shown.

.Parameters	Notation	Prior distribution	Hyper-parameters	Parameter value	Prior median	0.025	0.975
Survey precision (t)	ε_{st}	Fixed		$1 / (\text{Survey standard error})^2$	-	-	-
Process error (t)	ε_{pt}	Log-normal	μ_p / τ_p	0 / estimated	$1 / \text{inf}$	0	inf
Precision (Process)	τ_p	Gamma	α_p / β_p	1.5 / 0.005	236.6	21.6	934.8
Theta	θ	Fixed	-	-	2.39	-	-
Struck and loss 25%	SL	Beta	α_{sl} / β_{sl}	1.135 / 2.763	0.25	0.015	0.755
Initial population (BEL-EHB)	Start	Uniform	Nupp / Nlow	15,000 / 2,000	8,500	2,325	14,675
Carrying capacity (BEL-EHB)	K	Uniform	Nupp / Nlow	20,000 / 5,000	12,500	5,375	19,625
Initial population (JAM)	Start	Uniform	Nupp / Nlow	40,000 / 2,000	21,000	2,950	39,050
Carrying capacity (JAM)	K	Uniform	Nupp / Nlow	40,000 / 5,000	22,500	5,875	39,125
Maximum rate of increase	λ_{max}	Beta	α_{sl} / β_{sl}	15.618 / 373.015	0.039	0.023	0.062

Table 3b) Prior distributions used in the population model for the proportion of BEL-EHB animals harvested in Nunavik and Nunavut, by region. For each sub-region and season, the priors for the proportion of BEL-EHB belugas in the harvest are given. HSUB = prior to 2009 most samples were from the Hudson Strait-Ungava Bay area from the fall but harvest area is not known. These are assigned the same parameters as PHS_F. Prior median and 0.025 and 0.975 quantiles are shown.

Nunavut

Parameters	Notation	Prior distribution	Hyper-parameters	Parameter value	Prior median	0.025	0.975
Sanikiluaq (Spring)	PSAN_S	Beta	$\alpha_{san} / \beta_{san}$	45.778 / 27.164	0.629	0.515	0.734
Sanikiluaq (Fall)	PSAN_F	Beta	$\alpha_{san} / \beta_{san}$	8.194 / 5.323	0.6113	0.344	0.837
Sanikiluaq (Winter)	PSAN_W	Beta	$\alpha_{san} / \beta_{san}$	3.697 / 5.493	0.396	0.131	0.7151
Sanikiluaq (Summer)	PSAN_SU	Fixed	-	-	1	-	-

Nunavik

Parameters	Notation	Prior distribution	Hyper-parameters	Parameter value	Prior median	0.025	0.975
Hudson Strait (Spring)	PHS_S	Beta	$A_{hs_sp} / \beta_{hs_sp}$	32.11 / 229.09	0.122	0.086	0.165
Hudson Strait (Fall)	PHS_F	Beta	A_{hs_f} / β_{hs_f}	50.58 / 64.36	0.44	0.351	0.532
HSUB *	PHSF	Beta	α_{hs} / β_{hs}	50.58 / 64.36	0.44	0.351	0.532
Ungava Bay (Spring)	PUB_S	Beta	$\alpha_{ub_s} / \beta_{ub_s}$	3.13 / 57.43	0.047	0.015	0.12
Ungava Bay (Fall, used HS Fall)	PUB_F	Beta	A_{ub_f} / β_{ub_f}	50.58 / 64.36	0.44	0.351	0.532
Northeast Hudson Bay (used HS spring)	PNEHB_S	Beta	$A_{nehb_s} / \beta_{nehb_s}$	32.11 / 229.09	0.122	0.086	0.165
Northeast Hudson Bay (Fall)	PNEHB_F	Beta	$A_{nehb_f} / \beta_{nehb_f}$	6.228 / 6.20281	0.50	0.24	0.762

MANAGEMENT FRAMEWORKS

Sustainable Yield (SY)

The management objective for BEL-EHB stock is to maintain a stable abundance at or above the 2015 abundance estimate of 3,400 animals, where for a given harvest, the probability of a decline in abundance does not exceed 50% (Hammill et al 2017a, 2021). However, this objective does not provide a buffer for uncertainty in the assessment, population dynamics, or environmental conditions. It also does not define harvest levels or reference points associated with management actions ensuring that the population remains in or returns to a healthy state. Here, we present three precautionary approach frameworks and harvest levels that could be sustained using these approaches.

The Potential Biological Removal (PBR) is estimated using the equation:

$$PBR = 0,5 R_{max} \times FR \times N_{min}$$

where R_{max} is the maximum rate of population increase (set to cetacean default value of 0.04), FR is a recovery factor (between 0.1 and 1), and N_{min} is the estimated population size using the 20th percentile of the log-normal distribution (Wade 1998). The implicit management objective of the PBR approach is to identify harvest levels that have a 95% probability of the population being above the Maximum Net Productivity Level, defined as 50% of carrying capacity over a period of 100 years (Wade 1998).

DFO-Maximum Sustainable Yield (DFO-MSY)

The general DFO-MSY framework identifies a Limit Reference Level (LRL) and a Precautionary Reference Level (PRL), which define three zones of resource concern (Figure 3; DFO 2006, 2013). The objective using this framework is to manage the removal rate so that the population remains in the Healthy zone. A stock is considered healthy if there is at least a 50% probability that it is above the PRL. It is considered critical if there is a 50% probability that it lies below the

LRL. A stock is considered to be in the Cautious zone if its abundance lies between the LRL and PRL (Hammill et al. 2017b). This framework is based on the concept of maximum sustainable yield (MSY). For marine mammals, the PRL would be set at 80% of MSY, which occurs at 60% of estimated carrying capacity. The LRL and the PRL are calculated as 24% and 48% of K respectively.

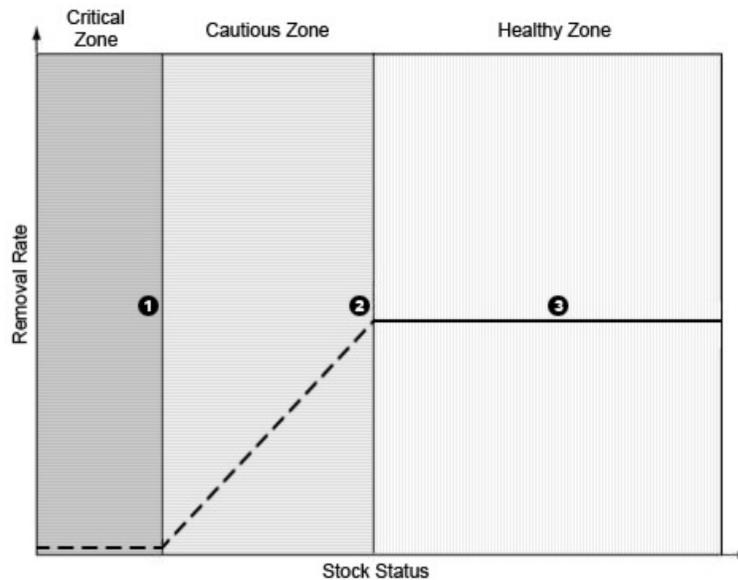


Figure 3. Suggested Precautionary Approach framework for fisheries in Canada. 1. The Limit Reference level (LRL). 2. The Precautionary Preference Level (PRL). 3. A removal rate identified to maintain the resource within the Healthy zone (DFO 2006).

DFO-Atlantic Seal Management (DFO-ASM)

The DFO-ASM framework is similar to the MSY framework, with a PRL, and a LRL and three zones of resource concern (Critical, Cautious and Healthy; Figure 3). However, in the DFO-ASM framework, the PRL is set at 70% of the highest population observed (N_{max}) from a survey or model estimate. The LRL is set at 30% of N_{max} . The management objective is to maintain a 95% probability that the population is above the LRL and 80% probability that the population is above the PRL (Hammill and Stenson 2003, 2007, 2009, 2013; Stenson et al. 2012).

Throughout this document, numbers greater than 1,000 are presented in the tables, but are rounded to the nearest 100 in the text.

RESULTS

HARVEST

A total of 366 belugas were reported harvested by Nunavik hunters, including 41 animals from the Long Island area during the 2021-22 season (Figure 4). Another 30 animals were reported harvested in Sanikiluaq, Nunavut (Figure 2). The 2021 harvest was close to the annual average of 344 animals taken over the last five years (Appendix A, Tables A1, A2). In a previous assessment it had been recognized that there were some genetic differences among animals harvested in the Sanikiluaq area, but these animals had not been grouped with the EHB animals (Hammill et al. 2017a). Using the proportions of EHB belugas in the catches from the last assessment, an estimated 112 EHB belugas were harvested, including one in Sanikiluaq (Figure 4; Hammill et al. 2021). The number of harvested EHB belugas is above the 5-year average of 89 belugas/year.

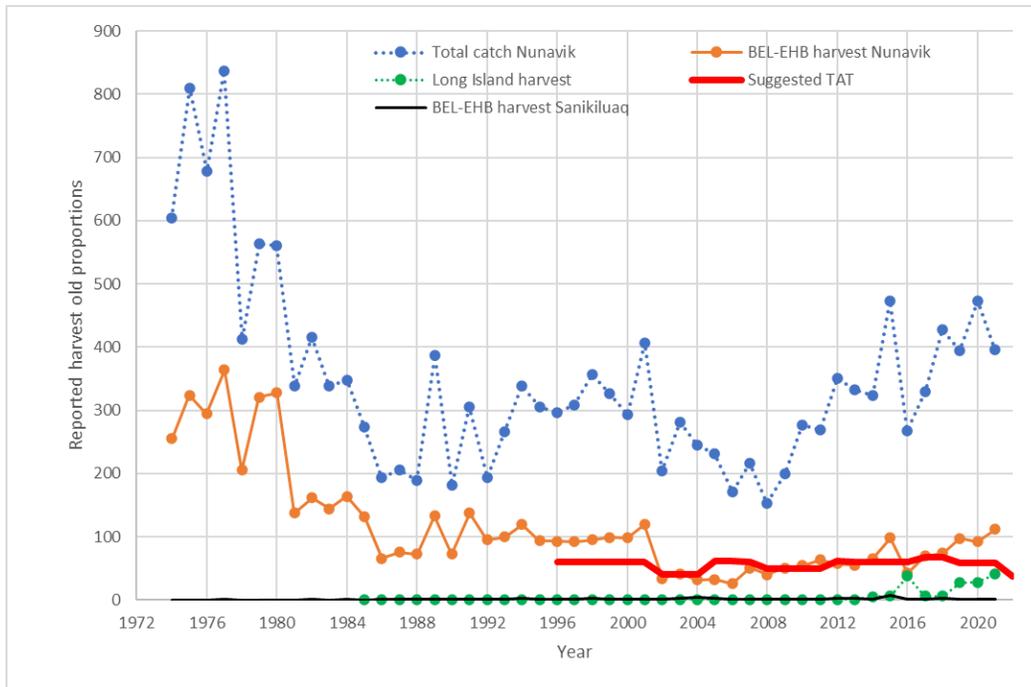


Figure 4. Harvest statistics derived using proportions from the 2017 assessment and found in Hammill et al. (2017a). Total reported harvest of beluga in Nunavik (blue), landings from Long Island area (green) and estimated landed harvest of the BEL-EHB stock by Nunavik (orange) and Sanikiluaq hunters (black). The BEL-EHB stock landings are based on reported harvest statistics for the area and the proportions from the genetic analysis used in Hammill et al. (2017a; Appendix A, Table A2). The red line represents the recommended Total Allowable Take (TAT) of BEL-EHB animals.

Using the new proportions of BEL-EHB animals in the harvest from Parent et al. (2023), an estimated 158 animals from the BEL-EHB stock were harvested, including 19 BEL-EHB animals from Sanikiluaq. The estimated number of BEL-EHB belugas harvested is above the five-year average of 119 BEL-EHB belugas harvested per year since 2016, including an average of 19 BEL-EHB belugas reported harvested in Sanikiluaq (Figure 5; Table 2; Appendix A, Table A1).

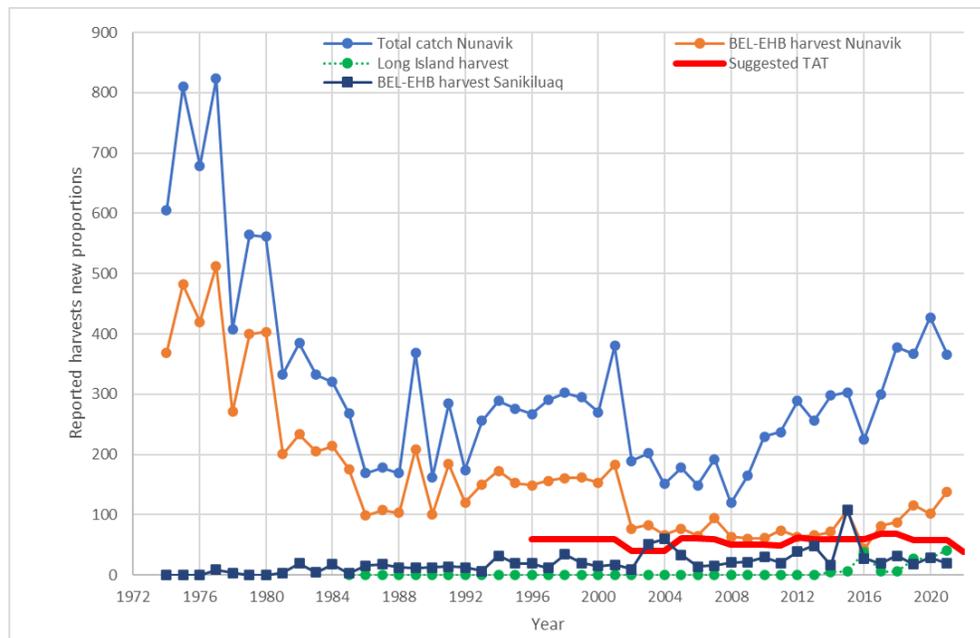


Figure 5. Harvest statistics derived using revised proportions from the new genetic analysis. Total reported harvest of beluga in Nunavik (blue), estimated landed harvest from the BEL-EHB stock (orange) and landings from Long Island area (green). The BEL-EHB landings are based on reported harvest statistics for the area and the proportions from the genetic analysis presented at this assessment (Table 2; Appendix A, Table A1; Parent et al. 2023). The red line represents the recommended Total Allowable Take (TAT) of BEL-EHB animals.

JAMES BAY POPULATION ABUNDANCE

The model converged rapidly and there were no signs of large autocorrelation among variables (all values < 0.5). The starting abundance was negatively correlated with carrying capacity and the maximum rate of increase. The 2021 abundance estimate was positively correlated with the estimated carrying capacity and the process error. Carrying capacity and the maximum rate of increase were negatively correlated (Appendix B). Significant updating of the priors was observed for carrying capacity and starting abundance. There was some updating of the prior for maximum rate of increase, but no change in the struck and loss prior was observed. The model estimated a carrying capacity of 21,000 (95% CI = 12,900–38,000), and a maximum rate of increase of 4.1% (95% CI = 2.4–6.4). The estimated starting abundance was 7,800 (95% CI = 5,000–10,400, rounded to the nearest 100), increasing to 18,200 in 2015 and then levelling off and declining slightly to 16,700 (95% CI = 11,600–21,300) in 2021 (Table 4; Figure 6; Appendix B, Table B1, Figures B1, B2).

