NWRT Project Number: **2-17-01**

Grizzly bear population and density estimates in Kivalliq, Nunavut, using DNA based mark-recapture method

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Analysis of Kivalliq grizzly bear monitoring 2016–2017

DRAFT: October 21, 2018

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Contents

Summary

1. The grizzly bear population of the Kivalliq region of Nunavut was sampled with DNA hair snare posts in 2016 and 2017. A total of 48 bears were recognised in samples from four 60-km x 60-km grids.
2. Spatially explicit capture–recapture analyses of the grid data indicated a density of 3.5 bears / 1000 km^2 (95% CI 2.1–6.1 bears / 1000 km^2). This corresponded to a population of 662 bears (95% CI 385–1135) in the 209 000 km^2 region as a whole, excluding zones within 50 km of settlements.
3. Supplementary intensive sampling around Henik, Oftedal and Roseblade Lakes in 2017 revealed 19 grizzly bears. To estimate density from these data it must be assumed that bear movements along the lake shore are indicative of movement perpendicular to the shore. With this assumption the estimated local density was 9.6 bears / 1000 km^2 (95% CI 4.4–20.9 / 1000 km^2). It is unsafe to incorporate these data in a region-wide capture–recapture analysis of density as the lakes are not representative of the region as a whole.
4. The goal of density estimates with 20% relative standard error (RSE) can probably be achieved with about 280 posts in about seven 60-km x 60-km grids arranged in a chequer-board pattern over the region and re-visited 3 times over 6 weeks. Post sites that fall in lakes should be omitted from the design, rather than seeking to relocate the entire grid to dry land.
5. If a 'clean start' systematic random design (4) is deemed unachievable then we suggest completing the original design over two years using only dry-land sites. Joint analysis of these data will yield an overall estimate of density with adequate precision, but it will be hard to interpret analyses of data combined across multiple years (2016–2020) because time and space are confounded.
6. The target of 20% RSE is unlikely to be achieved with the basic design (4) if the final analysis needs to allow for additional effects (e.g., sex differences or a learned response) or regional density is actually less than 3.5 / 1000 km^2. There is a strong argument for augmenting the sampling effort to provide a safety margin (e.g., 4 visits over 8 weeks, or sampling alternate sites in a second year).

Introduction

This report presents capture–recapture analyses of grizzly bear (*Ursus arctos*) data collected from hair snares in the Kivalliq area of Nunavut in 2016 and 2017. A framework for sampling in Kivalliq was established by Boulanger, Efford and Awan (2013); this entailed 60-km x 60-km grids in a systematic random design (Fig. 1). The original intention was to sample six grids in each of two successive years. For logistical reasons only two grids were sampled in 2016 and two in 2017.

