Estimates of wolverine density and abundance in Norrbotten county in Sweden and associated reindeer herding areas, 2023/2024

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Summary

Background Project RovQuant has produced density maps and abundance estimates for large carnivores (wolf, wolverine, and brown bear) throughout Scandinavia since 2019. These estimates are based on non-invasive genetic sampling (NGS) and dead recovery data collected annually by Swedish and Norwegian authorities. The spatial capture recapture (SCR) method used produces population-level estimates, as well as regional estimates of abundance. The Swedish Environmental Protection Agency (Naturvårdsverket), in coordination with the Sámi parliament (Sametinget), has expressed interest in obtaining updated wolverine abundance estimates in Norrbotten county in northern Sweden and associated reindeer herding areas for the winter 2023/2024. This demand coincides with the first comprehensive NGS conducted in Norrbotten county since 2019.

Approach Using NGS and a single-season Bayesian SCR model, we estimated the density of wolverines in Norrbotten county during winter 2023/2024. From this, we derived estimates of wolverine abundance within different administrative units associated with Sámi reindeer herding activity in the county.

Results The SCR model estimated that the total number of wolverines in Norrbotten during winter 2023/2024 was likely (95% credible interval) between 206 and 222 individuals. We provide tables with abundance estimates for the different Sámi villages, calving areas, and concessions within Norrbotten.

Discussion Wolverines are elusive and highly mobile. Estimates of wolverine density for very small areas, such as some Sámi villages, are thus associated with a high degree of uncertainty. The results from this analysis have therefore to be interpreted with caution. Nonetheless, the approach used here offers an alternative to inform the compensation scheme and facilitate co-existence between large carnivores and indigenous livestock husbandry practices. This year's intensive NGS sampling in Norrbotten county constitutes not only a necessary prerequisite for reliable abundance estimation in the county's reindeer herding areas, but is also a key step towards a comprehensive assessment of the wolverine population throughout Scandinavia.

Sammanfattning

Bakgrunn RovQuant forskningsprojektet har sedan 2019 tagit fram täthetskartor och populationsberäkningar för de stora rovdjuren varg, järv och björn i Skandinavien. Dessa uppskattningar bygger på DNA-data från spillningsinventeringar (NGS, non-invasive genetic sampling) och från döda rovdjur som årligen samlas in av svenska och norska myndigheter. Den tillämpade rumsliga fångst-återfångst metoden (SCR, spatial capture recapture) resulterar i beräkningar av respektive rovdjursstammens storlek på populations-, regional eller lokal nivå. Naturvårdsverket har i samarbete med Sametinget beställt nya populationsuppskattningar för Norrbottens läns järvstam både för länet i sin helhet och för norrbottniska samebyars svenska betesområden. Denna begäran samspelar med den heltäckande DNA-inventering av järv som har genomförts i Norrbottens län under vintersäsongen 2023/24. Mer riktade insatser med DNA-insamling har inte skett i länet sedan 2018/19.

Metod Med hjälp av en "enkel-säsongs" Bayesian SCR modell har vi uppskattat järvtätheten inom Norrbottens län för inventeringssäsongen 2023/24. Från detta resultat har vi sedan erhållit uppskattningar på antalet järvar i olika områden som används av respektive sameby vid olika årstider.

Resultat SCR-modellen uppskattade järvpopulationen i Norrbottens län under 2023/24 till 206 - 222 individer (95 % konfidensintervall).

Diskussion Järven är en skygg och mycket rörlig djurart. Uppskattningar på järvtätheter inom mindre områden, som exempelvis vissa samebyar, är därför förknippade med relativt hög osäkerhet. Resultaten enligt de här analyserna behöver därför tolkas med viss försiktighet. Oavsett så kan metoden som tillämpats i denna analys användas i syfte att informera ersättningssystemet och förbättra samexistensen mellan stora rovdjur och rennäringen. Denna säsongs intensiva DNA-insamling i Norrbottens län är inte bara en nödvändig förutsättning för säkra populationsuppskattningar i olika områden som används av samebyarna utan också ett stort steg i riktning mot en heltäckande inventering av järvstammen i Skandinavien.

Contents

1 Introduction

Sweden and Norway monitor large carnivores using non-invasive genetic sampling (NGS) and dead recoveries. Both countries have collected an extensive individual-based data set for the wolverine (*Gulo gulo*), which is stored in the Scandinavian large carnivore database Rovbase (www.rovbase.se, www.rovbase.no). Since 2017, project RovQuant has been developing statistical methods that allow a comprehensive assessment of the status and dynamics of large carnivore populations using NGS data and other sources of information stored in Rovbase (Bischof et al., 2019b, 2020). The analytical framework developed by RovQuant is based on spatial capture-recapture (SCR) models (Efford, 2004; Royle et al., 2009). These models use the spatial information contained in the repeated genetic detections of individuals to estimate various population parameters, including spatially-explicit abundance (i.e., density). Importantly, the approach accounts for imperfect detection during sampling (i.e., the fact that some individuals are not detected at all) and animal movement (i.e., the fact that individuals may use and be detected in multiple management units or countries). The SCR method brings along several advantages, including the ability to map density, derive jurisdiction-specific abundance, and yield tractable measures of uncertainty (Bischof et al., 2019a, 2020).

