



Preventing the extinction of the Dinaric-SE
Alpine lynx population through reinforcement
and long-term conservation



Action A6: Dispersal probability and potential connectivity between Dinaric-SE Alpine and neighbouring lynx populations and their consequent effect on their mutual viability: methodological perspective

Technical report

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1. Current state of Dinaric – SE Alpine population of Eurasian lynx

Following the extirpation of the Eurasian lynx (*Lynx lynx*) in the Dinaric region at the end of 19th century, it was reintroduced in Slovenia in 1973 by translocating 6 individuals from Slovakian Carpathian mountains (Čop and Frković 1998). The initial spread and population growth of the small and isolated population soon stagnated and began to decline, mainly due to the loss of genetic diversity and the increase in inbreeding (Sindičić et al. 2013; Skrbinšek et al. 2019).

To prevent further loss of genetic diversity and possible local extinction, 12 individuals were translocated from the Slovakian and Romanian Carpathians to the Dinaric population as part of the LIFE Lynx project (2017-2024) to reinforce the population (Fležar et al. 2023). The analysis of the population genetic status after the reinforcement actions showed a significant decrease in inbreeding to a degree where the population appears viable (Fležar et al. 2023), demonstrating the importance and success of the reinforcement.

However, the problems of low genetic diversity and inbreeding cannot be solved simply by reinforcement as long as the population remains small and isolated. Stepping stone populations are needed to improve the connections between the Dinaric and Alpine populations as well as other neighboring populations, which in the future would lead to a possible metapopulation structure that would allow populations to have sufficient gene flow to maintain the long-term viability of these connected subpopulations. As part of the LIFE Lynx project (Fležar et al. 2023), 6 individuals were therefore translocated to the SE Alpine region in Slovenia, which together with the individuals released in the SE Alpine region in Italy (as part of the UlyCA project) are to form the basis of a new stepping stone population.

Achieving a stable metapopulation of Eurasian lynx in Central Europe is a long and difficult process. Reinforcements alone can only increase the viability of the population in the short term (Pazhenkova and Skrbinšek 2021; Pazhenkova et al. unpublished), especially in isolated populations. In addition to translocating individuals to create stepping stone populations that could connect core populations in the future, careful spatial planning and management strategies are crucial. This report provides an overview of methods recently used in dispersal, habitat suitability and connectivity modelling studies, as well as population viability analyses, which can be used to determine and inform the management steps necessary for conservation of Eurasian lynx in Europe.

2. Methodological review

2.1 Dispersal

Dispersal, defined as the movement from the site of origin to the site of reproduction or new settlement (Howard 1960), is an important life-history trait that concerns not only the dispersing

individual but also the population and the species as a whole (Tesson and Edelaar, 2013), especially with regard to sufficient gene flow between (isolated) populations to prevent inbreeding and the resulting risk of local extinction (Woodroffe 2003). Dispersal allows individuals to colonize new areas and populations into a metapopulation to ensure their long-term survival. Understanding dispersal movements and their prerequisites is crucial for effective conservation management, such as protecting and enhancing landscape connectivity for dispersing individuals, especially in fragmented and human-dominated landscapes (Woodroffe 2003).

The studies that investigated the dispersal patterns of the Eurasian lynx focused on demographic characteristics (e.g. age, sex differences), dispersal distance and space use of dispersers (Schmidt 1998; Zimmermann et al. 2005; Zimmermann et al. 2007; Samelius et al. 2012; Herrero et al. 2020; Gajdárova et al. 2021; Krojerová-Prokešová et al. 2019; Herrero et al. 2021). The methodology was mostly based on acquired tracking data (from VHF and GPS telemetry) of dispersers, since the increase in accessible laboratory techniques also on genetic data and their analysis (e.g. Gajdárova et al. 2021; Krojerová-Prokešová et al. 2019; Herrero et al. 2021).