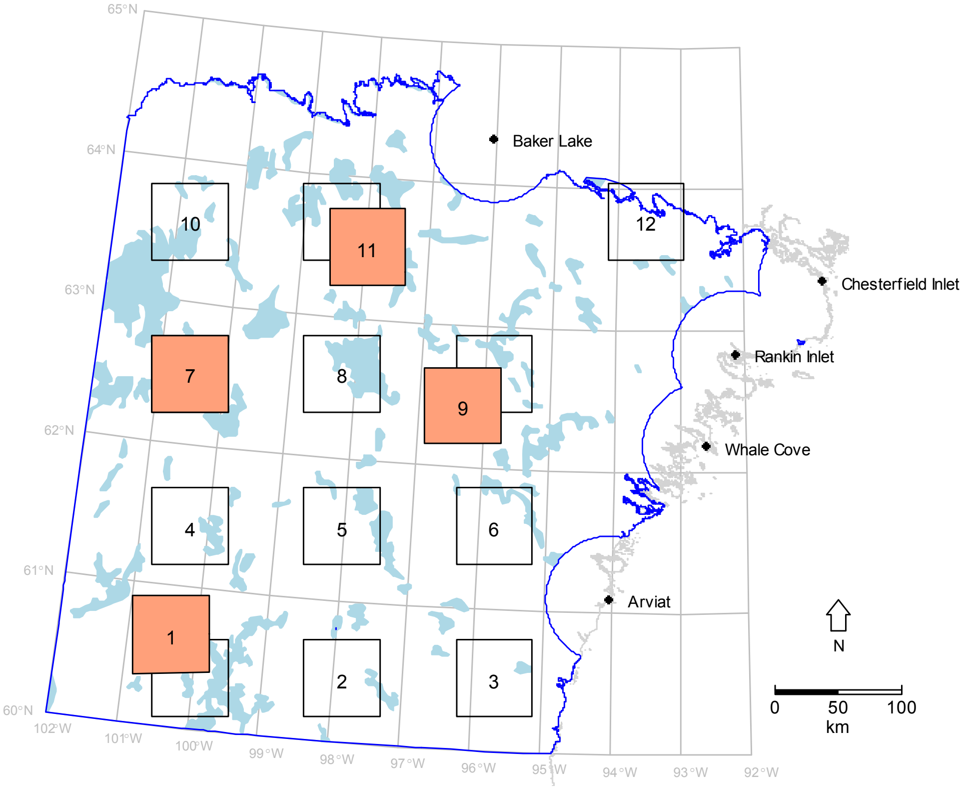

Fig. 1. Systematic sample of 60-km x 60-km study grids (open squares) proposed by Boulanger et al. (2013) to estimate grizzly bear density across Kivalliq region (blue outline; area including lakes 209 000 km^2) excluding sites within 50 km of settlements (black dots). Salmon-coloured squares indicate grids sampled in 2016–2017; three grids were shifted 28 km – 38 km to avoid lakes (pale blue).

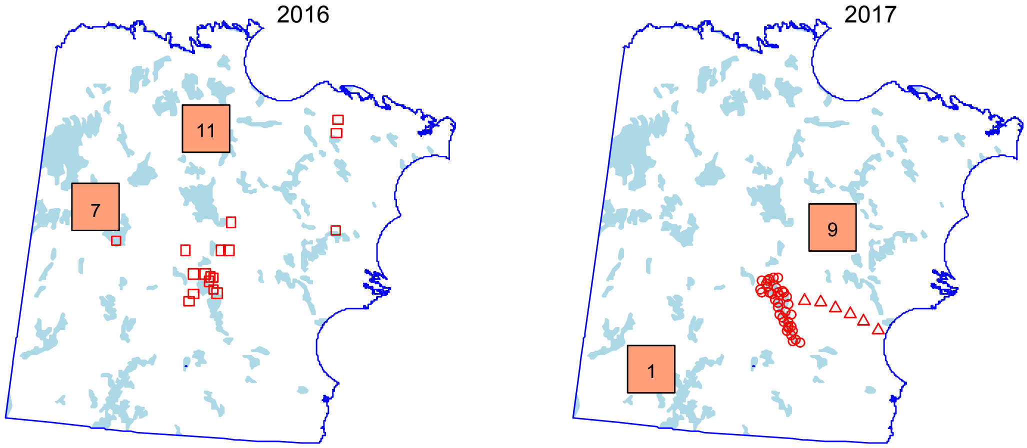

Fig. 2. Sampling sites. □ ad hoc samples 2016; ○ Henik, Oftedal and Roseblade Lakes 2017 (5 km spacing); Δ Transect posts Arviat–Henik 2017 (20 km spacing)

Methods

Field data collection

The four primary grids were each operated for about 6 weeks in one year, checked at approximately 2-week intervals. Data were also collected over 8 weeks in 2017 around Henik, Oftedal and Roseblade Lakes, and opportunistically at a few other sites in 2016 and 2017 (Fig. 2).

DNA records of hunted bears were not included in our summaries or analyses.

Laboratory analyses

Laboratory analyses by Wildlife Genetics International (Nelson, B.C.) used 8 barren-ground grizzly bear microsatellite markers and one sex marker. Potential genotyping errors were rigorously checked as described by Paetkau (2003).