Damages caused by large carnivores and wolverine predation (*Gulo gulo*) on semi-domestic reindeer are compensated through "conservation performance payments" in Sweden (Persson et al., 2015). The current compensation scheme is based on the recorded number of reproductions, but the Sámi parliament is seeking information about the distribution of wolverines across the various jurisdictions within the reindeer herding areas, in order to consider alternative ways of defining the compensation scheme (Dupont et al., 2023a).

In this context, Naturvårdsverket (Swedish Environmental Protection Agency), in coordination with Sametinget (Sámi parliament), tasked RovQuant at the Norwegian University of Life Sciences with obtaining abundance estimates of wolverines in Norrbotten county in Sweden, and its associated reindeer herding areas. This demand coincides with a comprehensive NGS conducted in Norrbotten county in northern Sweden during the winter 2023/2024, the first intensive sampling season since the winter 2018/2019. Between winter 2019/2020 and winter 2022/2023, no comprehensive NGS of wolverines was conducted in Norrbotten county. This made the estimation of density in this region challenging, as estimation relied solely on model prediction (Flagstad et al., 2021; Milleret et al., 2022a,b, 2023a).

Here, we analyzed the NGS data of wolverines collected in Norrbotten county during the winter 2023/2024 using a single-season SCR model. We provide the following information:

- Sex-specific estimates of the number of wolverines in 2023/2024 in Norrbotten county.

- Sex-specific estimates of the number of wolverines in 2023/2024 within different administrative entities associated with the Sámi reindeer herding areas in the county.

- Maps of wolverine density throughout Norrbotten county.

All estimates are accompanied by their 95% Bayesian credible intervals as a measure of uncertainty.

Box 1: Terms and acronyms used

AC: Activity center. Model-based equivalent of the center of an individual's home range during the monitoring period. "AC location" refers to the spatial coordinates of an individual AC in a given year and "AC movement" to the movement of an individual AC between consecutive years.
CAB: County Administrative Board ("Länsstyrelsen").
CrI: 95% credible interval associated with a posterior sample distribution.
Detectors: Potential detection locations in the spatial capture-recapture framework. These can refer to fixed locations (e.g., camera-trap locations) or, in this report, to areas searched (e.g., habitat grid cells where searches for genetic samples were conducted). The searched area was defined by the Norrbotten county border.
Habitat buffer: Buffer surrounding the searched area that is considered potentially suitable habitat but was not searched (60km in this report).
Legal culling: Lethal removal of individuals by legal means, including licensed recreational hunting, management removals, and defense of life and property.
Länsstyrelserna: Swedish County Administrative Boards, in charge of the monitoring of large carnivores at the county level.
MCMC: Markov chain Monte Carlo.
NGS: Non-invasive genetic sampling.
OPSCR: Open-population spatial capture-recapture
p_0: Baseline detection probability; probability of detecting an individual at a given detector, if the individual's AC is located exactly at the detector location.
σ: Scale parameter of the detection function; related to the size of the circular home-range.
RovQuant: Project at the Norwegian University of Life Sciences (Ås, Norway) that develops and applies SCR models.
SCR: Spatial capture-recapture.

2   Methods

2.1   Data

We used data from the Scandinavian large carnivore database Rovbase 3.0 (rovbase.se and rovbase.no; last extraction: 2024-08-28). This database is used jointly by Norway and Sweden to record detailed information associated with large carnivore monitoring, including, but not limited to, NGS data, dead recoveries, and GPS search tracks. In the following sections, we describe the various types of data used in the analysis. We used data collected in the winter 2023/2024 within Norrbotten county.

Non-invasive genetic sampling In Sweden, the collection of scat, secretion, urine, blood, and hair is managed by the County Administrative Boards (CAB) at the regional level and carried out by field officers from CAB, Sámi village members, and reindeer herders. NGS collection was conducted primarily between October 1 and May 15 in the winter 2023/2024. NGS data collected late in the monitoring season and suspected to be from cubs were not included in the analysis. This means that we only retained samples from individuals that were one year or older. DNA was isolated with an extraction robot (Maxwell 16, KingFisher or QIAsymphony instrument) and samples were genotyped using 96 SNPs (Single Nucleotide Polymorphism) on a microfluidic-based platform (Biomark X9 instrument) for sex determination and individual identification. For further details on the DNA analysis procedure see Flagstad et al. (2004), Flagstad et al. (2021), and Kleven et al. (2023).

GPS search tracks Government employees involved in structured searches for wolverine DNA following wolverine tracks (via snowmobiles, skis, snowshoes, etc.) document their effort with GPS track logs, which are registered in Rovbase 3.0. GPS search tracks were included in the SCR model to account for spatial and temporal variation in search effort during NGS.

2.2   Spatial capture-recapture model

We analysed the data collected in Norrbotten in the winter 2023/2024 using a Bayesian single-season spatial capture-recapture (SCR) model (Bischof et al., 2019b), which addresses two challenges associated with population-level wildlife inventories:

1. Detection is imperfect and sampling effort is heterogeneous in space: not all individuals present in the study area are detected (Kéry and Schaub, 2012).
2. Individuals that reside primarily outside the surveyed area may be detected within it. Without an explicit link between the population size parameter and the geographic area the population occupies, density cannot be estimated and population size is ill-defined (Efford, 2004).

