From reintroduction to extinction risk: past, present and future of the newly established population of Ospreys in southern Iberia

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ABSTRACT

Biodiversity is declining due to the ongoing environmental global change, and raptors are among the most threatened animal groups. To counteract their decline, birds of prey have frequently been the focus of reintroduction programs worldwide. However, newly established populations must be continuously monitored to assess both short- and long-term success. In this work, we investigate the case of the Osprey (*Pandion haliaetus*) in Andalusia (southern Iberia), a cosmopolitan species formerly extirpated as a breeder from the western Mediterranean in the late 20th century. We used a long-term demographic and reproductive dataset (2003-2024) from the reintroduced population to investigate historical trends and long-term future population viability with VORTEX. The population increased from zero territorial pairs in 2003 to 19 in 2024. We detected three phases in the evolution of the population: establishment (2003-2008), expansion (2009-2015), and stabilization (2016-2024). During the study period, annual productivity averaged 1.09 ± 0.32 (mean ± S.D.), breeding success 79.7 ± 13.6 %, and clutch size 2.20 ± 0.75 eggs. Our baseline stochastic simulations —assuming current reproductive and demographic parameters ('do-nothing scenario')— suggests that Andalusian Ospreys face a serious risk of extinction within the next decades —47% within the next 40 years— driven by negative population growth. Population dynamics of the species were especially sensitive to small changes in age-specific mortality rates —particularly those of adults—, breeding performance, and first age of reproduction. These findings highlight the disproportional vulnerability of small populations of long-lived birds to small environmental changes. Specifically, they underscore the urgent need for post-reintroduction management to secure the self-sustainability of the Iberian population of Ospreys and its role as a demographic bridge within the western Mediterranean.

Keywords: *Pandion haliaetus*; population viability; biological conservation; raptor; threatened populations; VORTEX; population dynamics.

1. INTRODUCTION

Biodiversity is globally declining because of the current global change, which involves climatic change (IPCC, 2021), species invasions (Didham *et al.* 2007; Lockwood *et al.*, 2013), disruption of biogeochemical cycles (Elser *et al.*, 2007), habitat loss and fragmentation (Wiegand *et al.*, 2005), or erosion of genetic diversity (Pauls *et al.*, 2013). Collectively, these processes are accelerating extinction rates worldwide, contributing to what has been described as the Sixth Mass Extinction (Cowie *et al.*, 2022).

Despite this global alarming context, some species have colonized new areas due to natural range expansion, human-promoted invasions, or targeted reintroduction programs. Several declining emblematic species have been successfully reintroduced or reinforced at regional scales, e.g. the Bearded Vulture (*Gypaetus barbatus*) in the Alps (Arroyo *et al.*¸2021; Santos-Cottin *et al.*, 2025), the Iberian lynx (*Lynx pardinus)* in southwestern Iberia (Simón *et al.*, 2012), or several at-risk butterfly species in Great Britain and North America (Schultz *et al.*, 2008). Beyond strict invasive species, some taxa are naturally shifting their ranges in response to large-scale environmental and climatic changes (McGeoch and Latombe, 2016). Studying and managing these newly established populations—alongside efforts to protect declining species—can play a key role in biodiversity conservation under the current global change.

Small populations of long-lived species with inherently low reproductive rates should be continuously re-evaluated at both the short- and long-term to assess the success of their reintroduction programs or management measures. This includes identifying demographic bottlenecks and implementing adaptive management when needed. The definition of “success” in reintroduction efforts has been widely debated (Robert *et al.*, 2015). Proposed criteria include: breeding by the first wild-born generation, a three-year period of population growth with recruitment exceeding adult mortality, a self-sustaining population exceeding 500 individuals, or evidence of long-term viability (Seddon, 1999). More robust definitions incorporate species-specific life history traits and quantitative population viability analyses. For example, Morandini & Ferrer (2017) defined reintroduction success as a population with <0.001 extinction probability over twice the species’ maximum lifespan and a positive population trend. Regardless of the specific criteria, there is broad consensus that successful reintroductions require populations to be ecologically functional—integrated into trophic networks and able to persist without continued human support. Accordingly, post-reintroduction monitoring and stochastic modeling are essential to evaluate self-sustainability and guide long-term conservation planning.

Birds of prey (*Accipitriformes*, *Falconiformes*, *Strigiformes*, etc.) have been among the most frequent targets of reintroduction programs globally. Raptors are usually long-lived species with low reproductive rates, small populations and delayed sexual maturation, therefore highly affected by small removals of individuals from their populations (Tack *et al.*, 2017). In addition to those biological constraints, raptors have historically suffered high mortality due to direct human persecution. More recently, the causes of raptors mortality shifted from direct to indirect ones towards the end of the 20th century, particularly mortality caused by human infrastructures (De Pascalis *et al.*, 2020; Šálek *et al.*, 2023; Serratosa *et al.*, 2024). Although direct persecution has declined, the changing nature of threats calls for renewed conservation strategies. In this context, science-based reintroduction programs remain a powerful tool to halt and reverse raptor declines at regional scales.

In this work, we investigate the long-term demographic and reproductive performance and future trends based on stochastic simulations of the Osprey (*Pandion haliaetus*) from Southern Iberia. The Osprey is a cosmopolitan species which inhabits a vast array of habitats throughout several continents, but it was regionally eradicated as a breeder within western Mediterranean in the late 20th century. Thus, part of the genetic flows and dispersal movements among European and Mediterranean populations was lost. A Spanish reintroduction project was implemented in 2003 leading to the settlement of a small population (~20 pairs) in southwestern Iberia, partially restoring historical connectivity and range. However, the long-term viability of this population remains unassessed, and the species faces multiple mortality risks in the region (García-Macía *et al.*, 2025). Therefore, this study aims to: (i) assess long-term (2003-2024) temporal trends in demographic and breeding parameters of the newly established population of Ospreys in southern Iberia; (ii) simulate population viability under baseline conditions using stochastic models; (iii) identify key demographic drivers of population growth via sensitivity analyses; (iv) to simulate plausible future scenarios under alternative management strategies; (v) evaluate potential conservation actions considering their priority and cost-effectiveness.

2. METHODS AND MATERIALS

2.1. Study species

The Osprey (*Pandion haliaetus*) is a medium-sized piscivorous raptor with a cosmopolitan distribution, inhabiting every continent except Antarctica. The species is found in a variety of habitats near water bodies such as rivers, lakes, coastal regions, and estuaries, where fish are abundant (Cramp and Simmons, 1982).

Within Europe, Ospreys populations are divided into the abundant and healthy northern populations, and the small and fragmented Mediterranean populations (Dennis, 2017). Northern European populations are usually long-distance migrators, overwintering in different regions of Africa and Mediterranean basin (Cramp and Simmons 1982; Crawford & Long, 2017; Monti, 2021; Bergier *et al*. 2022; Torralvo *et al*. 2022; Mackrill, 2024; Martín *et al.* 2019; Benjumea *et al*. 2024; Galarza *et al.*, 2025; Meyburg and Holte, 2023 & 2025; Torralvo *et al.*, 2025). The breeding Mediterranean populations usually show a higher diversity of movement strategies (Monti *et al.*¸2018). Those populations are mainly located in Iberia (~20-25 pairs; Siverio *et al.*, 2018), Balearic Islands (~25 pairs; Siverio *et al.*, 2018), Corsica (~30 pairs; Bretagnolle *et al.*, 2008), and the Mediterranean seashores of Algeria (<10 pairs) and Morocco (<15 pairs) (Monti *et al.*, 2012).

The breeding population in Iberia is relatively small and fragmentated (Siverio *et al.*¸2018): most of the territorial pairs (~20) are located in southwestern Andalusia (i.e. our study population), and a few territorial pairs or individuals have settled in the Cantabrian coasts of northern Spain and inner continental waters of Portugal after reintroduction programmes (Palma & Safara, 2018; Galarza *et al.*, 2025). In Andalusia (southern Spain), our study place, the species was extinct as a breeder in 1982 because of human persecution and habitat alteration (Torralvo *et al.*, 2018). In Portugal, the population was estimated in around 20 breeding pairs at the early 20th century, but it was also declared extinct at the end of that century (Palma & Safara, 2018). Thus, the existing population of Ospreys in mainland Iberia is the result of reintroduction projects, which aimed to connect the populations from continental Europe and the Mediterranean basin and improve the genetic status of these latter populations (Dennis, 2017).

2.2. Study area

The study was placed in Andalusia (Spain, southwestern Iberia) (Figure 1). The population of Ospreys in Western Mediterranean is delineated in two regions (Huelva and Cádiz), forming two sub-populations highly connected by demographic and genetic flows. We performed the analyses and stochastic simulations considering both sub-populations as a unit, as they work as a metapopulation with constant dispersal flows, specially through dispersal females, but we also showed demographic and reproductive parameters of both sub-populations separated in order to detect potential different trends and consider the implementation of specific conservation actions.

2.3. Background of the reintroduction project (2003-2012)

The reintroduction project of the Osprey in southwestern Spain started in 2003 and ended in 2012. Within this period, 191 Ospreys were released in Cádiz (‘Barbate’ and ‘Guadalcacín’ reservoirs) and Huelva provinces (‘Marismas del Odiel’ natural park) by using *hacking* —young individuals transferred to captivity where they were fed *ad libitum* until they reach complete independence— or *fostering* techniques —placement of chicks in nests of pairs that have already been formed—. 19.1 ± 5.9 individuals per year were released on average. 13 birds were released by fostering and 173 by hacking techniques. 144 birds were transferred from donor populations from Germany, 27 from Scotland, and 20 from Finland (Table S1). All individuals were ringed (metal and PVC), and some individuals were tagged with VHF or Argos remote transmitters. 152 birds were sexed using molecular techniques (82 females, 70 males, and 30 individuals with undetermined sex).

2.4. Fieldwork

Fieldwork involves recurrent visits to the nests by specialised observers to collect the following data: territory occupancy (yes/no), pair status (territorial, breeding/incubating, successful), clutch size, and number of fledglings. All the nests were delimited and visited each year, considering the small size of the population. Each nest was monitored weekly between February and August. This period covers nest occupation, courtship, incubation, chick-rearing, and post-fledging stages. In addition, all potential areas for settlement of the species (e.g. coastal areas and wetlands) were surveyed, especially those close to the reintroduction sites, in order to detect the settlement of new pairs.

A territory was considered as such when a pair settled there during the breeding period. We distinguished between ‘breeding pairs’ —starting incubation—, ‘successful pairs’ —chick-rearing—, and ‘non-breeding territorial pairs’ —settling in the territories but without incubating—. The sum of breeding pairs and non-breeding pairs resulted in the total number of ‘territorial pairs’. Territories in which only one individual settled, or individuals without a clear territorial behaviour, were discarded from the calculation of territorial pairs but were considered to set the initial population size of simulations (see Section 3.6).

As stated above, all reintroduced individuals were ringed (metal rings and PVC). Almost all wild-born chicks were also ringed, except occasionally due to physical inaccessibility to nests, so individuals recruited for the populations were also identified. When it was possible, the members of the pairs were identified by the observation of the distance-reading rings (PVC). On some occasions, rings could not be read because of absence (wild individuals dispersed from other populations) or deterioration (rings of old individuals).

2.5. Trends in demographic parameters and reproductive parameters

In order to detect different phases on the demographic trends of the Andalusian Osprey population, we performed a piecewise linear regression using the *“segmented”* R package (Fasola *et al.*, 2018). Piecewise regressions aim to systematically determine abrupt changes by extracting breakpoints and to estimate different linear coefficients for each phase. In our specific case, we aimed to determine in which years the evolution of the Osprey population abruptly shifted. We established two starting breakpoints for the model based on previous data exploration (2011 and 2015). Once the significance of the model was tested, another set of piecewise linear regressions was run with the number of breeding pairs, the number of successful pairs, and the number of non-breeding pairs, in order to determine differences in the breakpoints among distinct groups within the population. If simple linear models —without segmentation— were more parsimonious than segmented ones —higher R^2 values—, we considered that those variables did not show any abrupt shift, and the evolution was better explained by a simple linear trend.