However, finding and tagging dispersers for research can be very difficult. The problem is partly solved by genetic analyses on dispersers, but detailed data on animal movements across the landscape are therefore lacking. Thanks to large databases of tracking data (collected through projects such as Eurolynx) and advances in methods to quantify movement patterns (e.g. Bunnefeld et al. 2011), researchers are now able to identify dispersers from already existing tracking data (as in Meyer et al. unpublished). This can be done, for example, using the net-square displacement (NSD) method, which uses the straight-line distance between the starting and each subsequent location for the movement of each individual – the shape and slope of the curve can explain the movement type of the observed individual, with the dispersal fitting a logistic regression model (Bunnefeld et al. 2011) and thus showing a positive NSD slope over time (Meyer et al. unpublished). Additionally, research by Meyer et al. (unpublished) on dispersal patterns of translocated and remnant lynx individuals, based on the assumption that translocation can trigger dispersal or exploratory behavior in adult animals, demonstrates the importance of tracking data from translocated animals (which are often fitted with GPS collars to monitor translocation success) for research on dispersal, as well as understanding the movements and habitat use of forcefully dispersed (i.e. translocated) animals. (i.e. translocated) individuals (see e.g. Topličanec et al. 2022 for the early post-release movement of translocated lynx in the Dinaric Mountains after their release).

Research on dispersers and their movement across the landscape is important for constructing connectivity and landscape suitability models, especially under the assumption that dispersers use a different, often less suitable habitat compared to the habitat they choose when resident (e.g. Hemmingmoore et al. 2020), although recent studies comparing habitat use of dispersers and residents found no significant differences (Meyer et al. unpublished). Dispersal data are also important for evaluating constructed connectivity models and potential corridors (Zeller et al. 2018; Abrahms et al. 2016; Huck et al. 2010), modeling potential influences on dispersal, especially in fragmented landscapes (Kramer-Schadt et al. 2004; Kramer-Schadt et al. 2005) or determining potential release sites (e.g. Topličanec et al. (2022) recommend that the release site should be at least 60 km from the boundaries of the targeted settlement area, based on data on post-release movements of translocated individuals).

Studies on the dispersers' habitat selection and use in the case of the Eurasian lynx are rare and have only been conducted on a small (local) scale (Herrero et al. 2020; Hemmingmoore et al. 2020). While the resource selection functions (RSF; Manly et al. 2002) used in the previously mentioned studies are based on a rather static selection model of habitat characteristics and have a problem in defining habitat availability in relation to movement constraints (Fieberg et al. 2021), the combination with the function of movement by random walk theory resulted in step selection functions – SSF (Fortin et al. 2005; Avgar et al. 2015), in which observed steps from telemetry data are compared with random steps of available but unused locations (based on the habitat and movement characteristics of the observed steps), thus generating predictions of space use patterns projected across the landscape (Fortin et al. 2005; Avgar et al. 2015). The problem with SSF lies in its assumption of independence of movement from habitat selection. Therefore, it is recommended to use the integrated step selection function (iSSF) instead, as it includes both habitat variables and movement characteristics and therefore allows for simultaneous effects of habitat selection on movement and vice versa (Avgar et al. 2015; Signer et al. 2019).

Meyer et al. (unpublished) used the aforementioned iSSF via the amt package in R (Signer et al. 2019) to assess Eurasian lynx habitat selection and later to model landscape suitability at a larger scale (utilization distribution) across Europe via the diffusion-taxis equation (Potts and Schlägel 2020), thus incorporating specific movement characteristics into a habitat selection model. As habitat selection is often individual-specific and therefore varies between individuals, Meyer et al. (unpublished) also used a mixed-effects conditional Poisson regression in a Bayesian framework via an integrated Laplace approximation (Rue et al. 2009; Muff et al. 2019), which allows for the specification of random effects (depending on the individual) but still using the shared information in the population, which is very useful for geographically broad research (Meyer et al. unpublished).

