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# Estimates of wolf density, abundance, and population dynamics in Sweden and Norway, 2015–2025

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COVER PICTURE
Ridgeline plot of wolf density in 2024/2025.

NØKKELORD
*Canis lupus*, ulv, tetthet, populasjonsdynamikk, deteksjonssannsynlighet, ikke-invaderende innsamling av genetisk materiale, åpen populasjon romlig fangst-gjenfangst, rovdyrforvaltning

KEY WORDS
*Canis lupus*, wolf, population density, population dynamics, detection probability, non-invasive genetic sampling, open-population spatial capture-recapture, carnivore management

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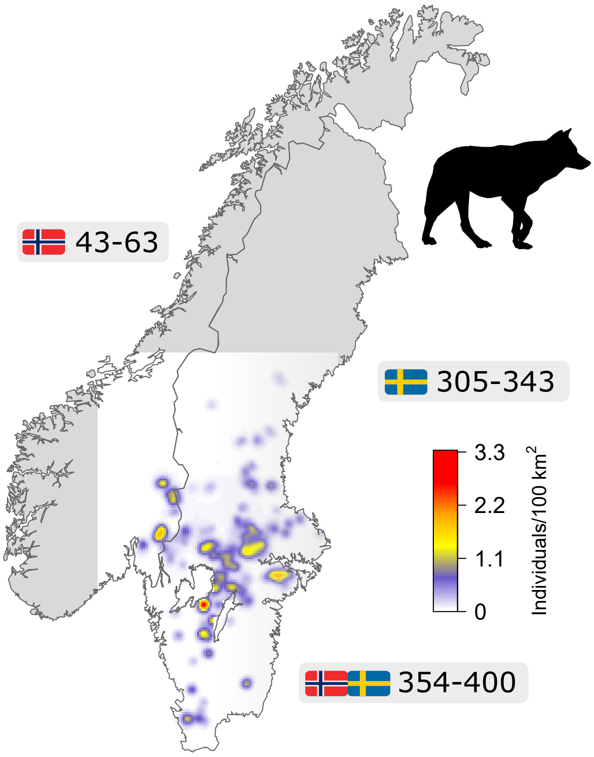
# Summary

**Background** The Scandinavian wolf (*Canis lupus*) population is being monitored annually using non-invasive genetic sampling (NGS) and recovery of dead individuals. DNA extracted from faeces, urine, hair, and tissue is used to identify the species, sex, and individual from which each sample originated. These data are compiled in the Scandinavian large carnivore database Rovbase 3.0.

**Approach** Using the Bayesian open-population spatial capture-recapture (OPSCR) model developed by RovQuant, we estimated annual density and vital rates of the Scandinavian wolf population for ten consecutive monitoring seasons from 2015/2016 to 2024/2025.

**Results** We generated annual density maps and estimated total and jurisdiction-specific population sizes for wolf from the winter 2015/2016 to 2024/2025 within the main population range. Based on the OPSCR model, the size of the Scandinavian wolf population was likely (95% credible interval) between 354 and 400 individuals in 2024/2025, with 305 to 343 individuals attributed to Sweden and 43 to 63 to Norway. During the past four years, the wolf population experienced a steady decrease from 495-528 individuals in 2021/2022 to 354-400 individuals in 2024/2025. In addition to annual density and jurisdiction-specific abundance estimates, we report annual estimates of cause-specific mortalities, recruitment, and detection probabilities.



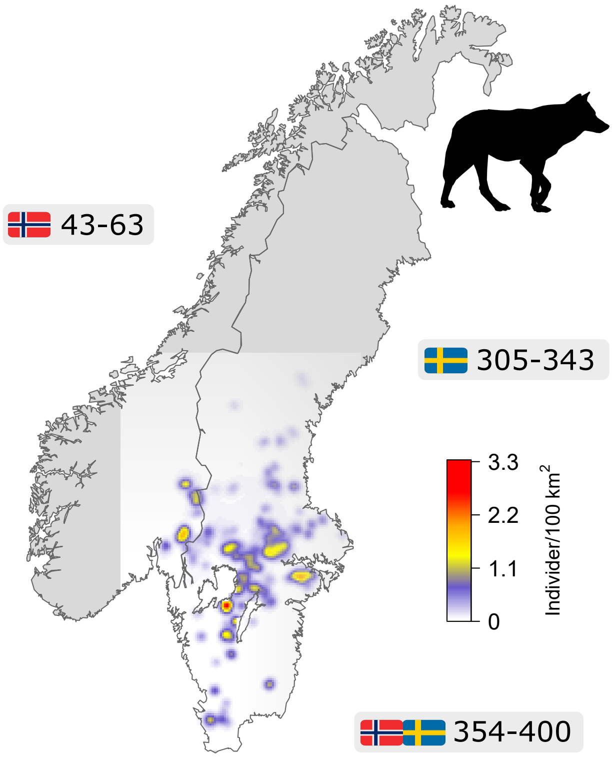
Density map and ranges of abundance estimated for wolves in 2024/2025

## Sammendrag

**Bakgrunn** Den skandinaviske ulvebestanden (Canis lupus) blir overvåket årlig ved bruk av ikke-invasiv genetisk prøveinnsamling (NGS) og gjenfunn av døde individer. DNA ekstrahert fra skit, urin, hår og vev brukes til å identifisere art, kjønn og individ for hver enkelt prøve. Denne informasjonen samles og ivaretas i den skandinaviske databasen for store rovdyr; Rovbase 3.0.

**Tilnærming** Ved bruk av en Bayesiansk åpen romlig fangst-gjenfangst populasjonsmodell (OPSCR), utviklet av RovQuant, estimerte vi årlige tettheter og demografiske rater i den skandinaviske ulvebestanden i ti sesonger fra 2015/2016 til 2024/2025.

**Resultater** Innenfor hovedutbredelsesområdet til ulvebestanden laget vi årlige kart over tettheten av ulv fra 2015/2016 til 2024/2025, som viser både total bestandsstørrelse og bestandsstørrelser innenfor ulike administrative enheter. Basert på OPSCR-modellen var den skandinaviske ulvebestanden mellom 354 og 400 individer i 2024/2025 (95% kredibelt intervall), med 305 til 343 individer i Sverige og 43 til 63 individer i Norge. De siste fire årene har ulvebestanden hatt en jevn nedgang fra 495-528 individer i 2021/2022 til 354-400 individer i 2024/2025. I tillegg til årlige tettheter og områdespesifikke bestandsestimater, gir rapporten estimater på dødelighetsfaktorer, rekruttering og oppdagbarhet.



Kart som viser tetthet av ulv i 2024/2025 sammen med intervaller for estimert antall ulv

# Contents

# 1 Introduction

Non-invasive genetic sampling (NGS) and dead recoveries, are central components of national and regional large carnivore monitoring in Norway and Sweden. Both countries have accumulated an extensive individual-based data set for wolf (*Canis lupus*) and plan to continue such transnational monitoring in the future.

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 collected and stored in Rovbase (www.rovbase.se, www.rovbase.no) by the national monitoring programs in Sweden and Norway. At the core of the analytical framework developed by RovQuant (Bischof et al., 2019b, 2020) are Bayesian open-population spatial capture-recapture (OPSCR) models (Ergon and Gardner, 2014; Bischof et al., 2016; Chandler et al., 2018). These models use the spatial and temporal information contained in the repeated genetic detections of individuals to estimate various population parameters, including spatially-explicit abundance and vital rates. Importantly, the approach accounts for imperfect detection (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 conventional approach for wolf population size estimation in Scandinavia since 2015/2016 entails the use of a static conversion factor to calculate the size of the wolf population from the number of observed reproductions (Wabakken et al., 2024). The conversion factor approach assumes that the relationship between total population size and the number of observed reproductions remains unchanged over time and between regions, which has led to criticism of the method (Chapron et al., 2016; Bischof et al., 2019a). Aside from relaxing this and several other assumptions (Bischof et al., 2019a), the OPSCR method brings along several advantages. These include the ability to map density, derive jurisdiction-specific abundance, estimate survival and recruitment (which are needed for making population projections), and yield tractable measures of uncertainty (Bischof et al., 2019a, 2020).

RovQuant reported its first results for wolves in 2019 (Bischof et al., 2019a,b, 2020) and on an annual basis since 2021 (Milleret et al., 2021, 2022b, 2023b, 2024). In the present report we summarize the analysis of a 10-year time series (2015/2016–2024/2025) using the latest available wolf monitoring data and the most recent version of the OPSCR model. We provide the following information:

- Annual estimates of the number of wolves within the main population range (with Bayesian credible intervals) for Sweden, Norway, and both countries combined, as well as estimates by county and by large carnivore management region in both countries.
- Annual maps of wolf density throughout the species' primary range in Scandinavia.
- Annual estimates of survival, cause-specific mortality, recruitment, and population growth rate (with Bayesian credible intervals).
- Estimated proportion of individuals detected through non-invasive genetic sampling (with Bayesian credible intervals).

## Box 1: Terms and acronyms used

**AC:** Activity center. Model-based equivalent to 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.

**CrI:** 95% Bayesian 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 to areas searched (e.g., habitat grid cells where searches for genetic samples were conducted; used in this project).

**Statsforvalteren:** Norwegian state's representative in the county, responsible for following up decisions, goals, and guidelines from the legislature and the government.

**Habitat buffer:** Buffer surrounding the searched area that is considered suitable habitat but was not searched.

**Legal culling**: Lethal removal of individuals by legal means including licensed recreational hunting, management removals, 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.

**p0:** Baseline detection probability; probability of detecting an individual at a given detector, if the individual's AC is located exactly at the detector location.

$\boldsymbol{\sigma}$: Scale parameter of the detection function; related to the size of the circular home-range.

**SCR:** Spatial capture-recapture.

**SNO:** Statens naturoppsyn (Norwegian Nature Inspectorate) is the operative field branch of the Norwegian Environment Directorate (Miljødirektoratet).

# 2 Methods

## 2.1 Data

We included data from multiple sources, the primary one being the Scandinavian large carnivore database Rovbase 3.0 (rovbase.se and rovbase.no; last extraction: 2025-04-23). This database is used jointly by Norway and Sweden to record detailed information associated with large carnivore monitoring, including, but not limited to, non-invasive genetic sampling (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 during winters 2015/2016 to 2024/2025.

**Non-invasive genetic sampling** Swedish and Norwegian management authorities, SNO (Norway) and Länsstyrelserna (Sweden) conduct annual searches for sources of DNA (primarily scats and urine) throughout the Scandinavian wolf range (Svensson et al., 2023). Although samples may be collected throughout the year, the official survey period starting with the 2015/2016 season has been Oct 1 – Mar 31. About one third (30%) of DNA samples originated from opportunistic searches (without associated information on search effort) conducted by hunters or other members of the public. See Liberg et al. (2012) and Bischof et al. (2019a) for further details about the data collection procedure. For individual identification, at least 17 microsatellite markers were amplified with PCR throughout the study period. Samples were amplified four times to account for the occurrence of allelic dropout and false alleles (Taberlet et al., 1996). Consensus genotypes were constructed from the replicated PCR runs using the threshold rule that the same alleles had to appear at least twice for a heterozygous genotype and three times for a homozygous genotype (Åkesson et al., 2016). Since 2017/2018, 90 single nucleotide polymorphisms (SNPs) were used for individual identification, in addition to microsatellites. Samples were amplified and genotypes visualized twice using nanofluid arrays (Fluidigm Inc.). Consensus SNP genotypes consisted of the markers with the same allele composition from the two amplifications (Åkesson et al., 2018).

**Dead recoveries** In Scandinavia, all dead large carnivores killed legally (e.g., legal hunting, management kills, defense of life and property) have to be reported to the state authorities (Statsforvalteren or SNO in Norway and Länsstyrelserna or the police in Sweden). All wolves found dead due to other reasons (e.g., natural deaths, vehicle and train collisions, illegal hunting) also have to be reported, but an unknown proportion remains undetected. Tissue is collected from all reported dead carnivores for DNA extraction and analysis. DNA from dead carnivores, if genotyped, can be linked with NGS data via individual IDs and provide definite information about the fate of individuals. Dead recoveries associated with GPS-coordinates also provide additional information for the estimation of individual locations, especially valuable for individuals with few or no NGS detections (Dupont et al., 2021).

**GPS search tracks** Government employees involved in systematic searches for wolf DNA along roads and following wolf tracks (e.g., via snowmobiles, skis, snowshoes) documented their effort with GPS track logs which were registered in Rovbase 3.0. GPS search tracks were included in the OPSCR model to account for spatial and temporal variation in search effort.

**Observation reports in Skandobs** We used all observation records available from Skandobs (skandobs.se; skandobs.no) that were recorded during the wolf monitoring seasons since Oct 1, 2015, (last extraction: 2025-04-23). Skandobs is a web application that allows anyone to anonymously register observations (e.g., visual, tracks, faeces) of bears, lynx, wolves, and wolverines in Scandinavia. This database consists of around 120 000 records of possible large carnivore observations. Although most observations are not verified, they offer the best available proxy for spatio-temporal variation in opportunistic search effort.

