

On the road to self-sustainability: reintroduced migratory European northern bald ibises *Geronticus eremita* still need management interventions for population viability

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SUPPLEMENTARY MATERIAL 1 Study species.

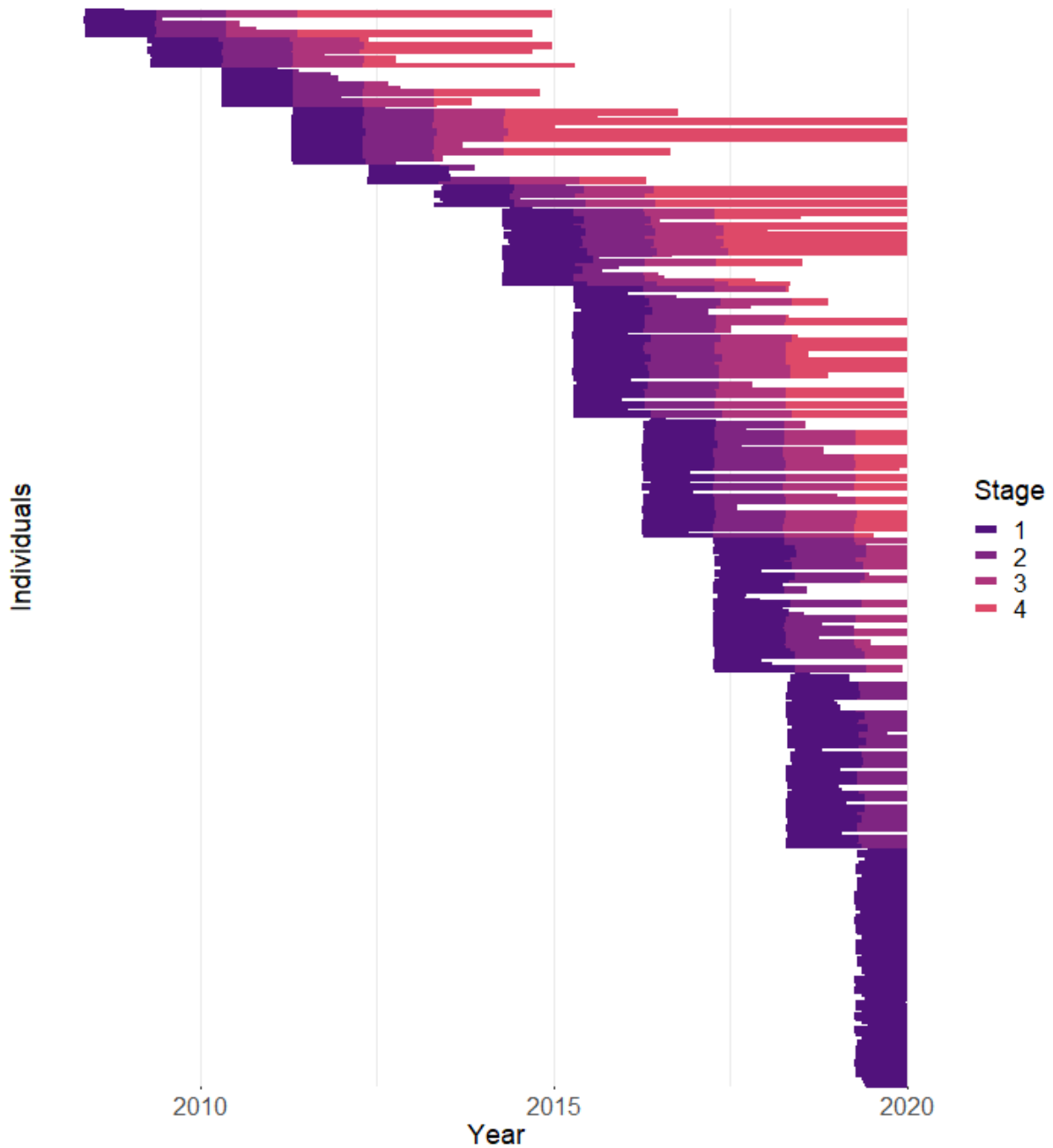
The Northern Bald Ibis (*Geronticus eremita*, hereafter NBI) is one of the most endangered bird species in the world: According to the IUCN Red List of Threatened Species, the NBI was critically endangered from 1994 (BirdLife International, 2017); since 2018 the species is listed as endangered due to management actions applied to the existing populations (BirdLife International, 2018).