A spatial capture–recapture dataset was assembled from the spreadsheets of DNA lab results (‘g1811 Results.xlsx’ from 2016 and ‘g1928 Results.xlsx’ from 2017). Repeat samples from the same individual, place and date were ignored. The resulting data match the binary proximity detector type used in SECR models (Efford et al. 2009; Efford 2018).

Spatially explicit capture–recapture (SECR) model

We estimated the population density (*D*) of grizzly bears by fitting spatially explicit capture–recapture (SECR) models to pooled data from the four grids sampled in 2016 and 2017. A SECR model has two components:

i. a model for the spatial distribution of activity (home range) centres, and
ii. an observation model that relates detection probability to the distance between a detector and an activity centre.

For computational convenience the distribution model is restricted to a region defined by a buffer around the detectors; the region is called the habitat mask or, when the model is fitted by Bayesian methods, the state space. In continuous habitat the buffer is made large enough that any further increase has a negligible effect on the estimates. For the Kivalliq analyses we chose a buffer of 60 km. The habitat mask was discretized as 2.5-km pixels; pixels were omitted if the centre fell in a lake as mapped in “AC_5M_Waterbodies.shp” (lakes comprised 10.5% of the land surface area).

The observation model may take various parametric forms. We used a (negative) exponential relationship between detection probability and distance: $g(d) = g_0\ e^{-d/\sigma}$ where g_0 and σ are parameters. The exponential accommodates occasional long movements, which we have found to be necessary in other grizzly bear analyses. Models using the exponential detection function were preferred to the more usual half-normal model (ΔAIC = 4.2; unpubl. results).

The basic observation model assumed g_0 and σ to be constant across individuals and sampling times. Failure of this assumption can cause bias in density estimates. We therefore considered possible sources of variation in g_0 and σ by fitting the following single-factor models and using Akaike’s Information Criterion (AIC) to compare them:

i. sex effect on scale of movement (g0~sex, σ~sex)
ii. general learned response (g0 ~ b)

iii. site-specific learned response (g0 ~ bk)
iv. temporal variation (g0 ~ session * t)

All these models used the 'hybrid mixture' formulation in secr (Efford 2018) which enables direct comparison of full-likelihood models with or without sex as a covariate.

Models were fitted by maximizing the integrated likelihood in version 3.1.7 of the R package 'secr' (Efford 2018).

Simulations of potential sampling across Kivalliq region

We undertook new simulations to determine the implications of the 2016–2017 results for region-wide sampling. The basic design was a systematic random sample of 60-km x 60-km subgrids at 120-km centres with random origin, following Boulanger et al. (2013). The earlier simulations were refined in these ways

i. A new systematic-random sample of locations was drawn for each replicate
ii. Post locations were dropped if they fell in a lake or outside the region boundary, and hence subgrids varied in shape and number of posts
iii. Grizzly bear activity centres were allowed to fall only on dry land
iv. Detection was modelled with an exponential function
v. Detection parameters were from a null (constant) model fitted to the 2016–2017 grid data ($g_0 = 0.12$, $\sigma = 7.0$ km) with the best density estimate (3.5 / 1000 km^2).

Across 1000 realisations the full systematic sample comprised on average 583 post locations (range 480–680, SD 44). We also considered a 50% subset of each sample – essentially the white squares of a chequerboard. These averaged 285 post locations (range 232–348, SD 25).

Data sets were generated with the functions sim.popn() and sim.capthist() in 'secr'. SECR estimates were calculated from each simulated dataset by maximising the conditional likelihood to estimate g_0 and σ and computing a derived estimate of density (Borchers and Efford 2008). We fitted a constant (null) model that did not include a sex effect or learned response.

Results

Data summary

Detections

A 'detection' represents the occurrence of a known individual at a particular post in a particular sampling interval (session); an individual may contribute more than one detection per session. A 're-detection' is any detection after the first (one less than the total number of detections for an individual). Over 2016 and 2017, 48 different bears were detected on the four grids; the total of 67 grid detections included 19 re-detections (Table 1). Bears were sometimes detected at more than one post per session; these re-detections accounted for 7 of the grid re-detections.