**Parentage analysis and social status assignation** Each year, field observations, genetic sampling data, dead recoveries, and parentage analysis (which resulted in a near-complete pedigree of the Scandinavian wolf population) are used to establish counts of pairs, packs, and reproductions (Svensson et al., 2014, 2015, 2017, 2019, 2021, 2023; Wabakken et al., 2016, 2018, 2020, 2022, 2024). The social status (adult scent-marking member in a pack/pair, or subadult member of a pack and vagrant individuals) was determined on a yearly basis for genetically identified individuals using the pedigree and tracking information from the monitoring (Åkesson et al., 2022). The identity of known adult scent-marking individuals was reported in the yearly monitoring reports (Svensson et al., 2014, 2015, 2017, 2019, 2021, 2023; Wabakken et al., 2016, 2018, 2020, 2022, 2024) and a detailed description of the method used for parental assignment was provided in Åkesson et al. (2016). We assigned individuals to two different states depending on whether the individual had been identified as an adult scent-marking member of a pair or a pack ("adult scent-marking") or not ("other"). See Bischof et al. (2019a) for further details.

**Study area** Although wolves can occur throughout the Scandinavian peninsula, we restricted the analysis to the core area (Figure 1). Following the recent wolf range expansion towards the south of Sweden, the Swedish Environmental Protection Agency requested a corresponding expansion of the study area to include southern Sweden (Milleret et al., 2022b, 2023b). Since 2022, the RovQuant models therefore include an additional 68 400 km$^2$ in the study area (total= 322 400 km$^2$), compared to the previous analyses of the Scandinavian monitoring wolf data by RovQuant (Bischof et al., 2019b, 2020; Milleret et al., 2021).

## 2.2 Open-population spatial capture-recapture model

We analysed the data using a Bayesian open-population spatial capture-recapture (OPSCR) model (Bischof et al., 2019b), which addresses three challenges associated with population-level wildlife inventories:

1. Detection is imperfect and sampling effort heterogeneous in space and time: 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 geographic space or area, density cannot be estimated and population size is ill-defined (Efford, 2004).
3. Non-spatial population dynamic models usually estimate "apparent" survival and recruitment, as these parameters include the probability of permanent emigration and immigration, respectively. By explicitly modelling movement of individuals between years, the OPSCR model can help return unbiased estimates of demographic parameters (Ergon and Gardner, 2014; Schaub and Royle, 2014; Gardner et al., 2018; Efford and Schofield, 2022).

The OPSCR model (Ergon and Gardner, 2014; Bischof et al., 2016; Chandler et al., 2018) is composed of three sub-models:

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

**Population dynamics and population size sub-model** We used a multi-state formulation (Lebreton and Pradel, 2002) where each individual life history is represented by a succession of up to five discrete states $z_{i,t}$: 1) "unborn" if the individual has not been recruited in the population (state "unborn" is required for the data augmentation procedure, see below); 2) "alive other" if it is alive and not assigned as an "adult scent-marking" individual; 3) "alive adult scent-marking" if it is alive and assigned as an "adult scent-marking" individual; 4) "culled" if it was culled and therefore recovered dead between the start of the previous and current monitoring season; 5) "Dead from other causes and recovered" if it died from other causes of mortality (e.g. disease, car collision, ...) and was reported to the authorities; and 6) “dead”: if it has died but was not recovered. We then modelled the transition between states from one monitoring season to the next ($t$ to $t + 1$) to estimate vital rates (recruitment and mortality). More details are available in Bischof et al. (2019b), and Bischof et al. (2020). We used data augmentation (Royle and Dorazio, 2012), whereby additional, undetected individuals are available for inclusion in the population at each time step.

**Density and movement sub-model** We used a Bernoulli point process to model the distribution of individual activity centers. In the first year, individuals were located according to an intensity surface, which was a function of the locations of known packs at time $t - 1$ (see Bischof et al., 2019b and Bischof et al., 2020 for more details). For all subsequent years ($t > 1$), the location of individual activity centers was a function of the distance from previous activity centers (at time $t - 1$), as well as a function of the locations of known packs (at time $t - 1$). As in previous analyses (Milleret et al., 2022b, 2023b, 2024), we used an exponential model to describe the movement of individuals between years, as it better accommodates distributions with long tails (i.e., a few individuals that make exceptionally long dispersal movements).

**Detection sub-model** SCR models take into account the spatial-variation in individual detection probability based on the distance between activity center 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 activity center and the detector.

In Scandinavia, DNA material from live wolves is collected following two main processes. First, authorities collect genetic samples and record the corresponding search effort during official searches ("structured sampling" thereafter). Second, DNA material can be collected by any member of the public (e.g., hunters) or by the authorities in a more or less opportunistic manner and associated search effort is not directly available ("unstructured" sampling thereafter). 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 "Statsforvalteren" or "SNO" in Rovbase) and if it was located within 500 m from a search track recorded on 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 study area and therefore used the same 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 the structured or unstructured sampling were assumed to be driven by different processes.

We accounted for spatio-temporal heterogeneity in detectability during ***structured sampling*** using:

- Spatial-temporal variation in effort using the length of GPS search tracks in each detector grid cell.
- Spatio-temporal variation in snow cover.
- Spatio-temporal variation in monitoring regimes between jurisdictions (groups of counties in Sweden, monitoring regions in Norway).

- Individual variation linked with the state of the individual (i.e., adult scent-marking individuals, other individuals).
- Individual variation linked with a previous detection that could be expected to positively or negatively influence the probability of being detected at subsequent occasions, depending on the state of knowledge in the territory or neighboring territories.

We accounted for spatio-temporal heterogeneity in detectability during ***unstructured sampling*** using:

- Spatio-temporal variation in unstructured sampling or carnivore observations (Figure A1). For each detector grid cell and during each monitoring season (Oct 1 – Mar 31), we identified whether a) any carnivore sample had been registered in Rovbase (excluding successfully genotyped wolf samples already used in the OPSCR analysis) or b) any observation of carnivores had been registered in Skandobs. Roughly, the variable distinguishes areas with very low detection probability from those with higher probability that carnivore DNA samples, if present in a detector grid cell, could have been detected and submitted for genetic analysis (Figure A1).
- Spatio-temporal variation in snow cover.
- Spatial variation in accessibility measured as the average distance to the nearest road.
- Spatio-temporal variation between countries.
- Individual and temporal variation linked with the state of the individual (i.e., adult scent-marking individuals, other individuals).
- Individual and temporal variation linked with a previous detection that could be expected to positively influence the probability of being detected at subsequent occasions.

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).

**Model fitting** We fitted sex-specific Bayesian OPSCR models using Markov chain Monte Carlo (MCMC) simulation with NIMBLE version 0.12.2 (Turek et al., 2021; de Valpine et al., 2017; de Valpine et al., 2022) and nimbleSCR (Bischof et al., 2021) in R version 4.1.0 (R Core Team, 2021). We ran 4 chains each with 30 000 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 from which abundance estimates were derived. We considered models as converged when the Gelman-Rubin diagnostics (Rhat, Gelman and Rubin, 1992) was $\leq$1.1 for all parameters and by visually inspecting the trace plots.

**Abundance estimates** To obtain an estimate of abundance for any given area, we summed the number of predicted AC locations (live individuals) that fell within that area for each iteration of the MCMC chains, thus generating a posterior distribution of abundance for that area. In this fashion, abundance estimates and the associated uncertainty can be extracted for any spatial unit, including countries or counties (Figure A2). Individuals detected near a border can have their model-predicted AC placed on different sides of that border in different model iterations (even if detections are only made on one side of the border). As a result, the probability of designating such individuals to either side of the border can be integrated into jurisdiction-specific abundance estimates. This is especially relevant for wolves detected along the Swedish and Norwegian border ("cross-boundary wolves", Wabakken et al., 2022); individual wolves can be partially designated to both countries (Bischof et al., 2016).

To ensure that abundance estimates for spatial sub-units (jurisdictions) add up to the overall abundance estimate, we used the mean and associated 95% Bayesian credible interval limits to summarize posterior distributions of abundance. Combined (female/male) parameter estimates were obtained by merging posterior samples from the sex-specific models.

**Density maps** We used both the distribution of model-estimated AC positions and the scale parameter ($\sigma$) of the detection function to construct density maps based on individual utilization distributions. These maps are not only based on the position of the center of an individual's home range, but also take into account the area over which that individual's activity is spread, i.e., its space use (Bischof et al., 2020). To do so, 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).

**Other derived parameters** The average proportion of individuals detected and the associated uncertainty were obtained by dividing the number of individuals detected through NGS sampling (Table A3) by the abundance estimates and their associated Bayesian credible intervals, respectively.

We derived the proportion of females in the population and the associated uncertainty by dividing the posterior distribution representing the number of females by the combined abundance estimate for males and females (Table A3). Yearly population growth rates were calculated as $\lambda_t = N_{t+1}/N_t$ (Table A7).

**Focus on uncertainty** Although we reported median (or mean for abundance; see above) estimates for all parameters in the tables, we intentionally focused the main results of this report on the 95% Bayesian 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 on a single point estimate (Milleret et al., 2022a).

# 3 Results

## 3.1 Non-invasive genetic samples and dead recoveries

A total of 20 844 (9 109 female; 11 735 male) genotyped wolf genetic samples were included in the analysis, of which 76% originated from Sweden. These samples were associated with 1 876 (868 female; 1008 male) individuals. We did not include individuals with unknown sex in this analysis. Among all genotyped samples, 9 274 (3838 female; 5436 male) were assigned to the structured sampling and 11 570 (5271 female; 6299 male) to the unstructured sampling. We also used 703 (312 female; 391 male) dead recoveries of wolves in the OPSCR model, of which 587 (258 female; 329 male) were due to legal culling and 116 (54 female; 62 male) due to other causes of mortality. The majority of dead recoveries (66%) originated from Sweden. Annual total and country-specific tallies of NGS samples and associated individuals, as well as dead recoveries included in the analysis are provided in the Appendices (NGS samples: Table A2 and Table A1, NGS individuals: Table A3, dead recoveries: Table A4)

## 3.2 Density and abundance

Wolf abundance for the entire study area (322 400 km$^2$, excluding the buffer area) was likely (95% Bayesian credible interval) between 354 and 400 individuals in 2024/2025 (Table 1, Figure 1). Estimates refer to the status of the population at the start of the annual sampling period (Oct. 1). The proportion of females in the Scandinavian wolf population was likely between 42% and 52% in 2024/2025. Based on the model-predicted location of ACs, we estimated that in 2024/2025, between 305 to 343 individuals could be attributed to Sweden and 43 to 63 to Norway (Table 1). See Table 1 for total and sex-specific abundance estimates for each country and management area. See Table A5 and Table A6 for annual wolf abundance estimates for all of Scandinavia, by region and by county between 2015/2016 and 2024/2025. During the past four years, the wolf population experienced a steady decrease from 495-528 individuals in 2021/2022 to 354-400 individuals in 2024/2025 (Figure 2, Table A5). Note that estimates for different years (Figure 2) shown here differ slightly from those provided in our previous report (Milleret et al., 2023b). This is due to the use of an updated OPSCR model and the inclusion of additional years of data. The analysis yielded annual density maps, which illustrate changes in the distribution of wolves over time (Figure A3).

**Table 1:** Wolf population size estimates in 2024/2025 within the study area by sex at several spatial scales: the entire study area, by country, by management unit (carnivore management regions in Norway and "Rovdjursförvaltningsområden" in Sweden), and counties (“Län” in Sweden); see also Figure A2. Only counties and management units that are within or that intersect the study area are included in the table. Readers should focus on the 95% Bayesian credible interval provided in parentheses, as these - unlike mean values - convey the uncertainty inherent in abundance estimates. Numbers are based on estimated activity center locations of wolves. Combined female-male estimates were obtained by joining sex-specific posterior distributions. Rounding may result in small deviations between total estimates and the sum of the estimates for constituent regions. Note that the numbers reported here are predictions from a statistical model which always represents an oversimplification of reality and is based on available data (NGS and dead recoveries). As a consequence, especially at the local scale, the model-estimated number of wolves based on DNA sampling can deviate from the number of wolves inferred from ancillary observations (e.g., camera traps). Estimates for Norwegian counties are provided in Table A6.