The SCR model is composed of three sub-models:

1. A model for population size.
2. A model for density.
3. A model for detections during DNA searches.

Population size sub-model We used data augmentation to estimate population size (Royle et al., 2014). Individual state z_i follows a Bernoulli distribution with probability ψ. Individual state z_i takes the value 1 if the individual is considered as part of the population and 0 otherwise.

Density sub-model We used a Bernoulli point process to model the distribution of individual ACs (Zhang et al., 2022). Individual ACs were located according to an intensity surface, which was a function of the locations of known dens (see Bischof et al., 2019b and Bischof et al., 2020 for more details).

Detection sub-model SCR models take into account the spatial variation in individual detection probability based on the distance between AC locations (estimated by the density sub-model) and a given detector. A half-normal function was used to express the declining probability of detection with increasing distance between the AC and the detector (Royle et al., 2014).

DNA material was collected following two main processes: 1) Authorities collected genetic samples and record the corresponding search effort during official searches ("structured sampling" hereafter). 2) DNA material was collected by members of the public such as e.g. Sámi reindeer herders, or by the authorities in a more or less opportunistic manner, which means that search effort is not directly available ("unstructured sampling" hereafter). Currently, it is not possible to unambiguously distinguish between samples collected by the authorities during the structured or unstructured sampling in Rovbase. We therefore assigned each sample to structured or unstructured sampling based on whether a given sample matched in time and space with recorded search tracks. A sample was assigned to the "structured" sampling if it was collected by the authorities (marked as collected by CAB in Rovbase) and located within 500 m of a GPS search track recorded the same day. All remaining samples were assigned to the unstructured sampling.

We assumed that both sampling processes could in theory occur within the entire Norrbotten county and therefore used the same 10×10 km detector grid for both observation processes. Samples were then assigned to the closest detector (see details in Bischof et al., 2019b, and Bischof et al., 2020). However, spatial and temporal variation in the probability to detect a sample during structured or unstructured sampling were assumed to be driven by different processes.

We accounted for spatial and individual heterogeneity in detectability during ***structured sampling*** using:

- Spatial variation in search effort represented by the length of GPS search tracks in each 10×10 km detector grid cell.

- Spatial variation in snow cover during the monitoring period calculated as the average percentage of snow cover in each detector grid cell (MODIS at 0.1 degrees resolution, https://cmr.earthdata.nasa.gov, accessed 2024-09-20).

- Individual variation linked with a detection during the previous occasion (2022/23 monitoring season) that could be expected to influence the probability of being detected at the next occasion.

We accounted for spatial and individual heterogeneity in detectability during ***unstructured sampling*** using:

- A binary covariate that represented the willingness (1) or unwillingness (0) of Sámi villages to contribute to NGS of wolverines (Figure 1). Some Sámi villages did not want to or did not have the capacity to participate to NGS of wolverines in Norrbotten County in 2023/2024. Note that further detail about the intensity of NGS from the different Sámi villages was not available.

- Spatial variation in snow cover during the monitoring period calculated as the average percentage of snow cover in each detector grid cell (MODIS at 0.1 degrees resolution, https://cmr.earthdata.nasa.gov, accessed 2023-09-29).

- Spatial variation in accessibility measured as the average distance to the nearest road.

- Individual variation linked with a detection during the previous occasion (monitoring season) that could be expected to influence the probability of being detected at the next occasion.

The different model components and data sources for covariates are described in detail in Bischof et al. (2019a), Bischof et al. (2019b), and Bischof et al. (2020).
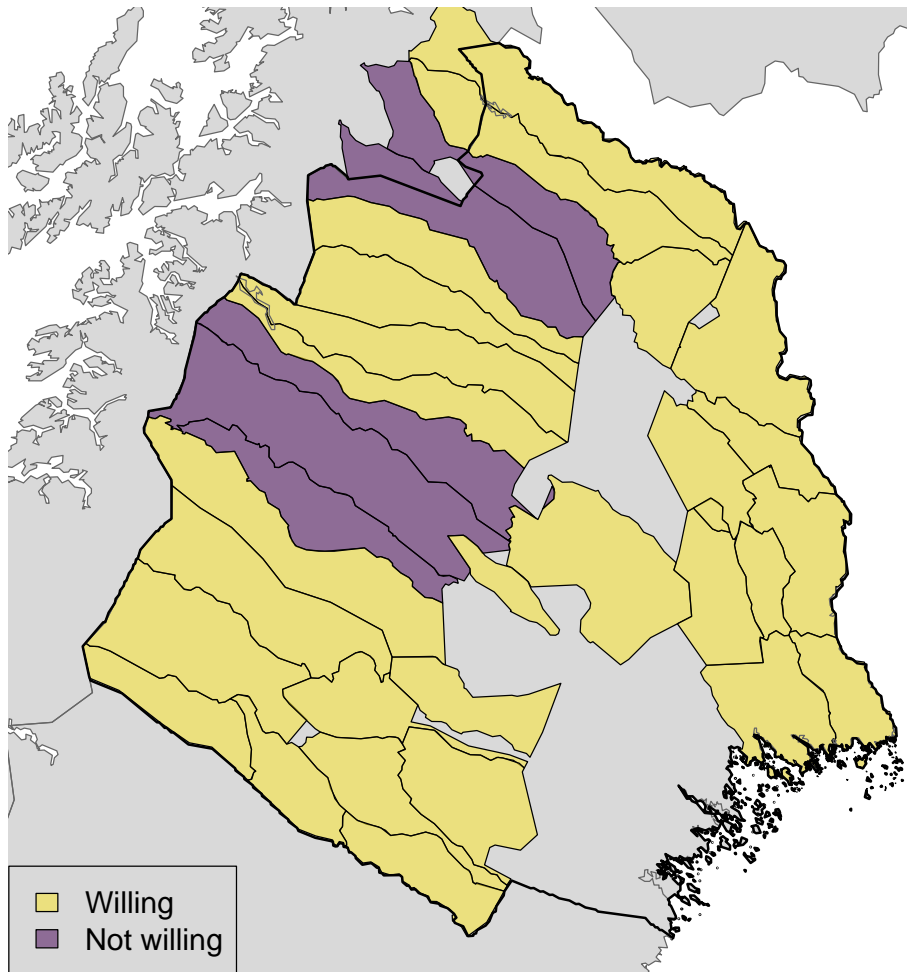