Table 1. Summary of data from 2016 and 2017. Grids 1, 7, 9 and 11 are mapped in Fig. 1.

	Posts	Sessions	Detections	Re-detections	Individuals
2016 Grid 7	49	3	27	7	20
2016 Grid 11	49	3	9	1	8
2016 Other	17	–[a]	8	0	8[b]
2017 Grid 1	49	3	10	5	5
2017 Grid 9	49	3	21	6	15
2017 Lakes	36	4	33	14	19
2017 Transect posts	6	3	2	0	2[c]

a. Timing of visits uncertain
b. Includes bear 1-7D3-X3a also detected on Grid 7
c. Includes bear 2-TP6-X2 also detected at Roseblade Lake

The sex ratio of detected bears was nearly even in 2016 (18 female, 17 male) and somewhat female-biased in 2017 (27 female, 13 male). The 2017 female bias applied to both grids (13 female, 7 male) and lakes (14 female, 5 male). Only one bear (female 3-WK1-G) was detected in both 2016 and 2017 (at non-grid site WK1 in 2016 and on Grid 9 in 2017).

Movements

Re-detections provided evidence for the scale of bear movements (Table 2, Fig. 3).

Table 2. Distances (km) between successive detections of Kivalliq grizzly bears.

	0–9.9	10–19.9	20–29.9	30–39.9	40–49.9	50–59.9
2016 grids	2	3	1	2	0	0
2017 grids	3	5	1	1	0	1
2017 lakes and TP	6	6	2	0	0	1
Total	11	14	4	3	0	2

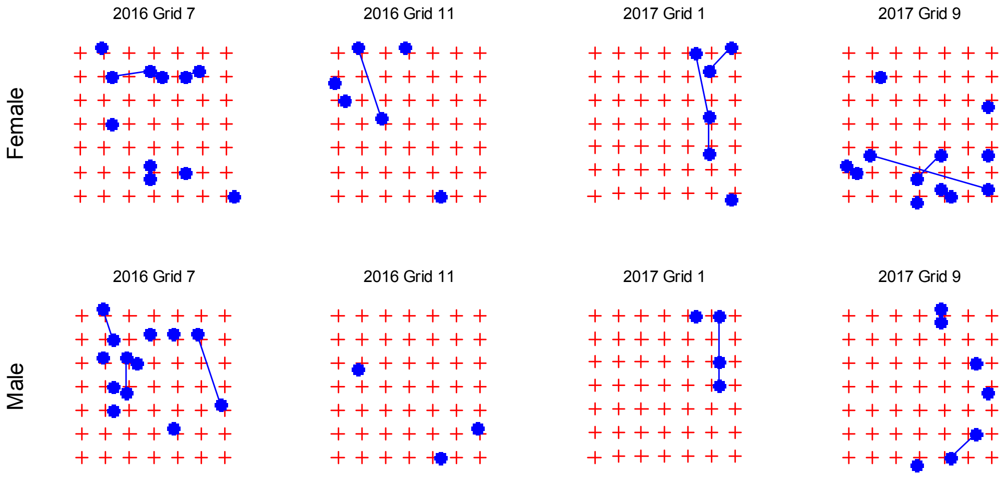

Fig. 3. Movements of individual grizzly bears on Kivalliq grids in 2016 and 2017. Hair snare posts (red crosses) were 10 km apart.

Results

SECR analyses

Choice of observation model

The model with a site-specific learned response showed a slight advantage over other models and estimated density differed only slightly among models (Table 3). The model-averaged estimate of density was 3.51 bears / 1000 km^2 (RSE 0.28; 95% CI 2.07–5.95 bears / 1000 km^2)

Table 3. Comparison of observation models. All models used the exponential detection function and included one parameter for density and one parameter for sex ratio. np is the number of parameters; LL is the maximised log likelihood; ΔAIC is the difference in AIC between each model and the best model; 'Weight' is the AIC model weight; $\widehat{D}$ is the estimated density in bears / 1000 km^2.

