# Title:

Predicting spatio-temporal recolonization of reintroduced large herbivore populations and zones of potential human wildlife conflicts: red deer in Corsica

# Running title:

Recolonisation of Corsica by red deer

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# Abstract

1. Trophic rewilding via the (re)introduction of keystone species and ecosystem engineer, such as large herbivores, is increasingly being considered in Europe to support nature recovery and improve the resilience of ecosystems in the face of rapidly changing environmental conditions. Large herbivore presence can however generate issues for local communities, making it important to anticipate likely expansion patterns and identify possible zones of human-wildlife conflicts
2. We used the recently developed integrated Step Selection Function approach to build a predictive, spatially explicit, individual-based model to examine reintroduced Corsican red deer (Cervus elaphus) population expansion in Corsica. We developed the model based on known demographic processes and habitat selection of reintroduced red deer collected during a xx-year intensive field study.
3. During model validation, our model accurately described the recolonization process in the three reintroduction sites, correctly predicting xxx. We then projected dispersers over the entire island for 2050. We predicted xxx. We identified xx as likely spatial barriers slowing the red deer expansion.
4. Synthesis and applications. As the number of trophic rewilding projects increases in Europe, there is a real need to anticipate how the (re)introduced populations are likely to expand their distribution to prevent avoidable human-wildlife conflicts.

**Keywords**

Trophic rewilding, adaptive management, recolonization, spatially explicit individual-based model, red deer

# Introduction

In the face of rapidly changing environmental conditions, increasing level of environmental predictability and dramatic loss of biodiversity, nature recovery has become a priority, with the United Nations for example declaring this decade as the Decade on Ecosystem Restoration to spur global actions to prevent, halt and reverse the degradation of ecosystems. In this context, trophic rewilding, a form of environmental management approach that aims to diversify and complexify ecological interactions through the (re)introduction of keystone species and ecosystem engineers, has gained significant traction in Europe. Trophic rewilding discussions have primarily focused on the necessity and feasibility of large herbivore (re)introductions, given their significant impacts on ecosystems. Through their presence and activities (e.g., feeding, trampling, urination and defecation), large herbivores indeed directly and indirectly influence ecosystem structure and processes, ultimately leading to changes in ecosystem composition and functioning.

The translocation of large species is, however, not without risks and can lead to conflicts with human populations as large species interact with human activities such as agriculture, logging, hunting, and development. In the United States, for example, the reintroduction of elks, Cervus canadensis, was associated with increased costs to local communities as they saw their fences being more damaged, their crops being more depredated, and their livestock catching more disease (Mc Cann et al, 2021; Hegel et al, 2009). One way to prevent the likely increases in human-wildlife conflicts following species translocations is to identify areas likely to be colonized by introduced individuals, so that targeted actions can be strategically deployed early enough to mitigate the risks associated with population expansion. This step is generally done by mapping habitat suitability at landscape scales using approaches such as species distribution modelling, and rarely, individual based modelling (see e.g., Marucco and McIntire 2010).

Mechanistic individual-based models can make readily interpretable predictions of population expansion (e.g. xxx). However their reliability depends on how accurately the set of “movement rules” for individuals reflects the true movement of individual animals. Developing such rules heuristically or based on separately defined habitat suitability maps has provided previous insights (e.g. xxx). An alternative approach, based more directly on animal movement, is to develop such rules directly from empirical movement data collected by animal GPS collars.

In this study, we aim to use the recently developed integrated Step Selection Function approach by Signer and colleagues (2023) to build a predictive, spatially explicit, individual-based model to examine reintroduced Corsican red deer (*Cervus elaphus*) population expansion in Corsica. The case of the Corsican red deer is particularly interesting as island fauna, in general, has been known to undergo a much higher extinction rate than continental fauna (Wood et al. 2017), and yet research on the consequences of species translocations within islands remains poorly studied. Although previously abundant, the Corsican deer completely disappeared from this highly topographically heterogeneous island in 1970 due to illegal hunting and habitat fragmentation (vineyards). Following its extinction in the wild, a conservation program started in the eighties (Mandas et al, 2017), with deer being translocated from Sardinia and raised in natural reserves in Corsica for several years before being released into the wild in 1998. Translocated individuals were released in three very different locations: Moltifau, in the North of the island; San Petru di venacu in the Centre; and Zicavu in the South.