Figure 1: Spatial covariate used to describe the willingness of Sámi villages to contribute to the NGS of wolverines in Norrbotten during the winter 2023/2024.

Model fitting We fitted sex-specific Bayesian SCR models using MCMC simulation with NIMBLE version 0.12.2 (de Valpine et al., 2017; Turek et al., 2021; de Valpine et al., 2022) and RovQuant's R package nimbleSCR version 0.2.0 (Bischof et al., 2021) in R version 4.1.0 (R Core Team, 2021). We ran 4 chains each with 25 000 iterations, including a 10 000-iterations burn-in period. Due to the computing challenge associated with post-processing large amounts of data, we thinned chains by a factor of 10 before deriving abundance estimates. We considered models as converged when the Gelman-Rubin diagnostics (Rhat, Gelman and Rubin, 1992) was ≤1.1 for all parameters and when mixing between chains was satisfactory based on visual inspection of trace plots.

2.3   Abundance estimates

Using SCR models, abundance for any arbitrary area can be easily derived by extracting the number of estimated individual activity centers (AC) that fall within the area of interest. However, the expansive home ranges of large carnivores and their capacity for long-distance movement are in stark contrast with the comparatively small areas (individual Sámi villages and reindeer calving areas) for which abundance estimates were to be generated in this project. The impact (e.g., predation on livestock) of a single large carnivore may readily spread over multiple jurisdictions/villages, and management may want to take this into account. Therefore, as an alternative to purely AC-based estimates, we calculated abundance based on individual space-use or utilization distributions (UD-based estimates, Dupont et al. 2023a). SCR models assume a bivariate normal model of individual space use whereby individuals spend most time near the center of their home range (AC), and space use intensity decreases as distance to the AC increases. The width of this individual space-use distribution, or home range, is determined by the standard deviation of the bivariate normal σ. Based on the AC locations and σ estimates, we can calculate individual space-use and the proportion of time an individual spends in a given region as the integral of its space-use distribution within this region. Abundance within a given region is then calculated as the sum of the individual utilization distributions within that region (see Dupont et al. 2023a for more details). This calculation can be done for each iteration of the MCMC algorithm, leading to a posterior distribution for the UD-based abundance in each region. As a result, in addition to the uncertainty in the location of the individual AC locations, the UD-based approach also takes into account individual space-use and therefore uncertainty in home range size. Combined (female and male) parameter estimates were obtained by merging posterior samples from the sex-specific models. In this study, we only estimated wolverine density in Norrbotten county.

To create density maps based on the UD approach, we constructed raster maps (5 km resolution) of individual utilization distributions, scaled values in each raster to sum to one, and then summed rasters across individuals to create a single population-level raster map for each iteration. An overall density map was derived by calculating the mean across iterations in each cell (Bischof et al., 2020).

Spatial extent and configuration of jurisdictions We extracted wolverine UD-based abundance estimates for multiple spatial subunits that were derived from multiple shapefiles (Figure 2) provided by P. Benson (Sametinget) to R. Bischof (RovQuant; NMBU) on September 28, 2021 (Dupont et al., 2023a):

1. Sámi reindeer calving areas within Norrbotten county (*"A.Kalv praxis by"*): 32 polygons associated with 32 Sámi village names.
2. Year-round Sámi villages (*"B.Åretrunt by"*): 24 polygons associated with 24 Sámi village names.
3. Sámi year-round counties (*"C.Åretrunt Lan"*): 1 polygon.

4. Sámi winter counties (*"D.Vinter Lan"*): 1 polygon.
5. Sámi concessions (*"G.Koncession by"*): 9 polygons associated with 9 Sámi concession names.