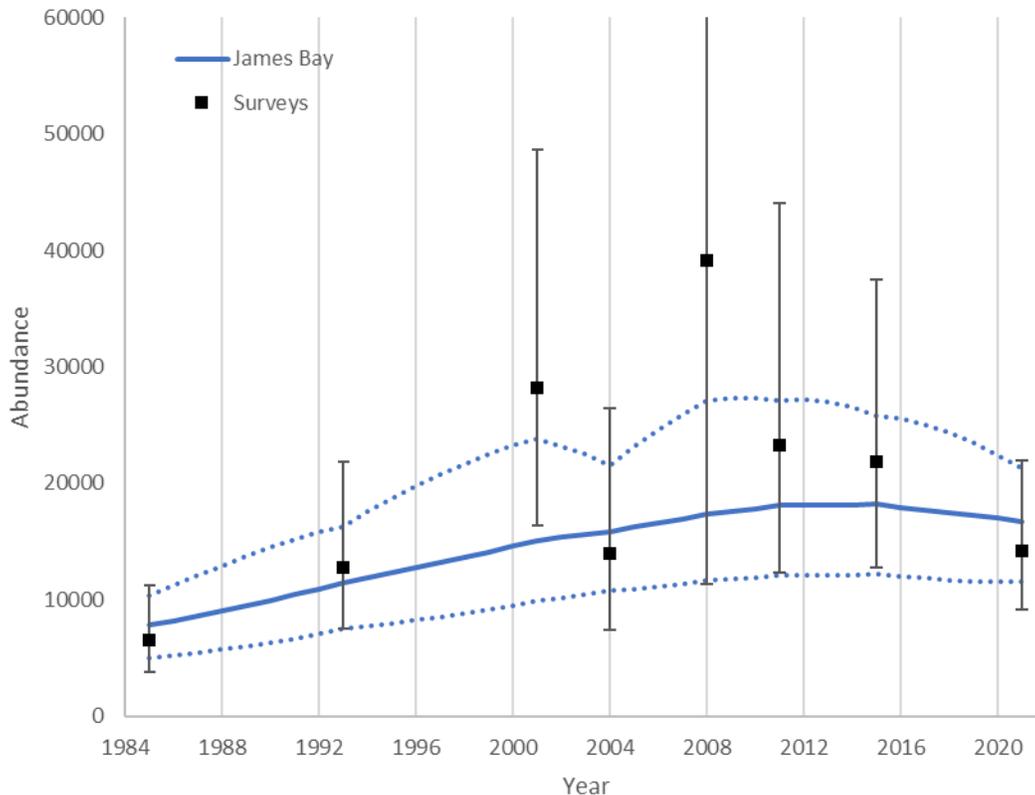


Figure 6. Aerial survey and model abundance estimates of James Bay beluga and 95% credibility intervals during 1985–2021.

BELCHER-EASTERN HUDSON BAY (BEL-EHB) STOCK ABUNDANCE

The model (referred to as model run 1, using the observed 2021 survey CV of 29%) fitted to the BEL-EHB data converged rapidly, with no signs of large autocorrelation among variables (Appendix B, Tables B2, Figures B3, B4). Negative correlations were observed between the starting population, the maximum rate of increase and the 2021 abundance estimate. Carrying capacity was negatively correlated with the maximum rate of increase and the 2021 abundance estimate, but positively correlated with starting population and struck and loss. The maximum rate of increase was negatively correlated with starting population and process error and positively correlated with struck and loss and the most recent abundance estimate (Appendix B, Figure B4). Significant updating of the priors was observed for the starting population, carrying capacity, and maximum rate of increase. Some updating of the prior also occurred for the struck and loss prior. The model estimated a starting population of 9,000 belugas (95% CI = 5,800–13,200, rounded to the nearest 100), a carrying capacity of 11,000 (95% CI = 6,400–19,400), and a maximum rate of increase of 3.5% (95% CI = 2.1–5.5%; Figure 7; Table 4). The median for the struck and loss prior was 25% (95% CI = 1.5–76%). The median posterior for struck and loss was 27% (95% CI = 1.7–76%). The estimated 2021 population is 2,900 (95% CI = 1,700–3,900). Using the updated abundance estimates, the abundance in 2015 was 3,600 (95% CI = 2,400–5,700). The rate of decline has increased from an average annual rate of decline of 1.1% between 2004 and 2014, to an average annual rate of decline of 3.0% between 2015 and 2021 (Figure 7).

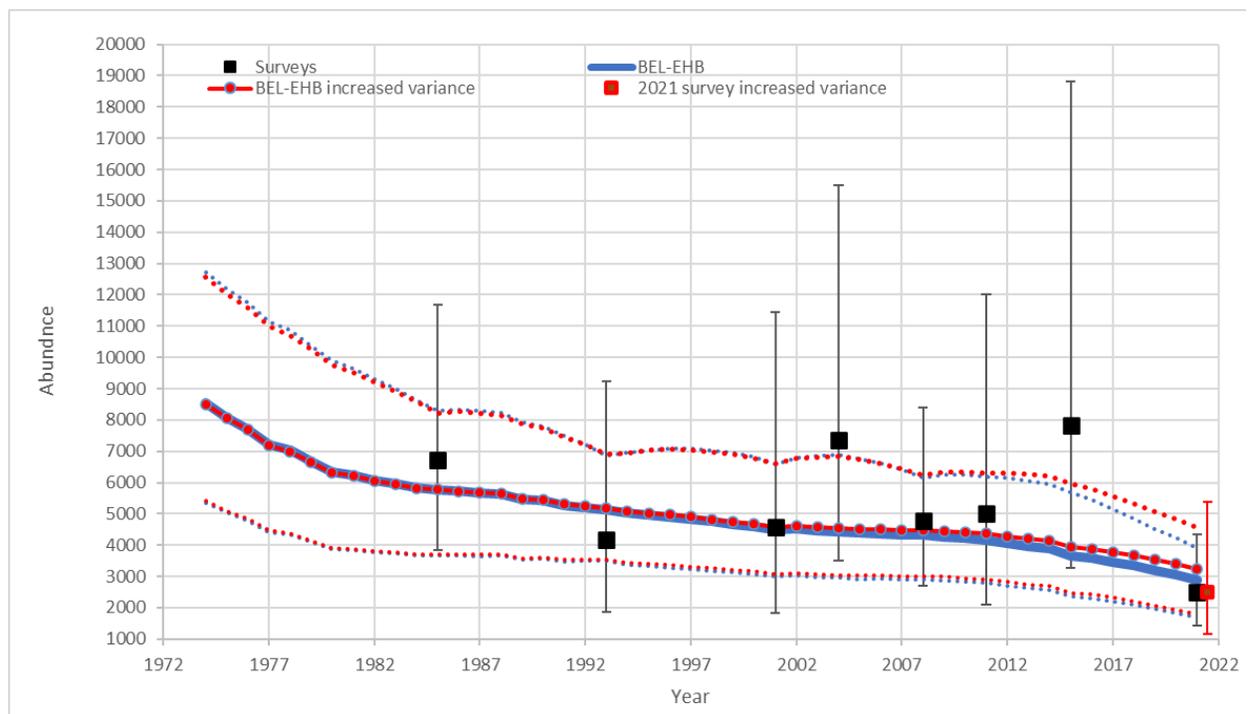


Figure 7. Aerial survey and population model estimates of Eastern Hudson Bay beluga abundance during 1974–2021 and 95% credibility intervals. Two runs were completed, assuming a struck and loss (SL) median prior of 25% (red) or 2 (blue).

The 2021 aerial survey estimates were the lowest in the time series and had the lowest coefficient of variation (greatest precision) in the time series as well. These characteristics, as well as being the last point in the survey time series, mean that this point had a major impact on model estimates of abundance and trend. The impact of this estimate was examined by increasing the survey coefficient of variation (CV) to a value equal to the coefficient of variation for the entire survey time series, excluding 2021, and the model was refitted to the time series of aerial survey estimates (referred to as model run 2, the 2021 survey CV increased to 40%). The model converged rapidly, with no signs of large autocorrelation among variables (Appendix B, Table B3; Figures B5, B6). The strength of the cross-correlations changed slightly, but the overall directions of the correlations remained the same (Appendix B). Significant updating of the priors was observed for the starting abundance, carrying capacity, and maximum rate of increase. There was no updating of the prior for the struck and loss (Table 4). The model estimated a starting abundance of 9,000 (95% CI = 5,800–13,100, rounded to the nearest 100), a carrying capacity of 10,900 (95% CI = 6,500–19,400), and a maximum rate of increase of 3.6% (95% CI = 2.1–5.6; Table 4, Figure 7). The estimated 2021 abundance was 3,200 (95% CI = 1,800–4,600) beluga. Abundance in 2015 was 3,900 (95% CI = 2,500–6,000). The rate of decline in the population under this scenario has increased from an average of less than 1% per year between 2004–2014, to 2.5% per year between 2015–2021 (Figure 7).

Table 4. Prior and posterior estimates of carrying capacity (K), maximum rate of increase (lambda), starting abundance (start.pop), struck and loss, and abundance in 2021 (N2021) for JAM and BEL-EHB beluga. Shown are mean and standard error (SE), and 0.025, 0.25, 0.5, 0.75, and 0.975 quantiles.

JAM

Parameters	Mean	SE	0.025	0.25	0.5	0.75	0.975
K	22536	6618	12873	17704	21016	26320	38031
K.prior	22484	10098	5872	13731	22493	31197	39121
Lambda _{max}	0.042	0.01	0.024	0.035	0.041	0.048	0.064
Lambda _{max} .prior	0.04	0.01	0.023	0.033	0.039	0.046	0.062
startpop	7792	1362	5050	6890	7813	8718	10400
startpop.prior	20994	10983	2949	11478	20985	30512	39047
struck.and.loss	0.29	0.21	0.02	0.12	0.25	0.43	0.76
struck.and.loss.prior	0.29	0.21	0.02	0.12	0.25	0.43	0.76
N2021	16662	2459	11555	15092	16742	18333	21252

BEL-EHB stock (CV =29%)

Parameters	Mean	SE	0.025	0.25	0.5	0.75	0.975
K	11860	3676	6435	8945	11049	14549	19395
K.prior	12503	4334	5375	8745	12507	16256	19630
Lambda _{max}	0.036	0.009	0.021	0.03	0.035	0.041	0.055
Lambda _{max} .prior	0.04	0.01	0.023	0.033	0.039	0.046	0.062
startpop	9158	1898	5776	7810	9033	10389	13236
startpop.prior	8495	3751	2318	5249	8501	11734	14672
struck.and.lost	0.305	0.205	0.017	0.137	0.273	0.444	0.756
struck.and.lost.prior	0.291	0.205	0.015	0.122	0.252	0.427	0.755
N2021	2859	571	1680	2490	2881	3250	3917

BEL-EHB stock (CV = 40%)

Parameters	Mean	SE	0.025	0.25	0.5	0.75	0.975
K	11763	3641	6487	8891	10910	14363	19365
K.prior	12493	4331	5373	8753	12480	16248	19632
Lambda _{max}	0.037	0.009	0.021	0.03	0.036	0.042	0.056
Lambda _{max} .prior	0.04	0.01	0.023	0.033	0.039	0.046	0.062
startpop	9111	1852	5832	7795	8983	10303	13110
startpop.prior	8495	3754	2321	5239	8492	11744	14668
struck.and.loss	0.29	0.20	0.02	0.13	0.26	0.43	0.74
struck.and.loss.prior	0.29	0.21	0.02	0.12	0.25	0.43	0.76
N2021	3228	706	1782	2766	3248	3711	4554

HARVEST IMPACTS

James Bay

No management objective has yet been identified for the James Bay population. If the current approach that the probability of a decline in abundance due to harvesting must not exceed 50% after 5 years is used, then the harvest should not exceed 190 belugas annually (Table 5). Applying a precautionary approach framework, the PBR would be 296 belugas with a recovery factor of 1. Using the DFO precautionary approach frameworks, harvest levels would be between 170 and 173 animals, depending on the framework, would have a 95% probability of remaining above the LRL over 50 years. At these harvest levels, the probability that the population would remain above the PRL was close to 80% (Table 6).

Table 5. Population model estimated abundance (Abund.) and standard error (SE) of the JAM population and BEL–EHB stock and harvest levels that would have a 50% probability of maintaining the population above the benchmark (Bench.) level and Potential Biological Removals (PBR). CV=Coefficient of variance

Area	Current management plan				PBR		
	Abund. 2021	SE	Bench.	Harvest for 50% pop > Bench.	N _{min}	Recovery Factor	PBR
JAM	16,662	2,459	16,662	190	14,800	1	296
BEL-EHB (base run, CV=29%)	2,859	571	3,650 3,400	0*(20**) 0*(38**)	2,254	0.1	5
BEL-EHB (CV = 40%)	3,248	1,013	3,936 3,400	0*(35**) 60*(70**)	2,752	0.1	5

* Evaluated over 5 years.

** Evaluated over 10 years.

BEL-EHB

Several different approaches were examined to evaluate the impacts of harvests on the BEL-EHB stock (Tables 5, 6). The potential biological removal (PBR) estimate is 5 belugas, assuming a recovery factor of 0.1. The current management objective is to maintain the stock at or above a benchmark of 3,400 animals. This is based on the estimated abundance of 3,400 belugas from the 2015 assessment (Hammill et al. 2017a). However, since the 2017 assessment, a new aerial survey was flown and new availability and perception bias correction factors were applied to the entire time series of aerial survey abundance estimates (1985–2021), which resulted in changes in the 2015 model estimate of abundance. In Model run 1 (CV_{2021 survey}=29%), fitting the population model to the new availability and perception bias-corrected aerial survey abundance estimates rescaled the 2015 abundance estimate of BEL-EHB beluga to 3,600 animals. This estimate is the benchmark identified when evaluating the impacts of different harvests on the stock. Model run 2 used a CV of 40% for the 2021 aerial survey estimate. Fitting the population model to the aerial survey time series with a less precise 2021 estimate of abundance, resulted in a 2015 estimated abundance of 3,900, which would be the benchmark in evaluating the impact of harvests on the stock in this second run.

In the first model run, no harvests from the BEL-EHB stock would respect the management objective to remain above the benchmark of 3,400 or 3,600 over a 5-year timeframe (Table 5, Figure 8). If the timeframe is increased to 10 years, a harvest of 20 animals per year would respect the benchmark of 3,600 and a harvest of 38 animals per year would respect the benchmark of 3,400. In the second model run, with the CV from the 2021 aerial survey increased to 40%, no harvest would respect the benchmark of 3,900 if evaluated over a timeframe of 5 years. If the benchmark is 3,400, then a harvest of 60 animals per year would respect the benchmark over 5 years (Table 5, Figure 8). Evaluating the impact of harvesting over 10 years, a harvest of 35 belugas per year would respect the benchmark of 3,900, while a harvest of 70 belugas per year would respect the benchmark of 3,400 animals.

Applying a precautionary approach framework, the population would fall into the cautious zone, between the precautionary level and the limit reference level (Figure 3). To maintain a 95% probability that the population would be above the LRL after 50 years, in model run 1, the harvest should not exceed 20 BEL-EHB animals per year. After 50 years, the probability that the stock would be above the PRL would be 70-78%. In model run 2, harvest estimates of 25 BEL-EHB belugas per year would have a 95% probability of being above LRL after 50 years. At this level, the probability of the population being above the PRL after 50 years is 73-82% (Table 6).