Model	Description	np	LL	ΔAIC	Weight	$\widehat{D}$	RSE($\widehat{D}$) %
g0~bk, sigma~1	Site-specific learned response	5	–308.5	0	0.708	3.54	28.1
g0~session*t, sigma~1	Temporal	9	–306.0	2.99	0.159	3.36	23.8
g0~1, sigma~1	Constant	4	–311.6	4.27	0.084	3.36	23.4
g0~b, sigma~1	General learned response	5	–311.6	6.25	0.031	3.44	29.9
g0~sex, sigma~sex	Sex-specific	6	–311.2	7.29	0.019	3.36	23.5

Grids

Analyses of the pooled grid data from 2016 and 2017 with the preferred observation model produced the estimates in Table 4.

Table 4. Kivalliq grizzly bear population density and related parameters estimated from hair posts on four 60-km x 60-km grids in 2016 and 2017. Estimates from model with site-specific learned response in g_0.

Parameter	Estimate	Relative SE %	95% CI
D	3.54 / 1000 km^2	28.1	2.06–6.08 / 1000 km^2
g_0 (initial)	0.068	–	0.028–0.157
g_0 (later)	0.350	–	0.126–0.628
σ	8.85 km	24.1	5.56–14.11 km

Extrapolating the estimated density to the entire Kivalliq region, excluding lakes, gives a population of 662 bears (95% CI 385–1135).

Lakes

We also analysed the 2017 data from Henik, Oftedal and Roseblade Lakes, using a habitat mask with 60-km buffer as before (Table 5). A model with site-specific learned response was essentially indistinguishable by AIC from the null (constant) model (ΔAIC = 0.1). Precision was poor and there were problems of interpretation (see Discussion).

Table 5. Grizzly bear population density and related parameters estimated from hair posts around Henik, Oftedal and Roseblade Lakes in 2017. Estimates from model with site-specific learned response in g_0.

Parameter	Estimate	Relative SE %	95% CI
D	9.55 / 1000 km^2	41.6	4.36–20.9 / 1000 km^2
g_0 (initial)	0.217	–	0.059–0.553
g_0 (later)	0.524	–	0.169–0.856
σ	4.76 km	29.3	2.71–8.37 km

Simulations

Fig. 4 illustrates some realisations of the systematic random design. The number of dry-land post sites is a random variable with mean 580 (282 for chequerboard designs) and coefficient of variation of about 8% between realisations (positions of array origin) (Table 6). The simulated relative precision of null-model density estimates from chequerboard designs with 3 sampling intervals was 20%. Precision may be improved by extending the sampling season to 4 intervals or by sampling all grids (Table 6).