| | Females | Males | Total |
|---|---|---|---|
| TOTAL | 176.2 (162-195) | 198.5 (184-216) | 374.7 (354-400) |
| NORWAY | 26.3 (21-34) | 25.7 (19-34) | 51.9 (43-63) |
| Region 2 | 0.3 (0-2) | 0.5 (0-2) | 0.8 (0-3) |
| Region 3 | 0.7 (0-3) | 1.1 (0-4) | 1.7 (0-5) |
| Region 4 | 6.9 (5-10) | 8 (6-11) | 14.9 (11-19) |
| Region 5 | 17.6 (14-23) | 14.8 (10-20) | 32.5 (26-40) |
| Region 6 | 0.8 (0-4) | 1.3 (0-4) | 2 (0-6) |
| SWEDEN | 149.9 (138-165) | 172.8 (161-188) | 322.8 (305-343) |
| Norra | 5.6 (1-12) | 10.8 (6-17) | 16.4 (10-25) |
| Jämtland | 3.3 (0-9) | 6.7 (3-12) | 10 (4-17) |
| Västerbotten | 0 (0-0) | 0 (0-0) | 0 (0-1) |
| Västernorrland | 2.3 (1-5) | 4.1 (2-7) | 6.4 (4-10) |
| Mellersta | 112.8 (104-124) | 124.5 (115-136) | 237.3 (224-253) |
| Dalarna | 17.8 (13-24) | 18.3 (13-25) | 36.1 (29-45) |
| Gävleborg | 9.4 (7-13) | 11.9 (9-16) | 21.4 (17-26) |
| Örebro | 21 (18-24) | 28.2 (25-32) | 49.2 (44-54) |
| Stockholm | 0.4 (0-2) | 3 (2-5) | 3.4 (2-6) |
| Uppsala | 4.5 (3-6) | 5.8 (5-8) | 10.3 (9-13) |
| Värmland | 20.9 (16-27) | 27.4 (22-34) | 48.3 (41-57) |
| Västmanland | 15 (12-18) | 13 (10-16) | 28 (24-32) |
| VästraGötaland | 23.7 (21-27) | 16.8 (14-21) | 40.5 (36-45) |
| Södra | 31.5 (29-35) | 37.5 (34-42) | 69.1 (64-75) |
| Blekinge | 0 (0-1) | 0.1 (0-1) | 0.2 (0-1) |
| Halland | 1 (0-2) | 1.9 (1-4) | 2.9 (1-5) |
| Jönköping | 5.3 (4-7) | 5.3 (4-8) | 10.6 (8-14) |
| Kalmar | 0.5 (0-2) | 1.1 (0-3) | 1.6 (0-4) |
| Kronoberg | 3.1 (2-5) | 2.5 (0-5) | 5.6 (3-8) |
| Östergötland | 4 (3-6) | 4.8 (4-7) | 8.8 (7-11) |
| Skåne | 6.2 (6-7) | 8 (7-10) | 14.2 (13-16) |
| Södermanland | 11.3 (10-13) | 13.8 (12-16) | 25.1 (23-28) |

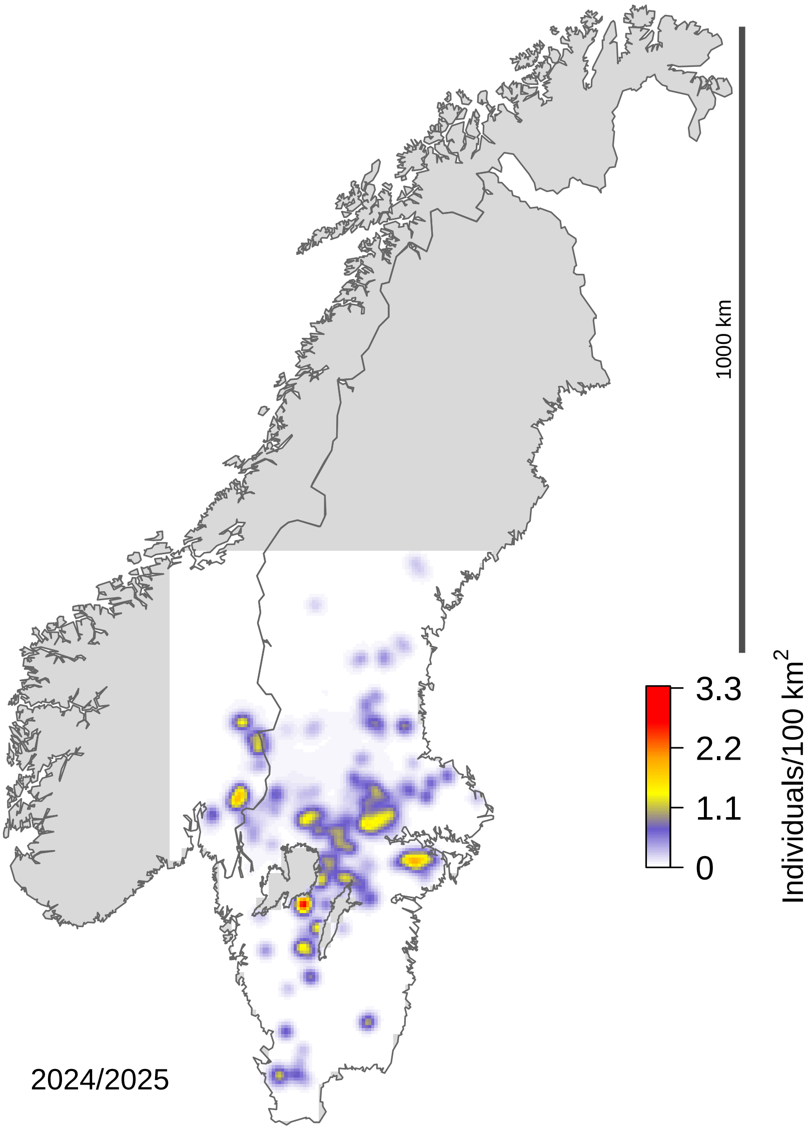


**Figure 1:** Wolf density based on individual utilization distributions throughout the study area (white background) in Scandinavia in 2024/2025. This map is available as a geo-referenced raster file at https://github.com/richbi/RovQuantPublic

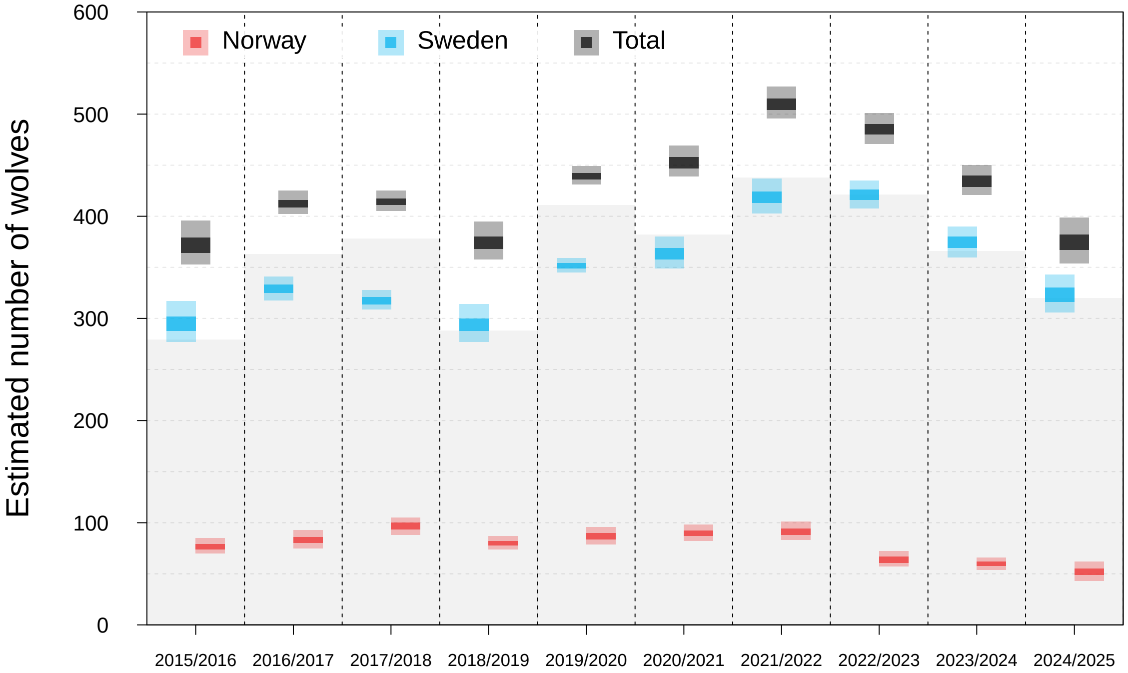


**Figure 2:** Annual wolf population size estimates within the study area by country (blue: Sweden, red: Norway), and total (black) between monitoring seasons 2015/2016 and 2024/2025. Darker and lighter bars show the 50% and 95% Bayesian credible intervals, respectively. Bayesian credible intervals indicate uncertainty in estimates given the model and data used to generate the estimates. Light grey bars in the background show the total number of individuals detected within the entire study area. Changes in the model and the data can result in different estimates and associated uncertainty compared with estimates provided in previous reports by RovQuant.

### 3.3 Vital rates

The OPSCR model produced annual estimates of legal hunting mortality, mortality associated with all other causes, and per capita recruitment rates (Figure 3; Table A8,Figure 4). There was temporal variation in mortality rates, with the risk of mortality from causes other than culling generally higher than the risk of mortality from culling. Overall, scent-marking adult individuals had a higher survival compared to other individuals, with no pronounced systematic difference between sexes (Figure A4). Recruitment experienced a steady decline since 2020/21 (Figure 4).

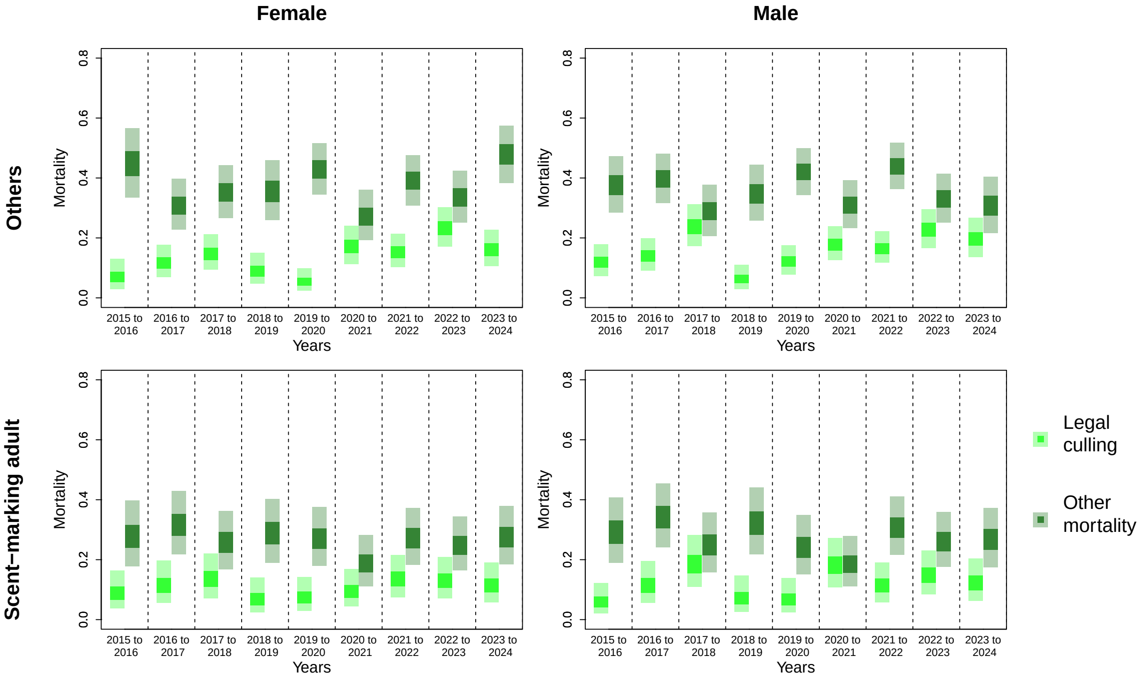


**Figure 3:** Mortality probabilities due to legal culling (light green) and all other causes (dark green) for female and male wolves. Darker and lighter bars show the 50% and 95% Bayesian credible intervals, respectively. Shown are overall estimates throughout the study area. Estimates refer to deaths occurring between the start of one sampling season and the start of the next.

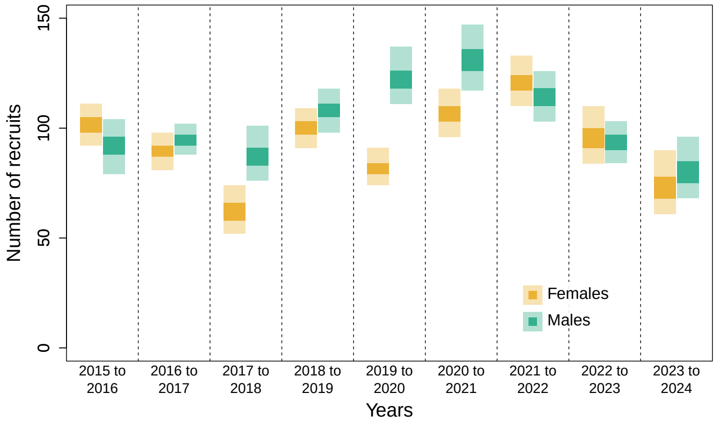


**Figure 4:** Estimated annual number of recruits of female and male wolves. Recruitment represents the number of new individuals present in the population on Oct 1 (i.e., individuals that were born between the two consecutive monitoring seasons and survived to Oct 1 or that immigrated in the study area). Darker and lighter bars show the 50% and 95% Bayesian credible intervals, respectively.

### 3.4 Detection probability

The overall proportion of detected individuals in the study area was likely between 80% and 90% in 2024/2025 (Table A12). The baseline detection probability during structured and unstructured sampling varied both in time and space (Figure A5 and Figure A6). More specifically, the length of recorded search tracks positively affected detection probability during structured sampling (2024/2025; males: $\beta_{2_{Structured}}$ =0.46, CrI: 0.38 - 0.55; females: $\beta_{2_{Structured}} = 0.42$, CrI: 0.33 - 0.52; Table A10). Previous detection of individuals and the average proportion of snow cover had no strong effect on detection probability for the structured sampling (Table A10). Unstructured search effort derived using the observation data in Skandobs and Rovbase had a strong positive effect on detection probability during unstructured sampling (2024/2025; males: $\beta_{4Unstructured} = 1.84$, CrI: 1.25 - 2.67; females: $\beta_{4Unstructured} = 1.63$, CrI: 0.99 - 2.32; Table A11). The effect of previous detection also tended to have a positive effect on detection probability during unstructured sampling, but the pattern was not consistent across years (Table A11).