The NBI is a migratory, mainly insectivorous, ibis species that reaches an age of up to 30 year in captivity (Böhm & Pegoraro, 2011). NBI breed in pairs that form each season and raise together up to four chicks in colonies of up to hundreds of birds (Fritz et al., 2017). Historic breeding grounds reached all around the Mediterranean, from Afrika to the Arabian Peninsula and Europe (Bowden et al., 2003; Bowden, 2015; Fritz & Unsöld, 2015; BirdLife International, 2017; Fritz et al., 2017; Böhm et al., 2020). A recent genetic study indicates a formerly contiguous population, only the extinction of the European population in the 17th century separated a western and eastern population. The study found no evidence of differentiation of two evolutionary significant units (Wirtz et al., 2018). An International Single Species Action Plan (ISSAP) was established to formulate conservation goals for the NBI in 2015 after years of consultation (Bowden, 2015). The ISSAP aims to increase the population size and breeding range of the species by means of improved survival and reproduction and the establishment of new colonies.

In autumn, all individuals migrate to the wintering grounds and they return to the same breeding area the next spring. Juveniles usually stay in the wintering grounds until they are adults (Fritz et al., 2019). Worldwide, only one wild, mainly sedentary population is remaining, with two breeding sites on the Atlantic coast in Morocco (Bowden et al., 2008; Schenker et al., 2020). A relict population in the Middle East, which bred in Syria and wintered in Ethiopia, went extinct in 2013 (Serra, 2015). In Turkey, a managed, sedentary population is remaining (Yeniyurt et al., 2017). Until the 17th century, NBI bred in Europe during summer, especially around the Alps or Andalusia (Schenker, 1977; Unsöld & Fritz, 2011; Bowden, 2015; Fritz et al., 2017). The European NBI population was migratory but the historical winter areas are unknown (Fritz et al., 2017; Schenker et al., 2020). The species went extinct in Europe due to human actions, especially hunting. Eradication was probably accelerated by the little ice age and the beginning of the Thirty Years' War (Schenker, 1977; Fritz et al., 2017). Currently, there are two on-going reintroduction projects in Europe. *Proyecto Eremita* reintroduce a sedentary NBI population in Andalusia (Spain; Bowden, 2015; López & Quevedo, 2016; Böhm et al., 2020), while the so called *Waldrappteam* establish a migratory population, with breeding sites North of the Alps and a wintering ground in southern Tuscany (Fritz et al., 2019).