Consideration of dispersal data (mainly based on dispersal distance and habitat selection) and the ability of dispersers to successfully travel between existing populations is crucial in establishing and conservation of potential Eurasian lynx metapopulations in Europe. This includes the identification and protection of potential corridors and the establishment of stepping stones between isolated populations with respect to the known dispersal distance and habitat selection of the species (Woodroffe 2003), forced dispersal in the form of translocations or reinforcement, and the identification and prevention of key threats to dispersal success. The latter includes threats from conflicts between humans and large carnivores (e.g. poaching; Heurich et al. 2018), as well as the presence of human-created barriers to connectivity such as highways or urban areas (Kramer-Schadt et al. 2004; Skrbinšek and Krofel 2008; Magg et al. 2016; Topličanec et al. 2022; Kuralt et al. 2023) as well as considering biological factors such as aggression and competition between species in the form of territorial behavior, which can act as a barrier to dispersal (e.g. Aspi et al. 2009 for wolves).

2.2 Habitat suitability modeling

Habitat suitability models (also referred to as species distribution models, ecological niche models, niche-based models, potential habitat distribution models, resource selection function, etc. (Guisan et al., 2017)) are a widely used analytical tool that quantifies the relationship between the distribution of the species under study in a given geographic area and various environmental variables (Guisan and Zimmermann, 2000; Guisan et al., 2017). They are an important conservation and management tool used to analyze and predict suitable habitat and can be crucial in spatial planning to prioritize

specific habitat patches for conservation, potential future distribution, as a basis for connectivity analyzes and the assessment of possible connections to different populations - to determine possible sites for the establishment of stepping stone populations for better connectivity between core populations (e.g. Schadt et al, 2002a) or for potential reintroduction (e.g. Hetherington et al., 2008; Guilfoyle et al. 2023). Habitat suitability modeling (using high quality data, e.g. from telemetry) is particularly important for species such as large carnivores due to their cryptic nature and low densities over large areas where acquiring empirical data on their actual distribution (census) is difficult (Zimmermann and Breitenmoser, 2002).

There are many different methods and approaches for modeling habitat suitability. Depending on the type of data used to create a habitat suitability model, they are either theoretical – based on literature reviews or expert opinion, rule-based (e.g. Schadt et al. 2002b; Hetherington et al. 2008; Guilfoyle et al. 2023) - or based on empirical data on occurrence (presence/absence or presence only), in the case of (large) mammal research typically from telemetry research (e.g. Zimmermann and Breitenmoser 2002). In the past, statistical regression models have been used to model habitat suitability for the Eurasian lynx, in particular general linear models (GLMs), also referred to as logistic regression when using binomial presence/absence data (e.g. Zimmermann and Breitenmoser 2002; Zimmermann and Breitenmoser 2007; Schadt et al. 2002a; Kramer-Schadt et al. 2004; Signer 2010; Skrbinšek 2004; Cristescu et al. 2019; Potočnik et al. 2020; Hemmingmoore et al. 2020). The problem of collecting absence data gave rise to models that work with presence-only data – one of the most commonly used methods for assessing habitat suitability of Eurasian lynx is ecological niche factor analysis (ENFA) (Zimmermann 2004; Basille et al. 2009; Huck et al. 2010). Recently, machine learning algorithms have been increasingly used for habitat suitability modeling, e.g. MaxEnt (Phillips et al. 2006; Phillips and Dudík 2008; Becker 2013 and Oeser et al. 2023 for the Eurasian lynx), Random Forest (Breiman 2001; Ripari et al. 2022 and Oeser et al. 2023 for the Eurasian lynx) and Boosted Regression Tree (Friedman 2001), all three of which are among the most powerful (presence-only) models currently available (Elith et al. 2006; Oeser et al. 2023; Valavi et al. 2021).

The MaxEnt (or Maximum Entropy) algorithm via the ENMeval R package (Kass et al. 2021) was used to assess the potential distribution of Eurasian lynx and suitable habitat in the Dinaric and south-eastern Alpine region (Kuralt et al. 2023). MaxEnt is a machine learning algorithm that uses presence-only occurrence data and a set of environmental variables to estimate the probability of distribution based on the probability distribution of maximum entropy constrained by the given data (Phillips et al. 2006; Phillips and Dudík 2008).