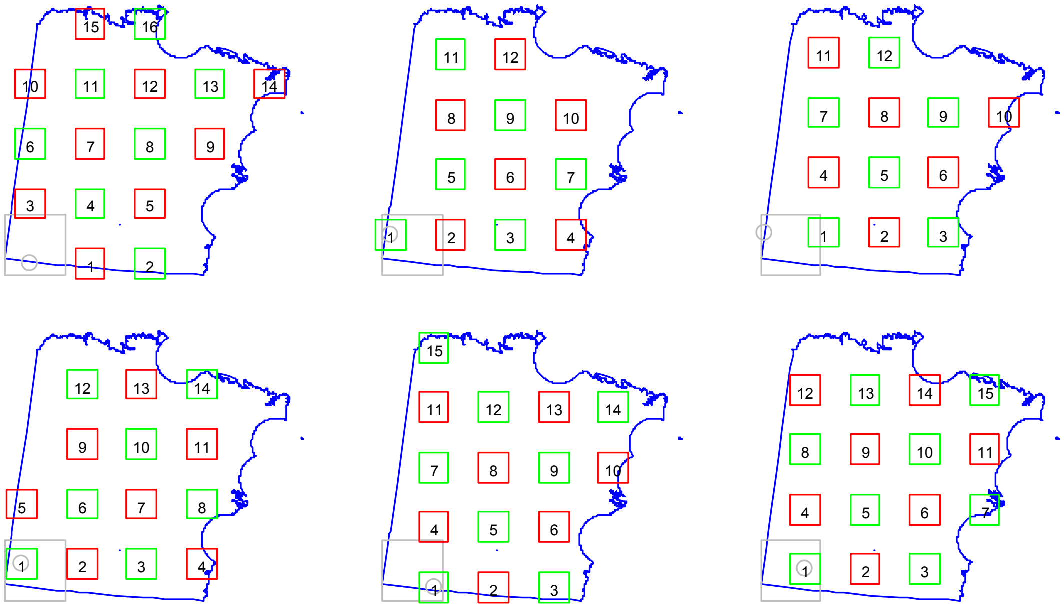

Fig. 4. Realisations of systematic random grid placement for sampling Kivalliq region. A rigid array of grid centres at 120-km spacing is placed at random across the region. The origin of the array (grey o) may lie anywhere within the grey square at the bottom left of each plot. Grids are rejected if their centre lies outside the region; accepted grids are numbered consecutively from the southwest corner. Grids corresponding to the white squares of a chequerboard are shown in red; the alternate subset (black squares) is shown in green. Each grid nominally comprises 49 posts at 10-km spacing, but sites in lakes (not shown) are omitted, as are any outside the region.

Table 6. Simulated DNA capture–recapture of grizzly bears in Kivalliq region (209 000 km^2) using systematic random post layouts as in Fig. 4. 'Odd grids' is shorthand for grids corresponding to the white cells of a chequerboard. The modal number of grids is 15 for all grids and 7 for odd grids; most grids are truncated (posts per grid < 49). True density 3.5 / 1000 km^2, exponential detection function g_0 = 0.12, σ = 7.0 km. *n* number of first detections of different bears; *r* number of detections after first. Mean of 50 replicates per scenario (SD in parentheses).

Scenario	Number of posts		Detections		Density estimate
	Total	Per grid	*n*	*r*	relative SE %
Odd grids, 3 x 2 weeks	282 (22.4)	38.0 (10.9)	75.6 (12.3)	26.8 (7.0)	20.2 (2.4)
Odd grids, 4 x 2 weeks	282 (22.4)	38.0 (10.9)	88.5 (14.6)	41.8 (10.8)	16.7 (2.1)
All grids, 3 x 2 weeks	580 (44.2)	35.5 (13.4)	153.3 (20.0)	54.2 (11.5)	13.9 (1.6)

Discussion

Review of assumptions

Habitat mask

Arbitrary truncation of the habitat mask (region of integration) potentially causes density estimates to be positively biased (i.e. exceed the true value). We checked the adequacy of the chosen truncation buffer (60 km) by re-fitting the model of Table 4 with a buffer 50% wider (90 km). Results were numerically indistinguishable from those in Table 4. Halving pixel size also had negligible effect on the estimates. We concluded that the 60 km buffer with 2.5-km pixels was appropriate.

Annual variation

Sampling took place in the summers of 2016 and 2017. We fitted models in which density was constant between years. This is likely to have been approximately true, given the likely high survival and low recruitment rates Schwartz et al. (2005). No grid was sampled in both years, and different subregions were sampled in the two years (Fig. 2), so we cannot separate geographic and temporal variation in density. We note that the sample of detected animals included more females in 2017 (grids 1 & 9) than in 2016 (grids 7 & 11).

Sex effect on observation model parameters

We expected male grizzly bears to have larger home ranges than females, and hence to show larger values of the spatial scale parameter σ. Boulanger et al. (2013) allowed for an approximately 2-fold difference in σ between the sexes in their simulations[1]. We did not detect a sex difference in σ estimated from the 2016 and 2017 grid data. This is most likely due to the limited sample of spatial recaptures. It was argued by Efford and Mowat (2014) that sex differences in σ have a little effect on density estimates when they are balanced by compensatory variation in g_0, as they found for one grizzly bear study, and we assume it is safe to proceed with observation models lacking a sex effect even if such an effect was present but not detected.