## 4 Discussion

The size of the wolf population on the Scandinavian peninsula steadily declined from 495-528 individuals in 2021/22 to 354-400 individuals in 2024/25 (Figure 2). This decline was pronounced both in Sweden, where population size decreased from 403-436 individuals in 2021/22 to 305-343 individuals in 2024/25, and in Norway, where population size decreased from 83-101 individuals in 2021/22 to 43-63 individuals in 2024/25 (Figure 2, Table A5). The reduction in the number of individuals may be mostly attributes to a reduction in recruitment of both females and males Figure 4). During the same period, the number of recorded packs dropped from 55 in 2021/22 (Wabakken et al., 2022) to 40 in 2024/25 (Svensson et al., 2025). Various factors can drive temporal variation in recruitment, but because packs are the reproductive units of wolf population, a reduction in the number of packs is likely at the origin of the decrease in recruitment (see also Chapron et al. (2016)).

## 5 Summary of improvements made

The analysis described in this report includes the following adjustments compared with previous analyses of wolf density in Scandinavia by RovQuant (Milleret et al., 2024):

1. Added of data from the 2024/2025 monitoring season.
2. Included of an additional state in the population dynamic model to explicitly model recoveries of individuals dead from mortality due to causes other than legal hunting.
3. Removed 1032 duplicated search tracks which represented approximately 0.008% of the total number of kilometers recorded.
4. Constrained the monitoring period to October 1- March 31. In previous reports, the period October 1- April 30 was used (Milleret et al., 2022b, 2023b, 2024). Note that apart from slight differences in the number of genetic samples used, this change had no noticeable impact on the results (Milleret et al., 2024).
5. Added of county-specific abundance estimates in Norway (Table A6).

## 6 Suggestions for future improvements

RovQuant continues to work on improving the functionality and efficiency of OPSCR models. We recommend the following developments for future analyses of the Scandinavian wolf monitoring data:

1. Review and adjust spatial covariates on density. This may involve the addition of land cover and topographic variables.
2. Account for individual heterogeneity in detectability/space use, for example by using a finite-mixture approach (Cubaynes et al., 2010).
3. Consider alternative detection models that do not assume a half-normal shape and/or circular home ranges (Sutherland et al., 2015).
4. Account for spatial variation in vital rates (i.e., survival, recruitment; Milleret et al. 2023a).

# 7 Acknowledgements

This work was made possible by the large carnivore monitoring programs and the extensive monitoring and observation data collected by Swedish (Länstyrelsena) and Norwegian (SNO) wildlife management authorities, as well as the public in both countries. Our analysis relied on genetic analyses conducted by the laboratory personnel at the DNA laboratories at the Swedish University of Agricultural Sciences, and the Norwegian Institute for Nature Research. We also thank Swedish and Norwegian wildlife managers for feedback provided during project RovQuant and the Research Council of Norway for partial funding (NFR 286886; project WildMap, NFR 345279: project PopFlow). The computations/simulations were performed on resources provided by NMBU's computing cluster "Orion", administered by the Centre for Integrative Genetics and by UNINETT Sigma2. J. Vermaat provided helpful comments on a draft of this report.

# 8 Data availability

Data, R code to reproduce the analysis, as well as figures, tables, and raster maps (Figure A3) are available at https://github.com/richbi/RovQuantPublic.

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# Appendices

**Figure A1:** Covariate used to account for spatio-temporal variation in unstructured sampling in the study area. Green cells (10 x 10 km) represent areas with at least one carnivore record in Rovbase (rovbase.no, rovbase.se, excluding the ones used in the OPSCR model) or an observation record from Skandobs (skandobs.se, skandobs.no) during a given monitoring season (Oct 1 – Mar 31).

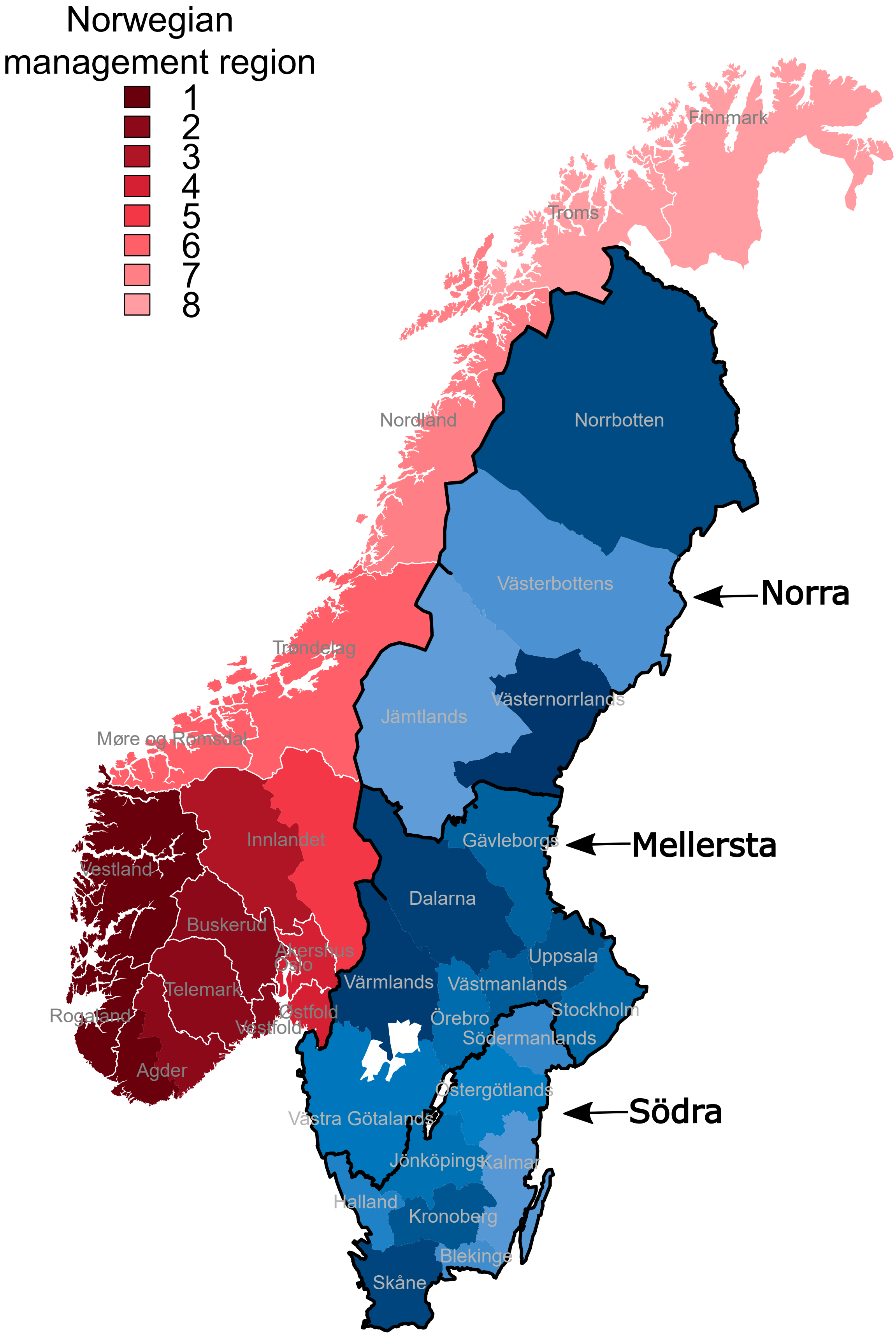

**Figure A2:** Management jurisdictions in Norway and Sweden. Shaded polygons show carnivore management regions in Norway and counties in Sweden. The Norwegian county borders used to extract abundance estimates presented in Table A6 are also displayed in white. Thick outlines delineate Swedish carnivore management regions ("Rovdjursförvaltningsområden") encompassing multiple counties.

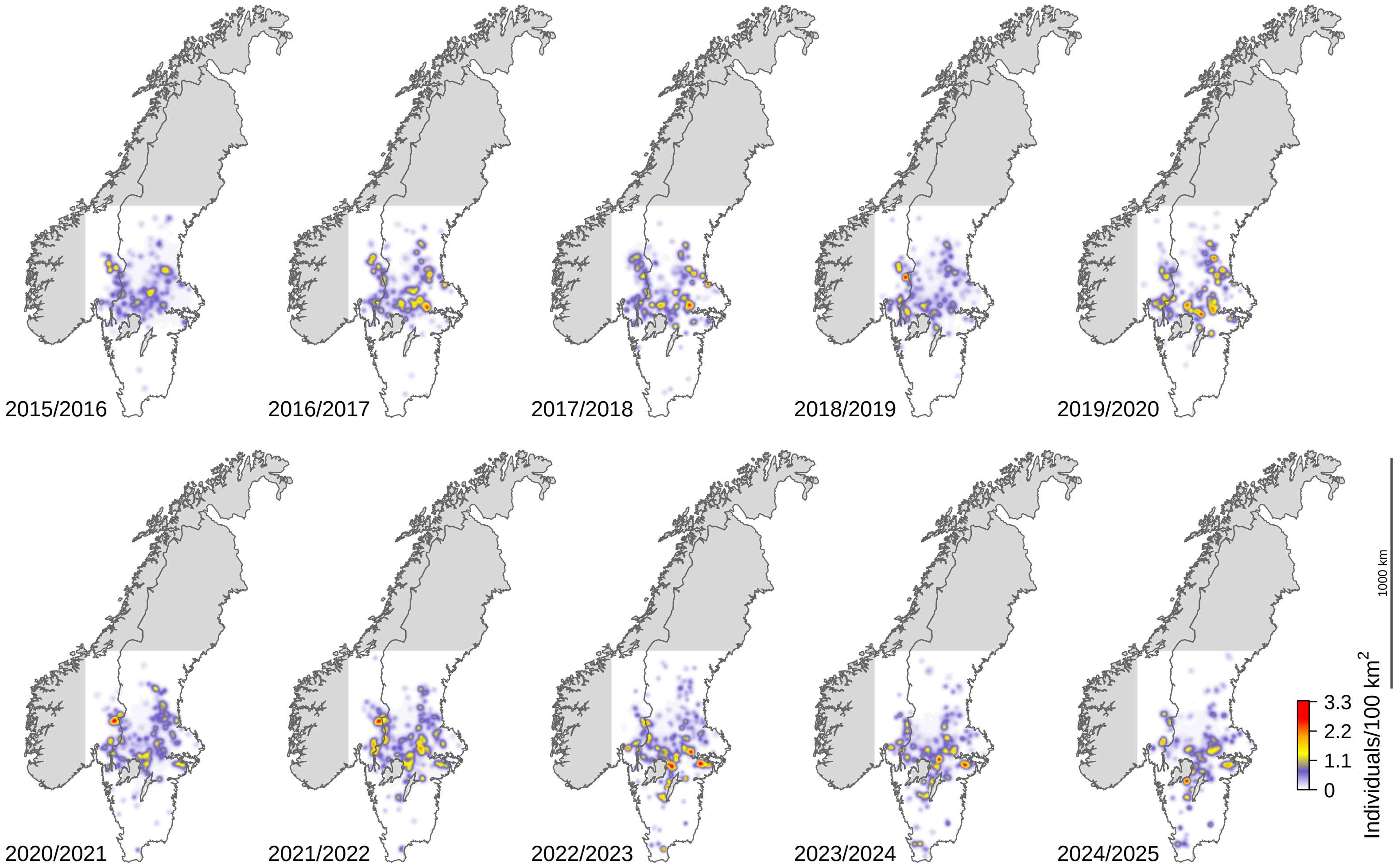

**Figure A3:** Wolf density based on individual utilization distributions throughout the study area (white background) in Scandinavia between 2015/2016 and 2024/2025. These maps are available as geo-referenced raster files at https://github.com/richbi/RovQuantPublic.