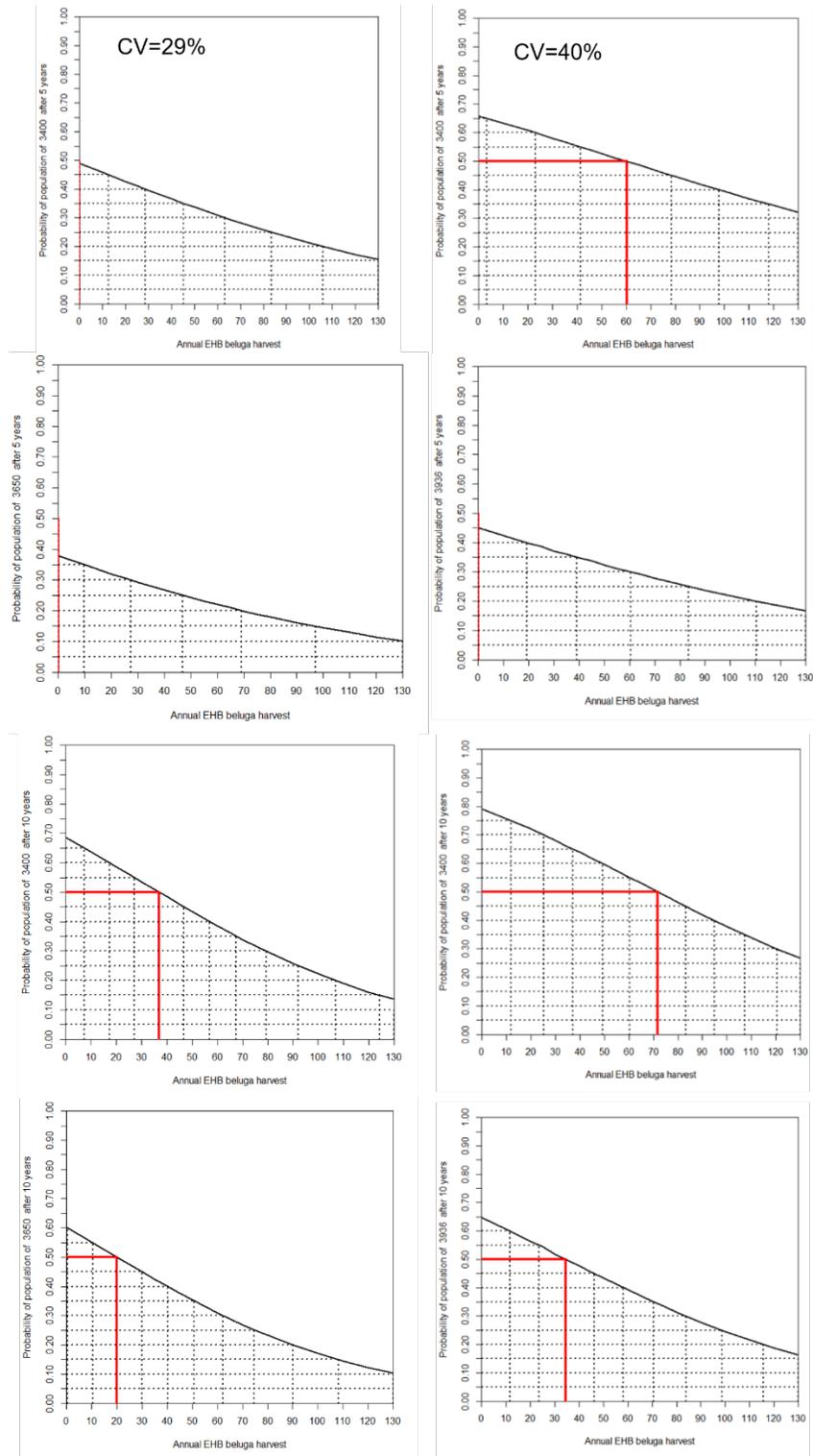


Figure 8. Probability that the BEL-EHB beluga stock would be greater than the benchmark identified on the y-axis after 5 years (first two lines) or 10 years (third and fourth lines). The red line identifies the level of harvest for a 50% probability that the stock will be greater than the benchmark. Harvest estimates from the base model run (Coefficient of variation (CV=29%) are shown in the left column, and from the increased variance run (CV = 40% for the 2021 survey in the right column.

Table 6. Reference levels and Total Allowable Take (TAT) obtained from two precautionary approach management frameworks. DFO-ASM uses the largest model population estimate (N_{max}) with Limit Reference Levels (LRL) at 30% of N_{max} (N30), and Precautionary Reference Levels (PRL) at 70% of N_{max} (N70)(DFO-ASM). DFO-MSY, an alternative approach, sets the LRL and PRL at 24 and 48% of the environmental carrying capacity (K). The TAT 95% prob. > LRL is the Total Allowable Take that maintains a 95% probability of the population remaining above LRL after 50 years. Prob. > PRL is the probability (%) of remaining above the PRL at the harvest level identified in the previous column.

Area	DFO-ASM					DFO-MSY				
	N_{max}	PRL (N70)	LRL (N30)	TAT 95% prob > LRL	Prob > PRL	K	PRL 48% K	LRL 24% K	TAT 95% prob. > LRL	Prob. > PRL
JAM	18,205	12,744	5,461	170	75%	21016	10,088	5,044	173	85%
BEL-EHB Model run 1 (CV _{2021 survey} =29%)	8,554	5,988	2,566	20	70%	11,048	5,303	2,652	20	78%
BEL-EHB Model run 2 (CV _{2021 survey} = 40%)	8,508	5,956	2,552	25	73%	10,909	5,236	2,618	25	82%

DISCUSSION

Several modifications occurred during this assessment, which had an impact on our understanding of beluga summering in eastern Hudson Bay. New genetic analyses identified a new genetic population of animals summering in the Belcher Island area (BEL), whose distribution also overlaps with beluga from the EHB population (Parent et al. 2023; St-Pierre et al. 2023). Combining the two populations into a BEL-EHB management stock improved the genetic assignment but also led to an increase in the estimated number of animals harvested from this stock. New estimates for availability bias and perception bias were applied to the aerial survey time series, increasing our estimates of beluga abundance compared to previous assessments. The most recent aerial survey had the lowest estimate of abundance in the time series and was the most precise (St-Pierre et al. 2023). Since it was also the most recent point in the time series it has had a major impact on the population model abundance estimates and trend.

The management of beluga harvesting in Nunavik is complex because the harvest impacts at least 5 beluga populations of differing conservation statuses, and involves 15 communities in two jurisdictions. The current management framework used genetic information obtained from skin samples provided by the hunters to direct harvesting towards the large WHB population, and away from the smaller BEL-EHB stock. The PBR for the WHB population is 753 animals (FR = 0.75), with total removal of 584 animals in 2015 (Hammill et al. 2017a). This leaves scope for higher harvests of WHB animals, although at some point harvests may reach levels requiring greater management of the population. For some communities in the Hudson Bay Arc, redirecting harvests towards beluga in James Bay provides access to needed subsistence resources, while favouring conservation of the BEL-EHB beluga stock summering in the eastern Hudson Bay area (Figure 1).

In previous assessments, it was assumed that animals seen during the summer surveys of eastern Hudson Bay had the same genetic composition as animals sampled from the two coastal EHB rivers (i.e., the Little Whale and Nastapoka Rivers). This was assumed although results from the genetic mixture analyses from past assessments indicated that most animals taken during the Sanikiluaq summer harvest had a non-EHB population signature (Hammill et al. 2017a, Hammill et al. 2021). During the 2017 review, it was highlighted that some samples from animals had haplotypes specific to the Belcher Islands, suggesting that the genetic composition of animals seen in these offshore areas was more complex than characterized by the typical EHB/WHB types. As a result, there was an inconsistency between the genetic definition of the BEL-EHB stock, comprised solely of EHB beluga, and the census from aerial surveys, which included EHB and Belcher Islands beluga. One consequence of this would be that the assessment underestimated the impact of harvests on the stock of beluga summering in the eastern Hudson Bay area (Hammill et al. 2017a). The re-examination of population structure in the Hudson Bay-Strait Complex shows that two distinct populations summer in eastern Hudson Bay (Parent et al. 2023). The eastern Hudson Bay surveys cover a large area and have consistently identified animals primarily in a zone between the coast and the Belcher Islands. Telemetry data from animals captured at the Nastapoka and Little Whale Rivers shows extensive offshore movement towards the Belcher Island area, which overlaps with the area where animals were seen during the surveys (Lewis et al. 2009; Bailleul et al. 2012). Assuming that there was no substantial shift in distribution to areas outside of those where belugas have consistently been observed during the summer surveys, the BEL population belugas must overlap with the EHB animals. Animals from both populations are taken in the summer harvests in Hudson Bay, and the fall and spring harvests in Hudson Strait. It was therefore logical to combine the BEL and EHB populations into one management stock, which also improves consistency with what is being evaluated by the summer aerial surveys. Moreover, this

combination allowed for an improved genetic definition of beluga summering in eastern Hudson Bay and reduced the number of belugas belonging to an unidentified group. The aerial surveys show that animals summering in eastern Hudson Bay are not abundant, and when combined with the new genetic information also indicates that the impact of harvests on animals summering in this area has been underestimated in previous analyses, particularly in the Sanikiluaq harvests (Parent et al. 2023).

Aerial surveys have been flown in James Bay and eastern Hudson Bay since 1985 at approximately 5 year intervals. The surveys have followed the same general design but changes in methods have occurred over time (St-Pierre et al. 2023). A significant change in 2021 was the use of three aircraft, which allowed the surveys to be completed before the end of August, when animals begin moving around (Bailleul et al. 2012). A second significant change was the change in the availability and perception bias corrections applied to the survey data. Previous surveys have used an availability correction factor of 2.09 based on data from the St. Lawrence beluga to account for animals that are diving, (Gosselin et al. 2017). In the 2021 survey, an availability correction factor of 1.97 was applied to the survey estimates based on telemetry data from satellite transmitters deployed on beluga in EHB in the early 2000s (Bailleul et al. 2012; St-Pierre et al. 2022). A perception bias correction factor based on data collected during the 2015 survey, but not analyzed at the time, was applied to the 2015 survey and a separate perception bias correction factor based on data collected in 2021 was also applied to the 2021 aerial survey estimates. The average of these two estimates (average perception bias = 1.23) was also applied to the 1985–2011 aerial survey time series. On average, the application of the two correction factors increased the abundance estimates in the time series by approximately 65% compared to previous assessments.

The aerial survey flown in 2021 in eastern Hudson Bay returned the lowest abundance estimate and with a CV of 29% (vs. CV = 51%, SE = 4%: 1985–2015) had the lowest CV in the 1985–2021 survey time series. This, along with the fact that it is the most recent point in the time series, has an important impact on model estimates of abundance and trend.

Using Bayesian methods to fit the population model to the aerial survey data allowed us to explicitly incorporate uncertainty around model parameters (Wade 2000), which are represented in the model by using stochastic distributions instead of single values. Bayesian fitting also ensured that uncertainty was propagated throughout the analysis, and that the correlations among parameters were preserved (Hoyle and Maunder 2004). However, there remains uncertainty associated with some of the information that has been collected and its impact on beluga management. For example, although abundance estimates for this stock are available from a time series of eight aerial surveys extending back to 1985, surveys have been flown at roughly 5 year intervals, which limits the number of points the model is able to fit to (St-Pierre et al. 2023). Beluga aerial survey estimates are highly uncertain due to the inherent challenges in estimating the abundance of a species that spends limited time at the surface, and whose behaviour affects diving activity, group size and distribution (Gosselin et al. 2014). Moreover, owing to the limited number of abundance estimates, the model is sensitive to the last estimate of abundance in the time series. The low estimate from the 2021 survey and especially the low CV associated with this survey, had a significant impact on model estimates of abundance and trend. To determine what these impacts might be, a second model run (Model run 2) was completed using a higher CV of 40% for the 2021 survey. This change did provide support for a slightly larger stock, but did not alter the fact that the BEL-EHB stock remains a relatively small and declining stock of around 2,900–3,200 beluga.

Additional uncertainty is related to the stock composition of harvests. Although we believe our understanding of stock structure in the Hudson Bay complex has improved, the number of samples returned by hunters does not reflect the majority of the hunt. In 2021, out of the 366 animals reported harvested in Nunavik, samples from only 87 animals had been received

by mid-January 2022. Additional information on age structure of harvests and demographic rates would also help improve our understanding of the dynamics of this stock.

In Hudson Bay, previous assessments have assumed a struck and loss prior of 42% (Doniol-Valcroze et al. 2012, 2013; Hammill et al. 2017a, 2021). This value lies at the upper end of the range of values found in literature and is more frequently associated with harvesting practices where animals are not harpooned first, but it also accounts for non-reporting. Conversations with hunters during the public hearings in Kuujjuaraapik, prior to the establishment of the new management plan, suggested that this assumption was too high. Consequently, we lowered the prior to values with a median of 25%, which is similar to Richard (2008), who estimated a struck and loss of 18% (CV = 6%; excluding non-reporting), but also did not make the prior too narrow to allow for non-reporting.

The process error term accounts for variability in the dynamics of the population. In this assessment, the process error has decreased markedly since 2000 (Appendix B; Figures B1 and B3). At this point, the reasons for this decrease are not known, but may include increased environmental stochasticity. Recent assessments have identified other stocks (e.g., Harp Seals; Stenson et al. 2020) for which recruitment and mortality may vary significantly between years due to variability in ice and food resource conditions. We have less information on variability in demographic rates of beluga, but the uncertainty associated with this parameter needs to be examined further. Beluga social structure is also quite complex, with other group members involved in calf care. A declining trend in mean age of harvested animals from the BEL-EHB stock since the 1980s may impact productivity if smaller animals have lower natality (Ferguson et al 2020). A declining age structure may have other implications as well. Emerging evidence of animal culture as a driving force in demographic processes suggests that the loss of older animals involved in the building of kinship relationships care of young and holders of ecological knowledge related to migration routes and favorable foraging areas will also contribute to a decline in stock productivity (i.e., Allee effects; O’Corry-Crowe et al. 2010, 2018, 2020; Brakes et al. 2021).

In James Bay, the population model fitted to the aerial survey estimates resulted in a 2021 estimate of 16,700 animals, making it one of the larger beluga populations in the world (NAMMCO 2018). The population abundance appears to have leveled off. Historically, belugas in James Bay were harvested for subsistence, and although there were attempts to develop commercial whaling in the area, these efforts were not successful and removals appear to have been insignificant (Reeves and Mitchell 1987). As a result, the James Bay population was never depleted to the extent seen in other populations, although significant habitat changes have occurred through very large-scale hydroelectric developments on the east side of James Bay (Reeves and Mitchell 1987). It is not known how or if these developments have impacted beluga in the James Bay and eastern Hudson Bay area. Harvesting activity in the James Bay / Long Island area in the current century has been limited to date, owing to the large distances that must be travelled by hunters from Nunavik communities to the Long Island area. No management objectives have yet been set for this population. However, the complex social development of beluga, and the importance of knowledge transfer (culture) to the development of beluga migration patterns, as outlined in recent research (Colbeck et al. 2013; O’Corry-Crowe et al. 2020; Ouellet et al. 2021; Bonnell et al. 2022) would argue for the development of harvesting strategies that will minimize chances of reducing the numbers of animals that favour the Long Island area.

Management efforts to limit the harvest of animals from the BEL-EHB beluga stock had some impact on slowing the population decline, with estimated annual declines of 1% or less between 2004 and 2014, but the rate of decline has increased since then (Figure 7). These declines in abundance are not unexpected since harvests have consistently exceeded the recommended TAT levels, but previous assessments have also under-estimated the proportions of animals

summering in eastern Hudson Bay that are removed by the harvest (Figures 4, 5). A precautionary approach framework would not have avoided the impacts of a greater proportion of belugas removed in the harvest, but would have lessened the impact because, by design, PA frameworks such as PBR or the DFO frameworks incorporate the risks of unknown errors in model parameters (Stenson et al. 2012; DFO 2013; Doniol-Valcroze et al. 2013; Hammill et al. 2017b).