MaxEnt is widely used due to its generative approach and consequent ability to work effectively with smaller data sets, its use of continuous and categorical values, its ease of use and use of presence-only data (Phillips et al. 2006), as well as its ability to fit complex responses (Elith et al. 2006). Overfitting caused by a limited amount of (training) data points can be avoided by using regularization mechanisms that penalize model complexity and strike a balance between fitting and model complexity (Phillips and Dudík 2008; Elith et al. 2011). The complexity of the model is also regulated by choosing a smaller number of different feature classes - dependencies on the environment described by simple functions (Phillips and Dudík 2008). When using small sample sizes, the use of linear features is recommended, while for larger sample sizes a combination of feature classes can be used (Phillips and Dudík 2008). In constructing the model of Kuralt et al. (2023), which used a fairly large amount of data points (3503), the model with an RM of 3.5 and a linear feature class was

selected among the models with a regularization multiplier (RM) of 2 to 5 in 0.5 steps and linear, quadratic and hinge features (Kuralt et al. 2023).

While overfitting, one of the main drawbacks of MaxEnt, can be avoided with the above-mentioned regularization, which is already an integral part of the model, some of the other drawbacks or threats of MaxEnt models can be avoided by extensions or simple manipulations of the background points. For example, bias in the occurrence data (e.g. due to biased data sampling due to better accessibility of certain areas, e.g. near roads, etc.) can be avoided by adding the occurrence sites to the background sample, which is then biased in the same way, so that the bias is factored out by the simple characteristic of choosing the distribution of maximum entropy relative to the background (Phillips and Dudík 2008). The use of telemetry data from relatively large amount of different individuals (45 in the case of the Kuralt et al. (2023) model) could also mean that the bias of the occurrence data is reduced, while the spatial autocorrelation of data points was avoided by spatial thinning (Kuralt et al. 2023).

Comparing the MaxEnt model (Kuralt et al. 2023) and extrapolated GLM (Potočník et al. 2020) in the study area of the LIFE Lynx project shows that the latter shows a more generalized prediction of habitat suitability and is more useful on a larger scale (Kuralt et al. 2023). This is particularly evident in the SE Alpine area, where the MaxEnt model (Kuralt et al. 2023) indicates strong fragmentation, while the GLM model classifies large parts of the area as more or less uniformly suitable (Kuralt et al. 2023). One explanation for this could lie in the high importance of the Tree Cover Density environmental variable in MaxEnt model, causing areas above the tree line to be less suitable (Kuralt et al. 2023).

A broader scale of habitat suitability models is increasingly necessary in order to assess potential future distribution sites that could represent important connections (in terms of stepping stone populations' areas) between existing Eurasian lynx populations. This is particularly important for the Dinaric – SE Alpine population, which has been reinforced in the LIFE Lynx project, as failing to connect with Alpine populations (and possibly the Balkan population) could mean a threat of repeated population declines due to inbreeding in the future (necessitating additional reinforcement, as shown in the viability simulations by Pazhenkova and Skrbinšek (2021) and Pazhenkova et al. (unpublished)). Extrapolation of existing models can generally be difficult due to environmental differences in broader areas (as in the case of the extrapolation of Signer's (2010) model, which was created based on data from the Jura mountains to the entire Alpine region, but without considering different environmental characteristics), especially when using a limited amount of data from a specific environment. However, Phillips et al. (2006) also caution against the MaxEnt exponential probability model, which can give large predictive values for environmental conditions outside the study range.

Using the largest available data sets when building large-scale habitat suitability models and testing different HSM approaches over large areas (Oeser et al. 2023) or even combining different modeling approaches into a single model (i.e. ensemble models) could be the solution for a sound ecologically informed basis for spatial planning and management at the metapopulation level.