We also computed reproductive parameters at a population-year scale to describe temporal trends at the population level. We calculated annual metrics by pooling data from all territories each year: (1) ‘Productivity’: number of fledglings per territorial pair (2): ‘Breeding success’: proportion of pairs that reared fledglings over total pairs incubating —breeding pairs—; (3) ‘Sex ratio’: proportion of male fledglings; (4) ‘Average laying and hatching dates’: calendar week in which laying and hatching of eggs occurred; (5) ‘Clutch size’: number of eggs laying by successful pairs. As above, we performed piecewise linear regressions with each breeding variable (productivity, breeding success, sex ratio, hatching and laying dates, and clutch size) to detect different phases in the year-to-year evolution of the reproductive parameters.

2.6. Apparent survival estimations

We estimated age-specific probability of apparent survival (Φ) by using "*RMark 3.0.0*" (Laake, 2013), an R package for model building in MARK (White and Burnham, 1999). We estimated this variable based on 427 birds ringed from 2003 to 2024 (191 reintroduced and 236 wild-hatched). We included the information of annual re-sightings of marked individuals during the entire study period, based on binary information (0 = no observed; 1 = observed). We run Cormack-Jolly-Seber (CJS) models, which allows for open population estimation of apparent survival. To estimate survival as a function of age (years), we included a covariate for age in the design data. We assumed that all individuals entered the population as nestlings, since the birds were tagged before they were able to fly. The survival parameter was modelled as a function of age using a *logit* link function. Confidence intervals were obtained via delta method from the model's real parameter estimates.

2.7. Stochastic models for population growth

We used VORTEX software (Vortex, version 10; Lacy *et al.*, 2005) to simulate the future growth of our study population. In VORTEX, a Monte Carlo simulation of demographic events, population processes are modelled as discrete, sequential events, with probabilistic outcomes determined by a pseudo-random number generator. We used stochastic rather than deterministic models, i.e., we incorporated mean values for parameters, but also dispersion metrics based on scientific literature and/or estimations using our study population. Stochastic models would be more adequate for our study population considering its small population size and the affections by both internal (e.g. pair constitution, years paired, etc.) and external factors (e.g. habitat-related and climatic factors) (own data).

We simulated a baseline scenario to study long-term viability of the population under current demographic and reproductive parameters. This baseline scenario was also used to evaluate the sensitivity of the population growth to deviation in specific parameters. Some species-related assumptions were made for all scenarios based on scientific literature or internal estimations: lifespan of 20 years, long-term monogamy, one brood per year, a maximum of three fledglings per brood, a sex ratio of fledglings of 1:1, etc. (Table 1). We performed 1,000 replicates of each scenario at long-term scale (40 years; twice the lifespan of the species, Morandini & Ferrer, 2017). For each scenario, we extracted the mean population size (number of individuals at the end of simulations), intrinsic growth rate of the population (r ± SD), the probability of extinction (i.e. proportion of iterations run before a population became extinct), and the mean time of extinction (years). We considered that a population became extinct when only one individual remained alive.

Two approaches were initially considered to conduct stochastic simulations, given that the Andalusian population is divided into two sub-populations (Huelva and Cádiz), which are separated by ~200km, occur in different environments, and show small differences in reproductive parameters (see Figure S2), yet are connected by female dispersal. The first approach treated the entire population as a single unit, while the second modelled each sub-population separately using distinct reproductive rates and incorporating female dispersal between them. We tested both approaches under various female-dispersal rates but found no meaningful differences in simulation outputs that would affect overall conclusions. Given the small sample size, the geographic proximity of the two sub-populations, the evidence of frequent female exchanges, and the lack of significant differences in simulation results, we opted for the simpler and more parsimonious approach: simulating the population as a single unit with averaged population reproductive parameters.

2.7.1. Baseline scenarios

Baseline scenario aimed to study population growth under a ‘do-nothing’ perspective, i.e. if its demographic and reproductive parameters remain stable in the future and new management measures are not implemented. In other words, the objective of the baseline scenarios was to assess the long-term viability of the population under its current conditions and test the sensitivity of the population to changes in specific parameters.

To run the baseline scenario, we extracted the reproductive and demographic parameters from the last phase of our population (2016-2024; see section 3.1.), when population growth was close to zero, i.e., the number of territorial pairs remained stable during almost a decade. Some parameters (i.e. clutch size) did not shift during the entire study period, so we extracted mean values from the period 2009-2024. Sex ratio slightly shifted during the study period (see Section 3.2.), but we also extracted the mean value for the entire study period (50%) considering that this variable is highly susceptible to change under different pair density (Morandini *et al.* 2019).

We estimated apparent survival probabilities from our population (see Section 2.6) using capture-recapture models. However, estimated survival rates had large confidence intervals (Figure 5, Table S4) and may underestimate survival at certain age-classes due to low detectability of non-territorial birds and the difficulty of reading old rings. To avoid underestimating survival, we used mortality rates from comparable well-studied populations, especially the Mediterranean ones. The selected values also aimed to be within the confidence intervals of our capture-recapture models, so they likely reflected plausible values of the local population. Thus, all baseline scenarios assumed that first-year juvenile mortality (1 calendar year -cy-) was 70 ± 15%, that of non-breeding sub-adults (2-3 cy) was 30 ± 10%, and that of adults (≥4 cy) was 10 ± 5% (Spitzer & Poole, 1980; Eriksson & Wallin, 1994; Klaassen *et al.*, 2014; Monti *et al.*, 2014; Väli *et al.*, 2021; Galarza *et al.*, 2025). We incorporated high standard deviation in mortality rates considering the uncertainty of our estimations, the ranges observed in literature, and the year-to-year environmental variability.

We only had specific data for territorial pairs, but lacked precise information on the sub-adult, non-territorial population—young dispersing individuals that do not yet display territorial behaviour but may be recruited into the breeding population in subsequent years. These individuals typically exhibit higher mobility and rarely settle in a specific site, making their identification and census through field methods particularly challenging. However, the stochastic simulations required an age-specific estimate of the initial population size. To address this, we assumed that during the previous two years (2022–2023), the population recruited individuals according to the age-specific annual survival rates defined in the baseline scenario: 30% survival during the first year, and 70% during the second and third years. Accordingly, we estimated that the number of individuals born in 2023 and surviving to 2024 was 22 × 0.3 = 7, and the number of birds born in 2022 and surviving to 2024 was 26 × 0.3 × 0.7 = 5. We also added the 23 fledglings (14 females and 9 males) born in 2024—the starting year of our simulations. We also included two adult floaters—non-territorial individuals—recorded in the study area in 2024. We assumed that age distribution of territorial adults beyond this threshold was balanced, considering the constant release of individuals throughout the reintroduction program and aiming for a parsimonious model structure. The maximum age considered was 16 years, based on demographic data from our population. In summary, simulations were initialized with a total of 75 individuals: 38 territorial adults (2024 records), 2 adult floaters (2024 records), and 35 sub-adults (23 first-calendar-year birds born in 2024, 7 second-cy born in 2023, and 5 third-cy born in 2022) (see Table S2). An equal sex ratio was assumed, except for fledglings born in 2024, whose sex was specifically known (Table S2).

Regarding emigration and immigration rates, long-distance dispersal and population exchange in Ospreys are well documented—particularly among females (Monti et al., 2018)—and have also been observed in our study population. For instance, some females from Morocco or the Balearic Islands have been recorded breeding in the Andalusian population, while others born in our study population have dispersed as far as France and Morocco. Thus, some events of both emigration and immigration are expected to occur in our population. However, data were insufficient to estimate precise exchange rates. In any case, our study population remains relatively isolated from the larger European populations (see Section 2.1), and is more likely to exchange individuals with smaller populations from Mediterranean islands, Morocco, or southern France. Therefore, overall immigration and emigration rates are expected to be low in absolute terms based on raw data. For the baseline scenario, we assumed a balanced exchange, with immigration and emigration rates cancelling each other out.

For the baseline scenario, we set the carrying capacity (*K*) at N ± 10 individuals, assuming current density-dependence growth under current environmental conditions and population spatial distribution (Bretagnolle *et al.*, 2008; García-Macía *et al.*, *In preparation*).

We also assumed that the first age of reproduction was 4 cy (calendar year), in line with the records of the stabilization phase of our population. However, population growth may be highly affected by the first age of reproduction, and raptors can breed earlier when population size is low (Morandini & Ferrer, 2017).

We also established a given frequency of catastrophic events as a proxy to simulate the negative effect of heat waves, storms and other environmental extreme events detected in the study area. We established 5% of annual probability of catastrophes with a negative effect of 5% over survival and 5% on reproduction.

To validate our baseline scenario, we simulated the historical evolution of the population from 2003 to 2024 (22 years) by running a deterministic model in VORTEX. This validation scenario used the same demographic parameters (mortality rates, productivity, carrying capacity, etc.) as the baseline scenario, but incorporated a reintroduction of 19 individuals per year (10 males and 9 females, matching the historical sex ratio) from 2003 to 2012 (Table S1). We then compared the model's output to empirical data by applying locally weighted regressions (LOESS) to both the number of observed territorial pairs (2003–2024) and the number of individuals projected by the validation model. To ensure comparability, both time series were normalized, as VORTEX outputs total individuals across age classes, whereas the observed data represented only territorial pairs. To quantify the similarity in temporal dynamics, we computed the annual root squared error (RSE) between LOESS-smoothed curves to identify the periods of greatest divergence. The overlapping smoothed trends allowed us to assess whether the model adequately captured the timing and trajectory of population growth leading to the observed present-day situation. Regardless of the specific approach, recommended practices in population modeling include validations based on the alignment of long-term trends and structural patterns rather than exact numerical fits (Lindenmayer *et al*., 2000; Wootton & Bell, 2014; Hale *et al*., 2023; Armstrong *et al*., 2021).

2.7.2. Sensitivity analysis

We conducted a sensitivity analysis based on the baseline scenario, modifying specific parameters to evaluate how changes in these variables influenced population growth. This analysis was carried out for three main reasons: (1) to address uncertainties surrounding certain demographic parameters (e.g., mortality rates, immigration rates); (2) to identify which parameters have the greatest influence on the population dynamics of our study population; and (3) to provide management-oriented insights, such as identifying threshold values (e.g., mortality or breeding success levels) that could lead to population decline and therefore require conservation action.

We first conducted a formal univariate sensitivity analysis using a one-at-a-time (OAT) approach in VORTEX. We selected eight biologically relevant parameters: adult mortality, immature mortality, juvenile mortality, breeding performance (=proportion of females in breeding pool, breeding success, and clutch size,), age of first reproduction, sex ratio, female immigration rate, and carrying capacity (K). Each parameter was varied across a biologically plausible range while holding all other parameters constant (Table S3), and 1,000 simulations of 40 years were run per value. We extracted two outputs: intrinsic population growth rate (r), and probability of extinction (PE). In order to allow comparison of the contributions made by different parameters to population growth (r), we performed simple linear regressions by using *lme4* R package (Bates *et al*., 2015). We established parameter values as explanatory variables, and population growth (r) as response variable.

We then performed a multivariate sensitivity analysis with juvenile mortality, adult mortality, breeding performance, and carrying capacity (K) based on best fitting variables within univariate analysis, biological relevance, susceptibility to being modified by management actions, and expected impact on long-term viability in small populations. Two complementary sensitivity analyses were implemented in VORTEX.

The first focused on the interaction between juvenile mortality (set at 50%, 70%, and 90%), breeding performance (−20%, −10%, 0%, +10%, +20% relative to baseline productivity), and K (75 and 150). The second examined the effects of adult mortality (5%, 10%, 15%) in combination with breeding performance and K, while holding juvenile mortality constant. This factorial approach aimed to disentangle the relative contribution of early-life and adult survival to population growth under varying reproductive and environmental scenarios. Results were summarized with response curves of population growth (r). Threshold values beyond which r became negative were identified and used to propose adaptive management indicators.

2.7.3. Management scenarios

Additionally, we use the parameters of baseline scenario increasing K up to 150 and modifying some specific variables to propose specific alternative management scenarios (Table 2):

- **M1:** Reduction of juvenile mortality (i.e. 60 ± 10%) and immature mortality (i.e. 20 ± 10%).
- **M2:** Reduction of adult mortality (i.e. 5 ± 3%).
- **M3:** Reduction of juvenile, immature and adult mortality (M1+M2).
- **R1.** Low-intensity reintroduction project within the current population. 10 fledglings per year (5 females, 5 males) incorporated into the population for 20 years.
- **R2.** Low-intensity reintroduction project within an additional site (simulated by an additional population in VORTEX). 10 fledglings per year (5 females, 5 males) incorporated into this new population for 20 years. We also increased carrying capacity (K = 100 for each sub-population), and assumed a rate of 40% of dispersal between sub-populations.
- **R3.** High-intensity reintroduction project within an additional site (simulated by an additional population in VORTEX). Same as above, but incorporating 20 fledglings per year (10 females, 10 males).