PBR

In addition to the harvest levels respecting the objective of the current beluga management plan, we presented three management approaches based on the precautionary principle. The PBR approach was developed in response to the United States Marine Mammal Protection Act (Wade, 1998) and is the main tool used to estimate a sustainable level of removals. The United States expect countries exporting fish products into their market to develop marine mammal monitoring systems and apply sustainable removals comparable to those currently in place in their country. The estimated PBR for the JAM population is 296 belugas, assuming a recovery factor of 1. The PBR for the BEL-EHB beluga stock is 5 animals assuming a recovery factor of 0.1 (Table 5).

PRECAUTIONARY APPROACH IN CANADA

Under the amended provisions of the [Fisheries Act](#) (2019), there is renewed emphasis on the sustainability of fisheries through the development of a management framework based on the Precautionary Approach and, in particular, calling on the Minister of DFO to establish a LRL. The LRL is considered a lower limit below which significant harm can occur to the stock, significantly complicating efforts for stock recovery (Stenson et al. 2012; Doniol-Valcroze et al. 2013; Hammill et al. 2017b). In this study, we presented two very similar precautionary management frameworks. Under both frameworks, the BEL-EHB stock lies in what can be considered the Cautious zone, below the PRL but above the LRL (Figure 3). Harvest strategies should focus on rebuilding the stock within a certain time frame. Under the frameworks we identified, annual harvests should decline to 20-25 BEL-EHB animals if the stock can be expected to have a 70% or greater probability of increasing above the PRL within 50 years (Table 6).

In 1984, the EHB beluga was designated as Endangered by COSEWIC because the population had declined significantly over a period of three generations and this decline was due primarily to overharvesting. In 2020, the status of EHB beluga was re-examined and revised to “Threatened” because of the perception that the population had stabilized. New genetic analyses identified that the BEL-EHB stock consists of two populations, whose aggregate abundance is approximately 2,900–3,200 animals, with a declining trend. This trend is due in part to underestimating the removals of animals belonging to the BEL-EHB stock and to consistent TAT overruns during consecutive management plans.

Limits on EHB beluga harvests were established in northern Quebec in the mid-1980s. Despite the last 30+ years of management and efforts to limit the removal of animals from the BEL-EHB stock, through the sampling program and redirecting harvesting to other populations, harvests have consistently exceeded the recommended levels and the stock continues to decline. All management frameworks point to the need for reduced harvests to stop the decline and to work towards recovery of this stock.

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APPENDIX A

Table A1. Reported harvests from communities in Nunavik and from Sanikiluaq (Nunavut). The ARC represents the communities of Kuujjuarapik, Umiujaq and Inukjuak. HSUB represents an early period where Hudson Strait and Ungava Bay catches were combined. HS represents Hudson Strait reported catches from spring (1 February–31 August) and fall (1 September–31 January). UBSP and UBFA are Ungava Bay spring and fall, respectively. NEHBSP and NEHBFA are northeastern Hudson Bay spring and fall, respectively.

YEAR	ARC	HSUB	Sanikiluaq (year-round)	HS spring	HS fall	UBSP	UBFA	NEHBSP	NEHBFA	Long Island	Annual total
1974	184	421	0	0	0	0	0	0	0	0	605
1975	224	586	0	0	0	0	0	0	0	0	810
1976	216	463	0	0	0	0	0	0	0	0	679
1977	269	554	14	0	0	0	0	0	0	0	837
1978	164	243	6	0	0	0	0	0	0	0	413
1979	271	293	0	0	0	0	0	0	0	0	564
1980	280	281	0	0	0	0	0	0	0	0	561
1981	97	236	6	0	0	0	0	0	0	0	339
1982	114	271	30	0	0	0	0	0	0	0	415
1983	105	227	7	0	0	0	0	0	0	0	339
1984	131	189	28	0	0	0	0	0	0	0	348
1985	103	166	5	0	0	0	0	0	0	0	274
1986	43	126	25	0	0	0	0	0	0	0	194
1987	53	125	28	0	0	0	0	0	0	0	206
1988	52	117	20	0	0	0	0	0	0	0	189
1989	84	284	19	0	0	0	0	0	0	0	387
1990	53	109	20	0	0	0	0	0	0	0	182
1991	106	178	22	0	0	0	0	0	0	0	306
1992	78	96	20	0	0	0	0	0	0	0	194
1993	67	189	10	0	0	0	0	0	0	0	266
1994	82	207	50	0	0	0	0	0	0	0	339
1995	55	221	30	0	0	0	0	0	0	0	306
1996	56	211	30	0	0	0	0	0	0	0	297
1997	51	239	19	0	0	0	0	0	0	0	309
1998	50	252	54	0	0	0	0	0	0	0	356
1999	57	238	32	0	0	0	0	0	0	0	327
2000	62	208	23	0	0	0	0	0	0	0	293
2001	73	241	27	0	0	66	0	0	0	0	407
2002	5	161	15	0	0	23	0	0	0	0	204
2003	8	168	80	0	0	26	0	0	0	0	282
2004	3	144	94	0	0	4	0	0	0	0	245
2005	1	172	53	0	0	5	0	0	0	0	231
2006	0	147	22	0	0	2	0	0	0	0	171
2007	21	165	24	0	0	6	0	0	0	0	216
2008	23	92	33	0	0	5	0	0	0	0	153
2009	21	0	34	68	70	6	0	0	0	0	199
2010	16	0	47	138	61	8	7	0	0	0	277
2011	19	0	32	115	86	0	17	0	0	0	269
2012	13	0	61	208	56	10	2	0	0	0	350
2013	8	0	76	150	90	8	0	0	0	0	332
2014	22	0	26	208	37	11	0	1	14	5	324
2015	36	0	170	106	94	28	3	0	30	6	473
2016	17	0	43	121	19	24	3	0	3	38	268
2017	18	0	30	150	85	23	4	0	13	6	329
2018	14	0	50	146	91	100	2	2	17	6	428
2019	35	0	28	144	110	23	2	2	24	27	395
2020	39	0	46	189	78	90	1	0	2	28	473
2021	28	0	30	51	160	20	0	0	66	41	366

Table A2. Results of the genetic mixture analysis (1982–2018) used in Hammill et al (2021) to determine the proportions of beluga (%) from each source stock in the harvest of Nunavik hunt areas (upper part) and Sanikiluaq harvest (lower part). N_{samp} : number of individual samples; N_{event} : number of different hunting dates; WHB: Western Hudson Bay; EHB: Eastern Hudson Bay; 95% CI: 95% confidence interval based on variance among hunting events; ND: not determined (small sample size). Unknown means samples could not be assigned to the WHB or BEL-EHB stock (from Hammill et al. 2021).

Nunavik management areas

Season	N_{samp}	N_{event}	% WHB	95% CI	% EHB	95% CI	CV (sample / event)	% Unk
Spring (Feb. 1–Aug. 31)								
Hudson Strait	770	347	82.9	78.5–87	11.7	8.1–16	0.15 / 0.17	5.3
NE Hudson	2	1	ND	-	ND	-	-	-
Ungava Bay	122	76	87.4	77.8–94.6	6.0	0.8–15.8	0.63 / 0.65	6.6
Fall (Sept. 1–Jan. 31)								
Hudson strait	454	180	67.6	60.3–74.5	29.1	22.4–36.3	0.09 / 0.12	3.3
NE Hudson	31	14	49.1	26.4–72	44.5	23.5–66.5	0.26 / 0.25	6.5
Ungava Bay	4	4	ND	-	ND	-	-	ND

Sanikiluaq (Nunavut)

Season	N_{samp}	N_{event}	% WHB	95% CI	% EHB	95% CI	CV (sample / events)	% Unk
Spring (Apr. 1–June 30)	301	107	76.8	69.2–83.7	1.6	0–6.6	1.01 / 1.17	21.6
Ext. spring (Apr. 1–July 14)	324	120	75.1	67.2–82.2	4.6	1.1–10.2	0.43 / 0.52	20.4
Summer (July 1–Aug. 31)	31	18	61.5	32.8–86.2	25.6	4.9–56	0.37 / 0.53	12.9
Fall (Sept. 1–Nov. 30)	45	30	97.8	91.8–99.9	0.0	-	-	2.2
Winter (Dec. 1–Mar. 31)	56	7	31.3	6.1–65.6	3.6	9–70.7	0.21 / 0.45	32.1

APPENDIX B

Table B1. Model priors and posteriors for parameters for James Bay model runs. The mean, standard error (SE), 2.5th, 25th, 50th, 75th and 97.5th quantiles are given for the following model parameters and their priors: maximum rate of increase (λ max), struck and loss (S&L) expressed as proportions, and population size in 2021. Rhat is the Brooks-Gelman-Rubin statistic; values near 1 indicate convergence of chains. N.eff is the number of effective runs after considering autocorrelation.

Parameter	Mean	SE	2.50%	25%	50%	75%	97.50%	Rhat	n.eff
K	22536	6618	12873	17704	21016	26320	38031	1.001	300000
K.prior	22484	10098	5872	13731	22493	31197	39121	1.001	290000
λ max	0.042	0.01	0.024	0.035	0.041	0.048	0.064	1.001	300000
λ max.prior	0.04	0.01	0.023	0.033	0.039	0.046	0.062	1.001	94000
startpop	7792	1362	5050	6890	7813	8718	10400	1.001	300000
startpop.prior	20994	10983	2949	11478	20985	30512	39047	1.001	300000
struck.and.lost	0.29	0.21	0.02	0.12	0.25	0.43	0.76	1.001	300000
struck.and.lost.prior	0.29	0.21	0.02	0.12	0.25	0.43	0.76	1.001	300000

Year	Abundance	SE	2.50%	25%	50%	75%	97.50%	Rhat	n.eff
1985	7792	1362	5050	6890	7813	8718	10400	1.001	300000
1986	8218	1527	5252	7208	8206	9213	11244	1.001	290000
1987	8660	1689	5479	7546	8614	9711	12081	1.001	300000
1988	9115	1843	5740	7906	9042	10219	12915	1.001	200000
1989	9588	1987	6034	8296	9484	10742	13741	1.001	250000
1990	10073	2103	6351	8703	9952	11276	14519	1.001	140000
1991	10571	2192	6705	9130	10435	11832	15228	1.001	99000
1992	11075	2227	7085	9591	10943	12399	15836	1.001	110000
1993	11588	2221	7480	10074	11488	12999	16242	1.001	180000
1994	12082	2499	7736	10406	11900	13528	17536	1.001	300000
1995	12577	2748	7994	10759	12322	14073	18715	1.001	300000
1996	13073	2981	8245	11129	12764	14614	19778	1.001	300000
1997	13565	3157	8556	11515	13208	15148	20749	1.001	300000
1998	14059	3314	8870	11909	13667	15694	21627	1.001	300000
1999	14555	3434	9195	12326	14141	16242	22486	1.001	300000
2000	15051	3521	9543	12747	14618	16798	23238	1.001	300000
2001	15535	3521	9904	13193	15101	17337	23866	1.001	300000
2002	15694	3343	10192	13474	15356	17490	23216	1.001	300000
2003	15837	3063	10493	13781	15608	17631	22488	1.001	300000
2004	15953	2733	10814	14090	15865	17741	21553	1.001	290000
2005	16439	3105	10956	14351	16223	18273	23157	1.001	300000
2006	16919	3453	11154	14642	16595	18796	24625	1.001	300000
2007	17392	3748	11388	14941	16977	19320	25915	1.001	300000
2008	17864	3992	11636	15264	17367	19826	27110	1.001	300000
2009	18081	4005	11761	15466	17598	20082	27360	1.001	300000
2010	18293	3943	11931	15685	17839	20344	27371	1.001	300000
2011	18479	3771	12089	15922	18088	20610	27149	1.001	300000
2012	18494	3835	12092	15952	18099	20565	27196	1.001	300000
2013	18487	3794	12111	15992	18120	20540	27017	1.001	300000
2014	18459	3651	12174	16049	18153	20501	26538	1.001	300000
2015	18411	3391	12262	16122	18205	20468	25753	1.001	300000
2016	18145	3426	12014	15900	17926	20113	25566	1.001	300000
2017	17903	3355	11851	15741	17719	19829	25068	1.001	300000
2018	17645	3228	11682	15577	17510	19540	24354	1.001	190000
2019	17344	3032	11570	15408	17277	19193	23438	1.001	300000
2020	17017	2774	11524	15240	17032	18800	22385	1.001	300000

Year	Abundance	SE	2.50%	25%	50%	75%	97.50%	Rhat	n.eff
2021	16662	2459	11555	15092	16742	18333	21252	1.001	300000

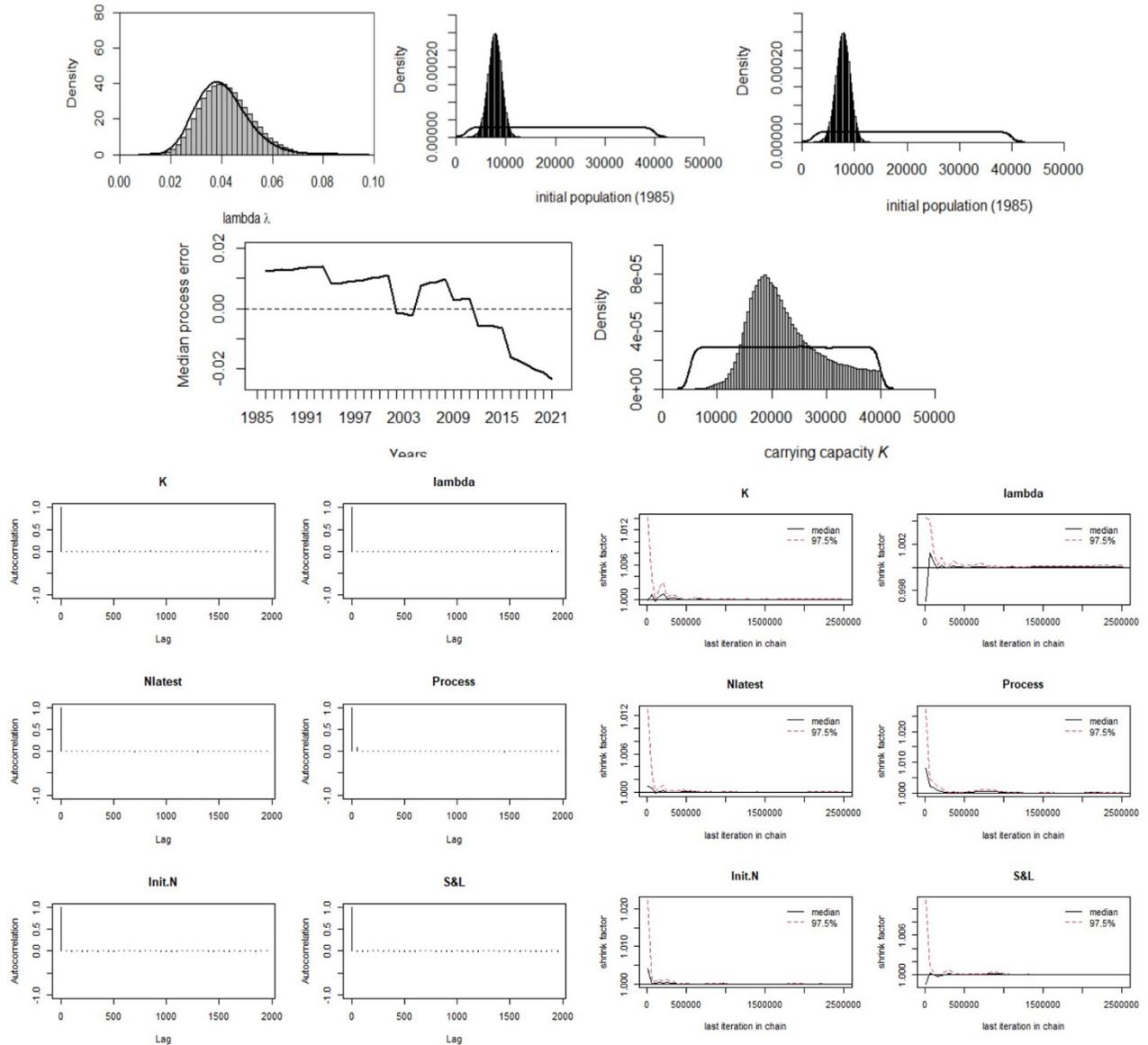


Figure B1. James Bay model run, model prior and posterior distributions. Priors are shown as dark lines, posterior values are columns for parameters: Maximum rate of increase (λ_{max}), initial population, struck and loss and process error and carrying capacity (K), autocorrelation and convergence also shown.