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[1] Note that they assumed a half-normal shape for the observation model where we assume a negative exponential shape.

Density models

We fitted only uniform-density models. SECR can be used to evaluate spatial variation in density, but we did not attempt this. The data were barely sufficient to fit a uniform-density model and cannot support more elaborate models. Each grid was sampled in just one year, so between-grid variation would be confounded with annual variation in density.

Inference from Lakes data

In 2017 interest focussed on the bears using a particular part of the Kivalliq region, specifically the shores of Henik, Oftedal and Roseblade Lakes. Sampling along lake shores used more closely spaced detectors than the grid sampling (5 km vs 10 km) and was conducted for longer (8 weeks as opposed to 6 weeks). This regime was efficient in terms of data accumulation (the number of bears and re-detections). However, sampling along selected lake shores does not lead to a credible estimate of density across the wider 2-dimensional region. For this some sort of representative sampling design is required, as proposed by Boulanger et al. (2013). We note in particular that the estimated Lakes density was high and imprecise.

The relatively rich data from the lakes might be considered as a way to strengthen estimates of the observation parameters g_0 and σ that could then be used to improve density estimates from grid sampling. This would require that grizzly movements along lake shores are representative of grizzly movements in the region as a whole, which seems implausible to us. It is especially problematic in the presence of behavioural responses as shown in our analysis of the 2016 and 2017 grid data.

Another possible use of lake-shore sampling would be to track changes in local population size over time using non-spatial open-population capture–recapture methods. This is feasible, but we warn that there are some difficulties of interpretation. Apparent changes in the local (lake-shore) population may be due to minor differences in the spatial distribution of bears, and the number of individuals of each sex is rather small for demographic (e.g., survival) analyses. Further consideration of actual designs of sampling for this objective would be needed to ensure that the lake-based sampling method would give reliable results

Recommendations for future monitoring

The choice of sampling design for future monitoring depends on the intended purpose of monitoring, and it is therefore desirable that this should first be clarified. The systematic design proposed by Boulanger et al. (2013) was intended to answer the question “How many bears have activity centres in the Kivalliq region?”. Widespread and representative sampling is needed to answer this question.

The partly-implemented systematic design performed much as would be expected from the earlier simulations. These had forecast that the relative standard error (RSE, aka CV) of density estimates would be 20% or better if six 60-km x 60-km grids were sampled in one year and density exceeded 3 bears / 1000 km^2. The density criterion appears to have been met (estimate 3.5 / 1000 km^2), but the realised precision was somewhat worse than forecast (RSE 28%). This can be explained by the reduced sampling (4 grids instead of 6) and the decision to fit a more elaborate observation model (site-specific learned response).

The original design proposed 12 subgrids sampled over two years, and the data from 2016 and 2017 confirm that this would provide the desired precision. However, the design was impractical in that some of the suggested sites fell in lakes. This problem was addressed in 2016–2017 by shifting each grid so that all sites were dry. A simpler approach for the future is simply to omit sites that fall in lakes. A slight reduction in the number of posts (11% based on the lake area as a proportion of the total) should have only minor effects on precision.

When sites are restricted to dry land the number of posts in any grid can vary. Dropping the requirement that grids are square and have the same number of posts allows us to aim for a more rigorous systematic random design – the one we simulated in this report (Fig. 4). This differs from the 2013 proposal in that grids may be truncated at the region boundary and sampling intensity is more uniform across the region. The ultimate choice of grid layout (e.g., from among panels in Fig. 4) is made by drawing random numbers for the origin of the systematic array after it has been decided to proceed with the survey. Given the cost and logistical difficulty of implementing the full design in one year, we envisage that one chequerboard subset (white-square grids) would be sampled in the first year, possibly followed by the alternate subset (black-square grids) in a second year.