- **P1.** Conservative increase of 10% in all breeding parameters: 85% of breeding pairs (incubating), 82% of breeding success (with fledglings), and mean clutch size of 2.3 eggs.
- **P2.** Large increase of 20% in all breeding parameters: 93% of breeding pairs (incubating), 90% of breeding success (with fledglings), and mean clutch size of 2.5 eggs.
- **P1 + M3.** Combination of *P1* and M3 scenarios.
- **R3 + P1 + M3.** Combination R3, P1 and M3 scenarios.

3. RESULTS

3.1. Trends in demographic parameters

The Andalusian Osprey population increased from zero territorial pairs in 2003 to 19 in 2024. We detected three phases in the evolution of the population: establishment (2003-2008), expansion (2009-2015), and stabilization (2016-2024) (Figure 2). The establishment phase (2003-2008) was characterized by the recruitment of the first territorial individuals after the reintroduction started in 2003, showing a slight increase of 0.51 pairs per year. The expansion phase (2009-2015) was characterized by the rapid recruitment of breeding individuals, displaying a very strong increase of 2.3 territorial pairs by year. In 2009, at the beginning of the expansion phase, the first wild Ospreys were hatched because of the reproduction between two reintroduced individuals. Finally, the stabilization phase (2016-2024) involved an abrupt stop of population growth, showing stabilization (Table S4, Figure 2). The adjusted R^2 (0.98) of the pairwise regression indicates good fitting, suggesting that the three estimated phases have biological relevance.

The number of breeding pairs —i.e., those which incubated— and successful pairs —i.e. those with fledglings— also showed the previous overall pattern; however, breakpoints approximately in 2010-2011 and 2015-2016 were estimated with those data (Table S4), i.e., the expansion of breeding and successful pairs started a few years later than that of territorial pairs. To homogenise data visualization (e.g. Figure 2) and discuss the results, we selected 2009 and 2015 as overall breakpoints of the population growth, i.e. those calculated with territorial pairs. On the other hand, the number of territorial non-breeding pairs did not show any trend or abrupt shift during the study period (Table S4).

The estimated survival probability varied with age: it was minimum for 1-year birds (0.16 ± 0.14; CI = 0.024-0.587), maximum for adults (> 5 years; mean values from 0.477 to 0.836), and intermediate for immatures (2-4 years, mean values from 0.37 to 0.57) (Table S5, Figure 5).

The size and growth trajectories of the two Andalusian sub-populations (Cádiz and Huelva) were broadly similar, despite interannual differences in the number of breeding pairs and reproductive parameters throughout the study period (Figures S1 and S2). While the Huelva sub-population exhibited slightly higher breeding success and productivity in some years, the overall demographic trends of both sub-populations were comparable.

3.2. Trends in reproductive parameters

Productivity (number of fledglings/territorial pairs) averaged 1.09 ± 0.32 (mean ± SD; range = 0.57 – 1.90) between 2009 and 2024, without any strong positive or negative trend or abrupt shift during the study period (Table S4, Figure 3). Breeding success (proportion of successful pairs/breeding pairs) averaged 79.7 ± 13.6 % (range = 60-100) during the study period, with a slight decrease between 2009 and 2024 but any abrupt shift (Table S4, Figure 3).

Incubation dates and clutch size were estimated considering 129 incubation events of breeding pairs from 2009 to 2024, excluding birds reintroduced by fostering. Ospreys started incubation (egg laying) during the 14.5 ± 2.0 calendar week, i.e. early April. On the other hand, eggs hatched during the 19.5 ± 1.9 calendar week, i.e. early May. The clutch size averaged 2.20 ± 0.75 (range 1 – 3). Pairs laid one egg in 20.2% of the incubation events (n = 26), two eggs in 39.5% (n = 51), and three eggs in 40.3% (n = 52). We did not detect any significant trend or abrupt shift on laying dates, hatching dates or clutch size throughout the study period (Figure 4, Table S4).

Finally, we estimated the sex ratio of fledglings (proportion of males over the total wild-hatched fledglings). The annual sex ratio averaged 50.5 ± 18.8 (range = 16 – 80) over the study period, but we detected a shift on sex ratio throughout the study period approximately between 2014 and 2016 (2014.7 ± 2.7) (Table S3, Figure 4). Sex ratios averaged 59 ± 20 from 2009 to 2015, and 43.9 ± 15.0 from 2016 and 2024, i.e., more males were born during establishment (I) and expansion (II) phases, while more females were born during the stabilization phase (III).

3.3. Population viability analysis: baseline scenario

Our baseline scenario (Tables 1 and 2) showed a mean intrinsic growth rate (r) of -0.039, an extinction probability of 47% within 40 years, and a mean population size of 16.71 ± 14.70 individuals at the end of the simulation. Therefore, the baseline scenario indicates that the population will probably decrease in the long term under the current breeding and demographic parameters (Table 3; Figure 6; Figure 8).

In order to validate the inputs of the baseline model, we examined observed and simulated population trajectories between 2003 and 2024 and calculated year-specific squared errors between them. As expected, the largest discrepancies occurred in the early stages of the reintroduction, when no territorial pairs were yet established, but the model simulated the presence of all age individuals. In contrast, the model showed lower discrepancies during the later stages, particularly after 2015, when both simulated and observed trajectories started to be stable (Table S6, Figure S3). This may indicate that the demographic and reproductive inputs selected for our baseline scenarios reflect the overall situation of the population at the onset of the simulations, so they can serve to test the sensitivity of the population under future management scenarios.

3.4. Sensitivity analyses

The univariate sensitivity analysis (Table S7, Figure 6) indicated that population growth was especially affected by changes in juvenile mortality (LM slope = -0.004), immature mortality (-0.003), adult mortality (-0.009), age of first reproduction (-0.055), immigration rates (0.024) and breeding performance (0.003). In contrast, sex ratio and carrying capacity (K) had negligible effects on population growth (slope ≈ 0.000).

Specifically, assuming all other baseline parameters remained constant, population growth became negative when annual juvenile mortality exceeded 53.8%, immature mortality exceeded 23%, adult mortality surpassed 6.3%, breeding performance declined by more than 8.6%, the age at first reproduction was greater than four years, or when the immigration rate fell below two females per year (Figure 6).

However, multiple parameters are likely to vary simultaneously. A multivariate sensitivity analysis incorporating variation in four key parameters—juvenile mortality, adult mortality, breeding performance, and carrying capacity—indicated that positive population growth ($r > 0$) would only be achievable under two plausible scenarios: (1) moderate mortality rates combined with a substantial increase in breeding performance, or (2) low mortality rates with no major decline in breeding performance (Figure 7).

3.5. Population viability analysis: management scenarios

Apart from formal viability analysis, we simulated a series of comparative management scenarios by modifying specific reproductive and demographic parameters to reflect plausible conservation interventions for the species (Table 2). All scenarios assumed a carrying capacity of $K = 150 \pm 10$, representing improved regional habitat suitability and enhanced dispersal opportunities.

First, we assessed how reductions in age-specific mortality rates would influence stochastic population growth rate (r) and extinction probability. A 10% reduction in juvenile and immature mortality (scenario *M1*) or a 5% reduction in adult mortality (*M2*) resulted in positive mean growth rates of $r = 0.033$ and $r = 0.014$, respectively. The combined reduction of both sub-adult and adult mortality (*M3*) yielded a higher growth rate (*r* = 0.072) and an extinction probability close to zero (Table 3, Figure 8).

A moderate 10% increase in breeding performance (scenario *P1*) did not result in positive population growth (*r* = –0.005), but it reduced extinction probability by up to 20%, primarily by slowing the rate of population decline (Table 3, Figure 8). In contrast, a more substantial 20% increase (*P2*) led to a positive growth rate (*r* = 0.029).

Reintroduction scenarios (*R1–R3*), which involved the supplementation of individuals without changes to reproductive or mortality parameters, supported population stability or growth during the release period (Table 3, Figure 8), and markedly reduced extinction risk over a 40-year horizon to near zero. However, once supplementation ceased, the intrinsic growth rate turned negative again, resulting in a sharp population decline (Table 3, Figure 8).

The most optimistic outcomes were achieved under combined management scenarios. Specifically, simulations that integrated increased breeding performance, reduced mortality rates, and active supplementation —alongside enhancements in carrying capacity— projected long-term population growth, with high positive growth rates and a negligible risk of extinction (Table 3, Figure 8).

4. DISCUSSION

In this study, we conducted a comprehensive analysis of the population dynamics of the newly established Osprey population in southern Iberia, a flagship species recently reintroduced yet demographically important within the Mediterranean basin. We examined long-term reproductive and demographic trends from 2003 to 2025, encompassing the reintroduction phase (2003–2012), and performed stochastic simulations in order to assess the viability of the population under future scenarios and the sensitivity of the population to alterations of breeding performance, age-specific mortality rates, demographic factors, and new human-induced inputs into the population.

Despite its small size, the Andalusian population is one of the most important breeding populations of the species within the Mediterranean basin, aimed to be a genetic and population link between other threatened Mediterranean populations (Dennis, 2017), so its long-term conservation is essential for the preservation of those. Therefore, the conservation of the Andalusian population, which represents a large proportion of the western Mediterranean population, is a major conservation issue. Furthermore, this study may serve to understand how small changes in demographic and reproductive parameters could trigger disproportionate effects on the viability of small populations of long-lived birds with low reproductive rates. This has particular relevance for the management of reintroduced and newly established populations, where early detection of demographic limitations and targeted interventions may determine long-term success.

4.1. Historical trends on demographic and reproductive parameters

We identified three demographic phases with biological relevance in the population growth of Andalusian Ospreys: establishment (2003-2008), expansion (2009-2015), and stabilization (2016-2024). These population dynamics and overall phases have already been found in increasing populations of Ospreys (Bretagnolle *et al.*, 2008) and other reintroduced birds (Evans *et al.*¸2009; Schaub *et al.*¸2009). The establishment phase — when individuals are recruited as territorial pairs at low annual rates— was expected given that first-year reintroduced birds usually require a few years to settle and acquire sexual maturity (Ewen *et al.*, 2012). Once there was a substantial breeding pool, many of the individuals were recruited as breeders and occupied the territories, leading to the expansion phase. Until then, the reintroduction project could be considered successful under some definitions since demographic growth was nearly exponential. However, the population growth stopped once reintroductions had ceased, with territories already occupied and intraspecific competition and density-dependent growth likely to occur (Bretagnolle *et al.*, 2008; own data). From that point onwards, a new context opened up in which the population needs to be demographically self-sustaining in the long term. The stabilisation of population levels may be caused by reaching the carrying capacity, but it may also be an early indicator that the population is not self-sustaining under its current demographic and reproductive conditions and new mitigation measures need to be implemented. Thus, stochastic simulations may help to understand plausible future scenarios and assess which conservation efforts are required to guarantee the long-term viability of the population (Andersen *et al.*, 2015; Morandini *et al.*, 2019).

While productivity (fledglings/territorial pairs) remains stable after 2011, breeding success (number of successful pairs/breeding pairs) decreased throughout the study period, with up to half of the territorial pairs with no fledglings production during the stabilization phase. This may indicate large variability between pairs and territories, with most of the fledglings reared by a small proportion of pairs settled in optimal territories, and many pairs with mating or incubation failure due to suboptimal conditions. The deeply study of intrinsic (pair constitution, breeders age, years paired, etc.) and extrinsic factors (climatic patterns, habitat, human disturbances…) affecting productivity and breeding success at territory level may help to understand why the Andalusian population of Ospreys stopped its growth and which conservation management actions should be implemented to facilitate the incorporation of more pairs to the breeding pool and increase breeding success.