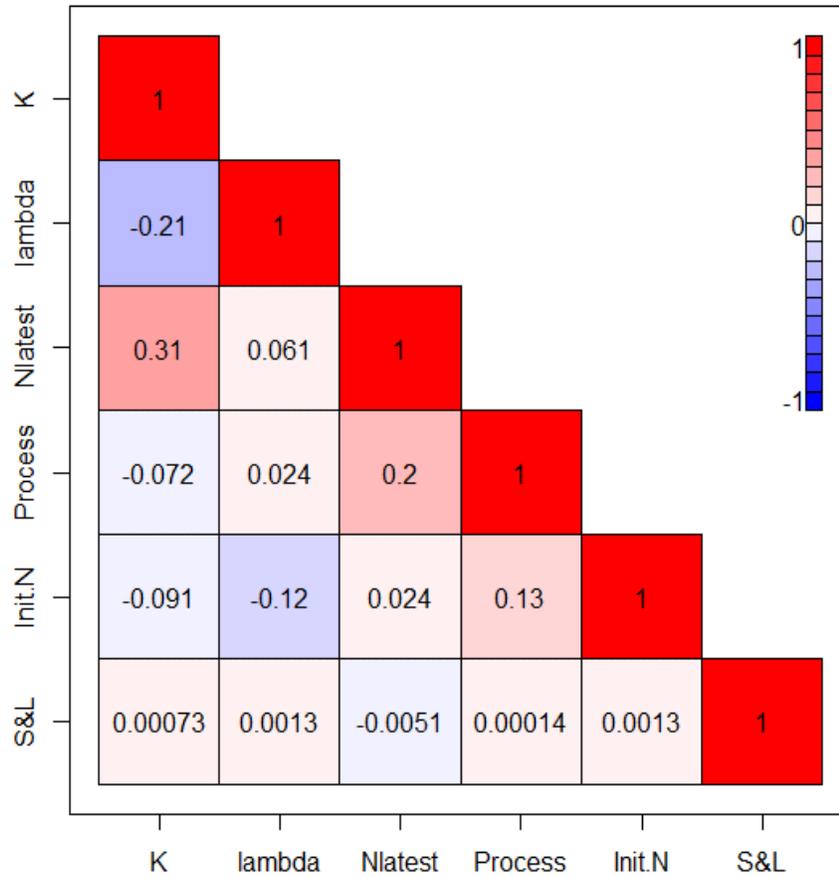


Figure B2. James Bay model run. Cross-correlation among model parameters carrying capacity (K), starting population ($Init.N$), struck and loss ($S\&L$), maximum rate of increase ($lambda_{max}$) and process error ($Process$), and 2021 abundance estimate (N_{latest}).

Table B2. Model priors and posteriors for parameters for the BEL-EHB beluga stock. The mean, standard deviation (SE), 2.5th, 25th, 50th, 75th and 97.5th quantiles are given for the following model parameters and their priors: maximum rate of increase (λ_{max}), struck and loss (S&L) expressed as proportions, and population size in 2021. Rhat is the Brooks-Gelman-Rubin statistic; values near 1 indicate convergence of chains. N.eff is the number of effective runs after considering autocorrelation.

Parameter	Mean	SE	2.50%	25%	50%	75%	97.50%	Rhat	n.eff
K	11860	3676	6435	8945	11049	14549	19395	1.001	300000
K.prior	12503	4334	5375	8745	12507	16256	19630	1.001	130000
λ_{max}	0.036	0.009	0.021	0.03	0.035	0.041	0.055	1.001	300000
λ_{max} .prior	0.04	0.01	0.023	0.033	0.039	0.046	0.062	1.001	270000
startpop	9158	1898	5776	7810	9033	10389	13236	1.001	140000
startpop.prior	8495	3751	2318	5249	8501	11734	14672	1.001	300000
struck.and.loss	0.305	0.205	0.017	0.137	0.273	0.444	0.756	1.001	300000
struck.and.loss.prior	0.291	0.205	0.015	0.122	0.252	0.427	0.755	1.001	300000

Year	Abundance	SE	2.50%	25%	50%	75%	97.50%	Rhat	n.eff
1974	8677	1866	5352	7357	8555	9880	12702	1.001	150000
1975	8226	1829	5032	6948	8090	9361	12196	1.001	180000
1976	7856	1787	4782	6620	7713	8930	11761	1.001	170000
1977	7356	1731	4419	6174	7209	8359	11147	1.001	280000
1978	7173	1680	4334	6033	7029	8138	10869	1.001	280000
1979	6824	1621	4104	5728	6679	7742	10384	1.001	240000
1980	6465	1553	3865	5418	6327	7340	9887	1.001	260000
1981	6362	1499	3841	5350	6232	7212	9648	1.001	300000
1982	6190	1430	3759	5226	6073	7011	9304	1.001	280000
1983	6068	1353	3733	5150	5968	6864	9000	1.001	220000
1984	5915	1267	3674	5049	5831	6684	8629	1.001	210000
1985	5826	1176	3679	5013	5770	6582	8294	1.001	300000
1986	5797	1190	3672	4986	5726	6526	8328	1.001	300000
1987	5747	1186	3654	4947	5670	6454	8286	1.001	270000
1988	5706	1166	3661	4920	5626	6395	8214	1.001	300000
1989	5527	1130	3541	4770	5451	6193	7942	1.001	300000
1990	5483	1082	3558	4758	5419	6125	7784	1.001	300000
1991	5325	1018	3487	4644	5272	5942	7481	1.001	300000
1992	5248	947	3500	4609	5212	5842	7215	1.001	260000
1993	5140	860	3499	4557	5122	5707	6868	1.001	190000
1994	5060	909	3387	4446	5023	5626	6953	1.001	300000
1995	5019	947	3333	4385	4963	5583	7036	1.001	300000
1996	4974	970	3283	4326	4904	5535	7084	1.001	260000
1997	4925	985	3248	4269	4845	5476	7099	1.001	210000
1998	4835	987	3171	4177	4746	5381	7020	1.001	190000
1999	4755	975	3120	4099	4662	5300	6939	1.001	150000
2000	4685	951	3077	4036	4597	5229	6809	1.001	170000
2001	4570	914	2993	3935	4492	5116	6597	1.001	240000
2002	4608	957	3020	3952	4511	5148	6784	1.001	300000
2003	4580	983	2983	3909	4469	5118	6848	1.001	300000
2004	4558	995	2953	3880	4439	5099	6877	1.001	300000
2005	4497	978	2916	3833	4383	5028	6750	1.001	300000
2006	4475	943	2926	3832	4373	4998	6618	1.001	300000
2007	4410	894	2899	3795	4326	4928	6408	1.001	300000
2008	4373	827	2909	3795	4313	4895	6147	1.001	300000
2009	4344	858	2878	3751	4268	4851	6243	1.001	300000
2010	4298	869	2835	3705	4214	4793	6248	1.001	300000
2011	4242	860	2789	3653	4156	4732	6198	1.001	300000
2012	4154	878	2713	3565	4060	4627	6159	1.001	300000
2013	4049	880	2624	3467	3953	4508	6064	1.001	300000
2014	3979	873	2570	3411	3886	4426	5966	1.001	300000
2015	3738	851	2352	3185	3650	4176	5668	1.001	300000
2016	3650	806	2298	3127	3581	4078	5441	1.001	300000
2017	3521	753	2207	3030	3471	3942	5144	1.001	300000
2018	3373	701	2093	2914	3342	3787	4840	1.001	300000
2019	3208	658	1966	2780	3196	3616	4520	1.001	300000
2020	3049	607	1842	2652	3054	3450	4227	1.001	300000
2021	2859	571	1680	2490	2881	3250	3917	1.001	300000

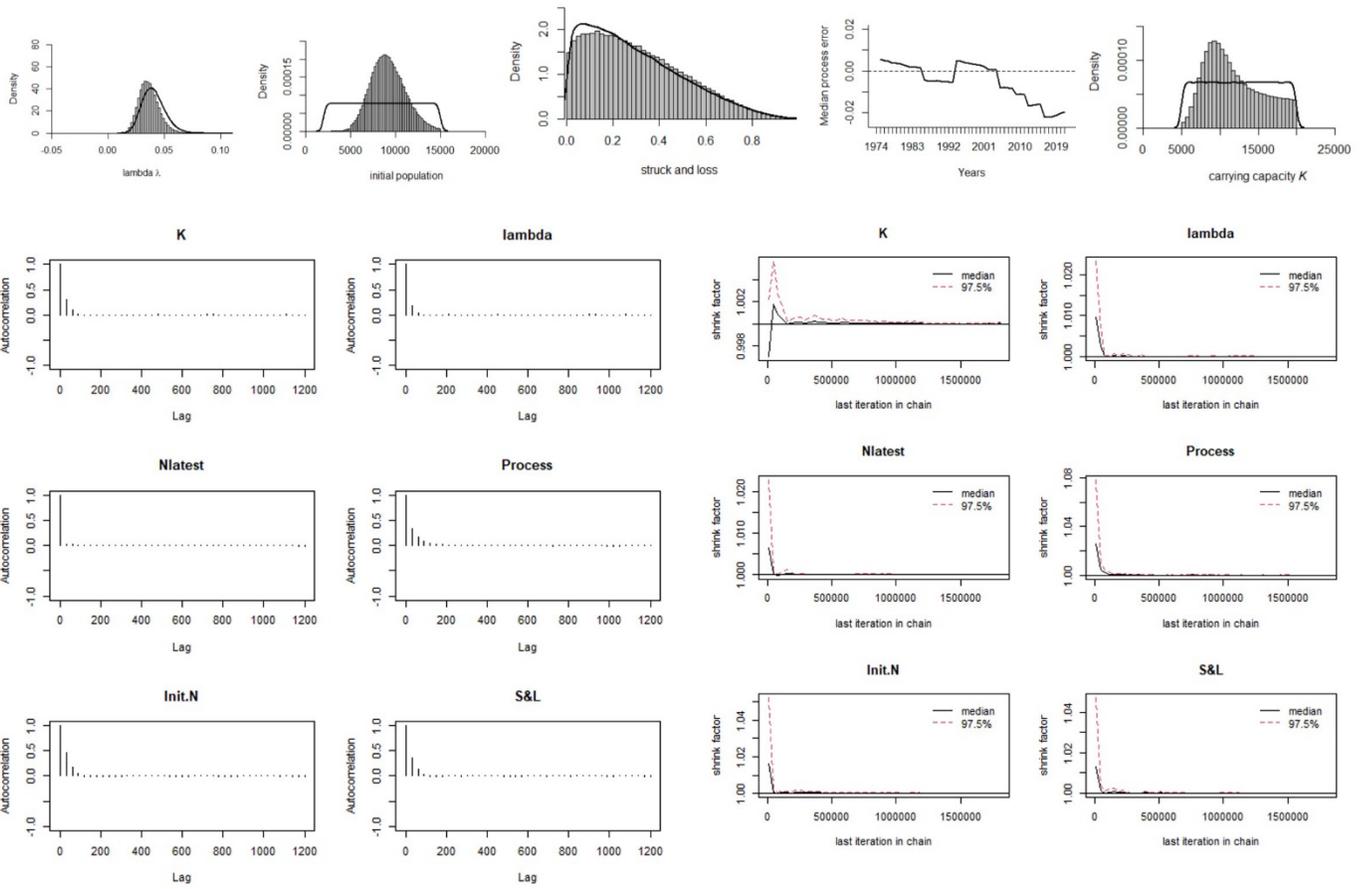


Figure B3. BEL-EHB model run. Priors are shown as dark lines, posterior values are columns for parameters: maximum rate of increase (λ_{max}), initial population, struck and loss and process error, carrying capacity (K), autocorrelation and convergence.

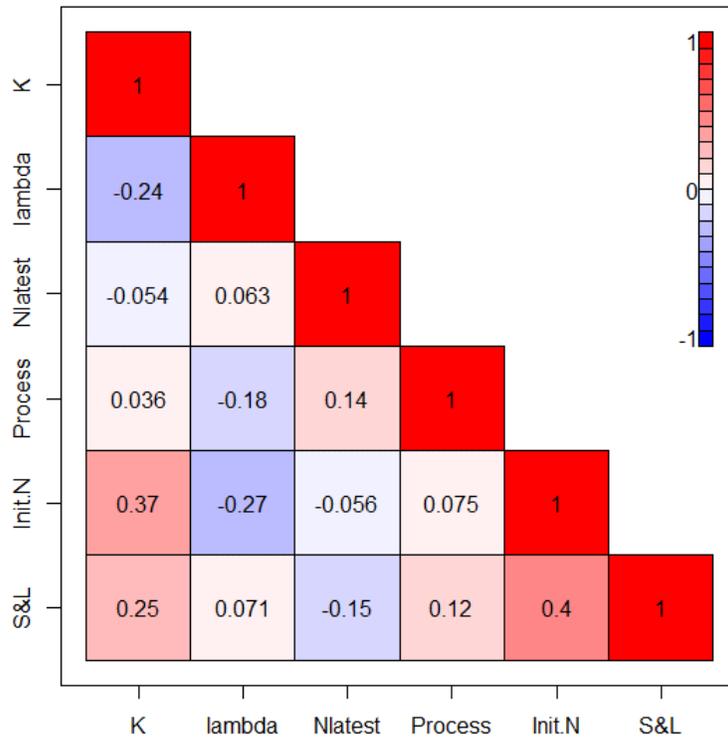


Figure B4. BEL-EHB model with median prior struck and loss of 25%. Correlation among model parameters carrying capacity (K), starting population ($Init.N$), struck and loss ($S\&L$), maximum rate of increase ($lambda_{max}$) and process error ($Process$), and 2021 abundance estimate (N_{latest}).

Table B3. Model priors and posteriors for parameters for the BEL-EHB model runs assuming a coefficient of variance of 40% on the 2021 survey. The mean, standard deviation (SE), 2.5th, 25th, 50th, 75th and 97.5th quantiles are given for the following model parameters and their priors: maximum rate of increase (λ), struck and loss (S&L), and population size in 2021. \hat{R} at the Brooks-Gelman-Rubin statistic; values near 1 indicate convergence of chains. N_{eff} is the number of effective runs after considering autocorrelation.