Focus on uncertainty Although we reported mean estimates for all parameters in the tables, we intentionally focused the main results of our report on the 95% credible interval limits of the estimates. We did so with the aim of drawing the reader's attention to the uncertainty around population size estimates, rather than a single point estimate (Milleret et al., 2022a).
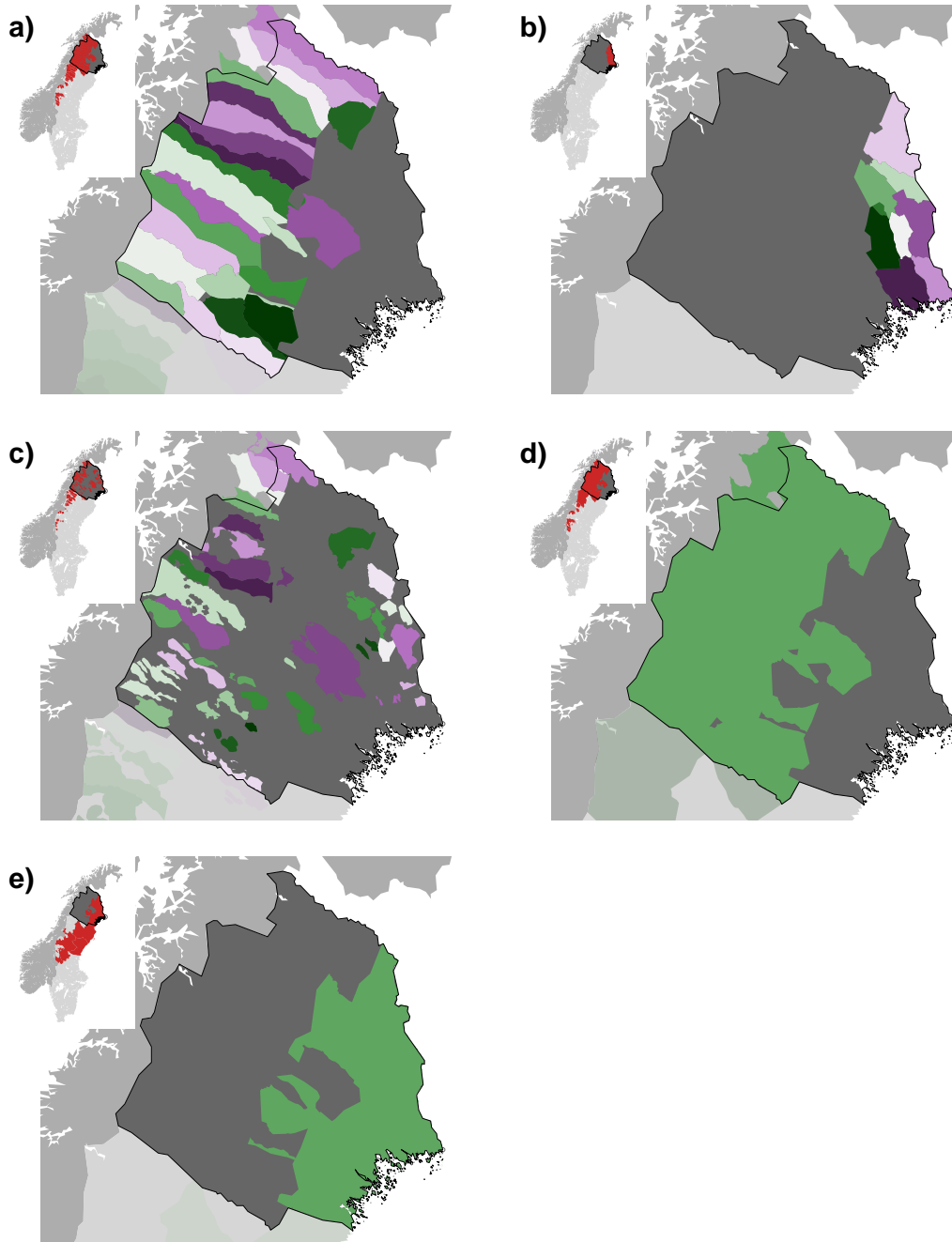

Figure 2: Shapefiles for which region-specific wolverine abundances were extracted: a) Year-round Sámi villages ("B.Åretrunt by"), b) Sámi concessions ("G.Koncession by"), c) Sámi reindeer calving areas ("A.Kalv praxis by"), d) Sámi year-round counties ("C.Åretrunt Lan"), and e) Sámi winter counties ("D.Vinter Lan").

3 Results

3.1 Non-invasive genetic samples and dead recoveries

A total of 1 417 (752 female; 665 male) genotyped wolverine genetic samples were collected in Norrbotten in the winter 2023/2024. These samples were associated with 227 (146 female; 81 male) individuals. Among all genotyped samples, 891 (463 female; 428 male) were assigned to structured sampling and 526 (289 female; 237 male) to unstructured sampling.

3.2 Density and abundance

In the winter 2023/2024, we estimated that wolverine abundance in Norrbotten county was likely (95% credible interval) between 206 and 222 (mean=213.7; Figure 3) individuals (Females: [132-147], mean=139.2; Males: [71-80], mean=74.6). Estimates refer to the status of the population at the start of the annual sampling period (October 1). Abundance estimates of wolverines extracted for the different administrative units associated with the Sámi herding activity are provided in Table 1, Table 2, and Table 3.