4.2. Future trends and management recommendations

We performed sensitivity analyses and several specific stochastic simulations under different management scenarios in order to investigate the potential growth of the population. Our baseline projections indicated that, under a 'do-nothing' scenario — assuming no improvement in reproductive success and age-specific mortality rates within the common ranges of the Mediterranean populations— the population is unlikely to remain viable in the long term. In fact, small reductions in breeding performance or small increases of age-specific mortality would be critical for growth rates considering the delicate demographic balance of the current population. However, the implementation of targeted conservation actions aimed to reduce mortality and enhance reproductive performance could promote population stability or even growth, particularly if such measures are accompanied by efforts to expand the species' range into additional suitable habitats. Our models suggested that a conservation program which integrate measures to improve breeding performance and decrease mortality rates would be the best approach to guarantee the self-sustainability —or potential expansion— of the population.

Breeding performance may be increased by a wide array of methods. Reduction of pairs density (intra-specific competition) by promoting the expansion of the population to nearby water bodies (e.g. unoccupied reservoirs) may help to improve the productivity at the nest-level (Bretagnolle *et al.*, 2008). Artificial nesting sites, when placed in appropriate areas, may contribute to the colonization of new habitats —as happened in our study population— and increase productivity (van Daele and van Daele, 1982; Forys *et al.*, 2016; Canal *et al.*¸2017). General habitat improvements related to food abundance and trophic quality, especially in the highly variable reservoirs of Cádiz, may also help to increase reproductive performance (Paviour, 2013). Artificial supplementary feeding during years of poor breeding conditions has been suggested to improve breeding performance (Academia & Watts, 2023); however, other works indicates that supplementary feeding does not influence nesting success (Sivonen, 2014), so it may be highly dependent on the environmental conditions at pair level. Regardless of the approach used to increase breeding performance, productivity of pairs could be highly influenced not only by current environmental conditions but also by harshness during early stages of development due to extreme events such as droughts or other poorly environmental conditions (Sergio *et al.*, 2022), mediated by lower prey availability and parental provisioning rates. The study area is increasingly suffering heat waves and droughts during the last decade, so actions to guarantee good body condition of nestlings may not decrease mortality rates but also increase long-term breeding performance when those individuals are recruited for the breeding population. In order to directly benefit breeders, along with both general improvements in habitat suitability and specific actions during environmentally poor years, human disturbances to breeding pairs should be decreased during the reproductive period, specially during the most sensitive phases (hatching, first stage of fledgling growth). Human disturbances have been widely observed in our study population (e.g. small boats, seaplanes, tourism, etc.), which may affect breeding performance (Monti *et al.*, 2018), so more restrictive exclusion protocols around nests might avoid excessive disturbances. On the other hand, white storks (*Ciconia ciconia*) have occupied several Osprey nests in Cádiz reservoirs prior to the breeding onset (inter-specific competition), thus reducing territory occupation and breeding pool, so future management measures should prevent storks from competing for nesting sites.

Despite the obvious importance of breeding performance, our stochastic simulations were more sensitive to reduction in age-related mortality —especially adult mortality — than to variations in reproductive parameters. This could indicate that maintaining sustainable mortality rates, in balance with the reproductive output of the population, may be more cost-effective. Specifically, efforts to reduce mortality in the study population should take into account age-specific mortality and differences in mortality rates among periods of the annual cycle in migratory raptors, which usually face population bottlenecks due to the juvenile mortality occurred during the first southward migration and the wintering period, but cumulative long-term mortality of both adults and sub-adults during the breeding period may be also important to understand population growth (Sergio *et al.*, 2018). Regardless of the age-specific rates and mortality across migratory flyways and wintering quarters—which may be more difficult to manage—, the Osprey face several mortality risks within their breeding quarters in southern Iberia (García-Macía *et al.*, 2025), mainly related to indirect impacts of human activities such as fish farms, powerlines, and wind farms. Although García-Macía *et al.* (2025) could not detail the origin of the dead individuals (breeders or wintering), the mortality of Ospreys in the region have increased in recent decades up to more than ten individuals death by year, with several deaths during the non-breeding periods suggesting the affection to the breeding population. As suggested by our simulations, small removals of individuals from the population may significantly alter demographic dynamics, so far-reaching mitigation measures should be implemented. Wind farms and power lines are under ongoing regional protocols to reduce mortality (Ferrer *et al.*, 2022a, b), but the continuing detection of annual deaths indicates that these both causes should still be reduced in the future. On the other hand, entanglement in fish farms —the main and fastest-growing cause of mortality in the region according to García-Macía *et al.* (2025) — have not received standardized protocols to reduce mortality until now. Thus, preventive and mitigation measures are urgently needed within these facilities.

The supplementation of more reintroduced birds, according to our simulations, may increase population growth while individuals are being released, but may be insufficient in the long term without the improvement of overall breeding performance and reduction of mortality. Thus, releasing birds may be a good tool to artificially increase productivity —specially in specific years—, or expand the population to new habitats, but breeding and mortality parameters should be improved too.

4.4. Limitations of the study

To properly interpret our results it is important to note and discuss the limitations of the study, mainly related to the approach of stochastic simulations. First, we used VORTEX Software to run simulations, a widely used software to conduct Population Viability Analysis (PVA) in raptors (e.g. Evans *et al.*, 2009; Andersen *et al.*¸2015; Morandini *et al.*, 2017, 2019), but with some inherent restrictions. PVA programs may produce different predictions for the same population (Brook *et al.*¸1999) depending on internal calculations, availability for parameters inputs and interpretation of stochasticity. Simplified models were found to be relatively congruent (Brook *et al.*, 1999), so to minimize model complexity and uncertainty, we opted for parsimonious scenarios validated with empirical data.

Second, we had uncertainty about certain demographic parameters, e.g. age-specific mortality rates, immigration rates, and carrying capacity. Further precise estimations of those parameters are needed, but we tried to solve this problem by using conservative values extracted from the exploration of our data, mean values of comparable Osprey populations from scientific literature, and incorporating high standard deviations.

Furthermore, we performed validation by comparing historical observed data with a simulated scenario which used the same inputs as our baseline scenario. In addition, sensitivity analyses were run to assess the influence of changes in specific parameters.

Finally, our simulations were performed considering Cádiz and Huelva sub-populations as a single metapopulation. This decision was made considering the high female dispersal rates observed between the sub-populations, the relatively low distance between them, the parallel evolution of both sub-population and the provenance of all individuals from the same reintroduction project. As stated in the Methods section, we performed several trials with the two different sub-populations and different values of female dispersal, but the difference in extinction probabilities, growth rates, etc. was not significant and would have complicated the model, so we decided to run the simulations by using a simpler unique population approach. However, different management measures may be applied within both sub-populations (or even in each specific habitat or nest), depending on the environmental evolution of their habitats or the different breeding parameters detected in future years.

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All authors revised and approved the content of this manuscript.

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Table 1. Summary of common values used in Vortex for all scenarios (baseline and comparative management scenarios).

Parameter	Value (±SD)	Source	Reference
Initial population size	75 individuals	Internal estimation	-
Lifespan	20 years	Literature	Poole (1989)
Reproductive system	Long-term monogamy	Literature and internal observations	Poole (1989)
Extinction definition	Critical size = 1	-	-
Catastrophes	Frequency= 5% Severity = 5%	Internal estimations to simulate the effect of climatic extreme events (e.g. heat waves, storms)	-
Inbreeding depression	Yes (default values in Vortex)	-	-
Mate monopolization	100%	-	-
Maximum number of broods per year	1	Literature and internal observations	Poole (1989)
Maximum number of fledglings per brood	3	Internal estimation	
Density dependent reproduction	No	We detected density dependence reproduction at the pair level, but productivity did not significantly shift at the population level.	-
Sex ratio of hatched fledglings	50/50	Internal estimation. Sex ratio shifted throughout the study period depending on demographic levels, but it averaged 50/50 at long-term.	-
Number of years of simulation	40 years	-	-
Number of iterations	1000	-	-

Table 2. Parameters used in Vortex for baseline and comparative scenarios. The comparative scenarios were built based on the baseline scenario assuming higher carrying capacity, so only the parameters changed are shown.

Scenarios	Parameter	Value (±SD)	Source	Reference
Baseline	First year mortality	70 ± 10	Internal estimations (values within confidence intervals), and scientific literature	Spitzer & Poole, 1980; Eriksson & Wallin, 1994; Klaassen *et al.*, 2014; Monti *et al.*, 2014; Väli *et al.*, 2021; Galarza *et al.*, 2025
	Immature (2-3 years) mortality	30 ± 10		
	Adult mortality	10 ± 5		
	% of females in breeding pool (breeding pairs)	78 ± 7	Internal estimation from 2016 to 2024 (see Results)	-
	% of successful pairs	74	Internal estimation from 2016 to 2024 (see Results)	-
	Clutch size	2.1	Internal estimation from the entire study period (see Results)	-
	Immigration/emigration rates	0 (balanced)	-	-
	Carrying capacity (K)	75 ± 10	Internal estimation, assuming density dependence of the population in its current phase	
	First age of reproduction	4 calendar year	Internal estimation from 2016 to 2024	-
M1, M3	First year mortality	60 ± 10	Internal estimations (values within confidence intervals), and scientific literature	Spitzer & Poole, 1980; Eriksson & Wallin, 1994; Klaassen *et al.*, 2014; Monti *et al.*, 2014; Väli *et al.*, 2021; Galarza *et al.*, 2025
	Immature (2-3 years) mortality	20 ± 10		
M2, M3	Adult mortality	5 ± 3		

Scenarios	Parameter	Value (±SD)	Source	Reference
P1	% of females in breeding pool (breeding pairs)	85 ± 7	Plausible values from scientific literature and maximum values from our study population	Judge, 1983; Thibault *et al.*, 1991; Bretagnolle *et al.*¸2008; Monti *et al.*¸2018; Siverio *et al.*¸2018
	% of successful pairs	82		
	Clutch size	2.3		
P2	% of females in breeding pool (breeding pairs)	93 ± 5		
	% of successful pairs	90		
	Clutch size	2.5		
R1	Supplementation of fledglings into the population	5 females and 5 males per year during the first 20 years	-	-
R2	Supplementation of fledglings into a new population	5 females and 5 males per year during the first 20 years; 30% of dispersal among population	-	-
R3	Supplementation of fledglings into a new population	10 females and 10 males per year during the first 20 years; 40% of dispersal among population	-	-

Table 3. Output of the stochastic simulations of alternative management scenarios. M1-M3 are scenarios related to reduction in mortality rates; P1-P2 are scenarios with an increase in reproductive parameters; R1-R3 are scenarios in which birds are reintroduced into the population. Intrinsic growth rate (r) > 0.05 are shown in dark grey, 0 < r < 0.05 are shown in light grey, -0.05 < r < 0 are shown in light orange, and r < -0.05 are shown in dark orange.