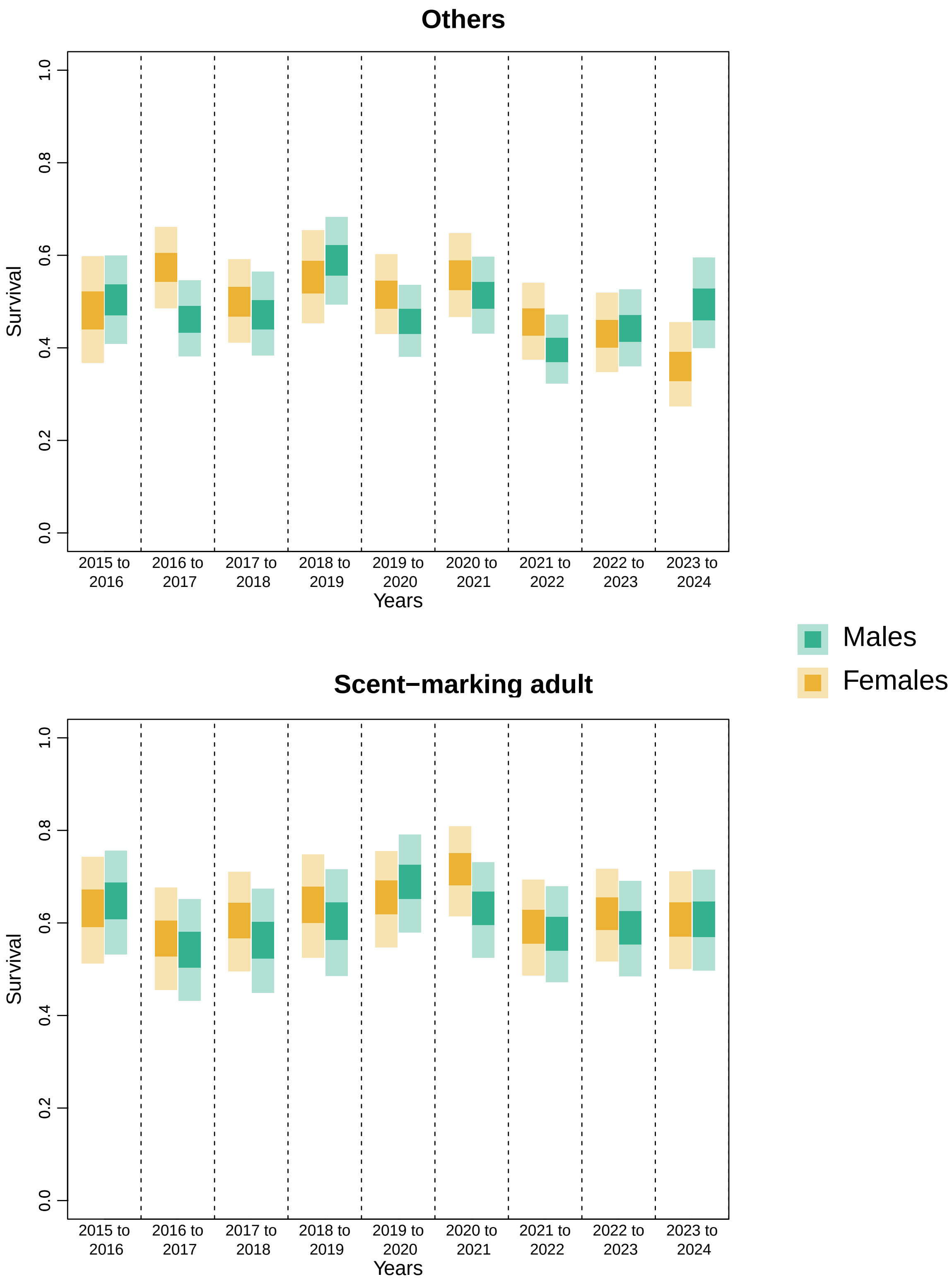

**Figure A4:** Annual survival probabilities for scent-marking adults and other individuals and for female and male wolves. Darker and lighter bars show the 50% and 95% Bayesian credible intervals, respectively. Combined mortality probabilities (and therefore overall survival) are obtained by adding the mortality probabilities due to legal culling and all other causes (Figure 3). Shown are overall estimates for the entire study area between 2015/2016 and 2024/2025.

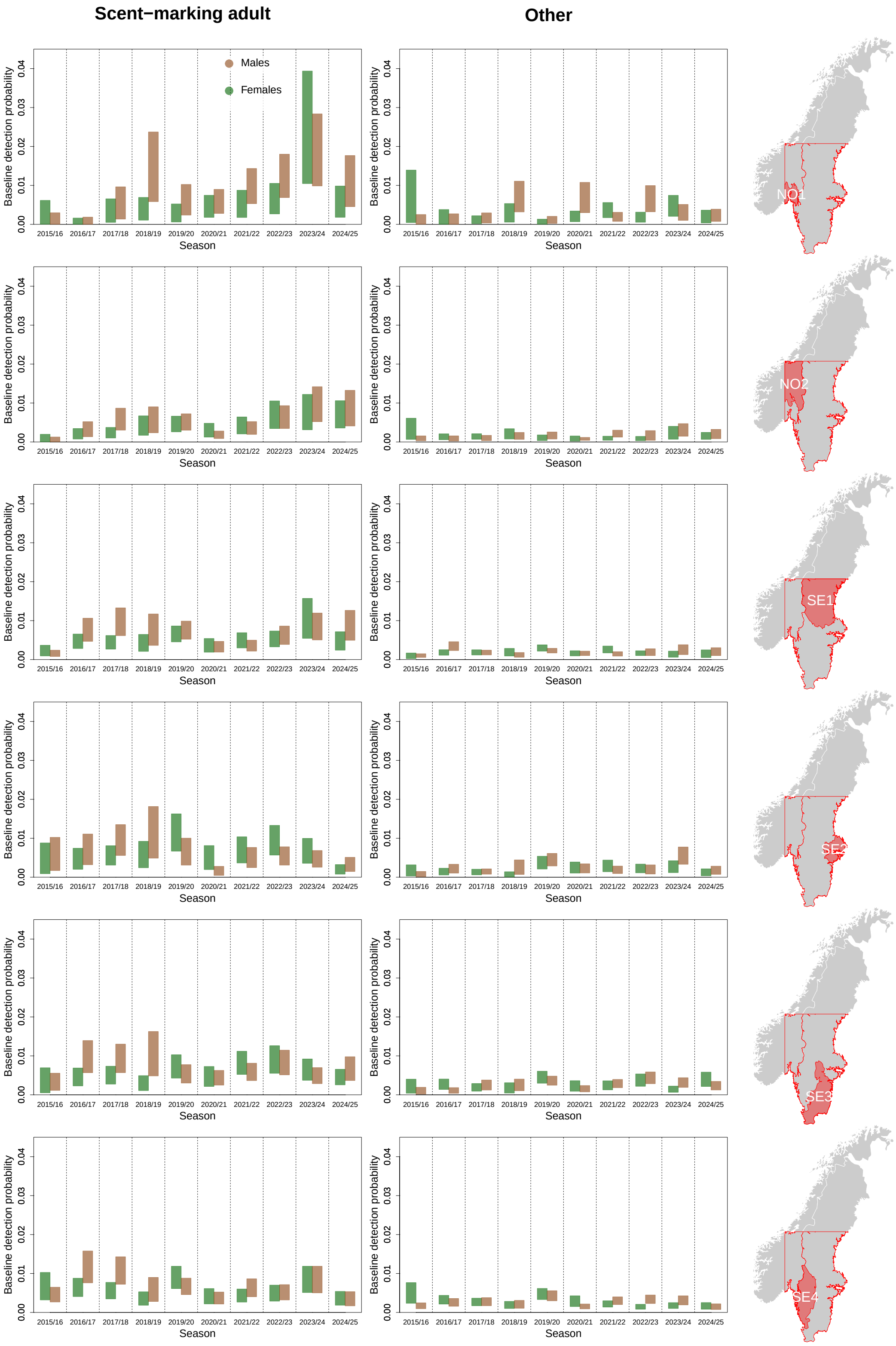

**Figure A5:** Sex-specific baseline detection probabilities ($p_{0_{structured}}$) of scent-marking adults and other individuals for the different Scandinavian jurisdictions during structured sampling as estimated by the open-population spatial capture-recapture model. Bars represent 95% Bayesian credible intervals. Results are separated into panels based on regions. Estimates are shown for the mean values of the detection covariates. Note that baseline detection probability ($p_0$) is a theoretical value of detection probability when a detector coincides with the location of an individual's activity center. It is not to be confused with detectability, i.e, the overall probability of detecting an individual.

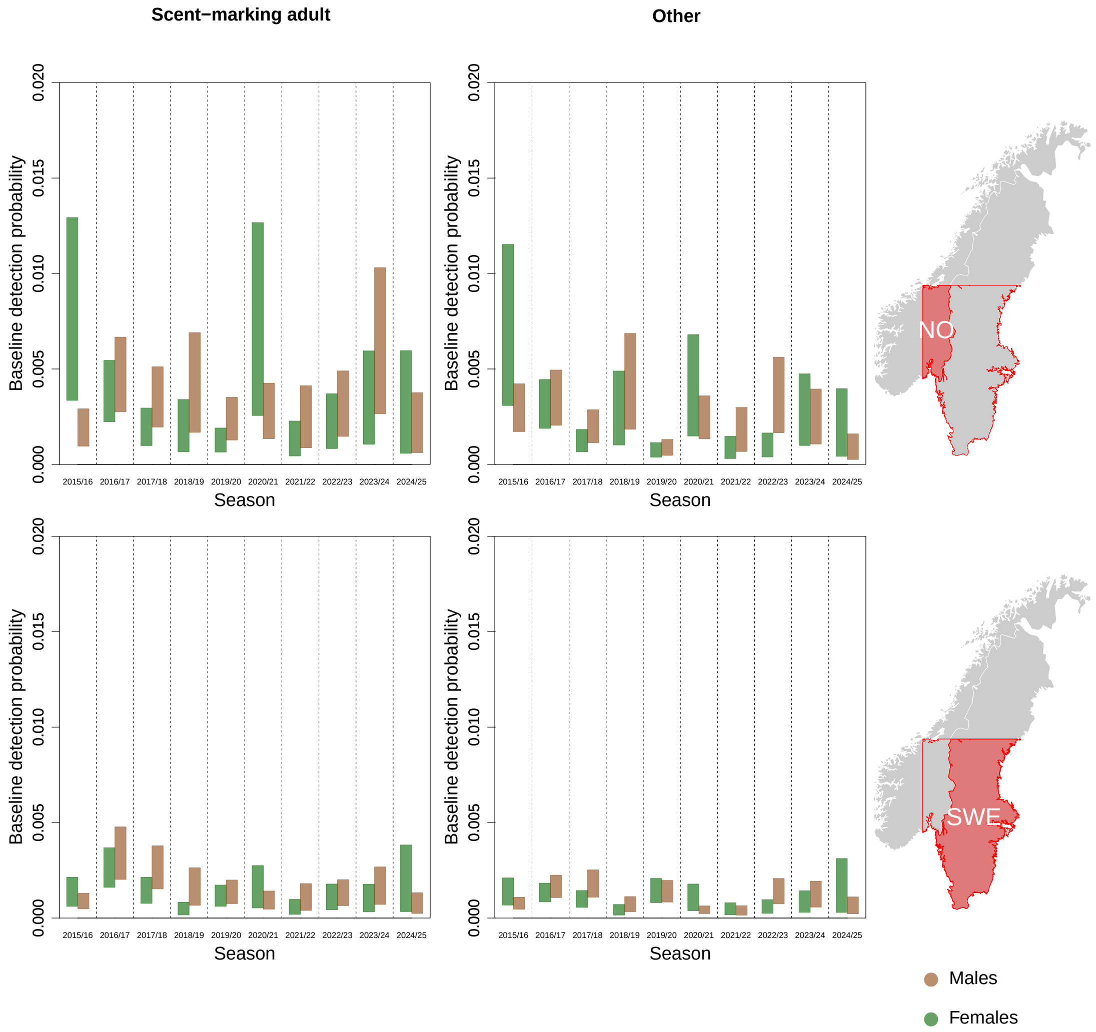

**Figure A6:** Sex- and country-specific baseline detection probabilities ($p_{0\,unstructured}$) of scent-marking adults and others individuals during unstructured sampling as estimated by the open-population spatial capture-recapture model. Bars represent 95% Bayesian credible intervals. Estimates are shown for the mean values of the detection covariates. Note that baseline detection probability ($p_0$) is a theoretical value of detection probability when a detector coincides with the location of an individual's activity center. It is not to be confused with detectability, i.e, the overall probability of detecting an individual.