Red deer are highly adaptable, occupying a range of habitats including forests, grasslands, and alpine meadows (ref). Their habitat preference can vary with season and geographic location and is influenced by the presence of both food and cover (Borowski and Ukalska, 2008). In general, they are known to seek cover in forested areas, and forage in open clearings. In topographically variable environments, red deer tend to move to higher elevations during the summer for better forage while occupying lower elevations during winter to avoid deep snow and harsh conditions (Dagtekin et al 2023). In Sardinia, the Corsican red deer has been shown to select areas with natural forests and/or Mediterranean maquis close to water sources; their tolerance to humans and roads has been previously described as low (Puddu et al. 2009). Because of this, we expected landcover type, topography, season and anthropogenic activity to strongly influence their movements, and therefore the connectivity of the landscape. We first calibrated and validated our model using data on 19 individuals from the three translocation sites; we then used this model to predict the potential future red deer recolonization to guide red deer conservation and management decisions. This included identifying critical areas for red deer establishment, which will be fundamental for future sources in the deer recolonization process of Corsica as a whole.

# Material and methods

## Study location and animal data

Corsican red deer were released into the wild in Corsica in three localities between 1998 and 2018: Moltifau (North), San Petru di venacu (Centre) and Zicavu (South). Moltifau is broadly characterized by shallow and arid soils on gneiss and granite bedrocks; the landscape combines open and wooded countryside, with grasslands and maquis covering the gentler slopes and forests growing on the steeper slopes. San Petru di venacu, in the Massif du Rotondo, is part of the geological series known as the "Medium-grained granite of central Corsica"; the area is characterized by mountain valleys covered by oaks, beeches, bushes, and scrubs. Zicavu, in the Plateau du Coscione, is a mid-mountainous site characterized by its Euro-Siberian physiognomy and features beech, fir, larch, and alder trees. The hilly and rugged landscape hosts numerous springs, streams, and marshes (LIFE financial instrument of the European Union, 2014, 2015).

Nineteen individuals (13 females and 6 males) were GPS collared to gather information on the animals' survival, dispersion, and habitat use in the three previously described localities (North site: 2F and 2M; Centre: 5F and 4M; South: 6F). The devices collected data for 5 years, between December 15th of 2015 until December 31st of 2020. Animals’ locations were recorded twice a day – at 10 a.m. and 10 p.m. for a minimum of 24 months.

## Environmental data

Elevation and landcover values are extracted from the Shuttle Radar Topography Mission (Jarvis et al., 2008) and the 2018 CORINE Land Cover inventory (https://doi.org/10.2909/960998c1-1870-4e82-8051-6485205ebbac), respectively. Distance to roads was calculated from a Corsican Road map (need the ref for this data which we received from the Corsica team).

## Movement data analysis

We followed Potts et al. (2022) in developing an initial step selection function, using this function to parameterise an IBM, identifying discrepancies between the IBMs predictions and empirical patterns, and then refining the step selection function. We iterate through this process until we arrive at a satisfactory IBM. Briefly a step selection analysis defines each “step” in an animals movement (over 12 hours in this case) in terms of its characteristics (e.g. distance travelled or some features of the area where the step begins, ends or passes through). The step selection function is fit to identify the characteristics of true steps, for each animal, from among a number of randomly generated steps (15 in our case).

We initially developed a theoretically-derived saturated model of what factors influence deer movement , this provided the structure of our initial step selection function. This model included environmental variables of landcover, slope, and the distance to roads; the individual variables of sex ; the temporal variable of season; and step specific variables of the log length of a step and the cosine of the turning angle of a step relative to a previous step. The model included both main effects and theory-based interaction terms (see supplementary for full details). We then applied step-wise model selection with AIC to simplify the model, and once the best model was found this was used as the initial step selection function

The full details of model selection results and SSF to IBM iteration are provided in the supplementary material. Briefly, the best model from the first round of model selection generated implausibly large home ranges we thus added the variable log distance to release site to the best model and repeated the model selection process.

Data and reproducible code are available on Github (<https://github.com/J-Cos/DeerMovement_paper>).

## Individual Based Model

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# Results

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# Discussion

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# Authors contributions

Study conceived and planned by xxx. Field data collected by xx. Xxx contributed substantively to the manuscript ideas. xxx conducted all analyses. xxx led paper writing. All authors reviewed drafts and approved manuscript for submission.

# Acknowledgments

TBD

# Data accessibility

Data will be made available via a digital repository.

# References

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