Scenario	Intrinsic growth rate (r ± SD)	Extinction probability (%) within 40 years	Mean time to extinction (years)	Mean population size at the end of simulation
BASELINE	-0.039 ± 0.186	47	35.8	16.71 ± 14.70
M1	0.033 ± 0.147	3	35.1	117.66 ± 30.46
M2	0.014 ± 0.146	4	40.0	97.56 ± 37.62
M3	0.072 ± 0.128	0	-	140.04 + 13.76
P1	-0.005 ± 0.173	20	39.1	65.54 ± 41.34
P2	0.029 ± 0.177	6	-	107.26 ± 34.92
R1	0.013 ± 0.174	4	-	72.45 ± 33.75
R2	-0.002 ± 0.147	0.1	-	68.71 ± 37.05
R3	0.012 ± 0.149	0.2	-	77.41 ± 37.34
P1 + M3	0.096 ± 0.137	0	-	141.95 ± 12.42
R2 + P1 + M3	0.118 ± 0.128	0	-	181.25 ± 19.59

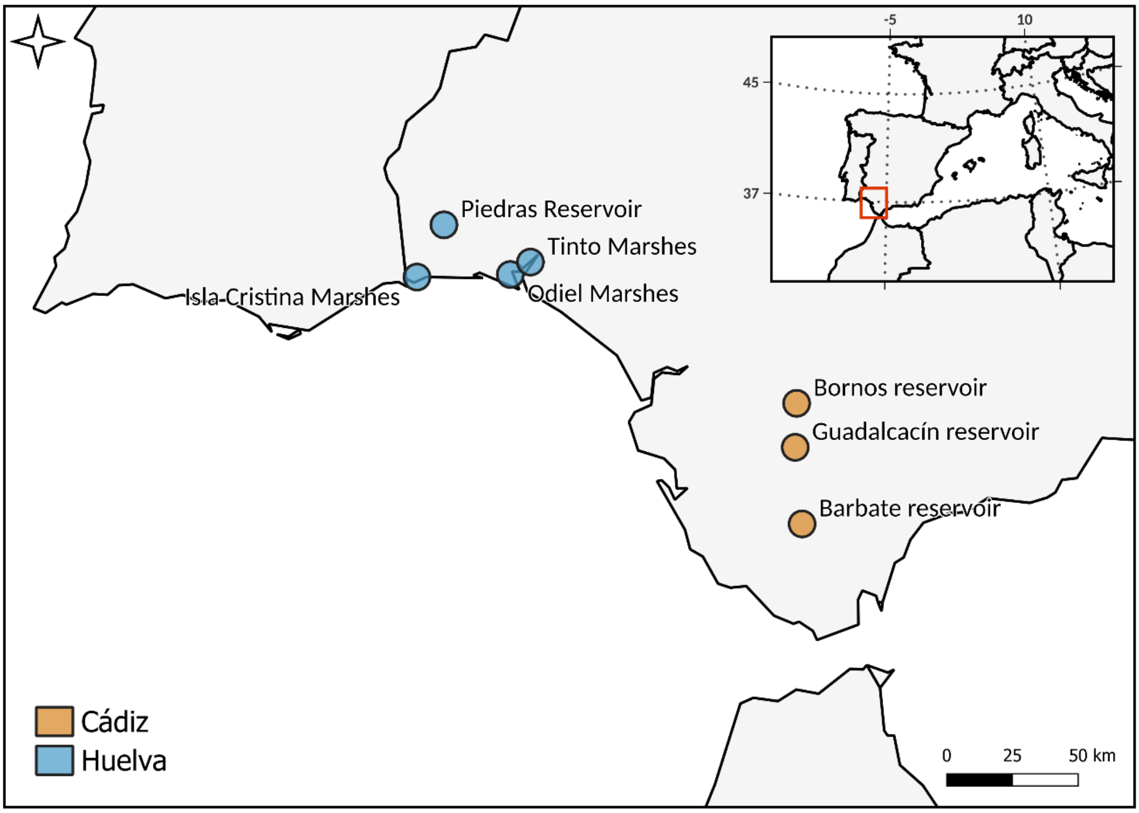

Figure 1. Map of the study area in Andalusia (southwestern Spain). The areas of Osprey territories are shown by a circle, each colour indicating a province (Cádiz or Huelva).

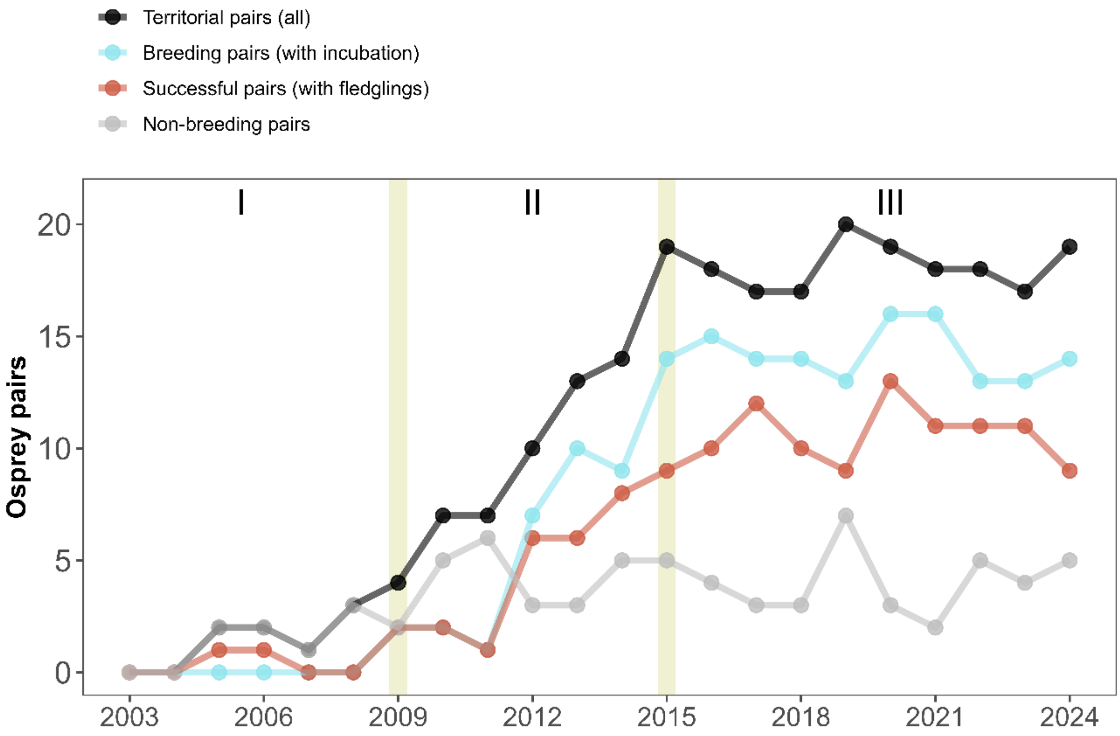

Figure 2. Evolution of the breeding population of Ospreys in southern Iberia from the beginning of the reintroduction project (2003) to last records (2024). The evolution of all territorial pairs (black dots) is shown, as well as that of breeding pairs (those incubating; blue dots), successful pairs (those rearing fledglings; red dots), and non-breeding pairs (those displaying territorial behaviour, but without incubation; grey dots). Two breakpoints (2009 and 2015) inferred from piecewise regression with territorial pairs are shaded, dividing the evolution into three phases: I (establishment, slight increase), II (expansion, strong increase), and III (stabilization). Note: some nestlings were incorporated into the nests (*fostering* technique) in some years (2005, 2006 and 2012), artificially increasing the number of successful pairs in 2005 and 2006.

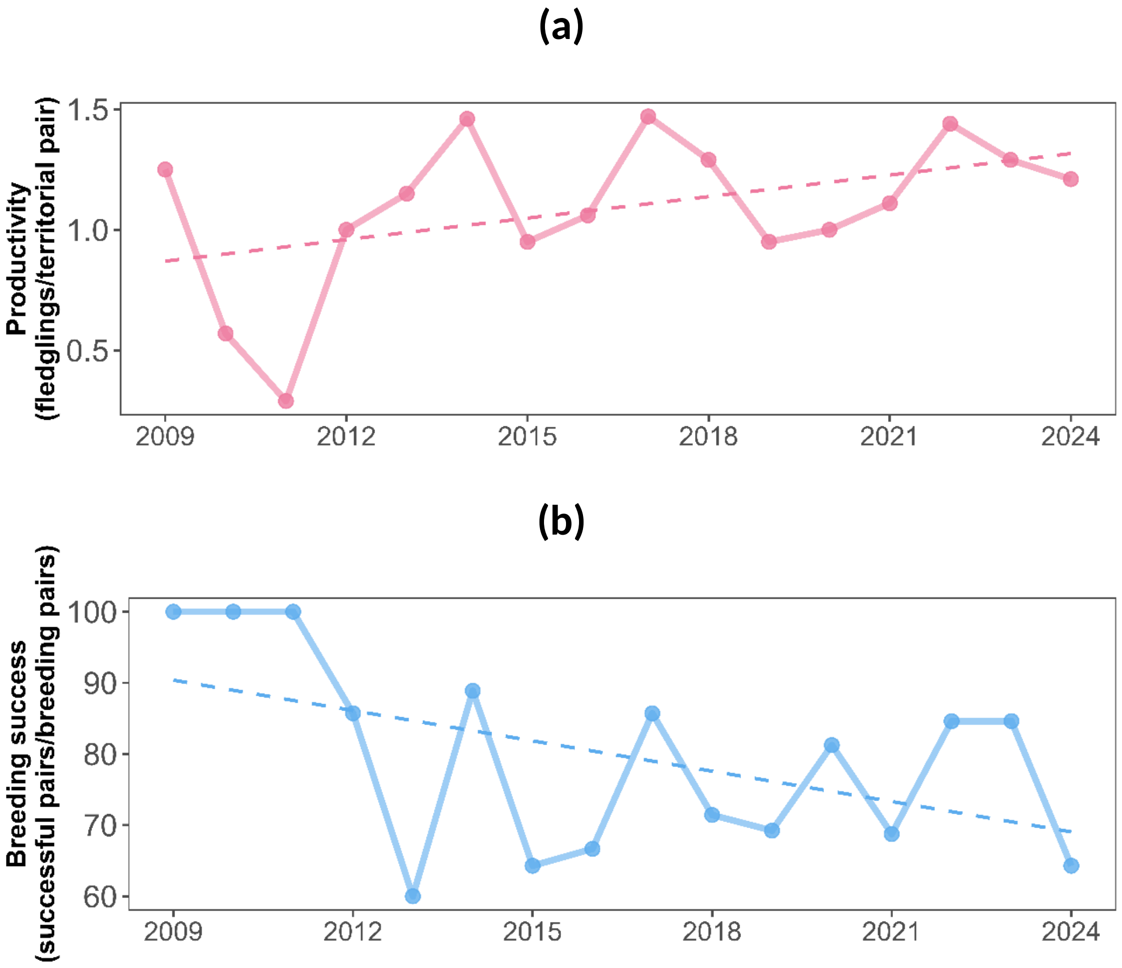

Figure 3. Evolution of the breeding parameters of Ospreys in southern Iberia from the first wild-hatched individuals (2009) to last records (2024). Productivity (a) and breeding success (b) are shown.

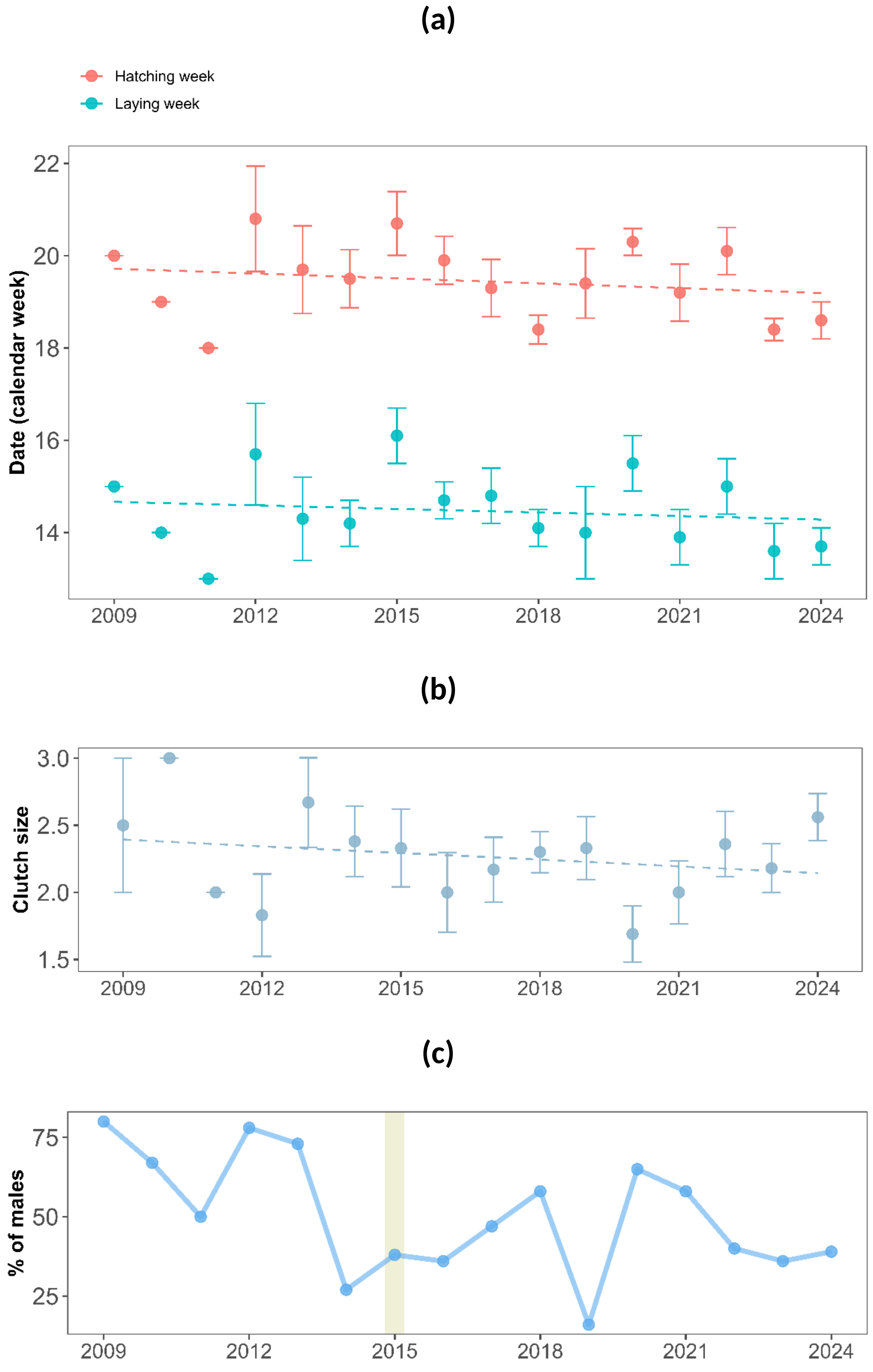

Figure 4. Evolution of laying/hatching dates (a), clutch size (b), and sex ratio (c) in Ospreys in southern Iberia from the first wild-hatched individuals (2009) to last records (2024). Dots indicate mean values, while vertical lines indicate standard errors. Dashed lines indicate linear predicted effects of mean values. Sex ratios were calculated considering wild-hatched birds, excluding fostering birds incorporated into the nests.