**Table A1:** Annual number of wolf non-invasive genetic samples included in the analysis. Numbers are reported by country, for females (F) and males (M), and for each type of sampling (structured and unstructured). We included only samples collected within the study area during the primary monitoring period (Oct 1 - Mar 31) between 2015/2016 and 2024/2025.

| | | 2015/2016 | | 2016/2017 | | 2017/2018 | | 2018/2019 | | 2019/2020 | | 2020/2021 | | 2021/2022 | | 2022/2023 | | 2023/2024 | | 2024/2025 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M |
| **Norway** | Structured | 6 | 9 | 20 | 10 | 36 | 42 | 53 | 93 | 44 | 75 | 51 | 130 | 73 | 162 | 56 | 116 | 90 | 155 | 81 | 105 |
| | Unstructured | 135 | 168 | 245 | 188 | 232 | 238 | 163 | 224 | 188 | 231 | 257 | 319 | 126 | 223 | 102 | 96 | 100 | 143 | 70 | 74 |
| **Sweden** | Structured | 137 | 200 | 373 | 582 | 474 | 665 | 221 | 293 | 597 | 717 | 280 | 456 | 416 | 498 | 364 | 457 | 261 | 371 | 205 | 300 |
| | Unstructured | 99 | 175 | 463 | 536 | 603 | 830 | 129 | 162 | 835 | 831 | 256 | 340 | 280 | 383 | 435 | 485 | 267 | 330 | 286 | 323 |
| **Total** | Structured | 143 | 209 | 393 | 592 | 510 | 707 | 274 | 386 | 641 | 792 | 331 | 586 | 489 | 660 | 420 | 573 | 351 | 526 | 286 | 405 |
| | Unstructured | 234 | 343 | 708 | 724 | 835 | 1068 | 292 | 386 | 1023 | 1062 | 513 | 659 | 406 | 606 | 537 | 581 | 367 | 473 | 356 | 397 |

**Table A2:** Annual number of wolf non-invasive genetic samples included in the analysis. Numbers are reported by country, for females (F) and males (M). We included only samples collected within the study area during the primary monitoring period (Oct 1 - March 31) between 2015/2016 and 2024/2025.

| | 2015/2016 | | 2016/2017 | | 2017/2018 | | 2018/2019 | | 2019/2020 | | 2020/2021 | | 2021/2022 | | 2022/2023 | | 2023/2024 | | 2024/2025 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M |
| **Norway** | 141 | 177 | 265 | 198 | 268 | 280 | 216 | 317 | 232 | 306 | 308 | 449 | 199 | 385 | 158 | 212 | 190 | 298 | 151 | 179 |
| **Sweden** | 236 | 375 | 836 | 1118 | 1077 | 1495 | 350 | 455 | 1432 | 1548 | 536 | 796 | 696 | 881 | 799 | 942 | 528 | 701 | 491 | 623 |
| **Total** | 377 | 552 | 1101 | 1316 | 1345 | 1775 | 566 | 772 | 1664 | 1854 | 844 | 1245 | 895 | 1266 | 957 | 1154 | 718 | 999 | 642 | 802 |

**Table A3:** Annual number of individual wolves detected via non-invasive genetic sampling and included in the analysis. Numbers are reported by country, for females (F) and males (M), and for each type of sampling (structured and unstructured). We included only individuals associated with samples collected within the study area during the primary monitoring period (Oct 1 - Mar 31) between 2015/2016 and 2024/2025. Some individuals were detected in both countries during the same year, hence the sum of the national counts can exceed the total number of unique individuals detected in Scandinavia.

| | | 2015/2016 | | 2016/2017 | | 2017/2018 | | 2018/2019 | | 2019/2020 | | 2020/2021 | | 2021/2022 | | 2022/2023 | | 2023/2024 | | 2024/2025 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M |
| **Norway** | Structured | 5 | 5 | 10 | 6 | 18 | 17 | 16 | 21 | 17 | 22 | 22 | 25 | 31 | 34 | 20 | 24 | 22 | 24 | 20 | 20 |
| | Unstructured | 29 | 44 | 46 | 36 | 47 | 44 | 31 | 43 | 36 | 44 | 37 | 53 | 40 | 48 | 27 | 20 | 23 | 31 | 22 | 19 |
| **Sweden** | Structured | 68 | 82 | 111 | 130 | 115 | 126 | 81 | 91 | 136 | 153 | 107 | 115 | 129 | 148 | 125 | 140 | 99 | 111 | 88 | 100 |
| | Unstructured | 53 | 85 | 104 | 123 | 120 | 144 | 69 | 69 | 146 | 158 | 98 | 115 | 122 | 130 | 136 | 142 | 100 | 111 | 89 | 110 |
| **Total** | Structured | 73 | 87 | 120 | 135 | 130 | 140 | 93 | 108 | 150 | 171 | 124 | 135 | 152 | 174 | 141 | 159 | 116 | 128 | 104 | 116 |
| | Unstructured | 80 | 123 | 142 | 154 | 161 | 178 | 96 | 107 | 178 | 194 | 134 | 163 | 154 | 168 | 160 | 160 | 123 | 139 | 108 | 127 |

**Table A4:** Number of cause-specific dead recoveries of wolves in Scandinavia between 2015 and 2025 that were included in the OPSCR analysis. Numbers are reported by country, for females (F) and males (M). Note that dead recovery data from the final season (2024/2025) were not used in this analysis because survival is modeled as part of the transition from the start of one monitoring season to the start of the next one.

|  | Country | 2015/2016 |  | 2016/2017 |  | 2017/2018 |  | 2018/2019 |  | 2019/2020 |  | 2020/2021 |  | 2021/2022 |  | 2022/2023 |  | 2023/2024 |  | 2024/2025 |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M | F | M |
| **Other** | Norway | 1 | 3 | 0 | 0 | 1 | 3 | 1 | 1 | 1 | 1 | 0 | 2 | 1 | 2 | 0 | 1 | 2 | 1 | 0 | 0 |
|  | Sweden | 8 | 6 | 4 | 5 | 8 | 2 | 4 | 5 | 5 | 7 | 8 | 5 | 1 | 6 | 3 | 2 | 5 | 6 | 1 | 4 |
| **Legal culling** | Norway | 5 | 1 | 6 | 6 | 18 | 16 | 10 | 8 | 6 | 12 | 11 | 16 | 13 | 23 | 10 | 9 | 11 | 11 | 2 | 3 |
|  | Sweden | 7 | 20 | 17 | 23 | 12 | 31 | 4 | 4 | 6 | 12 | 18 | 30 | 22 | 18 | 39 | 40 | 21 | 26 | 20 | 20 |
| **Total** | Total | 21 | 30 | 27 | 34 | 39 | 52 | 19 | 18 | 18 | 32 | 37 | 53 | 37 | 49 | 52 | 52 | 39 | 44 | 23 | 27 |

**Table A5:** Annual abundance estimates for wolf at several spatial scales: the entire study area, by country, by management unit (carnivore management regions in Norway and "Rovdjursförvaltningsområden" in Sweden), and counties ("Län" in Sweden); see also Figure A2. Only counties and management units that are within or that intersect the study area are included in the table. Estimates are based on model-estimated activity center locations. Bayesian credible intervals (95%) are shown in parentheses. Small deviations between the total estimate and the sum of abundance estimates from the constituent subregions may arise due to rounding. Note that the numbers reported here are predictions from a statistical model which always represents an oversimplification of reality and is based on available data (NGS and dead recoveries). As a consequence, especially at the local scale, the model-estimated number of wolves based on DNA sampling can deviate from the number of wolves inferred from ancillary observations (e.g., camera traps).

| | 2015/2016 | 2016/2017 | 2017/2018 | 2018/2019 | 2019/2020 | 2020/2021 | 2021/2022 | 2022/2023 | 2023/2024 | 2024/2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| TOTAL | 372.4 (353-395) | 412.7 (402-425) | 414.2 (405-424) | 374.4 (358-394) | 438.9 (431-449) | 452.7 (439-469) | 510.2 (495-528) | 485.3 (471-502) | 435.2 (421-452) | 374.7 (354-400) |
| NORWAY | 76.6 (70-85) | 83.4 (76-92) | 96.5 (88-105) | 80.2 (74-87) | 87.1 (79-96) | 89.5 (82-97) | 91.6 (83-101) | 64.5 (57-73) | 60.3 (54-67) | 51.9 (43-63) |
| Region 2 | 0.5 (0-2) | 0.9 (0-3) | 0.9 (0-3) | 0.9 (0-2) | 1.4 (0-4) | 0.3 (0-2) | 0.6 (0-2) | 0.7 (0-3) | 0.5 (0-2) | 0.8 (0-3) |
| Region 3 | 1.1 (0-4) | 1.4 (0-4) | 1.8 (0-5) | 1 (0-3) | 2.1 (0-5) | 1.4 (0-4) | 2 (0-5) | 2 (0-5) | 0.8 (0-3) | 1.7 (0-5) |
| Region 4 | 13.6 (11-17) | 16.6 (13-20) | 22.3 (18-27) | 23.9 (20-28) | 27.8 (23-33) | 23.2 (19-28) | 26.4 (22-31) | 24.2 (20-28) | 21.8 (18-26) | 14.9 (11-19) |
| Region 5 | 59.8 (55-66) | 62.6 (57-69) | 69.5 (63-76) | 52.5 (47-58) | 52.9 (47-59) | 63.3 (57-70) | 60.2 (53-68) | 36.3 (31-43) | 36.8 (32-42) | 32.5 (26-40) |
| Region 6 | 1.6 (0-5) | 2 (0-5) | 1.9 (0-5) | 2 (1-4) | 2.9 (1-6) | 1.2 (0-4) | 2.5 (1-5) | 1.4 (0-4) | 0.4 (0-2) | 2 (0-6) |
| SWEDEN | 295.9 (277-317) | 329.3 (318-341) | 317.7 (309-328) | 294.2 (278-313) | 351.8 (345-359) | 363.2 (349-379) | 418.5 (403-436) | 420.8 (408-435) | 375 (361-391) | 322.8 (305-343) |
| Norra | 23.8 (17-32) | 18.6 (13-25) | 8.6 (4-14) | 18.4 (12-26) | 18.1 (14-23) | 18.7 (14-25) | 12.5 (7-19) | 22.6 (17-29) | 15.2 (10-21) | 16.4 (10-25) |
| Jämtland | 18.3 (12-25) | 15.5 (10-21) | 7.6 (4-12) | 14.7 (9-21) | 16.7 (12-22) | 16.1 (11-21) | 9.8 (5-16) | 15.1 (11-20) | 9.8 (6-15) | 10 (4-17) |
| Västerbotten | 0.1 (0-1) | 0 (0-1) | 0 (0-0) | 0 (0-1) | 0 (0-0) | 0 (0-0) | 0 (0-1) | 0 (0-1) | 0 (0-1) | 0 (0-1) |
| Västernorrland | 5.5 (2-10) | 3 (1-6) | 0.9 (0-3) | 3.7 (1-8) | 1.3 (0-4) | 2.6 (0-6) | 2.6 (0-6) | 7.4 (5-11) | 5.3 (2-9) | 6.4 (4-10) |
| Mellersta | 256.6 (243-272) | 298.2 (288-309) | 288.6 (280-297) | 262.5 (249-278) | 312.2 (305-319) | 310.7 (298-325) | 357.5 (344-373) | 323.9 (312-337) | 282.8 (270-296) | 237.3 (224-253) |
| Dalarna | 75.2 (67-84) | 81.3 (75-88) | 62.4 (57-68) | 57.3 (48-67) | 70.2 (65-76) | 70 (62-79) | 78.9 (70-88) | 59.9 (53-68) | 50.3 (43-58) | 36.1 (29-45) |
| Gävleborg | 44.4 (38-52) | 50.3 (45-56) | 54.9 (50-59) | 45.9 (39-53) | 69.2 (65-74) | 61 (56-67) | 51.5 (46-57) | 33.8 (29-39) | 20.4 (16-26) | 21.4 (17-26) |
| Örebro | 24 (18-30) | 37.8 (33-43) | 34.8 (31-39) | 35.9 (30-43) | 49.8 (45-55) | 47.5 (41-55) | 56.9 (50-64) | 53.3 (48-59) | 56.5 (51-62) | 49.2 (44-54) |
| Stockholm | 5.5 (3-9) | 3 (2-5) | 4.7 (3-7) | 2.6 (0-5) | 3.4 (2-5) | 8.4 (5-12) | 7.2 (4-11) | 7.9 (5-11) | 3.7 (2-6) | 3.4 (2-6) |
| Uppsala | 6.4 (3-11) | 6.8 (4-10) | 9.1 (6-13) | 7 (4-11) | 4.9 (3-7) | 8.3 (6-12) | 13 (10-16) | 7.6 (5-11) | 10.2 (8-13) | 10.3 (9-13) |
| Värmland | 78 (71-85) | 87.4 (80-95) | 87.7 (82-94) | 84.6 (76-94) | 82 (77-88) | 78.3 (69-88) | 107 (97-117) | 101.8 (94-111) | 72.9 (65-81) | 48.3 (41-57) |
| Västmanland | 14.7 (11-20) | 25.9 (23-30) | 26.3 (23-30) | 15.6 (11-21) | 27.4 (23-32) | 18.5 (14-24) | 23.7 (19-29) | 27.6 (24-32) | 23.8 (20-28) | 28 (24-32) |
| VästraGötaland | 8.5 (5-13) | 5.7 (2-10) | 8.7 (5-13) | 13.5 (9-19) | 5.3 (3-9) | 18.7 (14-24) | 19.3 (14-25) | 31.9 (27-37) | 45.1 (40-51) | 40.5 (36-45) |
| Södra | 15.4 (8-25) | 12.4 (8-18) | 20.6 (18-25) | 13.4 (8-20) | 21.6 (18-25) | 33.8 (28-41) | 48.5 (42-56) | 74.3 (69-80) | 76.9 (71-83) | 69.1 (64-75) |
| Blekinge | 0.6 (0-2) | 1.2 (1-2) | 0.1 (0-1) | 0.1 (0-1) | 0.2 (0-1) | 0.2 (0-1) | 0.3 (0-2) | 0.1 (0-1) | 0.3 (0-2) | 0.2 (0-1) |
| Halland | 0.7 (0-3) | 0.3 (0-2) | 0.1 (0-1) | 0.4 (0-2) | 0.2 (0-1) | 1.5 (1-3) | 0.7 (0-3) | 1.2 (0-3) | 2.4 (1-4) | 2.9 (1-5) |
| Jönköping | 2.7 (1-6) | 1 (0-3) | 0.5 (0-2) | 1.2 (0-4) | 1.4 (0-3) | 2.7 (1-6) | 8.1 (5-12) | 14 (11-17) | 10.6 (7-14) | 10.6 (8-14) |
| Kalmar | 1.6 (0-5) | 0.6 (0-2) | 1.1 (0-2) | 1.6 (1-3) | 0.5 (0-2) | 1.7 (1-4) | 1.2 (0-4) | 0.8 (0-3) | 1.1 (0-3) | 1.6 (0-4) |
| Kronoberg | 2 (0-5) | 1.6 (1-3) | 0.5 (0-2) | 0.7 (0-3) | 0.8 (0-2) | 1.8 (1-4) | 2 (1-4) | 3.3 (2-5) | 5.9 (4-9) | 5.6 (3-8) |
| Östergötland | 2.7 (0-6) | 2.6 (1-5) | 3.6 (3-6) | 4.1 (2-7) | 10 (9-12) | 8.3 (6-11) | 12.2 (9-16) | 10.5 (9-13) | 10.7 (8-14) | 8.8 (7-11) |
| Skåne | 2.1 (0-5) | 1.6 (1-3) | 2.1 (1-3) | 0.6 (0-3) | 0.4 (0-2) | 2.8 (2-5) | 5 (4-7) | 12.4 (12-14) | 18.1 (16-21) | 14.2 (13-16) |
| Södermanland | 3 (0-7) | 3.6 (2-6) | 12.5 (11-15) | 4.7 (2-8) | 8.1 (6-10) | 14.8 (11-19) | 19.2 (16-23) | 32.2 (29-36) | 27.9 (26-31) | 25.1 (23-28) |