Between 94 - 99% of the wolverines estimated to have their activity center inside Norrbotten were detected during this study. In addition, NGS detected between 14 - 24 individuals that were estimated to have their activity center outside of Norrbotten (i.e. Norway, Västerbotten county or Finland), presumably because these individuals occasionally spend time inside of Norrbotten. In other words, it is possible to detect more individuals in an area than are estimated to live within that area. This is also the case for the brown bear in Norway, where a significant number of detections in Norway are attributed to individuals that likely have their activity center in Sweden (for further explanations see Bischof et al. 2016 and Dupont et al. 2023b).
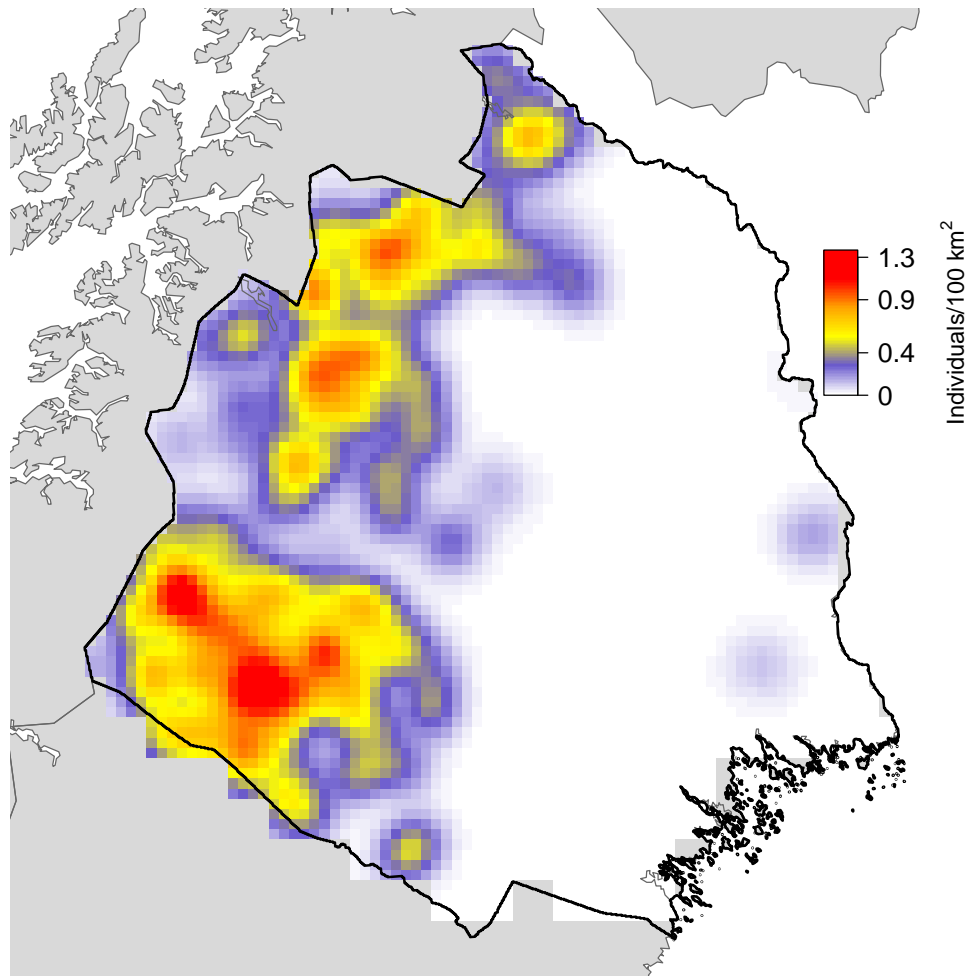
Figure 3: Wolverine density based on individual utilization distributions in Norrbotten during winter 2023/2024 based on a single-season spatial capture recapture model. This map can be accessed as a geo-referenced raster file at https://github.com/richbi/RovQuantPublic

3.3 Abundance in the reindeer herding areas

Table 1: Wolverine abundance estimates for the different Sámi villages (Figure 2.a) and concessions (Figure 2.b) in Norrbotten county in 2023/2024, based on estimated individual space use (UD-based abundance). For Sámi villages and concessions extending beyond the boundaries of Norrbotten county, estimates refer only to the area that is within Norrbotten county. Combined female-male estimates were obtained by joining sex-specific posterior estimates. Credible intervals (95%) are shown in parentheses. Sex-specific UD-based estimates are provided in https://github.com/richbi/RovQuantPublic.