2.3 Connectivity

As defined by Taylor et al. (1993), connectivity is the extent to which the landscape enables or hinders the movement of organisms between different areas with resources. Habitat loss and excessive fragmentation can reduce the size of habitats and populations, often splitting them into smaller segments that become more isolated and are prone to extinction due to loss of genetic variability (Frankham et al. 2010). An accurate assessment of landscape connectivity and potential barriers or corridors to animal movement is thus critical for the conservation and management of vulnerable populations.

There are various methods for modeling habitat connectivity. In the past, most studies on Eurasian lynx connectivity were based on a least cost path (LCP) analysis combining a cost grid (also called resistance or friction) and a cost distance function (e.g. Zimmermann 2004; Schadt et al. 2002b; Magg et al. 2016; Zimmermann and Breitenmoser 2007; Hemmingmoore et al. 2020; Johnson and Greenwood 2020). Kramer-Schadt et al. (2004) used a different approach based on a spatially explicit population simulation modeling approach, and introduced an individual-based, spatially explicit dispersal model to assess connectivity between habitat patches by the probability of dispersers reaching another suitable habitat patch. While this can result in a more accurate or realistic assessment of connectivity, individual-based models require an immense amount of data.

Recently, connectivity models (also referred to as permeability models, depending on the interpretation) based on circuit theory (McRae et al. 2008) have been increasingly used. Incorporating random walk theory (Newman 2005), they can provide a more accurate description of possible successful dispersal movements through a previously unknown landscape, in contrast to LCP analyses, which assume knowledge and overview of the landscape (McRae et al. 2008). The methods are relatively simple to apply and do not require much input data – the Circuitscape algorithm (Shah and McRae 2008; Anantharaman et al. 2020) requires a resistance grid (cost or friction; in some cases conductance is used as the opposite of resistance) and the focal nodes (habitat patches, areas or points) to be connected. Kuralt et al. (2023) also used the circuit theory-based methodology for modelling landscape connectivity (permeability) for the Eurasian lynx using the Omniscape algorithm (McRae et al. 2016) in the Julia programming language (Bezanson et al. 2017) – a newly developed algorithm that repeatedly runs Circuitscape the landscape using a moving window with a user-defined radius (set to correspond to known dispersal distances of the observed animals). Instead of focal nodes, grids of source strength are used, which define the amount of current – interpreted as the movement of dispersers or their density in an ecological sense (McRae et al. 2008) – that is injected into each pixel of the raster. These rasters are used to find source pixels (with values greater than 0), centering the moving window on a source pixel defined as a target and connecting all the surrounding source pixels to it in a process that is then repeated for an entire area (Kuralt et al. 2023; McRae et al. 2016; Landau et al. 2021). The result is a map of cumulative current flow that considers all possible paths (unlike LCP analyses), where current density is interpreted as the probability of animals moving through a given location through a random walk (McRae et al. 2008). By using an omnidirectional approach, it is not necessary to define core habitat patches, as is required in LCP analyses, for example.

Assessing landscape connectivity (permeability) is also important for landscape planning because it determines and maintains important corridors (or bottlenecks) for the dispersal and subsequent connectivity of adjacent habitat patches and populations at a broader scale, as discussed in Kuralt et

al. (2023) from the permeability of the landscape, where corridors in the form of narrow paths (bottlenecks for gene flow) are crossed by linear barriers such as the Ljubljana-Trieste highway, which prevent sufficient dispersal between the Dinaric and SE Alpine parts of the Eurasian lynx population in this area. Defining the spatial locations of corridors using connectivity modeling is not necessarily sufficient to assess their importance (e.g. Abrahms et al. 2016; Zeller et al. 2018). This can be done by combining different methods or validating the corridors with dispersal data (e.g. Abrahms et al. 2016; Zeller et al. 2018; Huck et al. 2010), telemetry data and/or genetic data – Kuralt et al. (2023) used the genetic data of Eurasian lynx in the Dinaric region to show the barrier effect of the Ljubljana-Trieste highway and the need for additional crossing structures to enhance movement through these corridors identified in the landscape permeability model. Corridors can also be assessed using the already mentioned spatially explicit individual-based dispersal models (e.g. Kramer-Schadt et al. 2005) and by combining connectivity analyses with (genetic) population viability analyses (see below).

