Monitoring standards for large carnivores in Europe

Agreements on objectives, categorization of data, criteria for data interpretation and quality levels of outputs

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1. INTRODUCTION

The low detectability of large carnivores necessitates intensive and often costly field efforts to obtain reliable data across appropriate spatial and temporal scales (Barea-Azcón et al., 2007; Kelly et al., 2012). When such population-level surveys are repeated over time to detect trends or changes, they form the basis of a monitoring program (Thompson et al. 1998). In this context, we focus on two fundamental parameters essential for assessing the status and dynamics of large carnivore populations: population size and distribution. Estimates of these parameters vary widely in quality among large carnivore populations, ranging from rough approximations to robust, science-based estimates that include measures of uncertainty (Kaczensky et al., 2013, 2024; Boitani et al., 2022). Data are often not comparable across neighbouring countries, which poses major challenges for developing transboundary population-level assessments (Kaczensky et al., 2013). In recent years, several European initiatives have produced guidelines and technical documents aimed at standardising data collection and evaluation to facilitate reliable, science-based population assessments (Molinari-Jobin et al., 2012; Reinhardt et al., 2015; WAG, 2023; Marucco et al., 2023a; Skrbinšek et al., 2024).

Within the framework of the LCIE, we developed harmonised monitoring standards to improve the robustness and comparability of population size and distribution estimates for European populations of wolves, lynx, wolverines, golden jackals, and bears. This document aims to present these standards and to define common quality levels applicable across diverse survey contexts, accounting for differences in effort and funding. Establishing such quality levels is essential to enable reliable comparisons of population size and distribution estimates among countries and to support coordinated transboundary management of large carnivore populations. In detail, chapters 2, 3, and 4 present the framework and methodological foundations of these standards. In particular, criteria of data categorization are adapted to each large carnivore species based on data categorised according to the SCALP criteria C1-C2-C3, which classify observations by their verifiability (Chapter 3; Molinari-Jobin et al., 2012). Furthermore, standard criteria for the interpretation of results have been defined for each species (Chapters 3 and 4), which are especially valuable for the joint assessment of transboundary populations. Finally, for the two population parameters considered (i.e. population size and distribution), we identified several key variables that influence the quality of estimates: small versus large populations, structured versus unstructured sampling effort, presence or absence of appropriate individual identification, and spatial extent of monitoring (e.g., modelled or extrapolated versus full range coverage). Based on these considerations, quality levels Q1-Q2-Q3 for population size and area of occurrence evaluations are defined and discussed in the final chapter.

2. DEFINITIONS

Hereafter we define the general terminology as used in this document:

- **Survey:** a survey is the assessment of the status of a population attribute (e.g., abundance, distribution) at one time and within a given geographic area, based on the data collection through some sampling scheme.

- **Monitoring**: the repetition of the same survey at the same geographic area that allows inference about change of a given population attribute. Hence, monitoring is composed of a series of surveys framed in a design aimed at answering specific management questions (Thompson et al. 1998; Elzinga et al., 2001; Boitani & Powell, 2012).

- **Objective of a survey or monitoring program**: objectives need to be explicitly stated in surveys and monitoring programs. This document aims to provide methods and guidelines to evaluate the status (and its change over time) of large carnivore populations in Europe by measuring the values of two attributes: distribution and abundance.

- **Population attributes or parameters**: are characteristics of a population we want to estimate through a statistical measure. In this document, the two attributes of interest are abundance and distribution. In particular, for abundance, we consider estimates of population size, and for distribution, estimates of area of occurrence/range. Other parameters of interest (not discussed in this document) may be related to the genetic status of the population, such as effective population size or level of inbreeding or hybridization; or related to the health status of the population.

- **Estimates**: all *estimates* of animal abundance (or occurrence) must account for the *detection probability* (the ability to observe or find signs of presence) to produce measures of *absolute abundance* with a level of precision (Nichols et al., 2000). The precision of an estimate could be measured through the Standard Error (SE), the standard deviation of the sample distribution (Sokal & Rohlf, 1995) or through Confidence or Credible Intervals (McCarthy, 2007) depending on the statistical framework used for analysis.

- **Index**: a feature of a population expected to have a fixed relation to a population attribute. An index can be used for comparison across time and space to infer quantitative variations of the population attribute but the index carries no information on the true quantitative value of the attribute (Thompson et al. 1998). An index can be transformed to an estimate of the population attribute when the relationship between the index and the attribute is known (conversion factor). It is possible to convert for example "reproductive units" to total population size if one knows the population structure at the time of monitoring. This conversion can include uncertainty (Andrén et al., 2002; Chapron et al., 2016).

- **Accuracy:** refers to how close a result comes to the true population parameter that is considered. Systematic error or inaccuracy is quantified by the average difference (bias) between a set of measurements obtained with the true population parameter value (Thompson et al. 1998).

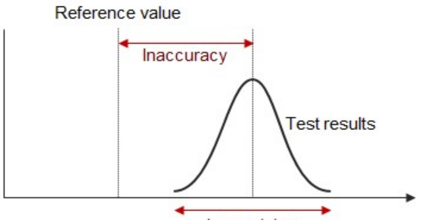

Figure 1 Representation of the differences between Inaccuracy and Imprecisions.

- **Precision:** refers to how well measurements agree with each other in multiple tests. Random error or imprecision is usually quantified by calculating the SE of a set of duplicate measurements (Sokal & Rohlf, 1995; Westgard, 2008).

- **Quality of estimates and of indices:** from the definitions above we consider estimates of true population parameters to be of higher quality than indices. However, estimates tend to be more expensive to obtain. The quality of indices must be judged against the objective of the study: for example, how well they track changes in absolute or relative abundance across time, space and management treatments (Mills, 2007). An index is of good quality if it can reliably indicate trends over time only if its relationship to true abundance remains constant, or at least does not change systematically. Hence, a good index requires a robust sampling design (Bart et al., 2004).

- **Mature/Adult individuals:** all individuals potentially able to reproduce due to physiological and behavioural/social factors. This is an operational definition for the monitoring standards of large carnivores, especially useful for the Red List Assessment (IUCN, 2022).

- **Home range vs. territory:** home ranges are fairly confined areas where non-nomadic animals enact their day-to-day activities (Powell et al., 2000) like food gathering, mating and caring for the young (Burt, 1943). Territories are per definition areas defended against conspecifics (Burt, 1943) and therefore show little overlap with neighboring territories. Territories can be feeding grounds, tiny mating areas or entire home ranges. Wolves and lynx are highly territorial (Mech & Boitani, 2003; Breitenmoser & Breitenmoser-Würsten, 2008) while bears are less (Powell, 1987). In wolves and lynx, the territory corresponds to their home range. However, young wolves still living in their natal pack and floaters can roam over areas much larger than an average wolf territory (Kojola et al., 2006). Therefore, for calculating the territory size of wolves or lynx in a given area, only data from territorial (breeding) individuals should be used. For robust calculation of territory sizes, telemetry data are mandatory.

- **Structured sampling** refers to a data collection approach in which sampling locations, timing, and methods are planned and standardized according to a predefined design. This structure ensures that observations are spatially and temporally representative of the population being studied, thereby reducing bias and increasing the comparability of results over time and across sites. It can include different specific designs (e.g. systematic, stratified, random, or mixed) as long as they are applied following a defined protocol.

- **Systematic sampling** is a specific type of structured sampling. In wildlife surveys is an approach in which sampling units (such as transects, camera traps, or observation points) are placed at regular, predetermined intervals across the study area. The first unit is typically located randomly within the initial interval, and subsequent units are positioned systematically at fixed spatial distances. This approach ensures uniform spatial coverage of the area of interest, reduces sampling bias associated with convenience or opportunistic placement, and facilitates comparability across sites and time periods. Systematic sampling is particularly useful for large-scale monitoring of wildlife populations, where consistent spatial representation is critical for estimating distribution and abundance.