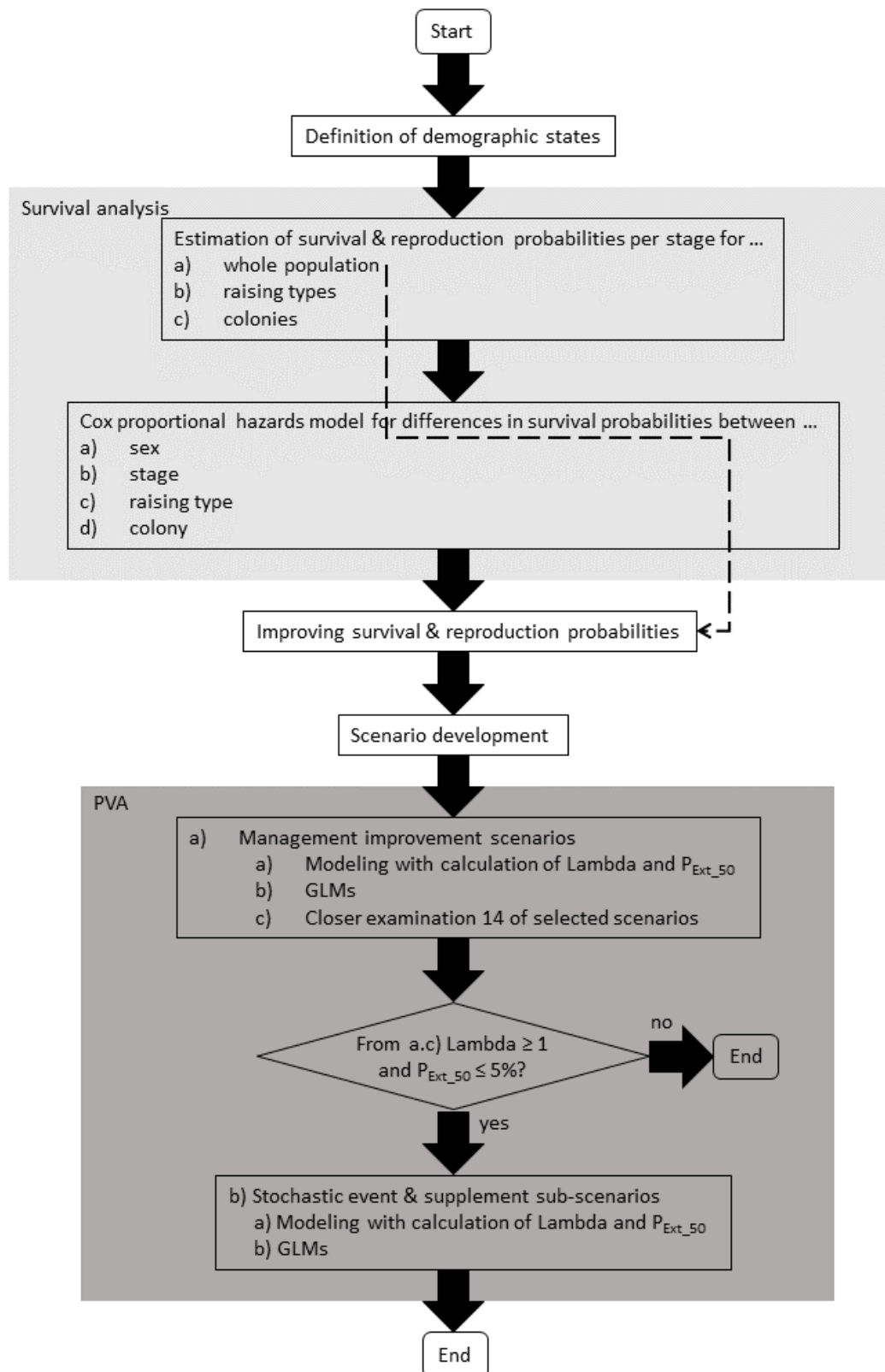
A group of scientists headed by J. Fritz founded the *Waldrappteam* in 2002. In the course of a feasibility study along the IUCN reintroduction guidelines (2002-2013) and during a subsequent LIFE+ biodiversity project (2014-2019; LIFE+12-BIO_AT_000143) the team released a total of 223 juveniles and reduced non-natural threats such as poaching and electrocution (Fritz et al., 2019). End of 2019, the *Waldrappteam* NBI population consisted of 143 individuals, which belong to four breeding colonies: Two well established colonies in Burghausen (Bavaria, Germany) and Kuchl (Salzburg, Austria) with 37 fledglings in 2019 and two colonies which consisted only of released and not yet adult birds in Überlingen (Baden-Württemberg, Germany) and Rosegg (Kärnten, Austria). All individuals are

migratory, with a migration tradition to the common wintering ground Laguna di Orbetello in the Tuscany, Italy (FIG. 1 of the main text) (Fritz, Kramer, et al., 2017; Fritz et al., 2019).