Parameter	Mean	SE	2.50%	25%	50%	75%	97.50%	Rhat	n.eff
K	11763	3641	6487	8891	10910	14363	19365	1.001	180000
K.prior	12493	4331	5373	8753	12480	16248	19632	1.001	240000
λ_{max}	0.037	0.009	0.021	0.03	0.036	0.042	0.056	1.001	260000
λ_{max} .prior	0.04	0.01	0.023	0.033	0.039	0.046	0.062	1.001	280000
startpop	9111	1852	5832	7795	8983	10303	13110	1.001	140000
startpop.prior	8495	3754	2321	5239	8492	11744	14668	1.001	300000
struck.and.loss	0.29	0.20	0.02	0.13	0.26	0.43	0.74	1.001	240000
struck.and.loss.prior	0.29	0.21	0.02	0.12	0.25	0.43	0.76	1.001	140000

Year	Mean	SE	2.50%	25%	50%	75%	97.50%	Rhat	n.eff
1974	8635	1820	5410	7347	8508	9799	12576	1.001	140000
1975	8183	1778	5080	6939	8050	9283	12036	1.001	140000
1976	7817	1737	4836	6618	7678	8857	11584	1.001	130000
1977	7319	1683	4462	6166	7176	8299	10998	1.001	220000
1978	7138	1636	4376	6025	6998	8074	10700	1.001	300000
1979	6794	1576	4148	5729	6653	7686	10245	1.001	300000
1980	6440	1513	3900	5421	6305	7293	9765	1.001	300000
1981	6338	1455	3877	5359	6213	7166	9528	1.001	300000
1982	6174	1391	3800	5234	6061	6974	9200	1.001	240000
1983	6057	1323	3771	5161	5957	6835	8909	1.001	170000
1984	5906	1239	3711	5057	5825	6659	8566	1.001	240000
1985	5820	1153	3708	5024	5767	6559	8227	1.001	300000
1986	5794	1162	3701	5001	5729	6510	8263	1.001	300000
1987	5749	1153	3694	4969	5680	6445	8210	1.001	300000
1988	5715	1134	3698	4951	5646	6393	8135	1.001	300000
1989	5542	1095	3586	4808	5477	6196	7873	1.001	300000
1990	5504	1053	3615	4798	5448	6139	7731	1.001	300000
1991	5354	994	3541	4685	5309	5963	7442	1.001	300000
1992	5286	930	3554	4659	5254	5875	7201	1.001	300000
1993	5186	852	3550	4609	5173	5748	6897	1.001	300000
1994	5108	894	3445	4505	5076	5668	6955	1.001	300000
1995	5068	925	3395	4446	5021	5629	7033	1.001	300000
1996	5028	946	3355	4396	4969	5583	7068	1.001	240000
1997	4981	956	3319	4342	4910	5530	7047	1.001	250000
1998	4894	955	3254	4256	4819	5439	6978	1.001	200000
1999	4819	944	3201	4184	4743	5360	6897	1.001	300000
2000	4757	924	3161	4130	4685	5298	6787	1.001	300000
2001	4650	891	3082	4036	4585	5191	6597	1.001	300000
2002	4693	928	3105	4060	4612	5230	6757	1.001	300000
2003	4671	951	3073	4025	4581	5209	6808	1.001	300000
2004	4655	960	3052	4001	4560	5193	6845	1.001	300000
2005	4604	947	3022	3963	4515	5136	6737	1.001	300000
2006	4592	922	3031	3971	4513	5118	6619	1.001	300000
2007	4539	894	3007	3943	4475	5060	6437	1.001	300000
2008	4513	816	3019	3951	4471	5037	6230	1.001	300000
2009	4500	849	2994	3921	4445	5019	6331	1.001	300000
2010	4469	865	2952	3881	4406	4985	6345	1.001	300000
2011	4428	861	2911	3841	4365	4942	6314	1.001	300000
2012	4361	887	2833	3766	4289	4866	6317	1.001	300000
2013	4276	897	2743	3678	4202	4777	6259	1.001	300000
2014	4226	902	2690	3629	4153	4724	6212	1.001	300000
2015	4005	893	2472	3414	3936	4503	5973	1.001	200000
2016	3935	867	2417	3364	3880	4429	5793	1.001	210000
2017	3824	831	2325	3277	3785	4316	5564	1.001	230000
2018	3694	795	2210	3169	3670	4186	5317	1.001	170000
2019	3546	762	2075	3044	3537	4035	5063	1.001	150000
2020	3403	732	1945	2921	3410	3889	4818	1.001	150000
2021	3228	706	1782	2766	3248	3711	4554	1.001	140000

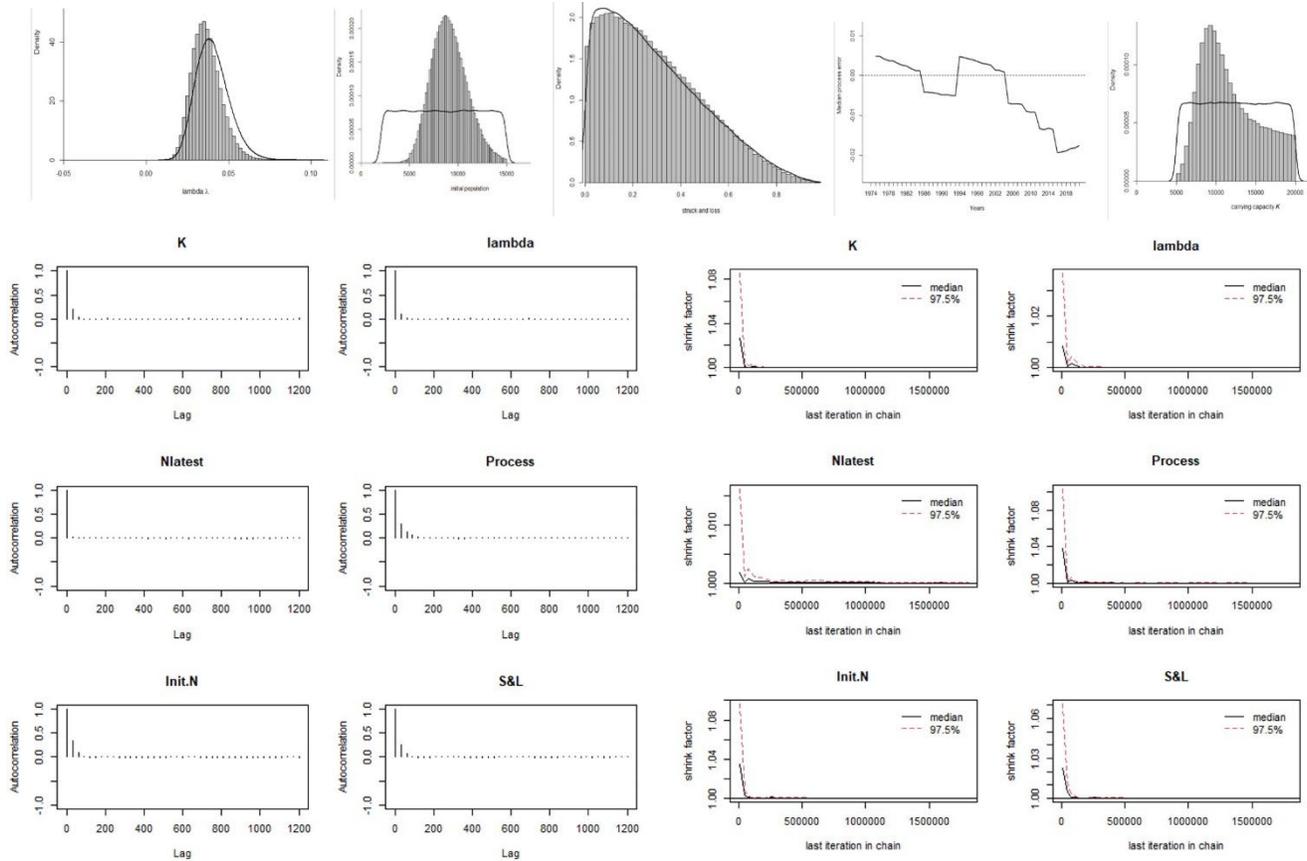


Figure B5. Model priors and posteriors for parameters for the BEL-EHB model runs assuming a coefficient of variance of 40% on the 2021 survey. Priors are shown as dark lines, posterior values are columns for parameters: maximum rate of increase (λ), initial population, struck and loss and process error carrying capacity (K), autocorrelation and convergence.

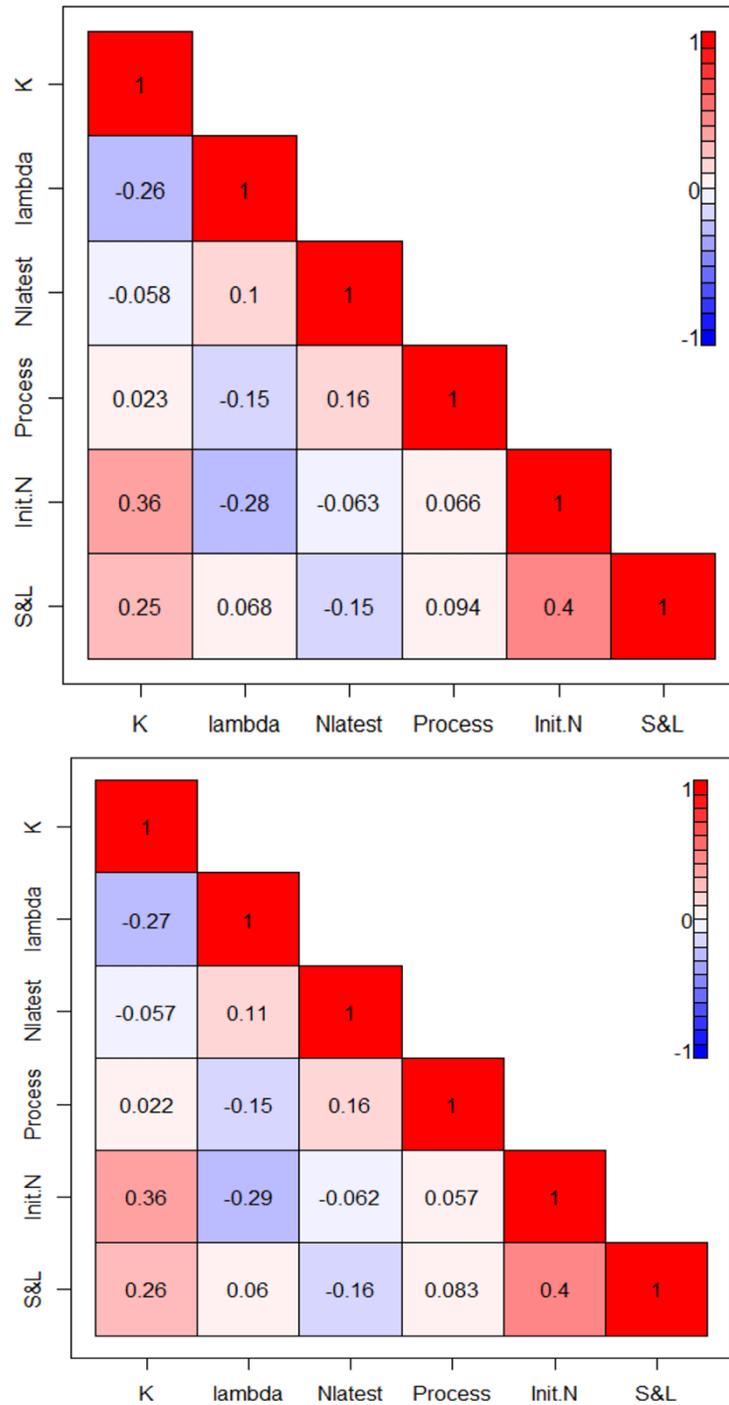


Figure B6. Model priors and posteriors for parameters for the BEL-EHB model runs assuming a coefficient of variance of 43% on the 2021 survey. Correlation among model parameters carrying capacity (K), starting population (Init.N), struck and loss (S&L), maximum rate of increase (lambda) and process error (Process), and 2021 abundance estimate (Nlatest).

Population model-JAGS code

```
#####  
##### Nunavik beluga model using R2jags assessment (all in R) #####  
#####  
rm(list=ls())  
setwd ("F:/Datas_whales/Beluga/Assessment 2022/JAGS")  
options(warn = -1)  
options(max.print=999999)  
library(R2jags)  
library(Hmisc)  
library(R.utils)  
library(R2WinBUGS)  
library(parallel)  
source("jags_modifications.r") ## modify original JAGS code to avoid auto-thinning, correctly handle the  
results from the parallelized version and add the potential to update this model afterward using parallel  
calculations - THIS SOURCE CODE MUST BE IN THE SAME DIRECTORY TO RUN IT  
sessionInfo()  
start.time1 <- Sys.time()  
  
#####  
### DATA ###  
#####  
# year range  
start.year=1974  
last.year=2021  
Nyears=last.year-start.year+1  
# surveys  
###Nunavik beluga Abundance Estimates #####  
survey.year=c(1985,1993,2001,2004,2008,2011,2015,2021)  
survey=c(6967,4061,4430,7153,4164,5060,8205,2315)  
survey.se=c(3240,1961,2427,3276,2265,2879,4053,734)  
  
###End of Nunavik beluga Data#####  
Nsurv=length(survey.year) # number of surveys  
surv.year=survey.year-start.year+1 # survey year number (i.e., 1 = starting year)  
#IMPORTANT WEIGHTING BY SURVEY SE  
survey.prec = 1/survey.se^2  
  
# catches  
catch<-read.csv2("catchSF_MOH1974update to 2021nov.csv", header=T)  
  
ARC=catch$ARC  
HSUB=catch$HSUB  
SAN=catch$SAN  
SPRING=catch$SPRING  
FALL=catch$FALL  
UBSP=catch$UBSP  
UBFA=catch$UBFA  
NEHBSP=catch$NEHBSP  
NEHBFA=catch$NEHBFA  
  
# projections  
N.fut.years=50 # number of years to project into the future  
Fut.lev=c(0,20,30,40,50,60,65,70,75,80,90,100,110,125,150,175,200,225,250,275,300) #future catch  
levels could be any number of scenarios  
N.lev=length(Fut.lev) # number of future catch levels
```

```

dataDL<-
list(Nyears=Nyears,Nsurv=Nsurv,N.fut.years=N.fut.years,N.lev=N.lev,Fut.lev=Fut.lev,surv.year=surv.year,
survey=survey,survey.prec=survey.prec,ARC=ARC,HSUB=HSUB,SAN=SAN,
SPRING=SPRING,FALL=FALL,UBSP=UBSP,UBFA=UBFA,NEHBSP=NEHBSP,NEHBFA=NEHBFA)

#####
### MODEL ###
#####

modelJAGS <- function(){

### PRIORS
# these are updated from file genetic results to provide rollover advice to board 16072019.xlsx
pSANSP~dbeta(45.77792,27.16434) #quantiles 0.5146050 0.5899003 0.6287670 0.6663520 0.7340679
pSANSP.prior ~dbeta(45.77792,27.16434)
pSANFA~dbeta(8.19355,5.32306) #quantiles 0.3436,0.5193,0.6113,0.6990,0.8370
pSANFA.prior ~dbeta(8.19355,5.32306)
pSANW~dbeta(3.69697,5.4934) #quantiles 0.1311,.2883, 0.3956, 0.5098, 0.7151
pSANW.prior ~dbeta(3.69697,5.4934)
pHSUB~dbeta(50.58324,64.36119) #quantiles are 0.351,0.408,0.4394, 0.4709,0.5318-changed to
assume the HS fall hunt,
pHSUB.prior~dbeta(50.58324,64.36119)

pSPRING~dbeta(32.11427,229.0895) #quantiles 0.086,0.109, 0.122, 0.136, 0.165
pSPRING.prior~dbeta(32.11427,229.0895)
pFALL~dbeta(50.58324,64.36119)
pFALL.prior~dbeta(50.58324,64.36119) #quantiles are 0.351,0.408,0.4394, 0.4709,0.5318
pUBSP~dbeta(3.13,57.43) #quantiles are 0.015 0.047 0.12
pUBSP.prior~dbeta(3.13,57.43)
pUBFA~dbeta(50.58324,64.36119) #0.0114,0.0912,0.19
pUBFA.prior~dbeta(50.58324,64.36119)
pNEHBSP~dbeta(32.11427,229.0895) #only 2 samples used HS spring
pNEHBSP.prior~dbeta(32.11427,229.0895)
pNEHBFA~dbeta(6.22767,6.20281) #quantiles are 0.2401,0.4047,0.5011,0.5978,0.762
pNEHBFA.prior~dbeta(6.22767,6.20281)

struck.and.lost~dbeta(1.13536, 2.76339) # 0.01504672 0.12269235 0.25276648 0.42599210
0.75316933 median based on Richard but was broadened
struck.and.lost.prior~dbeta(1.13536, 2.76339) #

prec.process ~ dgamma(1.5,0.005) #dgamma(1.5,0.00005)
prec.process.prior ~ dgamma(1.5,0.005) #dgamma(1.5,0.00005)

lambda ~dbeta( 15.61764, 373.015 ) # quantiles at 0.02299609 0.03308768 0.03934645 0.04637804
0.06159435
lambda.prior ~dbeta(15.61764, 373.015)

K~ dunif(5000,20000)#dgamma(12,0.001) # in assessment use upper of 25000
K.prior~dunif(5000,20000) #dgamma(12,0.001)

startpop1 ~ dunif(2000,15000)
startpop1.prior ~ dunif(2000,15000)
startpop <- min(startpop1,K)
startpop.prior ~ dunif(2000,15000)

R<-2.39