3. MONITORING STANDARDS FOR LARGE CARNIVORES IN EUROPE

3.1 Categories of large predator signs based on SCALP "C" criteria

The SCALP criteria were firstly developed in the framework of SCALP (Status and Conservation of the Alpine Lynx Population), a conservation initiative (www.kora.ch) that among other things developed standardised criteria for interpretation of lynx-monitoring data (Molinari-Jobin et al., 2012). These criteria have been adapted to other large carnivore species and to other countries in Europe (e.g. Kaczensky et al., 2009; Marucco et al., 2014; Reinhardt et al., 2015; Hatlauf & Böcker, 2022; Marucco et al., 2023a).

In the following, we define the SCALP criteria required for standardised monitoring of large carnivore populations in Europe.

A few preconditions apply:

- For the evaluation of field data, at least one experienced person must be available, or the sign of presence needs to be documented in order to be evaluated by experts.
- "Experienced" in this regard means having extensive field experience with the large carnivore species concerned.
- All observations must be checked for genuineness (i.e., the possibility of intentional deception must be ruled out).

The letter "C" stands for "category". The numbers 1, 2 and 3 below are not related to the observer's qualifications; rather, they are used to denote the level of validation for an observation.

C1: Hard evidence = hard fact i.e., evidence that unambiguously confirms the presence of a target species (live capture, dead animal, genetic proof, photo, telemetric location).

C2: Confirmed observation = indirect signs such as tracks, scats, kills and dens confirmed by an experienced person as being of the target species. The experienced person can either confirm the signs personally in the field or based on documentation by a third party.

C3: Unconfirmed observation = all observations that are not confirmed by an experienced person or observations which by their nature cannot be confirmed. This includes all sightings without photographic proof; all signs that are too old, unclear or incompletely documented; signs that, for other reasons, do not suffice to provide confirmation; and all signs that cannot be verified. Category C3 can be divided into the sub-categories "likely" and "unlikely".

False: false observations = observation for which a large carnivore can be ruled out as the cause.

Evaluation not possible = signs that cannot be evaluated because of lack of minimum information needed (e.g. reports of visual observations of tracks or kills).

WOLF

Table 1. Categories of wolf signs based on Reinhardt et al. (2015) and Marucco et al. (2023a).

C1 – Hard evidence	C2 – Confirmed observation	C3 - Unconfirmed observation
Captured or rescued alive animals	Tracks with typical pattern, followed for at least 100 meters	Tracks if followed < 100 m or single footprints
Dead animals	Scats or hairs with expert check	Scats not confirmed by an expert and not associated with snow tracks
GPS-collar localization	Predation signs with typical bites and/or consumption and/ or combined with other C2 data	Urine, hairs not associated with C2 tracks and without DNA evidence
High quality videos and photos	Howl with wolf pups' presence, assessed by an expert or recorder and assessed by acoustics analysis	Heavily eaten kills and/or livestock depredations not combined with other C2 data
Any DNA evidence that confirms the biological sample (e.g. scats, hairs, urine, saliva)		Howls by a single animal
Indirectly certified presence signs from DNA evidence (e.g. tracks on snow)*		Sightings not supported by photos and videos
		Poor quality videos and pictures

*If scat, hair, or urine is found along a C2 track, they are counted together as one C2 event (not as two independent signs). If the biological sample is genetically confirmed as C1, the track and sign together count as one C1 event.

LYNX

Table 2. Categories of lynx signs based on SCALP “C” criteria based on Molinari-Jobin et al. (2012)

C1 – Hard evidence	C2 – Confirmed observation	C3 - Unconfirmed observation
Captured or rescued alive animals	Tracks on snow documented and assessed by an expert	Tracks on snow not assessed by an expert
Dead animals	Prey remains with typical signs documented and assessed by an expert	Prey remains not assessed by an expert
GPS-collar localization		Sightings not supported by photos and videos
High quality videos and photos		Single footprint
Any DNA evidence that confirms the biological sample (i.e. scats, hairs, urine, saliva)		Presumed lynx scat not genetically analysed
Hair from lynx, identification based on hair structure		Vocalisations if not recorded
		Poor quality videos and pictures

BEAR

Table 3. Categories of bear signs based on SCALP "C" criteria

C1 – Hard evidence	C2 – Confirmed observation	C3 - Unconfirmed observation
Captured or rescued alive animals	Tracks on snow / sand / mud with typical pattern, assessed by an expert and documented by photo	Undocumented tracks on snow / sand / mud
Dead animals	Scats with expert check	Single footprint
GPS-collar localization	Hairs collected e.g., on a rubbing tree plus expert check	Urine, hairs not associated with DNA evidence
High quality videos and photos	Medium quality video and photos with expert assessment	Heavily eaten kills, livestock depredations not combined with other C2 data
Any DNA evidence that confirms the biological sample (i.e. scats, hairs, urine, saliva). Bear scat is quite distinct even without genetic confirmation.	Predation signs if combined with other C2 data and expert check	Inappropriate documentation provided by third party
Indirectly certified presence signs (e.g. tracks on snow). Bear footprints are quite distinct even without genetic confirmation.		Sightings not supported by photos and videos Poor quality videos and pictures

GOLDEN JACKAL

Table 4. Categories of golden jackal signs based on Hatlauf and Böcker (2022).

C1 – Hard evidence	**C2 – Confirmed observation**	**C3 - Unconfirmed observation**
Captured or rescued alive animals	Due to the high risk of confusion with other species in all categories, C2 records do NOT apply to the golden jackal	Sightings not supported by photos and videos
Recordings of group or single howling (BAM bioacoustics monitoring - sound recording) with typical yip howls		Single howls (without typical yip howls)
High quality videos and photos		Poor quality videos and pictures
GPS-collar localization		Urine, hairs without DNA evidence (or without structural analysis in case of hairs)
Any DNA evidence that confirms the biological sample (e.g. from scats, hairs, urine, saliva or livestock kills)		
Dead animals		

WOLVERINE

Table 5. Categories of wolverine signs based on SCALP “C” criteria

C1 – Hard evidence	C2 – Confirmed observation	C3 - Unconfirmed observation
Captured animals	Tracks on snow documented and assessed by an expert	Tracks on snow not assessed by an expert
Dead animals	Prey remains with typical signs documented and assessed by an expert	Single footprint
GPS-collar localization	Active natal dens site, e.g., tracks of wolverine cubs or den site clearly revisited by adult wolverine	Sightings not supported by photos and videos
High quality videos and photos		Prey remains not assessed by an expert
Any DNA evidence that confirms the biological sample (i.e. scats, hairs, urine, saliva)		Presumed wolverine scat not genetically analysed
Hair from wolverine, identification based on hair structure		Poor quality videos and pictures

3.2 Criteria for data interpretation and definitions

WOLF

Table 6. Definitions on wolf presence type

Wolf presence type in the area:	
Single wolf	Single wolf detected in an area
Single resident wolf	Single wolf living in an area for at least 6 months
Pair	Male and female wolves travelling together but not (yet) having reproduced
Pack	A group of more than two wolves living together in a territory
Reproductive pack	Consists of at least one mature wolf with confirmed reproduction
Age class of wolves:	
Mature/Adult (reproducing)	≥ 24 months
Pup	Wolf in its first year of life. The transition from pup to yearling is considered on 1st May
Yearling	Wolf in its second year of life
Monitoring year	1st May – 30th April
Wolf-dog Hybrid*	Wolf-dog hybrid documented with genetic analysis (Dziech, 2021; Stronen et al. 2022, 2025)

***If hybrids are detected, they should be excluded from the wolf population size estimate or index and reported separately. If hybrids are known to be present but cannot be excluded due to a lack of data on their proportion in the population, this should be clearly stated and reported.**

Table 7. Comparison of available methods for wolf detection

Method	**Possible applications in Surveying or Monitoring**	**Required investment of resources**	**SCALP category of data obtained**
Opportunistic sightings reported from the public/stakeholders	Where to concentrate monitoring efforts	Low	Not attributable
Questionnaires	Where to concentrate monitoring efforts	Low	Not attributable
Records on livestock damages	Where to concentrate monitoring efforts and conflict mitigation. If	Medium	C1, C2, C3

	C1 (because saliva samples confirm wolf presence), then used for distribution and trends		
Signs collection by travelling transects or opportunistic, snow tracking	Distribution, indications of population trend, reproduction	Medium	C1, C2, C3
Recovery of dead wolves	Distribution, mortality, health	Low	C1
Camera trapping	Distribution, abundance, population trend, demography, dispersal, reproduction	Medium to high	C1, C3
Genetic analysis on biological samples	Distribution, abundance, population trend, dispersal, reproduction	High	C1
Telemetry*	Distribution, territory size, habitat use and selection, dispersal, mortality causes, health and conflicts	Very high	C1

* Telemetry on its own is not a monitoring method, but it can provide valuable information on territory size (which can be used to estimate densities), habitat use or reasons for mortality that is otherwise difficult to obtain. Telemetry studies can be used to calibrate the results of a monitoring program.