**Table A6:** Annual abundance estimates for wolf at the county level in Norway; see also Figure A2. Only counties that are within or that intersect the study area are included in the table. Estimates are based on model-estimated activity center locations. Bayesian credible intervals (95%) are shown in parentheses. Small deviations between the total estimate and the sum of abundance estimates from the constituent subregions may arise due to rounding. Note that the numbers reported here are predictions from a statistical model which always represents an oversimplification of reality and is based on available data (NGS and dead recoveries). As a consequence, especially at the local scale, the model-estimated number of wolves based on DNA sampling can deviate from the number of wolves inferred from ancillary observations (e.g., camera traps).

| | 2015/2016 | 2016/2017 | 2017/2018 | 2018/2019 | 2019/2020 | 2020/2021 | 2021/2022 | 2022/2023 | 2023/2024 | 2024/2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| NORWAY | 76.6 (70-85) | 83.4 (76-92) | 96.5 (88-105) | 80.2 (74-87) | 87.1 (79-96) | 89.5 (82-97) | 91.6 (83-101) | 64.5 (57-73) | 60.3 (54-67) | 51.9 (43-63) |
| Innlandet | 60.9 (55-67) | 64 (58-71) | 71.3 (65-78) | 53.4 (48-59) | 55 (49-62) | 64.7 (58-72) | 62.2 (55-70) | 38.2 (32-45) | 37.6 (33-43) | 34.2 (27-43) |
| Buskerud | 0.3 (0-2) | 0.6 (0-2) | 0.6 (0-2) | 0.9 (0-2) | 1.1 (0-3) | 0.2 (0-1) | 0.4 (0-2) | 0.5 (0-2) | 0.4 (0-2) | 0.6 (0-2) |
| Vestfold | 0.2 (0-1) | 0.3 (0-2) | 0.3 (0-2) | 0.1 (0-1) | 0.3 (0-2) | 0.1 (0-1) | 0.1 (0-1) | 0.1 (0-1) | 0.1 (0-1) | 0.2 (0-1) |
| Oslo | 0.4 (0-1) | 0.1 (0-1) | 0.1 (0-1) | 0.9 (0-2) | 0.6 (0-2) | 0 (0-1) | 0 (0-1) | 0.1 (0-1) | 0.5 (0-2) | 0.2 (0-1) |
| Østfold | 2.5 (1-5) | 4.2 (2-7) | 9 (6-13) | 6.8 (4-10) | 9.5 (6-13) | 7.6 (4-11) | 6.6 (4-9) | 1.9 (0-4) | 2.4 (1-5) | 1 (0-3) |
| Akershus | 10.6 (8-14) | 12.3 (9-15) | 13.2 (10-17) | 16.2 (12-20) | 17.7 (13-23) | 15.6 (13-19) | 19.7 (16-24) | 22.2 (19-26) | 18.9 (15-23) | 13.7 (10-17) |
| Trøndelag | 1.6 (0-5) | 2 (0-5) | 1.9 (0-5) | 2 (1-4) | 2.8 (1-6) | 1.2 (0-4) | 2.5 (1-5) | 1.4 (0-4) | 0.4 (0-2) | 2 (0-6) |

**Table A7:** Annual population growth rate estimates for the wolf population in Scandinavia ("Total") and separately for Norway and Sweden. Estimates were derived using the posterior distributions of annual abundance estimates (Table 1) and indicate the change in estimated abundance at the start of one monitoring season to the start of the next one. Bayesian credible intervals (95%) are shown in parentheses.

| | 2015-2016 | 2016-2017 | 2017-2018 | 2018-2019 | 2019-2020 | 2020-2021 | 2021-2022 | 2022-2023 | 2023-2024 |
|---|---|---|---|---|---|---|---|---|---|
| Norway | 1.09 (0.95-1.25) | 1.16 (1.01-1.32) | 0.83 (0.74-0.94) | 1.09 (0.96-1.23) | 1.03 (0.91-1.16) | 1.03 (0.90-1.16) | 0.71 (0.60-0.82) | 0.94 (0.79-1.10) | 0.86 (0.70-1.07) |
| Sweden | 1.11 (1.03-1.20) | 0.97 (0.92-1.01) | 0.93 (0.87-0.99) | 1.20 (1.12-1.27) | 1.03 (0.99-1.08) | 1.15 (1.09-1.22) | 1.01 (0.95-1.06) | 0.89 (0.85-0.94) | 0.86 (0.80-0.92) |
| Total | 1.11 (1.04-1.18) | 1.00 (0.97-1.04) | 0.90 (0.86-0.95) | 1.17 (1.11-1.23) | 1.03 (0.99-1.07) | 1.13 (1.07-1.18) | 0.95 (0.91-0.99) | 0.90 (0.86-0.94) | 0.86 (0.80-0.92) |

**Table A8:** Estimates of the demographic parameters obtained from the sex-specific wolf OPSCR models. Parameters represent transition rates from Oct 1 to Sep 30 in the following year. State 2 and 3 represent other and scent-marking individuals, respectively. Median estimates and 95% Bayesian credible intervals (in parentheses) for per capita recruitment rate ($\rho$), survival ($\phi$), transition probability from other to scent-marking adult state ($\psi$), mortality due to legal culling (h), recovered mortality due to other causes (rw), and mortality due to other causes not recovered (w) are presented for males (M) and females (F).

| | State | 2015-2016 | | 2016-2017 | | 2017-2018 | | 2018-2019 | | 2019-2020 | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | M | F | M | F | M | F | M | F | M | F |
| $\rho$ | - | 0.66 (0.51-0.81) | 1.15 (0.92-1.38) | 0.65 (0.58-0.72) | 0.72 (0.62-0.81) | 0.63 (0.54-0.74) | 0.46 (0.38-0.56) | 0.81 (0.67-0.94) | 0.88 (0.73-1.02) | 0.75 (0.67-0.85) | 0.60 (0.54-0.68) |
| $\phi$ | 2 | 0.50 (0.41-0.60) | 0.48 (0.37-0.60) | 0.46 (0.38-0.55) | 0.57 (0.48-0.66) | 0.47 (0.38-0.57) | 0.50 (0.41-0.59) | 0.59 (0.49-0.68) | 0.55 (0.45-0.65) | 0.46 (0.38-0.54) | 0.52 (0.43-0.60) |
| | 3 | 0.65 (0.53-0.76) | 0.63 (0.51-0.74) | 0.54 (0.43-0.65) | 0.57 (0.45-0.68) | 0.56 (0.45-0.67) | 0.61 (0.49-0.71) | 0.60 (0.48-0.72) | 0.64 (0.52-0.75) | 0.69 (0.58-0.79) | 0.66 (0.54-0.76) |
| $\psi$ | - | 0.30 (0.19-0.42) | 0.53 (0.37-0.69) | 0.42 (0.30-0.54) | 0.44 (0.33-0.56) | 0.33 (0.23-0.46) | 0.27 (0.17-0.39) | 0.35 (0.25-0.46) | 0.48 (0.36-0.61) | 0.39 (0.28-0.50) | 0.38 (0.27-0.50) |
| **h** | 2 | 0.12 (0.07-0.18) | 0.07 (0.03-0.13) | 0.14 (0.09-0.20) | 0.12 (0.07-0.18) | 0.24 (0.17-0.31) | 0.15 (0.09-0.21) | 0.06 (0.03-0.11) | 0.09 (0.05-0.15) | 0.12 (0.08-0.18) | 0.05 (0.02-0.10) |
| | 3 | 0.06 (0.02-0.12) | 0.09 (0.04-0.16) | 0.11 (0.05-0.19) | 0.11 (0.06-0.20) | 0.18 (0.11-0.28) | 0.13 (0.07-0.22) | 0.07 (0.02-0.15) | 0.07 (0.02-0.14) | 0.06 (0.02-0.14) | 0.07 (0.03-0.14) |
| **rw** | 2 | 0.06 (0.03-0.10) | 0.09 (0.04-0.16) | 0.03 (0.01-0.06) | 0.02 (0.00-0.05) | 0.04 (0.02-0.08) | 0.06 (0.03-0.11) | 0.04 (0.02-0.08) | 0.05 (0.02-0.10) | 0.05 (0.02-0.09) | 0.03 (0.01-0.07) |
| | 3 | 0.02 (0.00-0.07) | 0.02 (0.00-0.07) | 0.02 (0.00-0.07) | 0.03 (0.01-0.09) | 0.01 (0.00-0.05) | 0.02 (0.00-0.07) | 0.02 (0.00-0.08) | 0.01 (0.00-0.05) | 0.01 (0.00-0.05) | 0.03 (0.01-0.09) |
| **w** | 2 | 0.32 (0.23-0.41) | 0.35 (0.24-0.48) | 0.37 (0.28-0.45) | 0.28 (0.21-0.37) | 0.25 (0.17-0.33) | 0.29 (0.21-0.38) | 0.30 (0.22-0.40) | 0.30 (0.21-0.41) | 0.37 (0.29-0.45) | 0.39 (0.31-0.48) |
| | 3 | 0.27 (0.17-0.38) | 0.25 (0.15-0.37) | 0.32 (0.22-0.43) | 0.28 (0.18-0.39) | 0.23 (0.14-0.34) | 0.23 (0.15-0.33) | 0.29 (0.19-0.41) | 0.27 (0.18-0.39) | 0.23 (0.14-0.33) | 0.23 (0.15-0.33) |

| | State | 2020-2021 | | 2021-2022 | | 2022-2023 | | 2023-2024 | |
|---|---|---|---|---|---|---|---|---|---|
| | | M | F | M | F | M | F | M | F |
| $\rho$ | - | 0.77 (0.65-0.89) | 0.84 (0.72-0.95) | 0.60 (0.51-0.68) | 0.78 (0.69-0.88) | 0.59 (0.51-0.67) | 0.60 (0.51-0.71) | 0.57 (0.47-0.70) | 0.53 (0.42-0.67) |
| $\phi$ | 2 | 0.51 (0.43-0.60) | 0.56 (0.46-0.65) | 0.40 (0.32-0.47) | 0.46 (0.37-0.54) | 0.44 (0.36-0.53) | 0.43 (0.35-0.52) | 0.49 (0.40-0.60) | 0.36 (0.27-0.46) |
| | 3 | 0.63 (0.52-0.73) | 0.72 (0.61-0.81) | 0.58 (0.47-0.68) | 0.59 (0.48-0.69) | 0.59 (0.48-0.69) | 0.62 (0.52-0.72) | 0.61 (0.50-0.71) | 0.61 (0.50-0.71) |
| $\psi$ | - | 0.35 (0.25-0.46) | 0.35 (0.25-0.47) | 0.43 (0.32-0.55) | 0.49 (0.37-0.61) | 0.37 (0.26-0.49) | 0.38 (0.27-0.50) | 0.37 (0.26-0.50) | 0.56 (0.41-0.71) |
| **h** | 2 | 0.18 (0.12-0.24) | 0.17 (0.11-0.24) | 0.16 (0.12-0.22) | 0.15 (0.10-0.21) | 0.23 (0.17-0.30) | 0.23 (0.17-0.30) | 0.20 (0.14-0.27) | 0.16 (0.11-0.23) |
| | 3 | 0.18 (0.11-0.27) | 0.09 (0.04-0.17) | 0.11 (0.06-0.19) | 0.13 (0.07-0.22) | 0.15 (0.08-0.23) | 0.13 (0.07-0.21) | 0.12 (0.06-0.20) | 0.11 (0.06-0.19) |
| **rw** | 2 | 0.03 (0.01-0.06) | 0.07 (0.03-0.11) | 0.04 (0.02-0.07) | 0.02 (0.00-0.04) | 0.02 (0.01-0.05) | 0.01 (0.00-0.03) | 0.04 (0.02-0.08) | 0.05 (0.02-0.09) |
| | 3 | 0.05 (0.01-0.10) | 0.01 (0.00-0.04) | 0.02 (0.00-0.06) | 0.01 (0.00-0.04) | 0.01 (0.00-0.04) | 0.03 (0.01-0.08) | 0.03 (0.01-0.09) | 0.02 (0.00-0.06) |
| **w** | 2 | 0.28 (0.20-0.36) | 0.20 (0.13-0.29) | 0.40 (0.32-0.48) | 0.37 (0.29-0.46) | 0.31 (0.23-0.39) | 0.32 (0.24-0.41) | 0.27 (0.18-0.36) | 0.43 (0.33-0.53) |
| | 3 | 0.14 (0.07-0.22) | 0.17 (0.10-0.27) | 0.28 (0.19-0.39) | 0.26 (0.17-0.36) | 0.25 (0.16-0.35) | 0.21 (0.14-0.31) | 0.23 (0.14-0.33) | 0.25 (0.16-0.35) |