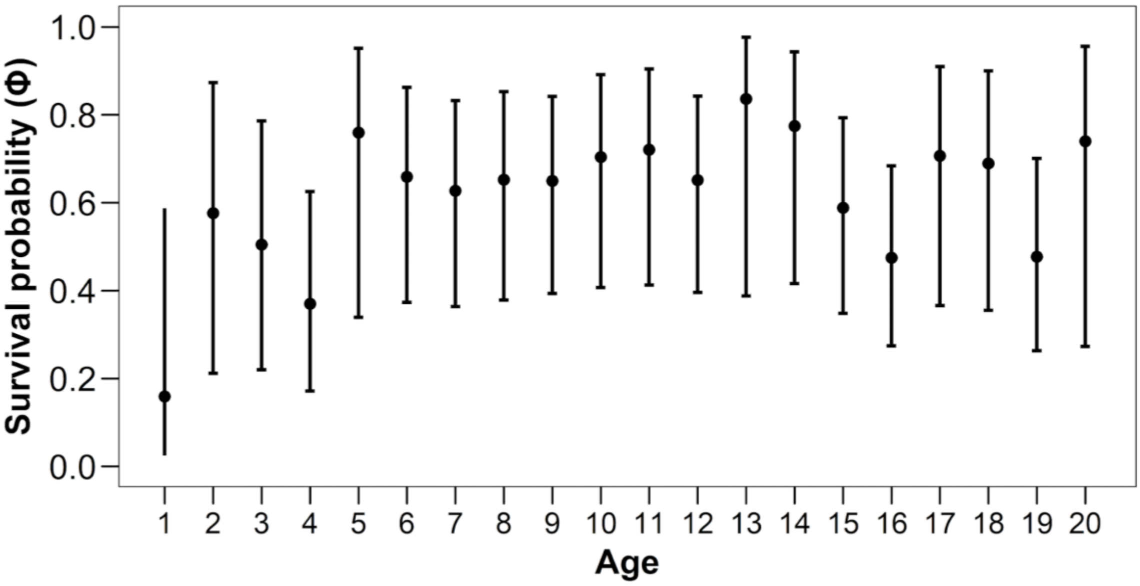

Figure 5. Survival probabilities of the Andalusian Ospreys among ages estimated by capture-recapture 'CJS' models.

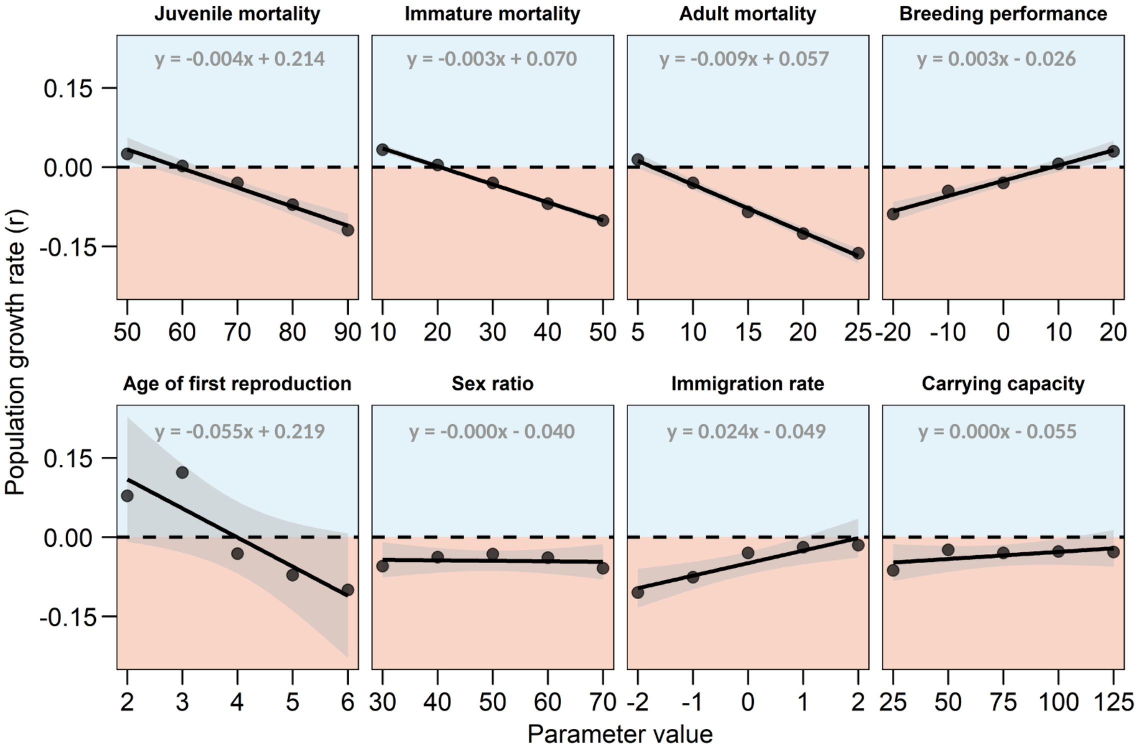

Figure 6. Sensitivity of the population growth (r) to variation in reproductive and demographic parameters. Coefficients of simple linear regressions are shown. Higher slopes indicate that the model is more sensitive to variations in that parameter. Positive and negative slopes indicate that increments in those parameters increase or decrease population growth, respectively. Positive population growth (r > 0) is shadowed in blue, while negative population growth (r < 0) is shadowed in red.

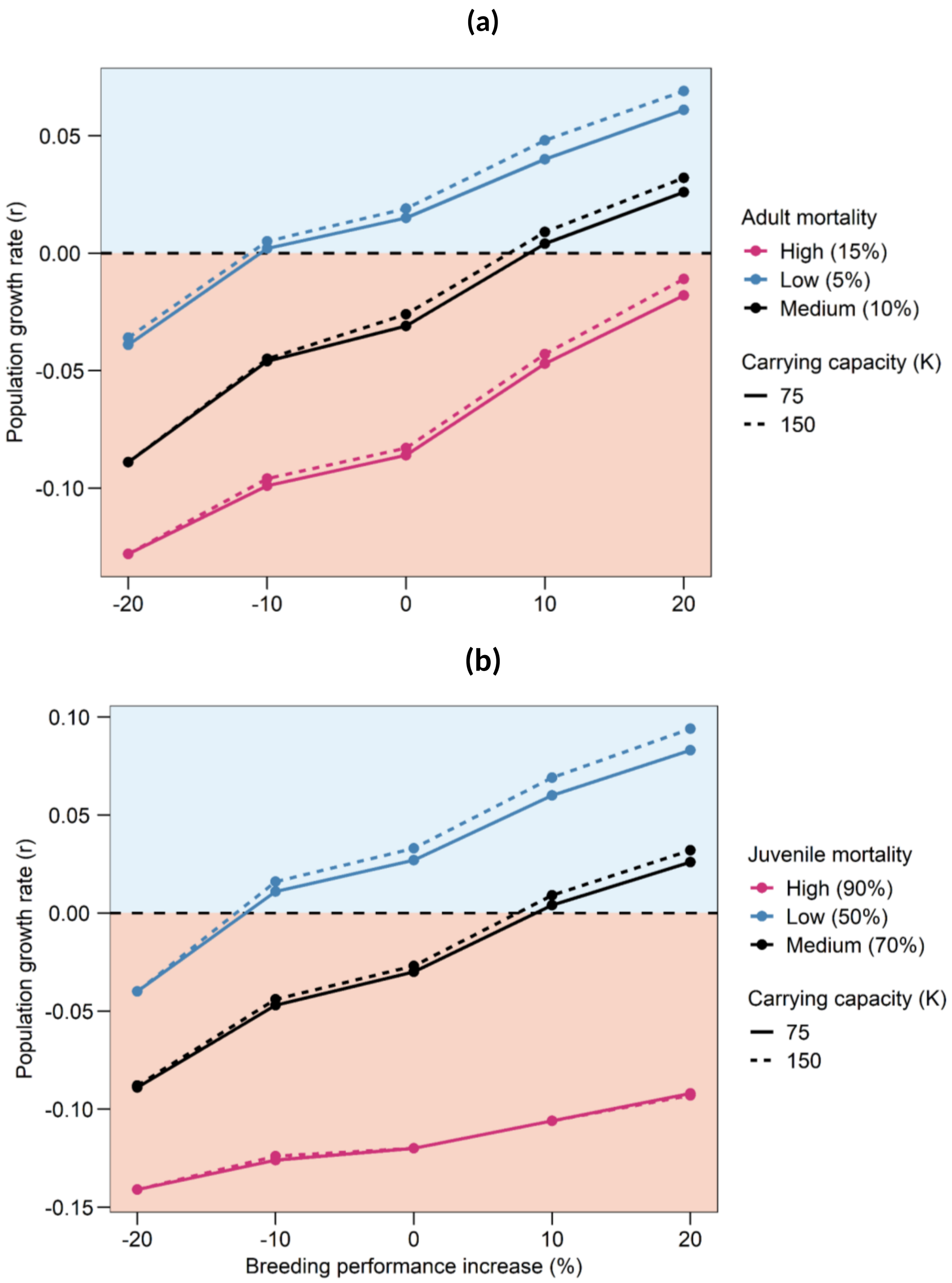

Figure 7. Sensitivity of the population growth (r) to variation in breeding performance (through breeding success and clutch size), carrying capacity (K), and annual mortality (a = adult; b = juvenile). Positive population growth (r > 0) is shadowed in blue, while negative population growth (r < 0) is shadowed in red.