Table 8. Parameters, recommended methods and data needed to estimate area of occurrence and population size for wolves in Europe

Measure	**Field Methods**	**Data needed**
Area of occurrence	Presence sign survey, camera trapping	At least one C1 hard fact, or two independent C2 signs, in a 10 x 10 km cell to define it as occupied
Number of reproductive units (packs and pairs) Number of individual territorial wolves	Presence sign survey, snow tracking, genetic analysis, howl survey, camera trapping, video / photo documentation	Occurrence of a pack, a pair or a territorial individual must be confirmed via C1 or C2 data
Population size	Capture-recapture methods or other modelling framework that accounts for imperfect detection	Individual identification from genetic analysis
Pack size	Presence sign survey, snow tracking, genetic analysis, howling survey, camera trapping, video/photo documentation	The minimum figure for pack size must be confirmed via C1 or C2 data

Reproduction	Presence sign survey with focus on pup signs (such as howling survey, photo/video documentation, camera trapping, snow tracking, genetic analysis)	Successful reproduction has to be confirmed via C1 or two C2 data
Distinguishing between adjacent territories	Genetic analyses, camera trapping, telemetry	Distinction possible by: genetic identification **OR** simultaneous proof of reproduction **OR** telemetry data from radio collared wolves belonging to one of the adjacent territories **OR** individuals are clearly identifiable (e.g. by camera trap pictures / videos)

*This distance is population specific, e.g. for CEP population a distance of 10km is used (Reinhardt et al., 2015).

LYNX

Table 9. Definitions about lynx presence type

Lynx presence type in the area:	
Lynx presence	Confirmed presence of a lynx
Family group	Confirmed reproduction
Age class of lynx:	
Kitten	Until the age of 1 year
Independent	Age 1 and older, cut-off date is 30th April
Monitoring year	1st May – 30th April; In Scandinavia 1st June – 31st May (Mattisson et al., 2022)

Table 10. Comparison of available methods for lynx detection

Method	**Monitoring/research questions to be answered**	**Required investment of resources**	**SCALP category of data obtained**
Opportunistic sightings reported from the public/stakeholders	Where to concentrate monitoring efforts	Low	Not attributable
Questionnaires	Where to concentrate monitoring efforts	Low	Not attributable
Collection of chance observations	Distribution, indications of population trend, reproduction, health and conflicts	Low	C1, C2, C3
Snow tracking	Distribution, population trend, reproduction	Medium	C2
Camera trapping	Distribution, abundance, population trend, demography, dispersal, reproduction	Medium to high	C1
Dead lynx	Distribution, mortality, health	Low	C1
Genetic analysis	Distribution, abundance, population trend, dispersal, health, reproduction	High	C1
Telemetry	Abundance, dispersal, health and conflicts	Very high	C1

Table 11. Parameters, recommended methods and data needed to estimate area of occurrence and population size for lynx in Europe

Parameter	**Field Methods**	**Data needed**
Area of occurrence	Camera trapping, presence sign survey	One C1 or C2 sign per 10 x 10 km cell
Population size	Opportunistic camera trapping to determine minimum size. For larger populations, systematic camera trapping for statistical capture-recapture estimation in reference areas. In Fennoscandia, number of family groups based on snow tracking	Minimum estimate based on C1 data, individual identification, tracks of family groups with distance criteria
Reproduction	Camera trapping, snow tracking, direct observation	Reproduction has to be confirmed via C1, C2

BEAR

Table 12. Definitions on definitions about bear presence type

Bear presence type in the area:	
Bear presence	Confirmed presence of a bear
Reproduction	Confirmed family group of a mother with cubs (which includes both cubs of the year & yearlings), or only cubs
Age class of bear:	
Cub of the year	Documented accompanied with the mother (or alone)
Yearling	Documented accompanied with the mother (or alone)
Adult female	Can be confirmed only if with cubs
Adult male	Confirmed by size (200+ kg)
Monitoring year	Spring and fall

Table 13. Comparison of available methods for bear detection

Method	**Monitoring/research questions to be answered**	**Required investment of resources**	**SCALP category of data obtained**
Opportunistic sightings reported from the public/stakeholders	Where to concentrate monitoring efforts	Medium	Not attributable
Questionnaires	Where to concentrate monitoring efforts	Low	Not attributable
Collection of chance observations	Distribution, indications of population trend, reproduction, health and conflicts	Low	C1, C2, C3
Snow tracking	Distribution, population trend, reproduction	Medium	C2
Camera trapping	Distribution, abundance, population trend, demography, dispersal, reproduction	Medium to high	C1
Dead bear	Distribution, mortality, health	Low	C1

Genetic analysis	Distribution, abundance, population trend, dispersal, health, reproduction	High	C1
Telemetry	Dispersal, health and conflicts	Very high	C1

Table 14. Parameters, recommended methods and data needed to estimate area of occurrence and population size for bear in Europe

Parameter	**Methods**	**Data needed**
Area of occurrence	Presence sign survey, camera trapping	One C1 hard fact, or two C2 signs per 10 x 10 km cell and year
Population size	Genetic analyses, documented counts at feeding sites	Minimum estimate based on C1 or C2 data
Reproduction	Tracks, photo/video, camera trapping	Reproduction has to be confirmed via C1 or C2 data

GOLDEN JACKAL

Table 15. Definitions about golden jackal presence type

Golden jackal presence type in the area:	
Single jackal	Single jackal detected in an area
Single resident jackal	Single jackal living in an area for at least 6 months.
Pair	Male and female golden jackal occupying a shared territory but not (yet) having reproduced
Group	A group of more than two golden jackals living together in a territory
Reproductive group	Consists of at least one mature golden jackal with confirmed reproduction
Age class of jackals:	
Mature/Adult (reproducing)	≥ 24 months (reproduction might already occur in yearlings, though)
Pup	Golden jackal in its first year of life. The transition from pup to yearling is considered on 1st May
Yearling	Golden jackal in its second year of life (reproduction is already possible)
Monitoring year	1st May – 30th April
Jackal-dog/jackal-wolf Hybrid*	Jackal-dog hybrid documented with genetic analysis (Galov et al., 2015; Stefanovic et al., 2024)

*If hybrids are detected they should be excluded from the golden jackal population size estimate/index but should be reported separately. If hybrids are known to be present but not excluded from the counts (because precise data of their proportion in the population are not available), then this should be declared and reported as well.

Table 16. Comparison of available methods for golden jackal detection

Method	**Monitoring/research questions to be answered**	**Required investment of resources**	**SCALP category of data obtained**
Opportunistic sightings reported from the public/stakeholders	Where to concentrate monitoring efforts	Low	Not attributable
Questionnaires	Where to concentrate monitoring efforts	Low	Not attributable
Howling surveys	Distribution, abundance, indications of population trend, reproduction	Medium	C1

Scats collected with scat detection dogs*	Distribution, reproduction, food ecology	High to very high	C1-C3
Signs collection by travelling transects or opportunistic, snow tracking	Distribution, indications of population trend, reproduction	Medium to high	C1, C3
Recovery of dead golden jackals (e.g., opportunistic, hunting bag)	Distribution, abundance, population trend, demography, reproduction, mortality, health	Low to medium	C1
Camera trapping	Distribution, abundance, population trend, demography, dispersal, reproduction	Medium to high	C1, C3
Genetic analysis on biological samples	Distribution, abundance, population trend, dispersal, reproduction	High	C1
Telemetry	Distribution, Dispersal, health and conflicts	Very high	C1

*Due to the difficulty of distinguishing golden jackals from fox scats, collection of scats is not possible without a scat detection dog.