2.4 Viability

Population viability analyses (PVA) represent a broad range of quantitative methods used to calculate the future of populations under various scenarios of change. This involves determining their demographic changes in the future, their survival rate under different scenarios, or identifying variables that are important for their population growth, which may prove crucial in determining future management steps or guidelines (genetic or spatial) for vulnerable populations, including reintroduced or reinforced ones (e.g. Pazhenkova and Skrbinšek 2021; Sanchez et al. Unpublished; Pazhenkova et al. Unpublished; Potočnik et al. 2009; Heurich et al. 2018; Kramer-Schadt et al. 2005) as well as for predicting viability for potential future reintroduction (Johnson and Greenwood 2020; Guilfoyle et al. 2023; Ovenden et al. 2019). Most recent advances in population viability analysis can be broadly categorized according to the type of data used into spatially explicit (e.g. spatially explicit individual-based models as in Kramer-Schadt et al. 2005 and Sanchez et al. unpublished) and genetic-demographic models (e.g. Pazhenkova and Skrbinšek 2021; Pazhenkova et al. unpublished).

Individual-based genetic-demographic models (as developed by Pazhenkova and Skrbinšek 2021 and Pazhenkova et al. unpublished) can be used to evaluate the success of past translocations (reintroductions or reinforcements) in terms of predicted long-term viability of populations based on reduction of inbreeding and enhanced genetic variability (Pazhenkova and Skrbinšek 2021; Pazhenkova et al. unpublished). Moreover, they can also be used to inform future genetic management strategies (e.g. additional reinforcements). For example, in the case of translocations to the Dinaric population of Eurasian lynx, Pazhenkova and Skrbinšek (2021) have shown using individual-based forward time simulations based on available genetic data that although the recent reinforcements done in the course of the LIFE Lynx project could increase the probability of population survival, the effect of lowering the inbreeding level lasts only for a short period (45 years until the increase in inbreeding levels reaching a critical level), so that repeated translocations are necessary. Pazhenkova and Skrbinšek (2021) estimate that 5-10 animals need to be translocated every 10-20 years to maintain a viable population if it continues to live in isolation. A significant drop of inbreeding levels in the Dinaric lynx population with inclusion of translocated animals and the short-term effect of the single reinforcement action was also shown also in the study by Pazhenkova et al. (unpublished), taking into account most recent genetic data.

Even though reinforcement actions are an important conservation tool for vulnerable, small and genetically less variable populations, their repeated implementation can be costly and energy consuming. Therefore, management measures aimed at establishing and maintaining a natural gene flow between populations are also important. Viability analyses that also incorporate a spatial dimension can be used as a tool to test the survival of populations under different scenarios of spatial connectivity. A spatially explicit individual-based model (SE-IBM) for the Eurasian lynx was first created by Kramer-Schadt et al. (2005) and has since served as the basis for other PVA analyses of Eurasian lynx populations (e.g. Sanchez et al. Unpublished; Heurich et al. 2018; Guilfoyle et al. 2023; Ovenden et al. 2019). In addition to estimating the probability of survival of populations under different scenarios, this model also provides a tool for determining potential reintroduction sites that can serve as stepping stones to connect small and isolated populations (Sanchez et al. Unpublished; Kramer-Schadt et al. 2005) and establish a metapopulation structure that reduces the risk of extinction of local populations (Hanski 1998; Sanchez et al. Unpublished). Additionally, it can also be used to determine the minimum number of translocated individuals at these sites (Kramer-Schadt et al. 2005; Sanchez et al. Unpublished).

The study by Sanchez et al. (unpublished) on Eurasian lynx populations in central Europe showed an improvement in the viability and connectivity of populations in the SE Alps, established and enforced by translocations under the LIFE Lynx and ULyCA projects, while the overall existing connectivity between the observed populations was very low overall and virtually non-existent at a larger Alpine scale. As highlighted in the study by Pazhenkova and Skrbinšek (2021), their analysis also calls for more translocations (with a focus on male individuals) in combination with ensuring better connectivity between populations via corridors and stepping stone populations. The model by Sanchez et al. (unpublished) also predicted the most reliable patches for the establishment of stepping stone populations and the minimum number of individuals that would need to be released in those patches to ensure their viability.