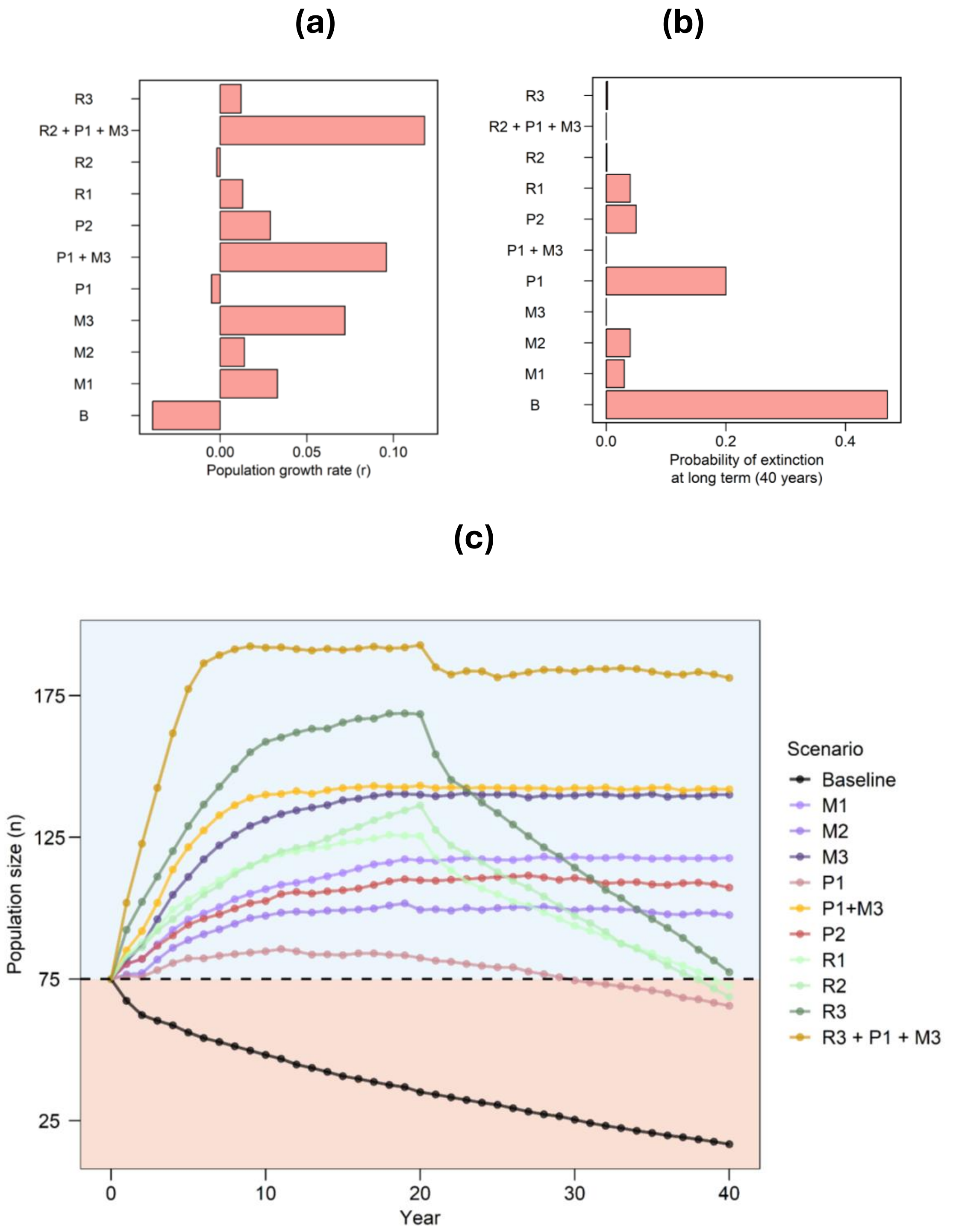

Figure 8. Outputs of the stochastic simulations under specific management scenarios: (a) Mean intrinsic growth rates; (b) Probability of extinction at long-term (40-year scale); (c) population size projections.

SUPPLEMENTARY MATERIALS

Table S1. Number and origin of the Ospreys reintroduced in Cádiz and Huelva (Andalusia) within 2003 and 2012, both through hacking and fostering.

Year	Number of reintroduced ospreys	+From Germany	+From Scotland	+From Finland
2003	4	0	0	4
2004	21	12	5	4
2005	20	12	5	3
2006	22	12	5	5
2007	21	12	5	4
2008	20	20	0	0
2009	27	20	7	0
2010	19	19	0	0
2011	19	19	0	0
2012	18	18	0	0
Total	**191**	**144**	**27**	**20**

Table S2. Age structure and population size input of females and males for our stochastic simulations.

Female age distribution (n = 40)	
Age	**Size**
1	14
2	4
3	3
4	2
5	2
6	2
7	2
8	2
9	2
10	1
11	1
12	1
13	1
14	1
15	1
16	1
Male age distribution (n = 35)	
Age	**Size**
1	9
2	3
3	2
4	3
5	3
6	2
7	2
8	2
9	2
10	1
11	1
12	1
13	1
14	1
15	1
16	1

Table S3. Inputs range of the univariate sensitivity analysis to test the variability of simulation models depending on one-step changes in specific parameters. Some of those parameters with high influence or biological relevance were also used in multivariate sensitivity analysis. *We increased all breeding-related inputs at the same time, i.e. proportion of breeding pairs, breeding success, and clutch size. Thus, each step of the analysis increased or decreased all those parameters by 10%.

Parameter	Base value (Baseline scenario)	Sensitivity range (step)
Adult mortality	10% ± 5	5 → 25% (5)
Immature mortality	30% ± 10	10 → 50% (10)
Juvenile mortality	70% ± 15	50 → 90% (10)
Breeding performance*	0	-20 → 20% (10)
Age of first reproduction	4 years	2 → 6 years (1)
Carrying capacity	75 ± 10 individuals	50 → 150 individuals (25)
Immigration rates	0	-2 → +2 ♀/year (1)
Sex ratio (proportion of males born)	50%	30 → 70% (10)

Table S4. Results of the piecewise regressions run to detect abrupt shifts in the tendencies of demographic and breeding parameters in our study population throughout the study period.

(a) **Territorial pairs** (Adjusted $R^2 = 0.98$)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2008.7	0.67
ps2.year	2015.3	0.53

	Estimate	Standard Error	T value	P-Value
Intercept	-1030.07	553.02	-1.863	0.008
Year	0.51	0.27	1.865	0.008
U1.year	1.73	0.35	4.938	NA
U2.year	-2.18	0.26	-8.270	NA

Residual standard error: 1.154

(b) **Breeding pairs** (Adjusted $R^2 = 0.96$)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2010.68	0.57
ps2.year	2015.32	0.49

	Estimate	Standard Error	T value	P-Value
Intercept	-572.79	394.12	-1.453	0.165
Year	0.29	0.20	1.455	0.165
U1.year	2.51	0.45	5.613	NA
U2.year	-2.90	0.44	-6.670	NA

Residual standard error: 1.273

(c) **Successful pairs** (Adjusted R^2 = 0.94)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2010.38	0.95
ps2.year	2016.4	0.73

	Estimate	Standard Error	T value	P-Value
Intercept	-476.98	365.48	-1.305	0.21
Year	0.24	0.18	1.307	0.21
U1.year	1.36	0.34	4.055	NA
U2.year	-1.74	0.34	-5.189	NA

Residual standard error: 1.18

(d) **Non-breeding pairs** (Adjusted R^2 = 0.49)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2014	1.89

	Estimate	Standard Error	T value	P-Value
Intercept	-1021.64	260.11	-3.928	<0.001
Year	0.51	0.13	3.939	<0.001
U1.year	-0.72	0.21	-3.348	NA

Residual standard error: 1.549

(e) **Productivity** (Adjusted R^2 = 0.16)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2010	0.68

	Estimate	Standard Error	T value	P-Value
Intercept	908.35	823.00	1.104	0.291
Year	-0.452	0.410	-1.102	0.291
U1.year	0.492	0.410	1.200	NA

Residual standard error: 0.289

(f) Breeding success (Adjusted $R^2 = 0.43$)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2013	1.62

	Estimate	Standard Error	T value	P-Value
Intercept	16761.69	9254.14	1.811	0.095
Year	-8.290	4.603	-1.801	0.095
U1.year	8.492	4.683	1.813	NA

Residual standard error: 10.29

(g) Laying date (Adjusted $R^2 = -0.087$)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2022.01	3.25

	Estimate	Standard Error	T value	P-Value
Intercept	-11.314	116.418	-0.097	0.924
Year	0.012	0.058	0.222	0.828
U1.year	-0.611	1.233	-0.496	NA

Residual standard error: 0.871

(h) Hatching date (Adjusted $R^2 = -0.091$)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2015.0	7.714

	Estimate	Standard Error	T value	P-Value
Intercept	-248.39	747.24	-0.332	0.742
Year	0.132	0.371	0.355	0.725
U1.year	-0.254	0.450	-0.564	NA

Residual standard error: 2.779

(i) **Sex ratio (**Adjusted $R^2 = 0.24$)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2014.68	2.72

	Estimate	Standard Error	T value	P-Value
Intercept	12648.74	7892.28	1.603	0.135
Year	-6.26	3.92	-1.595	0.135
U1.year	6.40	4.32	1.481	NA

Residual standard error: 16.41

(j) **Clutch size (**Adjusted $R^2 = 0.071$)

Estimated breakpoints		
	Est.	Standard error
ps1.year	2020.58	1.87

	Estimate	Standard Error	T value	P-Value
Intercept	95.24	53.44	1.782	0.100
Year	-0.04	0.03	-1.740	0.107
U1.year	0.19	0.14	1.359	NA

Residual standard error: 0.317

Table S5. Age-specific survival probability estimated by capture-recapture CJS models in MARK. Standard Error (SE) and Confidence Intervals (CI) are shown.

Age	Survival probability (Φ)	SE	CI (lower)	CI (upper)
1	0.159	0.138	0.024	0.587
2	0.576	0.202	0.212	0.873
3	0.504	0.164	0.220	0.786
4	0.370	0.124	0.171	0.625
5	0.760	0.169	0.339	0.951
6	0.659	0.135	0.373	0.862
7	0.627	0.129	0.363	0.832
8	0.652	0.130	0.378	0.853
9	0.650	0.122	0.393	0.842
10	0.704	0.132	0.407	0.891
11	0.721	0.134	0.412	0.905
12	0.651	0.121	0.396	0.842
13	0.836	0.146	0.388	0.976
14	0.774	0.140	0.416	0.943
15	0.588	0.122	0.348	0.793
16	0.475	0.111	0.274	0.684
17	0.707	0.151	0.366	0.910
18	0.689	0.152	0.355	0.900
19	0.477	0.120	0.263	0.700
20	0.740	0.199	0.273	0.956

Table S6. Results of model validation. We compared LOESS regressions of normalized observed values (territorial pairs) and estimated values (validation simulation). MSE = Mean Squared Error. LOESS = locally weighted regressions.

Year	Normalized observed value	Normalized simulated value (mean)	LOESS regression observed	LOESS regression simulated	MSE
2003	-1.48	-3.07	-1.45	-3.13	2.84
2004	-1.48	-2.04	-1.42	-2.06	0.41
2005	-1.21	-1.31	-1.37	-1.13	0.06
2006	-1.21	-0.43	-1.29	-0.35	0.90
2007	-1.34	0.37	-1.19	0.27	2.15
2008	-1.08	0.88	-1.09	0.76	3.43
2009	-0.94	0.96	-0.90	1.01	3.68
2010	-0.54	1.03	-0.67	1.10	3.15
2011	-0.54	1.03	-0.42	1.02	2.06
2012	-0.15	1.03	-0.13	0.83	0.92
2013	0.25	0.45	0.17	0.61	0.19
2014	0.25	0.30	0.49	0.41	0.01
2015	1.05	0.30	0.75	0.25	0.25
2016	0.92	0.23	0.86	0.20	0.44
2017	0.79	0.15	0.93	0.16	0.59
2018	0.79	0.15	0.95	0.13	0.67
2019	1.19	0.08	0.99	0.10	0.79
2020	1.05	0.08	0.99	0.06	0.86
2021	0.92	0.01	0.97	0.02	0.90
2022	0.92	0.01	0.96	-0.02	0.97
2023	0.79	-0.07	0.95	-0.07	1.04
2024	1.05	-0.14	0.93	-0.13	1.11

Table S7. Results of the univariate sensitivity analysis to test the variability of population growth (r) and probability extinction at long term (PE) under small changes of specific parameters.