Table 17. Parameters, recommended methods and data needed to estimate area of occurrence and population size for golden jackals in Europe

Measure	**Field Methods**	**Data needed**
Area of occurrence	Presence sign survey, howling survey, camera trapping	One C1 hard fact per 10 x 10 km cell and year
Number of groups	Howling survey, genetic analysis, camera trapping	Occurrence of a group, a pair or a territorial individual must be confirmed via C1 data
Population size	Capture-recapture methods or other modelling framework that accounts for imperfect detection. Minimum count from howling surveys	Individual identification from genetic analysis or recovery (e.g., hunting bag)
Group size	Howling survey, camera trapping, genetic analysis	Successful reproduction has to be confirmed via C1 data
Reproduction presence	Howling survey, camera trapping, genetic analysis, documented opportunistic observations	Successful reproduction has to be confirmed via C1 data

Distinguishing between adjacent territories	Howling survey, genetic analyses, camera trapping, telemetry, scats/hair (and following genetic analyses)	Distinction possible by: simultaneous response to howling survey OR genetic identification **OR** simultaneous proof of reproduction **OR** telemetry data from radio collared jackals belonging to one of the adjacent territories **OR** individuals are clearly identifiable (e.g. by camera trap pictures / videos)

WOLVERINE

Table 18. Definition about wolverine signs type

Wolverine presence type in the area:	
Wolverine presence	Confirmed presence of a wolverine
Reproduction	Confirmed reproduction (often den site)
Age class of wolverine:	
Kitten	Until the age of 1 year
Independent	Age 1 and older, cut-off date is 31st of January
Monitoring year	1st February – 31st January

Table 19. Comparison of available methods for wolverine detection

Method	Monitoring/research questions to be answered	Required investment of resources	SCALP category of data obtained
Reports from hunters	Where to concentrate monitoring efforts	Low	Not attributable
Questionnaires	Where to concentrate monitoring efforts	Low	Not attributable
Collection of chance observations	Distribution, indications of population trend, reproduction, health and conflicts	Low	C1, C2, C3
Snow tracking	Distribution, population trend, reproduction	Medium	C2
Camera trapping	Distribution, abundance, population trend, demography, dispersal, reproduction	Medium to high	C1
Genetic analysis	Distribution, abundance, population trend, dispersal, health, reproduction	High	C1
Telemetry	Abundance, dispersal, health and conflicts	Very high	C1

Table 20. Parameters, recommended methods and data needed to estimate area of occurrence and population size for wolverine in Europe

Parameter	**Field Methods**	**Data needed**
Area of occurrence	Camera trapping, presence sign survey	One C1 or C2 sign per 10 x 10 km cell and year
Population size	Opportunistic camera trapping to determine minimum size. For larger populations, systematic camera trapping for statistical capture-recapture estimation in reference areas. Number of reproductive units documented.	Minimum estimate based on C1 data, individual identification
Reproduction	Camera trapping, snow tracking, direct observation, active dens	Reproduction has to be confirmed via C1, C2 or C3 data, but needs to be distinguished

3.2.1 How to add numbers of individuals and social units from the different countries within a population

Most carnivore populations in Europe are transboundary; therefore, care must be taken to avoid double counting of cross-border territories and to ensure that national estimates of territories and individuals are not simply summed. Usually, the monitoring is conducted on country level or even on smaller monitoring units, for instance on the level of federal states, provinces or regions (Marucco et al., 2023b; Bischof et al., 2020; Bischof et al., 2016). When compiling these data, double counting must be avoided through the application of predefined rules. Several wolf monitoring programs conducting population assessments at the transboundary level regularly face this issue, for instance Sweden and Norway (Wabakken et al., 2022; Svensson et al., 2023), Slovenia and Croatia (Skrbinšek et al., 2024) and the wolf Alpine monitoring program where data from seven alpine countries are compiled (Marucco et al., 2023a). A pragmatic approach is to divide all transboundary territories equally to both monitoring units when the results are summarised. A transborder pack territory in Scandinavia will count half to Sweden and half to Norway when summarising the results and the same applies for the reproductions. On graphs showing population trends, the territories located entirely within national boundaries, as well as the transboundary ones, are displayed. Another way to handle transboundary territories is to decide, for each territory, which country will include it in its count, based either on where the majority of the territory lies or where reproduction was first confirmed. Obviously, this approach is much more labour-intensive than the first one and more applicable for intra-national monitoring programs where data has to be compiled on a national level. It is helpful when official agreements exist between the authorities of neighbouring countries to ensure that transboundary territories are clearly identified as such when population numbers are reported. In the absence of such agreements, scientists may have established a harmonised procedure that is not applied by national authorities, resulting in inflated population estimates when national data are aggregated without distinguishing transboundary packs or individual territories.

Compiling individual numbers at the transboundary population level is more complex. When these numbers are derived from minimum counts (e.g. average minimum pack size, see 4.1.2 Method B) or by applying a conversion factor (4.1.2 Method A), and the same methods are consistently used across all countries sharing the population, a joint estimate of individual numbers is feasible. In such cases, half of the individuals estimated to inhabit transboundary territories can be allocated to each neighbouring country. However, when estimates are obtained through statistical models, such as Capture-Recapture (CR), Individual-Based Models (IBM), Open-Population Spatial Capture-Recapture (OPSCR), or Spatial Capture-Recapture (SCR), and these analyses are conducted independently at national or regional levels rather than across borders, the results cannot be directly summed to produce a reliable population-level estimate, as an important portion of the population would be double-counted resulting in an overestimation.

4 ESTIMATION METHODS FOR LARGE CARNIVORE POPULATIONS

The frequent demand for population size estimates has sparked the development of numerous statistical techniques for robust and accurate estimates (Robinson, 2014; Blanc et al., 2014; Jiménez et al., 2016). Based on current practices, hereafter we define the possible methods of estimation of population size and area of occurrence for large carnivores in Europe. Approaches are either based on inference from marked animals (Thomson et al., 2008) or inference from unmarked ones (Chandler & Royle, 2013). In LC in Europe marked animals for population estimates are generally based on individual identification from non-invasive DNA samples (Solberg et al., 2006; Kindberg et al., 2009; Bischof et al., 2020) or from camera trap images when individuals are recognisable (O'Connell et al., 2011; Palmero et al., 2021; 2023).

Population size **(i.e. number of individuals) in a survey for large carnivore populations in Europe, given the sampling scheme applied, can be estimated by:**

- **Capture-recapture estimates, spatially explicit or not:** considering that population sampling is not comparable to a census, where every individual is counted, it becomes necessary to use analytical methods that consider the number of uncounted individuals, thus accounting for imperfect detection, to arrive at an estimate of the sampled population size (Kéry et al., 2009). Important advances have been made in understanding imperfect detection, in part due to the richness of capture-mark-recapture data generated either by non-invasive genetic sampling, where individual genotypes are identified from DNA extracted from samples (e.g., scats, hairs) left behind in the environment (Schwartz et al., 2007), or by using camera trap images, when individuals are recognisable (O'Connell et al., 2011). Large carnivore monitoring programs have greatly benefited from this approach, combining non-invasive genotyping as input data for the estimations of population size using capture-recapture models (Caniglia et al., 2012; Cubaynes et al., 2010; Marucco et al., 2009), or more recently, spatial capture-recapture (SCR) approaches (Bischof et al., 2020; Proffitt et al., 2015; Marucco et al., 2023b; Palmero et al., 2023).
  However, despite the abundance of datasets that have led to the development of these models, it is not always easy to obtain enough data to make accurate and reliable estimates. In fact, especially SCR models require large datasets with many recaptures at different locations of the same individual, in order to be able to estimate the ancillary parameters that are needed to obtain the population estimate (Dupont et al., 2021; Boiani et al., 2024).
  Furthermore, most large carnivores do not have distinguishable markings that allow for their recognition and thus allow for the use of camera traps and pictures/videos as input data for CR/SCR. In fact, only lynxes and wolverines can be distinguishable in most cases, the former because of their coat (Palmero et al., 2023) and the latter because of their gular patches (Royle et al., 2011). For wolves, bears and golden jackals, genetic analyses are still essential, but these data are considered expensive and demanding, in terms of effort to obtain them. However, for appropriate CR/SCR applications, important considerations have to be applied to properly sample over space and time, considering the size of the population and possible biases related to model-specific assumptions i.e., population closure assumption (Dupont et al., 2019) or large holes in the sampled area (Moqanaki et al., 2021).