		female	male	Total
Sámi villages	Baste cearru	4.7 (3-7)	1.4 (0-3)	6.1 (3-9)
	Gabna	9 (7-11)	3.6 (2-5)	12.6 (10-15)
	Gällivare	0 (0-0)	0 (0-0)	0 (0-1)
	Girjas	5.7 (4-8)	2.3 (1-4)	8 (5-11)
	Jåhkågaska tjiellde	3.1 (1-5)	1.5 (0-4)	4.6 (2-8)
	Könkämä	5.3 (3-8)	1.1 (1-2)	6.4 (4-9)
	Laevas	8 (6-11)	3.7 (2-5)	11.7 (9-15)
	Lainiovuoma	3 (1-5)	1.3 (1-2)	4.4 (2-7)
	Luokta-Mávas	17.5 (14-21)	8.3 (6-11)	25.8 (21-30)
	Maskaure	4.4 (3-6)	3.6 (2-5)	7.9 (6-10)
	Mausjaur	1.9 (1-3)	1 (1-1)	2.9 (2-4)
	Östra Kikkejaure	0.8 (0-2)	0 (0-0)	0.8 (0-2)
	Saarivuoma	0.9 (0-3)	2.1 (0-4)	3 (1-6)
	Semisjaur-Njarg	24.5 (21-27)	11.5 (9-14)	36.1 (32-40)
	Sirges	10.2 (8-13)	6.4 (4-9)	16.6 (13-20)
	Slakka	0.1 (0-1)	0.2 (0-1)	0.3 (0-2)
	Ståkke	4.4 (4-6)	5.2 (3-7)	9.6 (8-12)
	Svaipa	6.8 (4-10)	5.2 (4-7)	12 (8-15)
	Talma	8.5 (6-11)	3.2 (1-6)	11.7 (8-16)
	Tuorpon	6.6 (4-9)	3.8 (2-6)	10.4 (7-14)
	Udtja	1.8 (1-3)	1 (1-1)	2.8 (2-4)
	Unna Tjerusj	7.6 (6-10)	5 (3-7)	12.6 (10-16)
	Västra Kikkejaure	2.8 (2-4)	1 (1-2)	3.8 (3-5)
	Vittangi	0 (0-0)	0 (0-0)	0 (0-0)
Sámi concessions	Ängeså	0 (0-0)	0.2 (0-1)	0.2 (0-1)
	Kalix	0 (0-0)	0.7 (0-1)	0.7 (0-1)
	Korju	0.8 (0-1)	1 (0-1)	1.7 (1-2)
	Liehittäjä	0 (0-0)	0 (0-0)	0 (0-1)
	Muonio	0 (0-1)	0.2 (0-1)	0.2 (0-1)
	Pirttijärvi	0 (0-0)	0 (0-1)	0 (0-1)
	Sattajärvi	0 (0-1)	0 (0-0)	0 (0-1)
	Tärendö	0 (0-0)	0 (0-0)	0 (0-0)
	Tärendö, Ängeså	0 (0-0)	0 (0-0)	0 (0-0)

Table 2: Wolverine abundance estimates for the Sámi reindeer calving areas (Figure 2.c) in Norrbotten county in 2023/2024, based on estimated individual space use (UD-based abundance). For calving areas extending beyond the boundaries of Norrbotten county, estimates refer only to the area that is within Norrbotten county. Combined female-male estimates are obtained by joining the sex-specific posterior estimates. Credible intervals (95%) are shown in parentheses. Total and sex-specific UD-based abundance estimates are provided in https://github.com/richbi/RovQuantPublic.

	female	male	Total
Ängeså	0 (0-0)	0 (0-0)	0 (0-0)
Baste cearru	4.3 (2-7)	1.2 (0-3)	5.6 (3-9)
Gabna	5.3 (4-7)	1.9 (1-3)	7.3 (5-9)
Gällivare	0 (0-0)	0 (0-0)	0 (0-0)
Girjas	5.3 (3-7)	2.1 (1-4)	7.4 (5-10)
Jåhkågaska tjiellde	3 (1-5)	1.4 (0-4)	4.4 (2-7)
Kalix	0 (0-0)	0.1 (0-1)	0.1 (0-1)
Könkämä	4.2 (2-7)	1.1 (1-2)	5.2 (3-8)
Korju	0.4 (0-1)	0.7 (0-1)	1.1 (0-2)
Laevas	2.6 (0-5)	2.8 (1-4)	5.4 (3-8)
Lainiovuoma	0.5 (0-2)	0.7 (0-2)	1.1 (0-3)
Liehittäjä	0 (0-0)	0 (0-0)	0 (0-0)
Luokta-Mávas	5.7 (3-9)	2.2 (0-5)	7.9 (4-12)
Maskaure	0.4 (0-2)	0.4 (0-1)	0.8 (0-2)
Mausjaur	0.3 (0-1)	0.1 (0-1)	0.4 (0-2)
Muonio	0 (0-0)	0 (0-0)	0 (0-0)
Östra Kikkejaure	0 (0-1)	0 (0-0)	0 (0-1)
Pirttijärvi	0 (0-0)	0 (0-0)	0 (0-0)
Saarivuoma	0.2 (0-2)	0.5 (0-2)	0.8 (0-3)
Sattajärvi	0 (0-0)	0 (0-0)	0 (0-0)
Semisjaur-Njarg	8.2 (5-13)	3.8 (1-6)	12 (8-17)
Sirges	7.6 (5-11)	3.5 (1-6)	11.1 (7-15)
Slakka	0 (0-0)	0 (0-0)	0 (0-0)
Ståkke	1.2 (0-3)	3.1 (1-5)	4.3 (2-7)
Svaipa	2.8 (0-6)	3 (2-4)	5.8 (3-9)
Talma	2.3 (0-5)	1.2 (0-3)	3.5 (1-6)
Tärendö	0 (0-0)	0 (0-0)	0 (0-0)
Tuorpon	1.7 (0-4)	1.3 (0-3)	3 (1-6)
Udtja	0.7 (0-2)	1 (0-1)	1.6 (1-3)
Unna Tjerusj	2.8 (1-5)	1.3 (0-3)	4.1 (2-6)
Västra Kikkejaure	0.8 (0-1)	0.2 (0-1)	1 (0-2)
Vittangi	0 (0-0)	0 (0-0)	0 (0-0)