Parameter	Value	r	PE
Adult mortality	5	0.014	0
	10	-0.03	0.01
	15	-0.085	0,3
	20	-0.126	0,8
	25	-0.163	0.98
Immature mortality	10	0.033	0
	20	0.004	0
	30	-0.03	0.01
	40	-0.069	0.13
	50	-0.101	0.44
Juvenile mortality	50	0.025	0
	60	0.002	0
	70	-0.03	0.01
	80	-0.071	0.15
	90	-0.119	0.71
Age of first reproduction	2	0.078	0
	3	0.122	0
	4	-0.031	0.01
	5	-0.072	0.13
	6	-0.1	0.43
Sex ratio	30	-0.055	0.05
	40	-0.038	0.03
	50	-0.032	0.02
	60	-0.039	0.02
	70	-0.059	0.08

Immigration rate	-2	-0.105	0.58
	-1	-0.076	0.2
	0	-0.03	0.01
	1	-0.019	0
	2	-0.015	0
Breeding performance	-20	-0.089	0.29
	-10	-0.045	0.03
	0	-0.03	0.01
	+10	0.006	0
	+20	0.03	0
Carrying capacity	25	-0.063	0.41
	50	-0.024	0.05
	75	-0.03	0.01
	100	-0.027	0.01
	125	-0.028	0.01

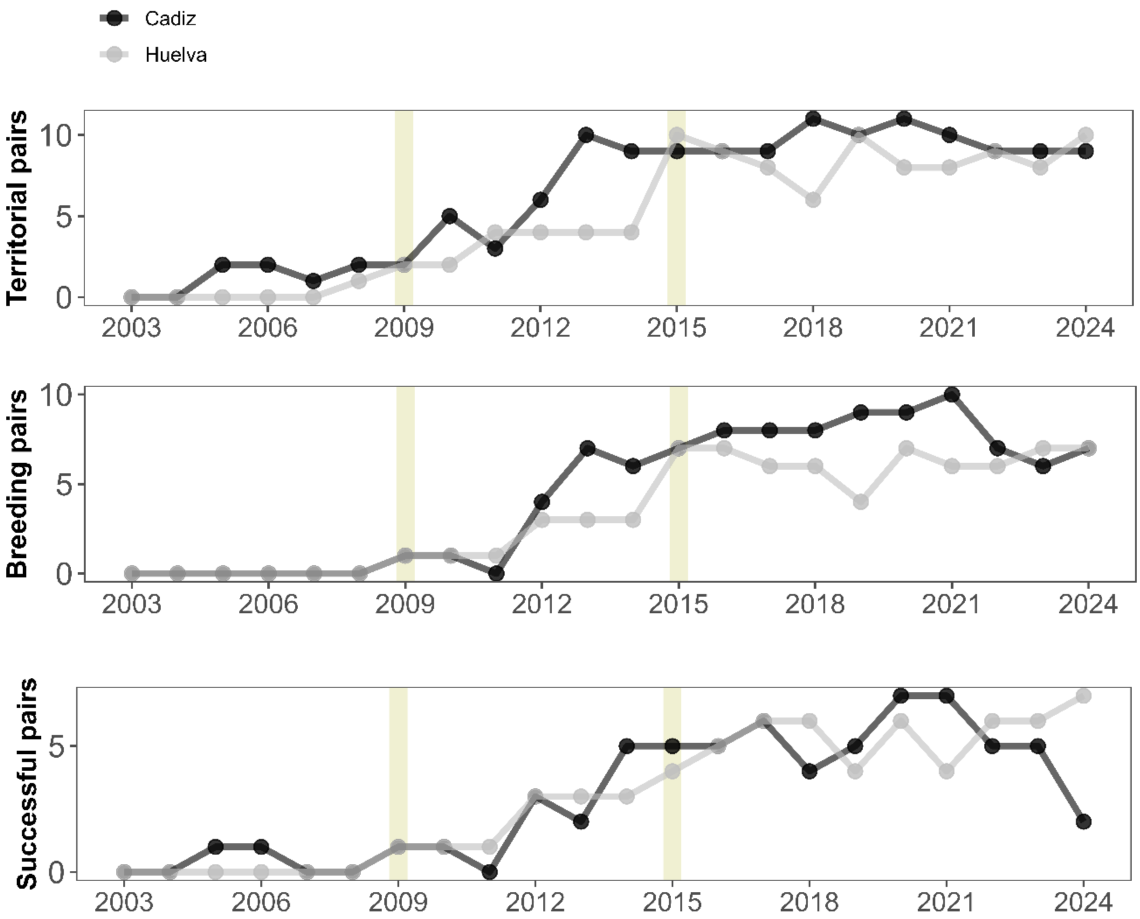

Figure S1. Evolution of the breeding population of Ospreys in southern Iberia from the beginning of reintroduction project (2003) to last records (2024), divided into Cádiz (black dots) and Huelva (grey dots) provinces. The evolution of the entire population is shown, as well as that of breeding pairs, and successful pairs. Two breakpoints inferred from piecewise regression, in 2011 and 2015, are shaded, dividing the evolution in three phases: I (establishment, slight increase), II (expansion, strong increase), and III (stabilization, slight decrease). Note: some nestlings were incorporated into wild nests (*fostering* technique) in some years (2005, 2006 and 2012), artificially increasing the number of successful pairs in 2005 and 2006.

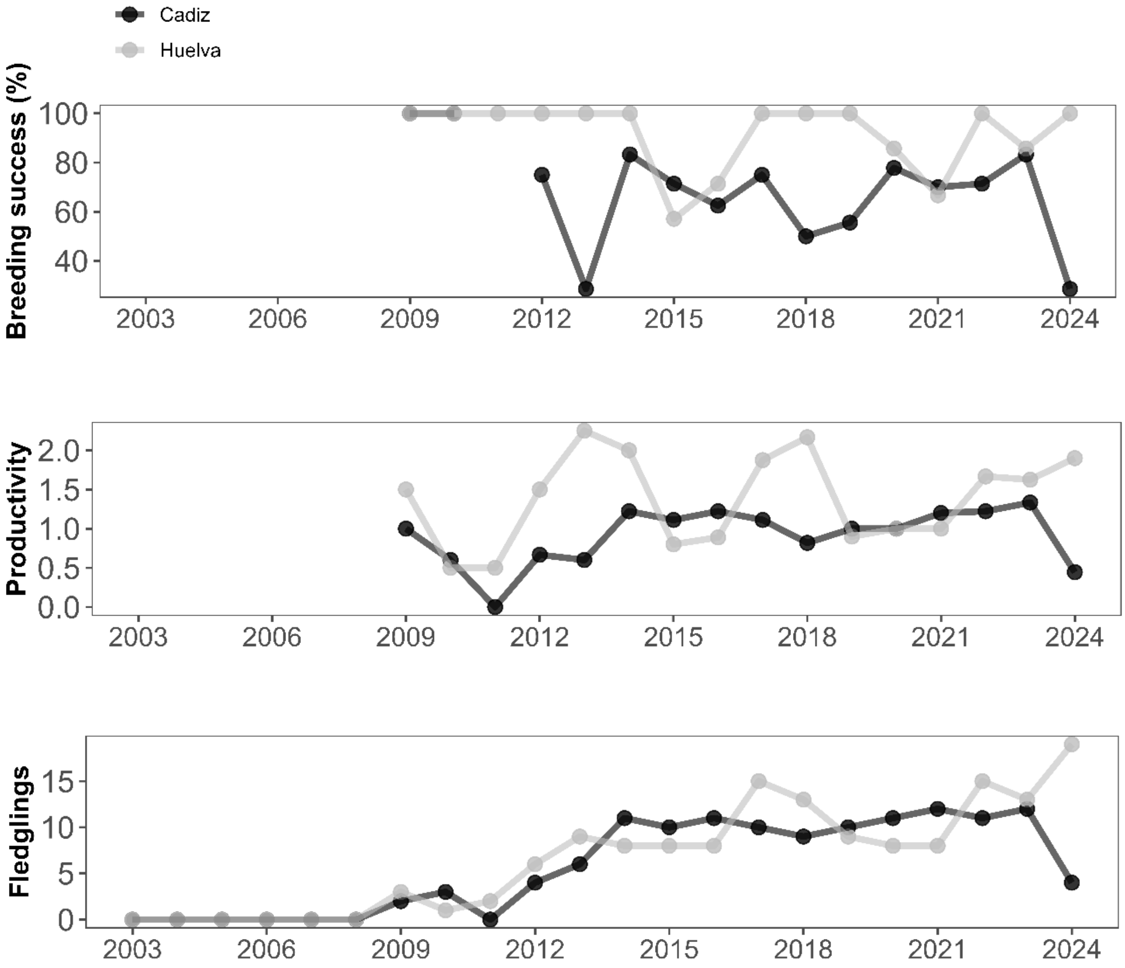

Figure S2. Evolution of the breeding parameters of Ospreys in southern Iberia from the beginning of the reintroduction project (2003) to last records (2024), divided into Cádiz (black dots) and Huelva (grey dots) provinces. The evolution of breeding success, productivity and wild-hatched fledglings are shown.

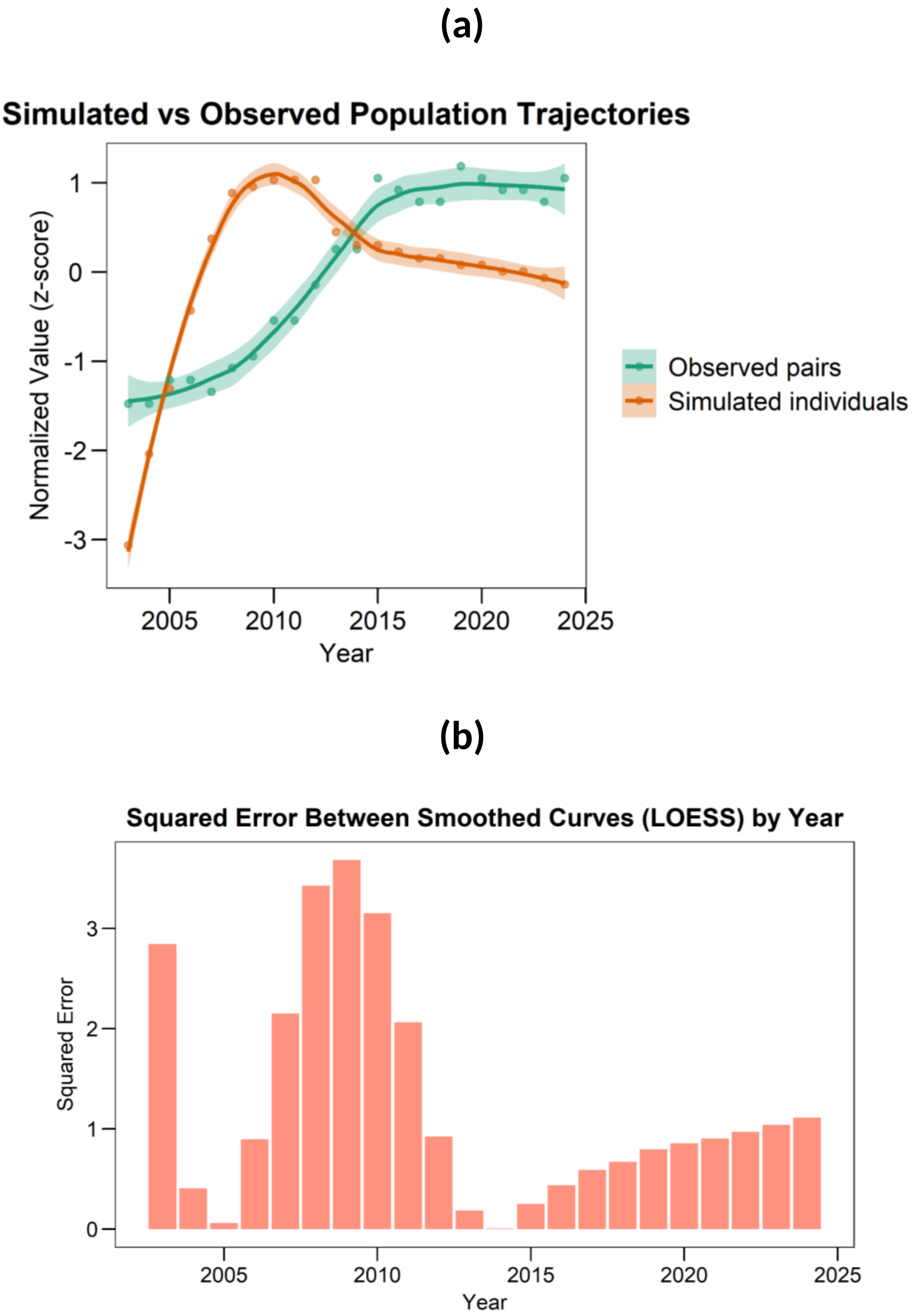

Figure S3. Results of model validation using smoothed curves and square errors comparison. a) LOESS adjustments (including 95% confidence intervals) of the normalized simulated individuals and observed pairs. (b) Year-specific squared errors between LOESS curves.