- **Individual Based models (IBM):** total population size can be estimated from an individual-based population model (IBM) parameterized with detailed demographic data. These models are built on ecological theory by considering population persistence as a bottom-up process emerging from individual variations and events. IBM indeed can encompass several ecological features of a species, such as the ability of dispersal, the genetic background, the probability of reproduction and so on (Grimm et al., 1999; Chapron et al., 2016; Hatlauf et al. 2024), and can use this information to predict the evolution of the population, allowing population-level characteristics to emerge from these individual interactions (Bauduin et al., 2020). IBM can also be spatially explicit and account for the preferential habitat in the modelling of the population (Marucco & McIntire, 2010). Again, however, these models are challenging to employ, mainly due to the quantity and quality of data required.

- **Integrated Population models (IPMs)**: these models combine different sources of data to build a more informative model. IPMs allow the exploitation of all or most data collected when surveying a population while improving the precision of the final estimate (Jimenez et al., 2022). The combining of an occupancy model and an SCR model has been used to produce wolf and lynx distribution and abundance estimates in different areas of Europe (Aragno et al., 2022; Gervasi et al., 2024; Blanc et al., 2014).

- **Population Distribution Models (PDMs)**, or **Abundance–Occupancy Models**: are analytical frameworks that integrate species' spatial occurrence with quantitative estimates of local abundance (Sells et al., 2022). These models extend the principles of species distribution modeling by explicitly linking the probability of occurrence to demographic patterns or population density across heterogeneous landscapes. By incorporating environmental, ecological, and sometimes demographic predictors, PDMs aim to characterize not only the geographic extent of suitable habitats but also spatial variation in density (Sells et al., 2022). The development of these explicit links are highly data demanding to be accurate, and the population estimates are totally dependent on the predefined population specific rules. Assumptions need to be clearly stated, and biases discussed.

- **Minimum counts of individuals (or packs for wolves and golden jackals, or family groups for lynx, or den site/reproductions for wolverines):** detected with the number of genotypes or via genetic pack reconstruction (Marucco et al., 2018; Jarausch et al., 2021), by counts of tracks with snow tracking (provided the sampling design prevents double counting) (Linnell et al., 2007; Kojola et al., 2014), by photos from camera traps (Rich et al., 2017), or by a combination of those data. When used as an index, sampling effort needs to be taken into account.

- **Guessed numbers**: in populations where surveys are not conducted and no estimation methods can be applied; experts may provide an approximate number based on their personal experience and knowledge. However, we strongly discourage such practice. Guessing numbers should be strictly avoided, and this approach is not further considered in this document.

Area of occurrence (i.e. distribution):

- **Minimum area of occurrence**: cells of a grid (ideally not coarser than 10x10 km) where presence signs have been detected and categorized using the SCALP criteria; LCIE recommends a 10x10 km grid for LC; it is an index.

- **Estimates of occurrence with an associated level of precision**: occupancy modelling (MacKenzie & Nichols, 2004; MacKenzie et al., 2006) allows researchers to combine detection/non-detection histories with spatial modelling to accurately estimate and predict species' occurrence across a landscape. These estimates, like CMR, therefore indicate estimates of precision. Occupancy models have, as their base unit, the grid of the study area. For each cell, they can accurately estimate the probability of presence based on repeated search events. By incorporating estimates of detectability from sign surveys directly, this approach corrects the inherent negative bias present in naïve occupancy estimates like the minimum area of occurrence (MacKenzie et al., 2003; Tyre et al., 2003).

- **Species specific indices:**
- **Wolves**: packs/pairs locations buffered with the average territory size; it is an index.
- **Golden jackal**: territorial group locations buffered with the average territory size; it is an index.
- **Lynx**: family groups locations buffered with the average female home range; it is an index.
- **Wolverine**: den site locations buffered with the average female home range; it is an index.

4.1 Conversion factors in population estimates

Introduction

This section primarily focuses on wolves, although several of the principles discussed may also be relevant to other large carnivores. Wolves live mostly in social units like packs (family groups) and pairs (a male and a female wolf that have not reproduced yet) (Mech & Boitani, 2003). Packs and pairs are the reproductive units of a wolf population that drive population dynamics and can offer valuable insights for monitoring population trends (Blanco & Cortés, 2012; Reinhardt et al., 2015; WAG, 2022; Marucco et al., 2023a). As discussed in the previous chapter, providing the size of a large carnivore population, even approximately, is not an easy task. For this reason, there is considerable variability in what each European country is able to achieve: some countries estimate the number of individuals, others the number of packs or pairs, and a few report both.

According to the European Habitats Directive, population size should be reported as the number of mature (adult) individuals (DG Environment, 2017). The same criterion applies to Red List assessments. However, both the public and the authorities often request information on the total number of wolves present in a given area. To meet the demand for these different types of population estimates, conversion factors are often applied to translate one measure into another (Svensson et al., 2013), for instance, converting the number of packs into an estimated total number of individuals (Chapron et al., 2016). It is important to underline that most conversion factors are population sensitive and cannot be transferred from one population to another (Chapron et al., 2016; Boitani et al., 2018; Bischof et al., 2019). Even for the same population, conversion factors have to be updated and evaluated over time and space as population density and distribution may change spatially and temporally (Chapron et al., 2016). This issue is especially critical for populations under hunting or culling regimes. As the number of assumptions within a model used to derive conversion factors increases, so does the need for precise and reliable input data. When the input data are rough or uncertain, the resulting estimates will inevitably be unreliable.

In the following, we introduce the most common types of conversion factors (A to D) used for wolf populations and refer to best-practice examples where available. It should be noted that the methods described below can be adapted to golden jackals which also live in social, territorial groups, and, in some cases, to other large carnivores as well.

4.1.1 Method A: Converting packs to adults / mature individuals (living in territories)

To convert the number of packs / pairs to the minimum number of mature individuals that are living in territories, the number of reproductive units can be multiplied by 2. In general, each wolf pack consists of the mature breeding pair and their subadult offspring of the last one or two years. Therefore, the minimum number of adults in a wolf pack is two. Given the relatively small pack size reported for wolves for many European countries (Fernández-Gil et al., 2020), most European wolf packs consist of no more than two adults. We propose to include the pairs in this conversion as well even if some pair individuals may not yet be 24 months old during the breeding season and a few pair bonded individuals may only be in their first year of life (Wikenros et al., 2021). Most breeding pairs will raise pups in the next monitoring year and become packs. Whenever more precise data on pack composition are available (e.g. due to genetic data allowing for age determination of pack members), the number of mature individuals per reproductive unit should be corrected accordingly. In some packs more than two adults (older offspring or adoptees) are recorded and some of these additional adult pack members may also reproduce (packs with multiple breeding). However, multiple breeding seems to be much rarer in Europe than observed in North America, but present (Ausband, 2018; Åkesson et al., 2022). Indeed, a conversion factor of 2 is suggested but should be supported by evidence.

This approach does not take into account adult individuals not associated with a wolf territory (so called floaters or dispersers) (Boitani et al., 2018). However, floaters do normally not contribute to wolf reproduction. They can do so if they take over a breeding position in an existing territory (Kojola et al., 2006; Caniglia et al., 2014). In this case they become part of the calculation via the pack / pair conversion. This conversion factor takes only into account adult individuals living in territories and thus being not only physiologically, but also socially capable of reproduction. Moreover, the number of packs approximately corresponds to the effective population size, which is another important parameter to estimate over time for assessing the status of the population (Mergeay et al. 2024).