Although the models used in the above studies are an important tool for assessing viability, potential threats and possible mitigation measures, using an immense conglomerate of different knowledge and information about the species observed, some caution is needed in their preparation and interpretation. Parameters and their values can quickly become arbitrary due to the lack of available data (Potočnik et al. 2009) and may be subject to uncertainty (e.g. Wiegand et al. 2004). The latter can be reduced by retrospectively calibrating the model for a time prior to the management action and with known parameters (Wiegand et al. 2004; inverse modeling – Bennett 2002, also used in SE-IBM by Sanchez et al. unpublished) and by evaluating the model parameters used through simulations set in the time prior to the period in question, as in the genetic-demographic viability models of Pazhenkova and Skrbinšek (2021) and Pazhenkova et al. unpublished.

An important additional limitation of the SE-IBMs mentioned above is also the omission of potential effects of low genetic variability (e.g. inbreeding or effects of genetic drift) and environmental stochasticity (e.g. habitat loss over time) (Kramer-Schadt et al. 2005; Sanchez et al. unpublished) and has to be considered especially when dealing with highly inbred populations (such as the Dinaric – SE Alpine lynx population; Sindičić et al. 2013; Skrbinšek et al. 2019). Sanchez et al. (unpublished) partially addressed the problem of low genetic variability by including it in the added mortality value, although the population size in the output could still be misleading. As for predicting the effects of

genetic variability on population viability, genetic-demographic models (Pazhenkova and Skrbinišek 2021; Pazhenkova et al. unpublished) are more useful and accurate.

Apart from the mentioned drawbacks of SE-IBMs (which can be addressed with additional analyses with other models, e.g. Pazhenkova et al. unpublished), spatially explicit individual-based population viability models are indispensable in management actions related to Eurasian lynx populations and can also be used to simulate population dynamics at a large (i.e. continental) scale, as was underlined in Sanchez et al. (unpublished) study.

Combining SE-IBMs with genetic-demographic population models may prove to be a sound solution for determining future management actions for Eurasian lynx populations in order to establish a viable metapopulation, taking into account most of the data available. Both the studies by Sanchez et al. (unpublished) and Pazhenkova et al. (unpublished) emphasise the importance of addressing the factors leading to lynx mortality (such as poaching and traffic mortality) in future management plans, as mentioned in the chapter on dispersal.

3. Conclusion

Establishing a viable metapopulation structure for the Eurasian lynx in Central Europe is important for its long-term survival in the fragmented landscape. The first steps in this process are to review all potentially important existing methods and research areas in order to establish comprehensive spatial planning and management guidelines. Combining research efforts on dispersal patterns with additional new approaches that bridge the obstacles in the lack of dispersers' data, habitat suitability modelling with machine-learning algorithms, connectivity analyses that go beyond simple least cost paths and population viability analysis methods that can round up the above-mentioned data and test different scenarios to predict future population viability can result in a powerful tool necessary to identify all possible threats and develop appropriate solutions on a broad (i.e. continental) scale.

The Dinaric – SE Alpine population of the Eurasian lynx has been existing in isolation since its reintroduction 50 years ago. The reintroductions carried out as part of the LIFE Lynx project have significantly reduced the problem of low genetic variability of the lynx. However, to ensure the long-term viability of the population, connections with neighboring populations, such as the Alpine and Balkan populations, need to be strengthened. Translocations to SE Alps has proven to be an important first step in establishing stepping stone populations to build a bridge to greater connectivity between populations in the region. However, the introduction of further measures, such as the creation of effective stepping stones through strategic, coordinated management guidelines, may be crucial in providing an invaluable foundation for future actions needed to ensure the long-term survival and viability of the Dinaric – SE Alpine populations.

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