SUPPLEMENTARY FIG. 1 Timelines of 250 northern bald ibises (NBIs) from 2008 to 2019. Graphical visualization of the lifetime of 384 NBI. The study period is represented on the x-axis and ranges from 2008 to 2019. Each line corresponds to one individual from its year of hatching to its year of death. The plot shows all females (N = 184), all males (N = 195) and individuals of unknown sex (N = 5) in 4 different stages (according to Figure 2) during their lifetime. Stage 1 (dark purple) corresponds to juveniles with their first migration to the wintering grounds. Stage 2 (plum) corresponds to 1 year old NBI that stay in the wintering grounds. Stage 3 (mallow) are 2 years old NBI with their first independent migration back to the breeding area. Stage 4 (coral) corresponds to reproductive adults. At the end of the data collection period the population consisted of 143 alive individuals (lines until the right border

of the figure; 74 f, 69 m). 71 individuals reached only stage 1 (37 f, 34 m), 28 individuals reached only stage 2 (11 f, 17 m), 13 individuals reached only stage 3 (8 f, 5 m), 31 individuals reached stage 4 (18 f, 13 m). The legend on the right side of the plot shows the colour code for the stages considered.



SUPPLEMENTARY FIG. 2 Flowchart of the study with an overview of the individual steps. Further details on the individual steps can be found in the main text. In light grey: steps of the survival analysis. In dark grey: steps of the population viability analysis (PVA). Dotted dark grey line: The estimated values for survival and reproduction are used for the steps after the survival analysis. P_{EXT_50} : extinction probability after 50 years.

2.1 Calculations

2.1.1 RR_{Baseline} and improvements

Here we counted only the female juveniles (raising type BP (biological parent raised)), that were born by the potential mothers (raising type BP or FP (foster parent raised)) per year and who were part of the migrating population and were not given to zoos or similar places:

$RR_{Baseline} = \frac{\text{no. of female BP fledglings p. a.} + \frac{1}{2} \text{ of BP fledglings of unknown sex p. a.}}{\text{no. of potential BP and FP mothers p. a.}}$	(1)
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~~□□□□□□□□□□~~

~~$$= \frac{\text{no. of female BP fledglings p. a.} + \frac{1}{2} \text{ of BP fledglings of unknown sex p. a.}}{\text{no. of potential BP and FP mothers p. a.}}$$~~

That means, also non-breeding adult females that stayed at the wintering grounds count in this analysis, hence this measure also includes the probability to breed. Additionally, we included one half of the juveniles of unknown sex. This would correspond to a scenario where any help from the Waldrappteam ended immediately. In addition, we calculated the standard deviation (SD) across years. For further scenarios regarding improvement in management e. g. in their breeding area we increased the baseline reproductive rate by 10%, 25% and 100%.

2.1.2 RR_{Status quo}

For this option we included the female juveniles that were born by the temporarily added females, but we did not include these females as potential mothers. This option includes all parent raised chicks per year that were part of the population and corresponds to the status quo of the population with active reproduction management:

$RR_{Status Quo} = \frac{\text{total no of female BP fledglings p. a. (from potential BP and FP mothers + chicks of added females)} + \frac{1}{2} \text{ of BP fledglings of unknown sex p. a.}}{\text{no. of potential BP and FP mothers p. a.}}$	(2)
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~~□□□□□□□□□□~~

~~$$= \frac{\text{total no of female BP fledglings p. a. (from potential BP and FP mothers + chicks of added females)} + \frac{1}{2} \text{ of BP fledglings of unknown sex p. a.}}{\text{no. of potential BP and FP mothers p. a.}}$$~~

2.1.3 RR_{All chicks}

For this option we summed up the chicks of RR_{Status quo} and the female foster parent raised chicks (raising type FP) per year. Again, we divided this number of chicks by the potential mothers:

$RR_{All Chicks} = \frac{\text{total no of female BP fledglings p. a.} + \text{no. of female FP fledglings p. a.} + \frac{1}{2} \text{ of BP fledglings of unknown sex p. a.}}{\text{no. of potential BP and FP mothers p. a.}}$	(3)
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$$\begin{array}{r}
 \square\square\square\square\square\square\square\square\square\square\square \\
 \text{total no of female BP fledglings p.a.} + \text{no. of female FP fledglings p.a.} \\
 + \frac{1}{2} \text{ of BP fledglings of unknown sex p.a.} \\
 \hline
 \text{no. of potential BP and FP mothers p.a.}
 \end{array} \quad (3)$$

2.1.4 Reproductive rate per raising type

Here we counted the number of female juveniles (raising type BP), that were born by the potential mothers (raising type BP or FP) per year and per raising type of the mother and that were part of the population and were not given to zoos or similar places, like the supplementary females. The calculation was the same than for 1.1.1, but we distinguished the numbers of the chicks and the potential mothers by the raising type of the potential mothers.