Best practice example: in Germany, for every monitoring year a minimum count of the number of packs, pairs and single territorial wolves is conducted. Sampling areas are the federal states and state data are compiled once a year on a national level according to national monitoring standards (Reinhardt et al., 2015). Every monitoring year, the number of wolf territories is converted to the number of mature individuals by multiplying the number of packs and pairs by two and adding the number of single territorial wolves. For territories with precise age data (genetic and photographic data) the number of mature individuals is corrected if differing from two (e.g. DBBW, 2024).

Recommendation: This rule of thumb conversion factor can be applied to all European wolf populations when pack / pair numbers are available as it is not population sensitive but based on wolf biology only.

4.1.2 Method B: Converting packs to individuals

It is not immediately straightforward to convert the number of packs to the number of the overall individuals of the population. A rigorous and accurate way of doing this conversion obviously requires an understanding of how the ratio of individuals to packs varies according to time and space (Chapron et al., 2016; Bischof et al., 2020). In addition, the ratio of individuals to packs is population-specific, depending on ecological conditions as well as management practices and cannot be transferred between populations (Boitani et al., 2018). When a population is subject to different management regimes or covers very large/different geographical regions each management unit therefore requires its own conversion factor.

Method B1: The ratio of individuals to packs or conversion factor can be evaluated using adequate modelling frameworks such as species-specific Individual Based Models (IBM e.g. in Scandinavia by Chapron et al., 2015; 2016; in the Alps by Marucco & McIntire, 2010; McIntire et al., 2017), or by Open-Population Spatial Capture-Recapture (OPSCR) models (Bischof et al., 2019), or by spatially explicit Capture-Recapture models (Marucco et al., 2023b). In the IBM developed by Chapron et al. (2015; 2016), the model incorporated data on the average number of pups per litter, estimates of the proportion of territorial wolves within the total population, as well as data on survival probability, dispersal and mortality rates for different age classes obtained from over 150 GPS-collared wolves. This information served as prior input for fitting the model to time series data using Approximate Bayesian Computation. In the OPSCR by Bischof et al. (2019), the population is considered as open, meaning individuals can enter or leave the population due to births (treated as immigration), deaths (mortality, legal and illegal), and emigration. In this framework, data on population size (number of packs) and population size dynamics, spatial distribution and movement of individuals between years (including dispersal), and detection probability of individuals based on genetic sampling and findings of dead wolves were included and adapted to a SCR model, that accounted for the movement (both spatially and in and out of the population) of the individuals over the years. This OPSCR model was run with monitoring data from five consecutive monitoring years and resulted in density maps from which population size estimates were derived. A probability distribution of conversion factor was then estimated from the ratio of counted packs number to the estimated number of individuals. However, these kinds of models require an enormous amount of updated biological data and a substantial modelling effort. Because conversion factors are probability estimates, they naturally differ according to modelling approaches and this can trigger credibility debates like in Sweden (Bischof et al., 2019). For example, an outdated conversion factor is still used in Scandinavia for the annual wolf status reports (Wabakken et al., 2022; Svensson et al., 2023), although there are more up-to-date and advanced conversion factors developed by Chapron et al. (2015, 2016) and Bischof et al. (2019, 2020).

Best practice example:

We list the published conversion factors that were derived with the different modelling approaches explained above by country, population, and year in Europe:

Table 21. Conversion factors obtained from modelling framework for wolf packs to overall wolf population size published in the scientific literature.

Publication	Population of interest	Country	Year	Conversion factor (and CI)	Notes/ Comments
Chapron et al., 2016	Scandinavia	Sweden	2003 - 2015	8.0 (95% CI = 6.62–10.07) 7.67 (95% CI = 6.26–9.89)	Derived from an IBM modelling approach
Bischof et al., 2019, 2020	Scandinavia	Sweden, Norway	2013 2014 2015 2016 2017 **5-year median**	8.6 (8.0 - 9.2) 8.6 (8.1 - 9.1) 9.0 (8.6 - 9.4) 8.7 (8.5 – 9.0) 9.8 (9.6 - 10.1) **8.8 (8.2 – 10.0)**	Derived from a OPSCR modelling approach
Derived from Marucco et al., 2023b	Italian Alps	Italy	2020-2021	7.1 (95% CrI = 5.9-8.5)	Derived from a SCR modelling approach. High spatial variability, i.e. large difference within East and West part of the Alps, not applicable at small scale

Recommendation:

If up-to-date and robust data on distribution and population parameters are present in addition to pack numbers, IBM / OPSCR / SCR models can be used to estimate individual numbers. However, these types of models require an enormous amount of extensive data and modelling capacities as well as long computation times (Milleret et al., 2018; Dupont et al., 2021), which for most countries is impossible to obtain and provide on a regular basis. The estimated conversion factors are specific for each population and for a certain period and can vary spatially and temporally; hence, they cannot be extrapolated to other cases.

Method B2: Another way of converting the number of packs to the number of individuals is to multiply the number of packs by the average pack size and add the proportion of floaters in the population (no. individuals = (no. packs * average pack size) + % floaters). At first glance, this approach seems to be strikingly simple. However, as Blanco & Cortes (2012) pointed out, it is extremely difficult to accurately get robust data on the average pack size and the proportion of floaters. Again, these data are population sensitive. In addition, the average pack size and the proportion of floaters will vary for each population not only from year to year and according to the management regime but also within any given year (Fernández-Gil et al., 2020). The pack size changes over the year with the birth of the pups, dispersal of older offspring and mortality of pack members. In late spring / early summer, after the pups are born, the pack size is the largest, while in late winter / early spring, it is the smallest (Fernández-Gil et al., 2020).

When reporting average pack size, it is crucial to specify whether the data refer to the summer or winter period, as seasonal variation strongly influences pack composition. Obtaining a robust estimate of average pack size is particularly challenging when relying on data derived from direct observations, camera trapping, or snow tracking (Barber-Meyer, 2022). In summer, pack size is mainly determined through direct observations, howling surveys or camera trap data. In Spain, the main factor affecting summer pack size was the number of times a pack was observed (Barrientos, 2000; Blanco & Cortes, 2012). In most monitoring programs, however, the main objective is not to quantify pack size but to determine pack status (i.e. whether reproduction has occurred). Consequently, reported pack sizes are often incidental findings, representing only a minimum count of individuals (Harrington & Mech, 1982). Observations at rendezvous sites, which could provide more accurate counts, are rarely feasible at large spatial scales. Llaneza et al. (2023) calculated the average minimum summer pack size for wolves in Iberia based on an extensive 35-year dataset, with an average of 2.77 packs surveyed per year. Despite the long-term effort, interannual variation could not be assessed. Obtaining accurate data on winter pack size is even more demanding, even in areas where snow tracking is possible. Because members of a pack often search for food alone or in small groups during winter, it is unusual to observe all or most pack members together (Mech & Boitani, 2003; Blanco & Cortes, 2012). As a result, reliable estimates of winter pack size derived from snow tracking, sign surveys, or camera trapping remain difficult to obtain. Assessing the number of floaters, the non-territorial individuals within a population, is even more complex. This requires extensive genetic sampling and pack reconstruction to assign individuals confidently to either resident packs or the floater/disperser category, a task that is unrealistic to perform regularly at large spatial scales.

Recommendation:

Method B1 is the preferred method for converting the number of packs to the number of individuals. However, if up-to-date data or modelling capacities for developing IBM / OPSCR / SCR models are not available, method B2 may be used instead. It is crucial that in these cases, the underlying methodology of how the average minimum pack size was calculated is documented, as well as the period of pack size estimation.

4.1.3 Method C: Converting individuals to adults / mature individuals

To robustly convert the number of individuals into an estimate of adults or mature individuals, extensive data are required. This data must be updated over time and across space as populations increase or decrease. In this context, the conversion factor may vary among years and populations (Boitani et al., 2018), a consideration that applies to all large carnivore species, not only wolves.

For lynx and wolverine, the conversions from family groups (for lynx) or reproduction occurrences (natal den site for wolverine) to total population size have been estimated using survival and reproduction estimates in a population matrix. This approach allowed us to define the population structure during the monitoring period by also making it possible to estimate the number of mature individuals/adults (for lynx: Andrén et al., 2002; for wolverine: Persson & Brøseth, 2011).