**Table A9:** Estimates of the spatial and movement process parameters obtained from the sex-specific wolf OPSCR models. $\beta_{dens}$ represents the effect of the number of known wolf packs on AC locations (Bischof et al., 2020). The scale parameter $\sigma$ of the detection function is expressed in kilometers and estimated separately for other ($\sigma_1$) and scent-marking ($\sigma_2$) individuals. $\tau$ represents the mean of the exponential movement parameter, describing individual movement distances between years, estimated separately for other ($\tau_1$) and scent-marking ($\tau_2$) individuals. Bayesian credible intervals (95%) are shown in parentheses. Parameters that were assumed to be constant across years are marked with $^*$.

| | 2015/2016 | | 2016/2017 | | 2017/2018 | | 2018/2019 | | 2019/2020 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | M | F | M | F | M | F | M | F | M | F |
| $\beta^*_{dens}$ | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) |
| $\sigma_1$ | 8.06 (7.43-8.78) | 6.31 (5.69-7.07) | 7.43 (7.01-7.90) | 7.92 (7.47-8.42) | 7.68 (7.31-8.07) | 8.09 (7.68-8.52) | 7.08 (6.53-7.68) | 6.73 (6.15-7.42) | 7.83 (7.52-8.15) | 7.55 (7.25-7.89) |
| $\sigma_2$ | 8.31 (7.69-9.01) | 7.41 (6.81-8.12) | 7.91 (7.58-8.27) | 7.90 (7.54-8.29) | 7.90 (7.60-8.22) | 7.33 (7.01-7.67) | 8.48 (8.02-8.99) | 8.10 (7.59-8.69) | 8.06 (7.73-8.42) | 7.72 (7.41-8.05) |
| $\tau^*_1$ | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) |
| $\tau^*_2$ | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) |

| | 2020/2021 | | 2021/2022 | | 2022/2023 | | 2023/2024 | | 2024/2025 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | M | F | M | F | M | F | M | F | M | F |
| $\beta^*_{dens}$ | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) | 0.28 (0.26-0.30) | 0.31 (0.29-0.34) |
| $\sigma_1$ | 7.74 (7.27-8.26) | 7.33 (6.82-7.91) | 6.86 (6.44-7.31) | 7.81 (7.32-8.35) | 6.25 (5.87-6.66) | 7.39 (6.91-7.94) | 6.76 (6.28-7.30) | 7.31 (6.72-7.97) | 7.30 (6.75-7.94) | 7.56 (6.93-8.27) |
| $\sigma_2$ | 7.62 (7.27-8.00) | 7.10 (6.72-7.52) | 7.61 (7.28-7.96) | 7.77 (7.36-8.22) | 7.38 (7.04-7.75) | 6.56 (6.24-6.91) | 8.30 (7.89-8.74) | 6.98 (6.60-7.41) | 7.55 (7.15-7.99) | 7.33 (6.89-7.82) |
| $\tau^*_1$ | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) | 68.35 (66.01-70.92) | 61.46 (59.04-64.04) |
| $\tau^*_2$ | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) | 7.83 (7.27-8.42) | 4.27 (3.91-4.67) |

**Table A10:** Estimates of the detection process parameters for the structured sampling $\beta_{1\,Structured}$ corresponds to the effect of previous detection of an individual on detection probability, $\beta_{2\,Structured}$ to the effect of search-effort (track length) on detection probability, and $\beta_{3\,Structured}$ to the effect of average snow cover during the monitoring period on detection probability ($p_{0\,Structured}$). Coefficients are associated with scaled covariates. Bayesian credible intervals (95%) are shown in parentheses.

| | 2015/2016 | | 2016/2017 | | 2017/2018 | | 2018/2019 | | 2019/2020 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | M | F | M | F | M | F | M | F | M | F |
| $\beta_{1_{Structured}}$ | -0.08 (-0.46-0.30) | -0.09 (-0.54-0.37) | 0.11 (-0.19-0.41) | 0.23 (-0.06-0.53) | -0.10 (-0.37-0.17) | 0.33 ( 0.06-0.61) | -0.35 (-0.82-0.10) | -0.04 (-0.43-0.34) | 0.07 (-0.17-0.30) | 0.04 (-0.19-0.28) |
| $\beta_{2_{Structured}}$ | 0.39 (0.29-0.48) | 0.39 (0.26-0.52) | 0.26 (0.19-0.33) | 0.31 (0.24-0.37) | 0.33 (0.27-0.39) | 0.32 (0.26-0.38) | 0.32 (0.23-0.40) | 0.35 (0.27-0.44) | 0.39 (0.33-0.45) | 0.34 (0.27-0.41) |
| $\beta_{3_{Structured}}$ | 0.08 (-0.35-0.52) | -0.58 (-1.16-0.00) | -0.23 (-0.48-0.03) | -0.11 (-0.42-0.20) | 0.16 (-0.17-0.52) | 0.02 (-0.38-0.44) | 0.17 (-0.15-0.50) | -0.01 (-0.42-0.41) | 0.05 (-0.13-0.24) | 0.04 (-0.16-0.24) |

| | 2020/2021 | | 2021/2022 | | 2022/2023 | | 2023/2024 | | 2024/2025 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | M | F | M | F | M | F | M | F | M | F |
| $\beta_{1_{Structured}}$ | 0.74 ( 0.41-1.07) | 0.28 (-0.11-0.67) | 0.42 ( 0.13-0.71) | -0.03 (-0.31-0.24) | 0.19 (-0.09-0.47) | 0.12 (-0.17-0.42) | -0.02 (-0.35-0.31) | -0.11 (-0.48-0.27) | -0.04 (-0.43-0.34) | 0.01 (-0.36-0.37) |
| $\beta_{2_{Structured}}$ | 0.24 (0.18-0.30) | 0.24 (0.17-0.31) | 0.29 (0.23-0.36) | 0.29 (0.23-0.35) | 0.34 (0.27-0.42) | 0.33 (0.26-0.40) | 0.16 (0.11-0.21) | 0.24 (0.17-0.33) | 0.46 (0.38-0.55) | 0.42 (0.33-0.52) |
| $\beta_{3_{Structured}}$ | 0.35 ( 0.15-0.55) | 0.32 ( 0.08-0.57) | 0.38 ( 0.17-0.58) | 0.13 (-0.10-0.36) | 0.09 (-0.09-0.27) | 0.14 (-0.07-0.35) | 0.22 ( 0.04-0.40) | -0.14 (-0.33-0.04) | -0.13 (-0.38-0.12) | -0.06 (-0.32-0.21) |

**Table A11:** Estimates of the detection process parameters for the unstructured sampling $\beta_{1Unstructured}$ corresponds to the effect of previous detection of an individual on baseline detection probability, $\beta_{2Unstructured}$ to the effect of distance to the nearest roads on detection probability, $\beta_{3Unstructured}$ to the effect of average snow cover during the monitoring period on detection probability, and $\beta_{4Unstructured}$ to the effect of spatio-temporal heterogeneity in unstructured sampling derived using the observation data in Skandobs and Rovbase. Coefficients are associated with scaled covariates. Bayesian credible intervals (95%) are shown in parentheses.

| | 2015/2016 | | 2016/2017 | | 2017/2018 | | 2018/2019 | | 2019/2020 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | M | F | M | F | M | F | M | F | M | F |
| $\beta_{1_{Unstructured}}$ | 0.57 ( 0.26-0.87) | -0.07 (-0.43-0.29) | 0.09 (-0.15-0.33) | 0.32 ( 0.09-0.55) | 0.25 ( 0.05-0.44) | 0.67 ( 0.45-0.88) | 0.03 (-0.32-0.39) | 0.82 ( 0.44-1.24) | 0.26 ( 0.07-0.46) | 0.58 ( 0.40-0.76) |
| $\beta_{2_{Unstructured}}$ | -0.22 (-0.80- 0.28) | -0.49 (-1.23- 0.10) | -0.64 (-1.20–0.19) | -0.50 (-1.04–0.07) | -1.28 (-2.10–0.60) | -0.71 (-1.31–0.22) | -0.26 (-0.86- 0.19) | 0.27 (-0.36- 0.89) | -0.65 (-1.39–0.06) | -0.41 (-1.24- 0.24) |
| $\beta_{3_{Unstructured}}$ | 0.42 ( 0.10- 0.77) | -0.04 (-0.48- 0.41) | -0.13 (-0.31- 0.06) | -0.08 (-0.28- 0.13) | -0.23 (-0.44–0.01) | -0.25 (-0.51- 0.01) | -0.29 (-0.55–0.02) | -0.58 (-0.87–0.29) | -0.01 (-0.11- 0.10) | 0.07 (-0.04- 0.19) |
| $\beta_{4_{Unstructured}}$ | 0.82 (0.52-1.13) | 0.86 (0.49-1.25) | 1.13 (0.81-1.45) | 1.23 (0.89-1.59) | 1.38 (1.03-1.76) | 1.70 (1.30-2.16) | 1.24 (0.77-1.77) | 1.69 (1.11-2.39) | 1.80 (1.44-2.23) | 1.99 (1.57-2.45) |

| | 2020/2021 | | 2021/2022 | | 2022/2023 | | 2023/2024 | | 2024/2025 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | M | F | M | F | M | F | M | F | M | F |
| $\beta_{1_{Unstructured}}$ | 0.77 ( 0.49-1.06) | 0.51 ( 0.20-0.84) | 0.15 (-0.14-0.43) | 0.43 ( 0.14-0.72) | 0.50 ( 0.24-0.75) | 0.44 ( 0.18-0.71) | 0.04 (-0.29-0.36) | 0.78 ( 0.44-1.11) | 0.47 ( 0.14-0.81) | 0.48 ( 0.15-0.81) |
| $\beta_{2_{Unstructured}}$ | -0.94 (-1.82–0.25) | 2.02 (-0.01- 3.49) | 0.07 (-0.50- 0.51) | -1.56 (-3.74–0.10) | 0.45 (-0.31- 1.17) | -0.24 (-1.52- 0.85) | 0.28 (-0.47- 0.91) | 0.96 ( 0.09- 2.89) | 0.09 (-0.69- 1.15) | 0.27 (-1.41- 4.43) |
| $\beta_{3_{Unstructured}}$ | -0.22 (-0.38–0.06) | -0.33 (-0.50–0.15) | -0.10 (-0.24- 0.05) | -0.23 (-0.39–0.07) | -0.50 (-0.61–0.38) | -0.34 (-0.46–0.22) | -0.18 (-0.31–0.04) | -0.38 (-0.51–0.24) | -0.19 (-0.38–0.01) | -0.20 (-0.39–0.02) |
| $\beta_{4_{Unstructured}}$ | 1.29 (0.90-1.72) | 1.66 (1.15-2.26) | 2.04 (1.44-2.85) | 1.54 (0.97-2.19) | 1.39 (0.90-1.93) | 1.85 (1.32-2.48) | 1.28 (0.76-1.89) | 1.52 (0.97-2.20) | 1.84 (1.25-2.67) | 1.63 (0.99-2.32) |

**Table A12:** Average proportion of individuals detected via non-invasive genetic sampling (NGS) in Scandinavia. Values were calculated as the number of individuals detected with NGS (Table A3) divided by the total and sex-specific abundance estimates obtained from the OPSCR models (Table A5). Bayesian credible intervals (95%) are shown in parentheses.

| | 2015/2016 | 2016/2017 | 2017/2018 | 2018/2019 | 2019/2020 | 2020/2021 | 2021/2022 | 2022/2023 | 2023/2024 | 2024/2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| M | 0.77 (0.71-0.83) | 0.88 (0.85-0.91) | 0.92 (0.90-0.95) | 0.78 (0.72-0.83) | 0.94 (0.91-0.96) | 0.83 (0.78-0.86) | 0.85 (0.81-0.89) | 0.89 (0.85-0.92) | 0.88 (0.84-0.92) | 0.85 (0.78-0.91) |
| F | 0.72 (0.66-0.78) | 0.88 (0.84-0.91) | 0.90 (0.87-0.93) | 0.76 (0.71-0.81) | 0.93 (0.90-0.96) | 0.87 (0.83-0.90) | 0.87 (0.83-0.90) | 0.85 (0.81-0.89) | 0.80 (0.75-0.84) | 0.86 (0.78-0.94) |
| Total | 0.75 (0.71-0.79) | 0.88 (0.85-0.90) | 0.91 (0.89-0.93) | 0.77 (0.73-0.80) | 0.94 (0.92-0.95) | 0.84 (0.81-0.87) | 0.86 (0.83-0.88) | 0.87 (0.84-0.89) | 0.84 (0.81-0.87) | 0.85 (0.80-0.90) |