Relationship of proposed design to 2016–2017 sampling

The proposed systematic random design is similar in approach to that recommended in 2013. Because the sample of sites is representative by design, it is expected to deliver an unbiased estimate of the regional grizzly bear density. A theoretical alternative is to construct a model of bear density across space, using local caribou and musk ox abundance as covariates. However, that would also require substantial hair-snare sampling (across gradients in the covariates) and it is not clear that there are reliable covariate data for any given year.

The proposed design has these advantages over the previous layout, while using a similar number of posts –

i. The design explicitly allows lakes to be excluded
ii. The design is more representative because grid centres may be placed right up to the boundary of the region (with possible truncation of some grids)
iii. It meets the requirements for rigorous calculation of sampling variance (next section).

We recommend that an entire chequerboard subset should be sampled in one year. This removes the risk of confounding between spatial and temporal variation that exists when sampling is conducted over multiple years. However, grids for a new systematic random design are likely to overlap in part with the grids sampled in 2016–2017. This may appear inefficient – why not just exclude those areas from new sampling? A clean start is preferred because it will lead to a clear, defensible density estimate at the time of the new sampling. Attempts to marry old data to a new rigorous sample will inevitably seem ad hoc, and an estimate from cobbling together data over several years will be suspect because of the probability that population has changed over time.

Completion of modified original design

In the previous section we advocated a ‘clean start’ systematic random design. If this is deemed impractical there is a further compromise option: to complete the original (2013) array of grids using only dry-land sites in the remaining grids. Supposing this was carried out over two years, grids 3, 5 and 12 could be completed in the first year and 2, 4, 6, 8 and 10 in the second year (Fig. 5). This would provide representative coverage of the entire region (slightly compromised by edge effects). Sampling would span a minimum of 5 years (2016–2020). Density estimates from a joint analysis would have good nominal precision (RSE about 14% as in the ‘all grids’ scenario of Table 6). Spatial patterns in the data could not be interpreted owing to confounding with temporal variation.

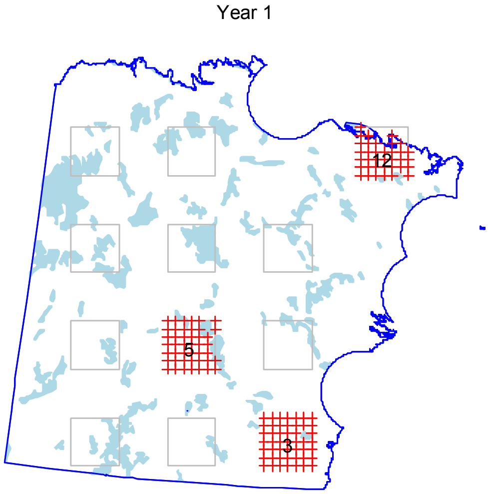

Fig. 6. Phased completion of original design over 2 years, using only dry-land sites. Grids 3, 5 and 12 have 48, 44 and 36 sites respectively (total 128). Grids 2, 4, 6, 8 and 10 have 48, 45, 43, 35 and 39 sites respectively (total 210). For more equal effort in the two years, Grid 10 could be transferred to Year 1.

Calculation of spatial variance

Our calculations of the precision of density estimates (Table 6) rest on the assumption of a uniform Poisson distribution of bear activity centres across the Kivalliq region. We believe this is near enough for most purposes, but note that our new systematic random design is also amenable to more rigorous calculations as developed for distance sampling by Fewster (2011). The number of individuals detected on each (possibly incomplete) grid (*n*) corresponds to the encounter rate from distance sampling on transects that may vary in length. Variance in *n* is one component of the sampling variance of density. Its calculation should include stochasticity from the random placement of the systematic array (Fewster 2011); the exact method requires further development.

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Acknowledgments:

Funding was provided by the Government of Nunavut Department of Environment (DOE) and the Nunavut Wildlife Management Board (NWMB). Arviat HTO provided logistical support for the study. DOE staff from the Kivalliq Region assisted in many ways including: M. Campbell, R. Harmer, F. Mikeeuneak, L. Savikataaq and R. Toolooktook. Wildlife Genetics International conducted genetic analysis of all hair samples.