For wolves, in some countries, mature individuals have been considered only as the adult individuals living in reproductive units, which are at least two per pack and always two per pair (e.g. DBBW 2024). In other studies, the number of mature individuals does not only consider the potentially breeding individuals within packs and pairs, but also the dispersers and floaters older than two years. For instance, in 2020-2021, for the Italian Alpine region, mature individuals (everyone except the offspring) accounted for 33–45% of the entire wolf population (Marucco et al., 2023b).

In contrast to method A, this approach takes into account the percentage of adult floaters. However, this percentage is population-specific and applies to a particular point in time. Additionally, it can vary spatially across different regions, meaning it should not be extrapolated to other populations or situations. In addition, the percentage of floaters may be influenced by management regimes. Where hunting or culling quotas are high, the high turnover of breeding wolves ensures many vacant breeding positions allowing most floaters and dispersers to settle within a short time in a territory.

Recommendations:

The estimated percentage of mature individuals from modelling frameworks also considers floaters in the percentage, compared to method A. However, these percentages are specific for any population and for a given time and can vary spatially and temporally; hence, they cannot be extrapolated to other cases.

4.1.4 Method D: Converting area of occurrence to number of packs

In large, saturated populations, the number of packs may be extrapolated from the area of occurrence, provided that sufficient up-to-date data on wolf territory size are available (Sells et al., 2022). The prerequisite for calculating the number of packs as a function of the area of occurrence is that the estimate of the area of occurrence is robust and unbiased. For the development of a conversion factor to estimate pack numbers based on the area of occurrence, sufficiently robust and up-to-date data of territory sizes that also account for habitat and density variations are needed. In addition, the ratio of pack numbers to pair numbers should be known. Even in saturated areas, territory size can vary widely (Mattison et al., 2013), and for this seemingly simple approach, it must be ensured that the data are collected from a sufficient number of breeding animals from different territories and densities; moreover, data need to be up to date. Particular care should be taken when using this approach in expanding populations, as the variation in territory sizes is expected to be even larger (Mattison et al., 2013; Fernández-Gil et al., 2020). The territory size can be significantly smaller in the core areas than at the population in the front of expansion. In this case, more data from different areas with different saturation levels and habitats are needed for such a modelling approach.

Recommendations:

This simplified approach is not recommended and relevant for the highly heterogeneous habitat of the European ranges of large carnivores, especially in case the population is subject to hunting / culling schemes.

5 POPULATION PARAMETERS' EVALUATION AND QUALITY LEVELS (Q1-Q2-Q3)

The quality of population estimates refers to the accuracy and reliability of statistical approaches and data collection methods used to describe the number, distribution, and characteristics of a population at a given time and place. Here we focus on the two most important parameters for assessing large carnivores' population:

- abundance (population size)
- distribution (area of occurrence)

Assessing the quality of population estimates for large carnivores requires evaluating the sampling design, methodologies, data sources, and modelling approaches used, as discussed in the previous chapters. Based on these considerations, we defined the **LCIE Quality Levels in three categories (Q1–Q2–Q3),** to classify both population size and occurrence estimates, thereby enabling comparisons among estimates of comparable quality across time and space. The LCIE Quality Levels are useful when presented together with LCIE population estimates, as they indicate the corresponding level of confidence in the data.

5.1 Quality levels for population size

Assessing the quality of population size estimates involves several important considerations, each aimed at ensuring that the estimates reflect true population dynamics accurately. To assign meaningful quality levels to population size estimates, we emphasize the importance of clearly evaluating:

1. **Sampling Design**:

Evaluate the design of the study used to estimate the population. Consider whether it was a complete structured survey or an unstructured sampling (i.e. the collection of opportunistic direct observations of animals or their indirect signs for a portion of the study area). This last haphazard collection of signs does not allow robust inference, but has other advantages such as providing preliminary information to a more structured plan, picking up on expansion into unmonitored areas, and building trust with local people and stakeholders. However, this opportunistic data is highly dependent on the presence of people and among other variables, depends on ease of access to an area and the motivation of people to document and communicate LC observations. Structured sampling, on the other hand, implies an inventory design aimed at documenting the detection or not-detection of the target species and thus providing the population abundance in an area. Differences in the quality of the outputs can be related both to sampling intensity and to the types of designs applied, which in most cases imply extrapolation by modelling approaches. Unstructured sampling can lead to indexes like minimum counts, while structured sampling can lead to estimates with CI if the sampling effort is controlled. Indeed, accounting for effort within the modelling framework allows the estimation of detection probability for individuals in the population and thus the application of the most robust techniques discussed in Chapter 4 (Kéry and Schmidt, 2008).

2. **Data Collection Methods and type of data**:

Assess the methods used for data collection based on chapter 3, and evaluate if C1 and C2 data are collected and used for the estimates. A majority of C1 data indicate a higher quality of data. Many C1 data allow for individual identifications: genetic analysis on biological samples and/or photos for lynx allows for individual recognition which provides higher accuracy in indexes and estimates, especially if CR/SCR models are applied (Burgar et al., 2018; Sun et al., 2022). It is also important to underline that methods that allow practitioners to obtain information on the heterogeneity of the population, i.e. sex or social status of the individuals allow for higher precisions in the estimate (Cubaynes et al., 2010).

3. **Sample Size and Area**:

Consider the sample size and the area covered in the study. A larger sample size and coverage tend to improve the robustness of population estimates. Larger sample sizes, in relation to the expected population size, indicate higher quality of the estimates. The extent to which the population has been counted or represented in the data is crucial. Undercoverage of certain groups or regions can lead to biased estimates, if the sampling design is not structured. It is fundamental to examine how well the study area represents the larger habitat of the target population. Intensive monitoring of one study area and extrapolation to a much larger distribution range without structured monitoring and confirmation of presence or reproduction may easily result in overly optimistic or pessimistic estimates and risks to fail to detect overall population changes.

5. **Error and Uncertainty**:

Estimating the levels of error associated with estimates is crucial for assessing quality. Population size estimates that report the uncertainty associated (Confidence Intervals or Credible Intervals) are considered better in quality as they allow us to assess how precise a population estimate is. Although a population estimate without uncertainty may seem more robust, it actually misses the information about how precise it is. This information is critical for understanding the reliability of the estimates and allows for comparisons over the years.

6. **Modeling Approaches**:

Assess the statistical models used to derive population estimates as discussed in chapter 4. It is important to consider the assumptions made in these models, and evaluate whether they hold true for the study area and the extent of extrapolation applied. Consider if conversion factors have been applied, based on the best practices highlighted in chapter 4.1. Models also need to be regularly validated with underlying field data.

7. **Stakeholder involvement and transparency**:

It is fundamental to engage with local wildlife managers, conservationists, and stakeholders for qualitative assessments of population status, in order to define the quantitative assessment. Engaging with local communities or stakeholders can enhance the accuracy of estimates by providing insights into the definition of the sampling designs. Guessed numbers of population size based on experts' opinions/questionnaires are not acceptable for population size estimates and quality cannot be even measured; however, they could be useful to define the sampling strategy. Ensuring open methodologies and transparent reporting standards further strengthens the credibility of population assessments, in line with the guidance provided in chapter 3.

Indicating the quality of population estimates is essential for large carnivores' effective management and conservation, in fact using high-quality demographic data can lead to better decision-making and resource allocation. However, low quality and medium quality estimates might be of extreme importance, especially where no other information is available. Regular and transparent reporting of the quality associated with each population estimate is essential to ensure proper interpretation of the data and to guide effective conservation and management actions.

In the following tables, we present the defined quality levels for evaluating population size estimates, building upon the definitions presented in Chapter 2, the criteria described in Chapter 3, the considerations discussed in Chapter 4, and the summary of key aspects provided above. **The LCIE quality levels (Q1, Q2, and Q3)** will be reported in LCIE assessments to differentiate the reliability of population estimates, thereby allowing meaningful comparisons among estimates of comparable quality and ensuring that data are considered and treated appropriately according to their assessed quality level. All estimates, including those of lower quality, hold significant value for informing an overall understanding of population status and trends; however, it is essential that their quality classification is explicitly stated to enable accurate interpretation and responsible use of the data. Moreover, these quality levels can be applied in other population assessment contexts to ensure methodological coherence and transparency.