```

STATE PROCESS

```
Nstart[1] <- startpop
```

```
Nfin[1] <- Nstart[1] - (ARC[1]+HSUB[1]*pHSUB+ (0.16*SAN[1])+ (.54*SAN[1]*pSANSP)+  
(.12*SAN[1]*pSANFA)+  
(.18*SAN[1]*pSANW)+SPRING[1]*pSPRING+FALL[1]*pFALL+UBSP[1]*pUBSP+UBFA[1]*pUBFA+NEHB  
SP[1]*pNEHBSP +NEHBFA[1]*pNEHBFA)* (1+struck.and.lost)
```

```
for (year in 2:9)
```

```
{ proc.error[year] ~ dlnorm(0,prec.process)
```

```
Nstart[year] <- (Nfin[year-1]*((1+lambda*(1-(Nfin[year-1]/(K))^R))))*(proc.error[year] ) #density dependent  
growth
```

```
Nfin[year] <- max(.01,Nstart[year] - (ARC[year]+HSUB[year]*pHSUB+ (0.16*SAN[year])+  
(.54*SAN[year]*pSANSP)+ (.12*SAN[year]*pSANFA)+  
(.18*SAN[year]*pSANW)+SPRING[year]*pSPRING+FALL[year]*pFALL+UBSP[year]*pUBSP+UBFA[year]  
*pUBFA+NEHBSP[year]*pNEHBSP  
+NEHBFA[year]*pNEHBFA)* (1+struck.and.lost) )  
}
```

```
for (year in 10:Nyears)
```

```
{ proc.error[year] ~ dlnorm(0,prec.process)
```

```
Nstart[year] <- (Nfin[year-1]*((1+lambda*(1-(Nfin[year-1]/(K))^R))))*(proc.error[year] ) #density dependent  
growth
```

```
Nfin[year] <- max(.01,Nstart[year] - (ARC[year]+HSUB[year]*pHSUB+ (0.16*SAN[year])+  
(.54*SAN[year]*pSANSP)+ (.12*SAN[year]*pSANFA)+  
(.18*SAN[year]*pSANW)+SPRING[year]*pSPRING+FALL[year]*pFALL+UBSP[year]*pUBSP+UBFA[year]  
*pUBFA+NEHBSP[year]*pNEHBSP  
+NEHBFA[year]*pNEHBFA)* (1+struck.and.lost) )  
}
```

OBSERVATION PROCESS for weighted fit where the surveys are weighted by the se

```
for (surv.ser in 1:Nsurv)
```

```
# NOTE: *** adjusted expected log N for variance/2, so mean survey will equal estimated N
```

```
{  
  survey.pred[surv.ser] <- (Nstart[surv.year[surv.ser]])  
  rate[surv.ser] <- survey.pred[surv.ser] * survey.prec[surv.ser]  
  survey[surv.ser] ~ dgamma(survey.pred[surv.ser] * rate[surv.ser], rate[surv.ser])  
}
```

FUTURE PREDICTIONS

```
for (lev in 1:N.lev)
```

```
{ for (year in 1:1)
```

```
{ fut.error[lev,year] ~ dlnorm(0,prec.process)
```

```
fut.Nstart[lev,year] <- (Nfin[Nyears]*((1+lambda*(1-(Nfin[Nyears]/(K))^R))))*fut.error[lev,year]
```

```
fut.Nfin[lev,year] <- max(1,(fut.Nstart[lev,year] - Fut.lev[lev]* (1+struck.and.lost) ) )
```

```
P.less[lev,year] <- step(Nfin[Nyears]-fut.Nfin[lev,year])  
}
```

```
for (year in 2:N.fut.years)
```

```
{ fut.error[lev,year] ~ dlnorm(0,prec.process)
```

```
fut.Nstart[lev,year] <- max(1,(fut.Nfin[lev,year-1]*((1+lambda*(1-(fut.Nfin[lev,year-  
1]/(K))^R))))*fut.error[lev,year] )
```

```
  fut.Nfin[lev,year] <- max(1,(fut.Nstart[lev,year] - Fut.lev[lev]* (1+struck.and.lost) ) )
```

```
  P.less[lev,year] <- step(Nfin[Nyears]-fut.Nfin[lev,year])  
}
```

```
}
```

```

####end of model
}

write.model(modelJAGS, modelJAGS <- paste0(getwd(),"/modelJAGS.bug")) ####this line is needed to
allow the parallel function to work

#####
### INITS ###
#####

Nchains = 5
Final_Nlter = 2000 #60000 #25000 good number at 20k iter
Thining = 50 #50
Burnin = 2000 #25000 #50000 #10000
Effective_Nlter = Burnin + Final_Nlter * Thining
Inits <- rep(list(list()),Nchains)

#####
### RUN ###
#####

print(paste("run time elapsed:", round(system.time(
m <- jags.parallel(model.file=modelJAGS,
  n.chains = Nchains,
  n.thin = Thining,
  n.iter = Effective_Nlter,
  n.burnin = Burnin,
  dat = dataDL,
  inits = Inits,
  parameters.to.save= c("K","K.prior","R","R.prior","lambda.prior","lambda",
    "rr.prior","rr","startpop.prior","startpop", "var.inflat.fact","prec.adj" ,
    "struck.and.lost.prior","struck.and.lost","histo","histo.prior",
    "prec.process.prior","prec.process", "proc.error" ,
    "Nfin","fut.Nfin","HARVEST","survey.prec",
    paste("P.less[", 1:N.lev, ", ",N.fut.years,"]", sep=""),

    "pSANSP","pSANFA","pSANW","pHSUB","pSPRING","pFALL","pUBSP","pUBFA","pNEH
BSP","pNEHBFA"))
)[3],"seconds"))

a<-sapply(rownames(m$BUGSoutput$summary), function(x) { temp <-
as.numeric(unlist(strsplit(substr(x,regexpr("\\[", x)+1, regexpr("\\]", x)-1), ","))) ;
as.numeric(paste(ifelse(temp<10, paste("0", temp, sep=""), temp), collapse="")) })

b<-substring(rownames(m$BUGSoutput$summary), 1,as.numeric(regexpr("\\[",
rownames(m$BUGSoutput$summary))-1)

mod.summary<-round(m$BUGSoutput$summary[order(b,a),],3)

##### Genetic proportions and total harvest #####

pSANSP<-mod.summary[substr(rownames(mod.summary),1,6) == "pSANSP","50%"]
pSANFA<-mod.summary[substr(rownames(mod.summary),1,7) == "pSANFA","50%"]
pSANW<-mod.summary[substr(rownames(mod.summary),1,6) == "pSANW","50%"]
pHSUB<-mod.summary[substr(rownames(mod.summary),1,6) == "pHSUB","50%"]
pSPRING<-mod.summary[substr(rownames(mod.summary),1,10) == "pSPRING","50%"]
pFALL<-mod.summary[substr(rownames(mod.summary),1,5) == "pFALL","50%"]
pUBSP<-mod.summary[substr(rownames(mod.summary),1,12) == "pUBSP","50%"]

```

```

pUBFA<-mod.summary[substr(rownames(mod.summary),1,11) == "pUBFA","50%"]
pNEHBSP<-mod.summary[substr(rownames(mod.summary),1,8) == "pNEHBSP","50%"]
pNEHBFA<-mod.summary[substr(rownames(mod.summary),1,7) == "pNEHBFA","50%"]

HARVEST<-
ARC+((0.16*SAN)+(0.54*SAN*pSANSF)+(0.12*SAN*pSANFA)+(0.18*SAN*pSANW)+HSUB*pHSUB+SPRING*pSPRING+FALL*pFALL+UBSP*pUBSP+UBFA*pUBFA+NEHBSP*pNEHBSP+NEHBFA*pNEHBFA)

##### priors and posteriors #####

K<-m$BUGSoutput$sims.list$K
K.prior<-m$BUGSoutput$sims.list$K.prior
R<-m$BUGSoutput$sims.list$R
R.prior<-m$BUGSoutput$sims.list$R.prior
lambda<-m$BUGSoutput$sims.list$lambda
lambda.prior<-m$BUGSoutput$sims.list$lambda.prior
startpop<-m$BUGSoutput$sims.list$startpop
startpop.prior<-m$BUGSoutput$sims.list$startpop.prior
struck.and.lost<-m$BUGSoutput$sims.list$struck.and.lost
struck.and.lost.prior<-m$BUGSoutput$sims.list$struck.and.lost.prior
prec.process<-1/sqrt(m$BUGSoutput$sims.list$prec.process)
prec.process.prior<-1/sqrt(m$BUGSoutput$sims.list$prec.process.prior)
proc.error<-(m$BUGSoutput$sims.list$proc.error)-1

# calculate log-normal CI around survey estimates
cvalue <- function(CV) { exp(1.96 * sqrt(log(1 + CV^2))) }
Nvec<-survey
CVvec<-survey.se/survey
Cvec<-cvalue(CVvec)
lcl_vec <- Nvec/Cvec
ucl_vec <- Nvec*Cvec

##### Abundance estimates and plot #####

dev.new(width=12,height=10)
par(mar=c(5, 4, 4, 4) + 0.1, bty="l")
plot(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin","50%"]~seq(start.year,start.year+Nyears-
1),type="l",lwd=2,xlim=c(start.year,start.year+Nyears),ylim=c(0,15000),yaxp=c(0,15000,15),ylab="Abundance",
xlab="Years",xaxt="n")
par(xaxp=c(1974,2022,15))
lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin","2.5%"]~seq(start.year,start.year+Nyears-1),lty=2)
lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin","97.5%"]~seq(start.year,start.year+Nyears-1),lty=2)
lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin","25%"]~seq(start.year,start.year+Nyears-1),lty=2)
lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin","75%"]~seq(start.year,start.year+Nyears-1),lty=2)
points(survey.year, survey, pch=19)
errbar(survey.year, survey, ucl_vec, lcl_vec, add=T)
axis(1,at=seq(start.year,start.year+Nyears-1),lab=as.character(seq(start.year,start.year+Nyears-1)))

##### Projections #####

Nfin<-m$BUGSoutput$sims.list$Nfin
fut.Nfin<-m$BUGSoutput$sims.list$fut.Nfin
Fut.catch<-m$BUGSoutput$sims.list$Fut.catch
dev.new(width=21,height=14)

```

```

par(mfrow=c(2,3),cex.lab=1.5,cex.axis=1.5, bty="l")
# choose future harvest level to plot
h<-9
plot(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin", "50%"]~seq(start.year,start.year+Nyears-
1),type="l",lwd=2,xlim=c(start.year,start.year+Nyears+N.fut.years+2),ylim=c(-
10000,15000),ylab="Abundance", xlab="Years",xaxt="n", yaxs="i", yaxt="n")
mtext(side=3,text=paste("Future harvest = ",Fut.lev[h],"/year",sep=""),col="red",adj=1)
axis(2, at=seq(0,15000,500))
abline(h=0)
lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin", "2.5%"]~seq(start.year,start.year+Nyears-1),lty=2)
lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin", "97.5%"]~seq(start.year,start.year+Nyears-1),lty=2)
points(survey.year, survey, pch=19)
errbar(survey.year, survey, ucl_vec, lcl_vec, add=T)
axis(1,at=seq(start.year,start.year+Nyears+N.fut.years-
1),lab=as.character(seq(start.year,start.year+Nyears+N.fut.years-1)))
#future starts here
abline(v=2021,lty=3)
#medians
lines((start.year+Nyears-1):(start.year+Nyears),c(median(Nfin[,Nyears]),median(fut.Nfin[,h,1])), col="red",
lwd=2)
lines(seq((start.year+Nyears),(start.year+Nyears+N.fut.years-1)),apply(fut.Nfin[,h,],2,median), col="red",
lwd=2)
#quantiles 2.5 97.5
lines((start.year+Nyears-
1):(start.year+Nyears),c(quantile(Nfin[,Nyears],probs=c(0.025)),quantile(fut.Nfin[,h,1],probs=c(0.025))),
lty=2, col="red", lwd=1)
lines((start.year+Nyears-
1):(start.year+Nyears),c(quantile(Nfin[,Nyears],probs=c(0.975)),quantile(fut.Nfin[,h,1],probs=c(0.975))),
lty=2, col="red", lwd=1)
lines(seq((start.year+Nyears),(start.year+Nyears+N.fut.years-1)),apply(fut.Nfin[,h,],2,function(x)
quantile(x,probs=c(0.025))), lty=2, col="red", lwd=1)
lines(seq((start.year+Nyears),(start.year+Nyears+N.fut.years-1)),apply(fut.Nfin[,h,],2,function(x)
quantile(x,probs=c(0.975))), lty=2, col="red", lwd=1)
par(new=T)

plot(seq(start.year,start.year+Nyears+N.fut.years-
1),rep(1,Nyears+N.fut.years),type="n",xlim=c(start.year,start.year+Nyears+N.fut.years),ylim=c(0,1000),
yaxt="n",ylab="", xaxt="n", xlab="")
lines(seq(start.year,start.year+Nyears-1),HARVEST)
points(seq(start.year,start.year+Nyears-1),HARVEST,pch=21,bg="white")
axis(4,
at=c(0,10,20,25,30,35,40,45,50,55,60,65,70,75,100,300),labels=c(0,10,20,25,30,35,40,45,50,55,60,65,70
,75,100,300), line=-5,cex.axis=1)
mtext(side=4,text="landed catch", adj=0.075, line=-3, cex=0.75)

### alt version with multiple catch levels
plot(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin", "50%"]~seq(start.year,start.year+Nyears-
1),type="l",lwd=2,xlim=c(start.year,start.year+Nyears+N.fut.years+2),ylim=c(0,15000),ylab="Abundance",
xlab="Years",xaxt="n", yaxs="i")
lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin", "2.5%"]~seq(start.year,start.year+Nyears-1),lty=2)