Table 3: Wolverine abundance estimates for the Sámi "year-round counties" (Figure 2.d) and "winter counties" (Figure 2.e) in Norrbotten county in 2023/2024, based on estimated individual space use (UD-based abundance). Estimates refer only to the area that is within Norrbotten county. Combined female-male estimates are obtained by joining the sex-specific posterior estimates. Credible intervals (95%) are shown in parentheses. Total and sex-specific UD-based abundance estimates are provided in https://github.com/richbi/RovQuantPublic.

	female	male	Total
Year-round	137.7 (131-145)	72.5 (69-77)	210.3 (203-218)
Winter	2 (0-5)	2.4 (2-4)	4.4 (2-7)

4   Discussion

The primary motivation behind the analysis presented here was to provide information to guide the allocation of compensation to reindeer herding operations in Norrbotten. Thus, estimates provided here may have direct policy implications and we feel obligated to repeat the following points from Dupont et al. (2023a):

1. Many of the regions for which estimates were generated are small compared to wolverine home range sizes, and certainly small compared to the area used by the wolverine population. At such a fine spatial grain, the ability of the model to make unbiased and precise inferences is limited. Mean estimates for very small areas will be disproportionately small relative to the associated uncertainty, making inferences unreliable. We urge users to focus on the upper and lower credible intervals provided here, instead of the point estimates.

2. Use of region-specific abundance estimates for disbursement of financial compensation also assumes that there is no overlap between different polygons/regions; overlap will lead to double-counting of animals and thus duplicate compensation (i.e., more than one jurisdiction receives compensation for the same wolverine's activity in the same area).

3. In this analysis, we only estimated region-specific abundances of wolverines and did not take into account actual damages inflicted. The relationship between wolverine abundance and risk of damages to reindeer husbandry operations will depend both on large carnivore activity and on the presence of reindeer and their vulnerability.

4. Our model makes a number of simplifying assumptions, the impact of which would need to be further evaluated. Among these assumptions are: circular home ranges and negligible variation in space use between individuals of the same sex. Again, the finer the spatial scale for which estimates are derived, the greater the expected impact of violations of these and other model assumptions.

Due to a lack of comprehensive DNA sample collection between the winter 2019/2020 and 2022/2023, wolverine estimates in Norrbotten were derived using predictions from the range-wide OPSCR analysis during this period (Milleret et al., 2023a). Using this indirect approach, the wolverine population size in Norrbotten was estimated to be between 157 and 211 individuals in 2022/2023 (Milleret et al., 2023a). In 2023/2024, the analysis of NGS data collected in Norrbotten with the single-season SCR model indicated that the number of wolverine was likely between 206 and 222 individuals. It is challenging to compare these estimates as they refer to different years, and they were obtained using different datasets and modeling approaches. However, population size estimates can be expected to be more robust when based on NGS data instead of spatial and temporal interpolation and prediction (Milleret et al., 2020).

The involvement of Sámi villlages in NGS in Norrbotten county boosted the amount of data collected. We treated these data as 'opportunistic' because the underlying search effort was not documented. The distinction between structured (with a recorded search effort) and opportunistic data collection is also used when estimating wolverine and wolf abundance at the Scandinavian level using open-population SCR models (Milleret et al., 2023a,b).

Once the rangewide NGS data from 2023/2024 are available for analysis, we will be able to generate new and potentially improved abundance estimates for Norrbotten county (results to be published by the end of 2024). Range wide sampling of wolverines within all Scandinavian regions is a requirement for reliable assessment of the Scandinavian wolverine population. Improved NGS sampling in Norrbotten in 2023/2024 constitutes an important step towards a

comprehensive and coordinated monitoring of wolverine in both Norway and Sweden.

NGS of wolverines in Norrbotten during the winter 2023/2024 occurred between October 1 and May 15. This monitoring period differs from the one used in other Swedish and Norwegian counties, which extends from December 1 to June 30 (Milleret et al., 2023a). Although we are aware that specific challenges and constraints occur in some regions, we recommend a coordination of NGS strategies between all regions of Scandinavia. This is key for a comprehensive estimation of wolverine population size and dynamics, not only at the Scandinavian level, but also for a given region of interest.

5 Acknowledgments

6 Data availability

Data, R code to reproduce the analysis, as well as figures, tables, and raster maps (Figure 3) are available at https://github.com/richbi/RovQuantPublic.

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