In order to translate the above quality assessment framework into a practical tool for evaluation, **Tables 22 and 23** summarize its main components. **Table 22** outlines the logical foundation for distinguishing between quality levels based on sampling characteristics, and **Table 23** expands on this by detailing the corresponding quality descriptions associated with different sampling strategies and data processing methods.

Table 22. Logical framework for differentiating quality levels of population size estimates, ranging from 1 (high quality) to 3 (low quality), based on the two key sampling conditions: the presence of individual identification and the type of sampling employed.

	Individual identification	**Unstructured sampling** (only a part of the population is opportunistically sampled, no extrapolation is possible)	**Structured sampling** (either the entire population is sampled, or only a part but with a structured approach to apply modelling for extrapolation)
Population size estimate	**NO**	LOW QUALITY - **Q3**	MEDIUM QUALITY - **Q2**
	YES	MEDIUM QUALITY - **Q2**	HIGH QUALITY - **Q1**

Table 23. Based on the logical framework presented in Table 22, this table provides a description of the quality levels Q1-Q2-Q3 associated with different sampling strategies and data categories used for estimating population size.

Quality level	**Description**
Q1 **HIGH Quality**	● Structured sampling based on individual identifications: (1) Population size estimates with CI based on a structured sampling, based on C1/C2 and individual identification, applicable both for small and large populations (2) Minimum population size estimated from structured counts (index) based on C1/C2, with individual identification. Applicable mainly for small populations
Q2 **MEDIUM Quality**	● Structured sampling not based on individual identifications, or unstructured sampling based on individual identification: (1) Structured sampling but not based on individual identifications, which do not allow the total avoidance of double counting (2) Minimum population size estimated from counts based on C1/C2 data and individual identification, but collected with unstructured sampling over the area of presence of the population (3) Use of science-based recent conversion factors
Q3 **LOW Quality**	● Unstructured sampling and no individual identification: Only a part of the population is directly sampled, no extrapolation is possible, no individual identification allows avoidance of double counting. It includes basic minimum counts.

5.2 Quality levels for the area of occurrence

In Kaczensky et al. (2024), a methodological framework was established to define the principles for producing large-scale species occurrence maps, incorporating a first evaluation of data quality based on the documentation and reliability of occurrence records within each grid cell. Building upon this approach, in the present chapter we further developed the concept of quality assessment by extending it from the grid cell to the overall population scale. Specifically, we introduce a classification of overall area-of-occurrence quality into three categories, **the quality levels (Q1, Q2, and Q3) for the area of occurrence** (Table 24), reflecting the general robustness and coherence of occurrence data across the LC populations' distributions. In this context, the quality levels of distribution outputs are directly derived from, and conceptually consistent with, the detailed criteria defined by Kaczensky et al. (2024), while providing an integrated framework for population-level interpretation and application.

5.2.1 Presence status of a 10 x 10 km grid cell as defined by Kaczensky et al. 2024

For the LCIE mapping of large carnivore distribution, the area of occurrence at a broad spatial scale is derived by intersecting GPS locations of large carnivore signs with the 10 × 10 km ETRS89-LAEA Europe grid (Kaczensky et al. 2024). Kaczensky et al. (2024) recommend distinguishing between these presence categories:

- **Permanent** = suggesting an established population which is reproducing but also including cells with continuous presence in the absence of documented reproduction.
- **Sporadic** = suggesting only occasional presences of dispersers or lone individuals.
- **Undefined** = presence confirmed but not known if it is permanent or sporadic.

"Permanent" is equivalent to the status of "Present regularly" (PRE) as used in Article 17 reporting to the Habitats Directive, while "Sporadic" corresponds to the status of "Occasional" (OCC) in the same system.

Kaczensky et al. (2024) recommend the use of the following data categories for each 10 x 10 km grid cell:

- **Confirmed presence:** based on C1 & C2 signs
- **Extrapolated presence:** cells which don't have LC signs but are intersected by buffered C1 & C2 signs or have a high probability of large carnivore presence based on documented modelling approaches.
- **Unconfirmed presence:** cells with only C3 signs (including interview data) and previously confirmed presence data (from the last reporting), where presence is still assumed to persist based on expert assessment.

If individual categorisation of cells is not possible, the following mixed categories are indicated for the larger occurrence area:

- **Confirmed and extrapolated presence:** mixed layer with buffered C1 & C2 signs and/or documented modelling approach, or when data was only available at the level of hunting grounds which are significantly larger in size than the underlying 10 x 10 km. This approach no longer shows how much was extrapolated and in what spatial arrangement making it less transparent how robust the extrapolation most likely is.

- **Confirmed and unconfirmed presence:** a mixed layer with C1-C3 signs; for these datasets it can be assumed that the majority are C1 and C2, but that documentation is not available; these data sources include undocumented direct observations and some damage inspection data. This approach no longer allows to differentiate between areas with high confidence of presence and those with low confidence, making it differentiate whether changes in range are confirmed or unconfirmed.

Depending on the spatial scale, large carnivore distribution maps can be a patchwork of the above categories (Kaczensky et al. 2024).

5.2.2 Quality levels Q1 - Q2 - Q3 for the area of occurrence of a LC population

The levels of quality of the evaluation for the area of occurrence have been defined in Table 24, based on the definitions provided in Chapter 2, the criteria described in Chapter 3, and the considerations outlined in Chapter 4. As outlined above, **the LCIE quality levels Q1 - Q2 - Q3 for the area of occurrence** represent an extension of the methodological framework defined in Kaczensky et al. (2024), providing a structured means to evaluate and communicate the overall reliability of area-of-occurrence estimates. By differentiating the quality of the distribution outputs, these levels allow for meaningful comparisons across populations and regions, while ensuring that each dataset is interpreted and used in accordance with its assessed level of confidence. All estimates, including those of lower quality, remain essential for describing population status and trends, as they contribute to a more comprehensive understanding of large carnivore distribution patterns. Nevertheless, explicit declaration of their quality classification is crucial to ensure transparency, facilitate appropriate data interpretation, and support consistent methodological standards. Moreover, the LCIE quality framework can be applied more broadly in other population assessment contexts to promote coherence and comparability across monitoring programmes and reporting schemes.

Table 24. Description of LCIE quality levels Q1-Q2-Q3, in relation to the corresponding sampling strategies and data elaboration methods applied for defining population occurrence.

Quality level	Description
Q1 **HIGH Quality**	● Confirmed presence: (1) Distribution is based primarily on validated data (C1 and C2 data) collected over the entire distribution range (2) Distribution based on validated data (C1 and C2 data) collected (ideally systematically) over most of the distribution range and either buffered (e.g., by the average home range of the species) or modelled to extrapolate to cells without presence data. Grid cells show whether they are based on validated data or extrapolation. The proportion of extrapolated to validated cells is less than 50% and the spatial arrangement shows no regional clustering.
Q2 **MEDIUM Quality**	● Mix of confirmed and unconfirmed presence: (1) Range-wide robust monitoring is documented, but the distribution is based on a mix of validated (C1 and C2 data) and limited unvalidated data (C3 data) without differentiating between the categories at the cell level. This approach should prove from the documentation that most cells are based on C1 and C2 data. (2) Distribution is based on robust sampling and monitoring over most of the distribution range and distinguishes between cells with validated data (C1 and C2 data) and extrapolation. However, extrapolated cells make up for more than half of the range or show regional clusters. (3) Only a minimum distribution is available based on validated data (C1 and C2 data) from part of the known or expected distribution range.
Q3 **LOW Quality**	● Unconfirmed presence: (1) Distribution is primarily based on a small study with validated data (C1 and C2) and extrapolation to a much wider range without validated data. (2) Distribution is based primarily on unvalidated data (C3 data, including interview data) and past presence.

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Appendix 1

Documents on “Monitoring standards for large carnivores in Europe”

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