```

```

lines(mod.summary[substr(rownames(mod.summary),1,4) ==
"Nfin", "97.5%"]~seq(start.year,start.year+Nyears-1),lty=2)
points(survey.year, survey, pch=19)
errbar(survey.year, survey, ucl_vec, lcl_vec, add=T)
axis(1,at=seq(start.year,start.year+Nyears+N.fut.years-
1),lab=as.character(seq(start.year,start.year+Nyears+N.fut.years-1)))
#future starts here...
abline(v=2022,lty=3)

#medians
nofurther=F
for(h in 1:N.lev){
  lines((start.year+Nyears-1):(start.year+Nyears),c(median(Nfin[,Nyears]),median(fut.Nfin[,h,1])),
col="red", lwd=2)
  lines(seq((start.year+Nyears),(start.year+Nyears+N.fut.years-1)),apply(fut.Nfin[,h,],2,median),
col="red", lwd=2)
  if(median(fut.Nfin[,h,N.fut.years])>0){
    text(label=as.character(Fut.lev[h]),x=start.year+Nyears+N.fut.years+1.5,
y=median(fut.Nfin[,h,N.fut.years]),col="red",cex=1)
  }
  if(median(fut.Nfin[,h,N.fut.years])<=0 & nofurther==F){
    text(label=bquote(">=(.Fut.lev[h])"),x=start.year+Nyears+N.fut.years+1.5, y=800,col="red",cex=1)
    nofurther<-T
  }
}
}

# K
hist(K,freq=F,n=50,col="gray",xlim=c(0,1.5*max(max(K.prior),max(K))),ylim=c(0,1.3*max(max(hist(K,n=50
,plot=F)$density),max(density(K)$y))),xaxs="i",yaxs="i",main="",ylab="Density",xlab=expression(paste("ca
rrying capacity ",italic(K))))
#lines(density(K.prior,adjust=1.5,cut=-1), lwd=2)
lines(density(K.prior), lwd=2)

#prec process
plot(1,20,type="n",xlim=c(0,0.4),ylim=c(0,50),xaxs="i",yaxs="i",main="",ylab="Density",xlab=expression(p
aste("Prec ",italic(process))))
hist(prec.process, freq=F, n=50, col="gray", add=T)
lines(density(prec.process.prior), lwd=2)

# Proc error
plot(1,1,type="n",xlim=c(-
0.5,0.5),ylim=c(0,6),xaxs="i",yaxs="i",main="",ylab="Density",xlab=expression(paste("proc.error
",italic()))))
hist(proc.error, freq=F, n=50, col="gray", add=T)

# lambda
plot(1,1,type="n",xlim=c(-
.05,0.11),ylim=c(0,80),xaxs="i",yaxs="i",main="",ylab="Density",xlab=expression(paste("lambda
",italic(lambda))))
hist(lambda, freq=F, n=50, col="gray", add=T)
lines(density(lambda.prior), lwd=2)

# start.pop
hist(startpop,freq=F,n=50,col="gray",xlim=c(0,1.5*max(max(startpop.prior),max(startpop))),ylim=c(0,1.3*
max(max(density(startpop.prior)$y),max(hist(startpop,n=50,plot=F)$density))),xaxs="i",yaxs="i",main="",yl
ab="Density",xlab="initial population (1985)")

```

```

#lines(density(startpop.prior,adjust=1.5,cut=-1), lwd=2)
lines(density(startpop.prior), lwd=2)

# struck and lost
hist(struck.and.lost,freq=F,n=50,col="gray",xlim=c(-
.01,max(max(struck.and.lost.prior))),ylim=c(0,1.2*max(max(density(struck.and.lost.prior)$y),max(hist(stru
ck.and.lost,n=50,plot=F)$density))),xaxs="i",yaxs="i",,main="",ylab="Density",xlab="struck and loss")
#lines(density(struck.and.lost.prior,adjust=1.5,cut=-1), lwd=2)
lines(density(struck.and.lost.prior), lwd=2)

# time-series of median process errors (don't forget that proc.error begins at year 2)
plot(apply(proc.error,2,median)~seq(start.year+1,start.year+Nyears-1),type="l",lwd=2,ylim=c(-
0.025,.02),xlim=c(start.year,start.year+Nyears),ylab="Median process error", xlab="Years",xaxt="n")
abline(h=0, lty=2)
axis(1,at=seq(start.year,start.year+Nyears-1),lab=as.character(seq(start.year,start.year+Nyears-1)))

##### plot prob of decrease after XX years #####
dev.new(width=7,height=7)
par(mar=c(5, 4, 4, 4) + 0.1, bty="l")
#XX <- N.fut.years
XX <-5
meanp<-mod.summary[substr(rownames(mod.summary),1,6) == "P.less","mean"]
newprobs <- matrix(data=meanp,nrow=1,ncol=N.lev,dimnames=list(start.year+Nyears-1+XX,Fut.lev))
xxx<-as.numeric(colnames(newprobs))
yyy<-as.numeric(newprobs[1,])
interpol<-approx(xxx,yyy,n=2000)
print( p10<-which.min(abs(interpol$y-0.10)) )
print( p15<-which.min(abs(interpol$y-0.15)) )
print( p20<-which.min(abs(interpol$y-0.20)) )
print( p25<-which.min(abs(interpol$y-0.25)) )
print( p30<-which.min(abs(interpol$y-0.30)) )
print( p35<-which.min(abs(interpol$y-0.35)) )
print( p40<-which.min(abs(interpol$y-0.40)) )
print( p45<-which.min(abs(interpol$y-0.45)) )
print( p50<-which.min(abs(interpol$y-0.5)) )
print( p55<-which.min(abs(interpol$y-0.55)) )
print( p60<-which.min(abs(interpol$y-0.6)) )
print( p65<-which.min(abs(interpol$y-0.65)) )
print( p70<-which.min(abs(interpol$y-0.7)) )
print( p75<-which.min(abs(interpol$y-0.75)) )
print( p80<-which.min(abs(interpol$y-0.8)) )
print( p85<-which.min(abs(interpol$y-0.85)) )
print( p90<-which.min(abs(interpol$y-0.9)) )
print( p95<-which.min(abs(interpol$y-0.95)) )
plot(xxx,yyy, type="n",
      xlab="Annual landings of EHB beluga", ylab=paste("Probability of stock decrease from current
levels",start.year+Nyears-1,"to",start.year+Nyears-1+XX),
      ylim=c(0,1),xlim=c(0,200), xaxp=c(0,200,20),xaxs="i", yaxs="i", yaxp=c(0,1,20), cex=1.5)
lines(xxx,yyy, col="black", lwd=2, lty=1)
segments(interpol$x[p10],0,interpol$x[p10],0.1, lty=3, lwd=2)
segments(interpol$x[p15],0,interpol$x[p15],0.15, lty=3, lwd=2)
segments(interpol$x[p20],0,interpol$x[p20],0.2, lty=3, lwd=2)
segments(interpol$x[p25],0,interpol$x[p25],0.25, lty=3, lwd=2)
segments(interpol$x[p30],0,interpol$x[p30],0.30, lty=3, lwd=2)
segments(interpol$x[p35],0,interpol$x[p35],0.35, lty=3, lwd=2)
segments(interpol$x[p40],0,interpol$x[p40],0.40, lty=3, lwd=2)

```

```

segments(interpol$x[p45],0,interpol$x[p45],0.45, lty=3, lwd=2)
segments(interpol$x[p50],0,interpol$x[p50],0.5, lty=3, lwd=5)
segments(interpol$x[p55],0,interpol$x[p55],0.55, lty=3, lwd=2)
segments(interpol$x[p60],0,interpol$x[p60],0.6, lty=3, lwd=2)
segments(interpol$x[p65],0,interpol$x[p65],0.65, lty=3, lwd=2)
segments(interpol$x[p70],0,interpol$x[p70],0.7, lty=3, lwd=2)
segments(interpol$x[p75],0,interpol$x[p75],0.75, lty=3, lwd=2)
segments(interpol$x[p80],0,interpol$x[p80],0.80, lty=3, lwd=2)
segments(interpol$x[p85],0,interpol$x[p85],0.85, lty=3, lwd=2)
segments(interpol$x[p90],0,interpol$x[p90],0.90, lty=3, lwd=2)
segments(interpol$x[p95],0,interpol$x[p95],0.95, lty=3, lwd=2)
segments(0,0.1,interpol$x[p10],0.1, lty=3, lwd=2)
segments(0,0.15,interpol$x[p15],0.15, lty=3, lwd=2)
segments(0,0.2,interpol$x[p20],0.2, lty=3, lwd=2)
segments(0,0.25,interpol$x[p25],0.25, lty=3, lwd=2)
segments(0,0.30,interpol$x[p30],0.30, lty=3, lwd=2)
segments(0,0.35,interpol$x[p35],0.35, lty=3, lwd=2)
segments(0,0.40,interpol$x[p40],0.40, lty=3, lwd=2)
segments(0,0.45,interpol$x[p45],0.45, lty=3, lwd=2)
segments(0,0.50,interpol$x[p50],0.50, lty=3, lwd=5)
segments(0,0.55,interpol$x[p55],0.55, lty=3, lwd=2)
segments(0,0.60,interpol$x[p60],0.60, lty=3, lwd=2)
segments(0,0.65,interpol$x[p65],0.65, lty=3, lwd=2)
segments(0,0.70,interpol$x[p70],0.70, lty=3, lwd=2)
segments(0,0.75,interpol$x[p75],0.75, lty=3, lwd=2)
segments(0,0.80,interpol$x[p80],0.80, lty=3, lwd=2)
segments(0,0.85,interpol$x[p85],0.85, lty=3, lwd=2)
segments(0,0.90,interpol$x[p90],0.90, lty=3, lwd=2)
segments(0,0.95,interpol$x[p95],0.95, lty=3, lwd=2)

```

```
#####
```

```

stop.time1 <- Sys.time()
runtime<-start.time1-stop.time1
runtime

```

```
##### plot prob of staying above a management target WHERE TARGET AND NUMBER OF YEARS ARE STATED###
```

```
# input 1: after how many years (by default = N.fut.years)
```

```
#XX <- N.fut.years
```

```
XX<-10
```

```
# input 2: reference point / target
```

```
#target <- 0.24*median(K) # can replaced by a single value of K eg 0.69*median(K) or a fixed value
```

```
target <-3464
```

```
# get N estimates for year XX (a matrix with [i=n.iter,j=N.lev]
```

```
pop.matrix<-m$BUGSoutput$sims.list$fut.Nfin[,XX]
```

```
# for each harvest level, how many iterations are above target
```

```
probs.target <- apply(pop.matrix,2,function(x) {length(which(x>=target))/length(x)})
```

```
# interpolate probabilities
```

```
interpol<-approx(Fut.lev,probs.target,n=2000)
```

```
print( p05<-which.min(abs(interpol$y-0.05)) )
```

```
print( p10<-which.min(abs(interpol$y-0.10)) )
```

```
print( p15<-which.min(abs(interpol$y-0.15)) )
```

```
print( p20<-which.min(abs(interpol$y-0.20)) )
```

```

print( p25<-which.min(abs(interpol$y-0.25)) )
print( p30<-which.min(abs(interpol$y-0.30)) )
print( p35<-which.min(abs(interpol$y-0.35)) )
print( p40<-which.min(abs(interpol$y-0.40)) )
print( p45<-which.min(abs(interpol$y-0.45)) )
print( p50<-which.min(abs(interpol$y-0.5)) )
print( p55<-which.min(abs(interpol$y-0.55)) )
print( p60<-which.min(abs(interpol$y-0.6)) )
print( p65<-which.min(abs(interpol$y-0.65)) )
print( p70<-which.min(abs(interpol$y-0.7)) )
print( p75<-which.min(abs(interpol$y-0.75)) )
print( p80<-which.min(abs(interpol$y-0.8)) )
print( p85<-which.min(abs(interpol$y-0.85)) )
print( p90<-which.min(abs(interpol$y-0.9)) )
print( p95<-which.min(abs(interpol$y-0.95)) )
dev.new()

```

```

#plot(Fut.lev,probs.target, type="l",xlab="Prélèvements annuels de béluga de l'EBH ", ylab=paste("«
Probabilité d'avoir une population de ",target,"
après",XX,"ans"),ylim=c(0,1),xlim=c(0,300),xaxp=c(0,300,10), xaxs="i", yaxs="i", lwd=2, yaxp=c(0,1,20),
cex=1.5)
plot(Fut.lev,probs.target, type="l",xlab="Annual EHB beluga harvest", ylab=paste("Probability of
population of ",target," after",XX,"years"),ylim=c(0,1),xaxp=c(0,300,30), xaxs="i", yaxs="i", lwd=2,
yaxp=c(0,1,20), cex=1.5)
#plot(Fut.lev,probs.target, type="l",xlab="Annual EHB beluga harvest", ylab=paste("Probability of staying
above target ", "population", " after",XX,"years"),ylim=c(0,1),xaxp=c(0,100,50),# xaxs="i", yaxs="i", lwd=2,
yaxp=c(0,1,20), cex=1.5)

```

```

segments(interpol$x[p05],0,interpol$x[p05],0.05, lty=3, lwd=2)
segments(interpol$x[p10],0,interpol$x[p10],0.1, lty=3, lwd=2)
segments(interpol$x[p15],0,interpol$x[p15],0.15, lty=3, lwd=2)
segments(interpol$x[p20],0,interpol$x[p20],0.2, lty=3, lwd=2)
segments(interpol$x[p25],0,interpol$x[p25],0.25, lty=3, lwd=2)
segments(interpol$x[p30],0,interpol$x[p30],0.30, lty=3, lwd=2)
segments(interpol$x[p35],0,interpol$x[p35],0.35, lty=3, lwd=2)
segments(interpol$x[p40],0,interpol$x[p40],0.40, lty=3, lwd=2)
segments(interpol$x[p45],0,interpol$x[p45],0.45, lty=3, lwd=2)
segments(interpol$x[p50],0,interpol$x[p50],0.5, lty=1, lwd=4,col='red')
segments(interpol$x[p55],0,interpol$x[p55],0.55, lty=3, lwd=2)
segments(interpol$x[p60],0,interpol$x[p60],0.6, lty=3, lwd=2)
segments(interpol$x[p65],0,interpol$x[p65],0.65, lty=3, lwd=2)
segments(interpol$x[p70],0,interpol$x[p70],0.7, lty=3, lwd=2)
segments(interpol$x[p75],0,interpol$x[p75],0.75, lty=3, lwd=2)
segments(interpol$x[p80],0,interpol$x[p80],0.80, lty=3, lwd=2)
segments(interpol$x[p85],0,interpol$x[p85],0.85, lty=3, lwd=2)
segments(interpol$x[p90],0,interpol$x[p90],0.90, lty=3, lwd=2)
segments(interpol$x[p95],0,interpol$x[p95],0.95, lty=3, lwd=2)
segments(0,0.05,interpol$x[p05],0.05, lty=3, lwd=2)
segments(0,0.1,interpol$x[p10],0.1, lty=3, lwd=2)
segments(0,0.15,interpol$x[p15],0.15, lty=3, lwd=2)
segments(0,0.2,interpol$x[p20],0.2, lty=3, lwd=2)
segments(0,0.25,interpol$x[p25],0.25, lty=3, lwd=2)
segments(0,0.30,interpol$x[p30],0.30, lty=3, lwd=2)
segments(0,0.35,interpol$x[p35],0.35, lty=3, lwd=2)
segments(0,0.40,interpol$x[p40],0.40, lty=3, lwd=2)
segments(0,0.45,interpol$x[p45],0.45, lty=3, lwd=2)
segments(0,0.50,interpol$x[p50],0.50, lty=1, lwd=4,col='red')

```

```
segments(0,0.55,interpol$x[p55],0.55, lty=3, lwd=2)
segments(0,0.60,interpol$x[p60],0.60, lty=3, lwd=2)
segments(0,0.65,interpol$x[p65],0.65, lty=3, lwd=2)
segments(0,0.70,interpol$x[p70],0.70, lty=3, lwd=2)
segments(0,0.75,interpol$x[p75],0.75, lty=3, lwd=2)
segments(0,0.80,interpol$x[p80],0.80, lty=3, lwd=2)
segments(0,0.85,interpol$x[p85],0.85, lty=3, lwd=2)
segments(0,0.90,interpol$x[p90],0.90, lty=3, lwd=2)
segments(0,0.95,interpol$x[p95],0.95, lty=3, lwd=2)
```

```
#####
```