2.1.5 Reproductive rate per colony

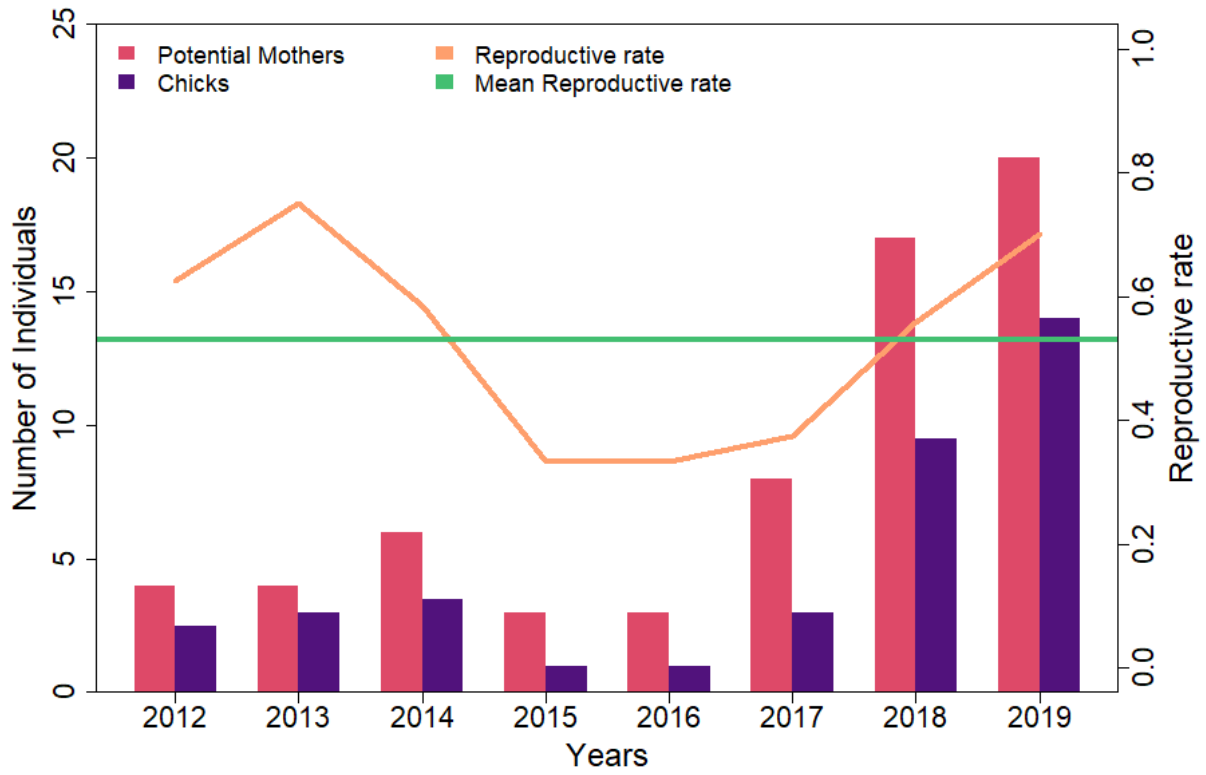
Here we counted the number of female juveniles (raising type BP), that were born by the potential mothers (raising type BP or FP) per year and per colony and who were part of the population and were not given to zoos or similar places. The calculation was the same as for 1.1.1, but we distinguished the numbers of the chicks and the potential mothers by the colony of the potential mothers.

2.2 Results

For RR_{Baseline} and $RR_{\text{Status quo}}$ we did not start before 2012 with the calculations of RR, because there were no potential mothers before 2011, and in 2011 there was only one potential mother. For $RR_{\text{All chicks}}$ we did not include the years 2011 to 2013, as there was only one potential mother in 2011 and no FP chicks were added in 2012 and 2013.

2.2.1 RR_{Baseline} and improvements

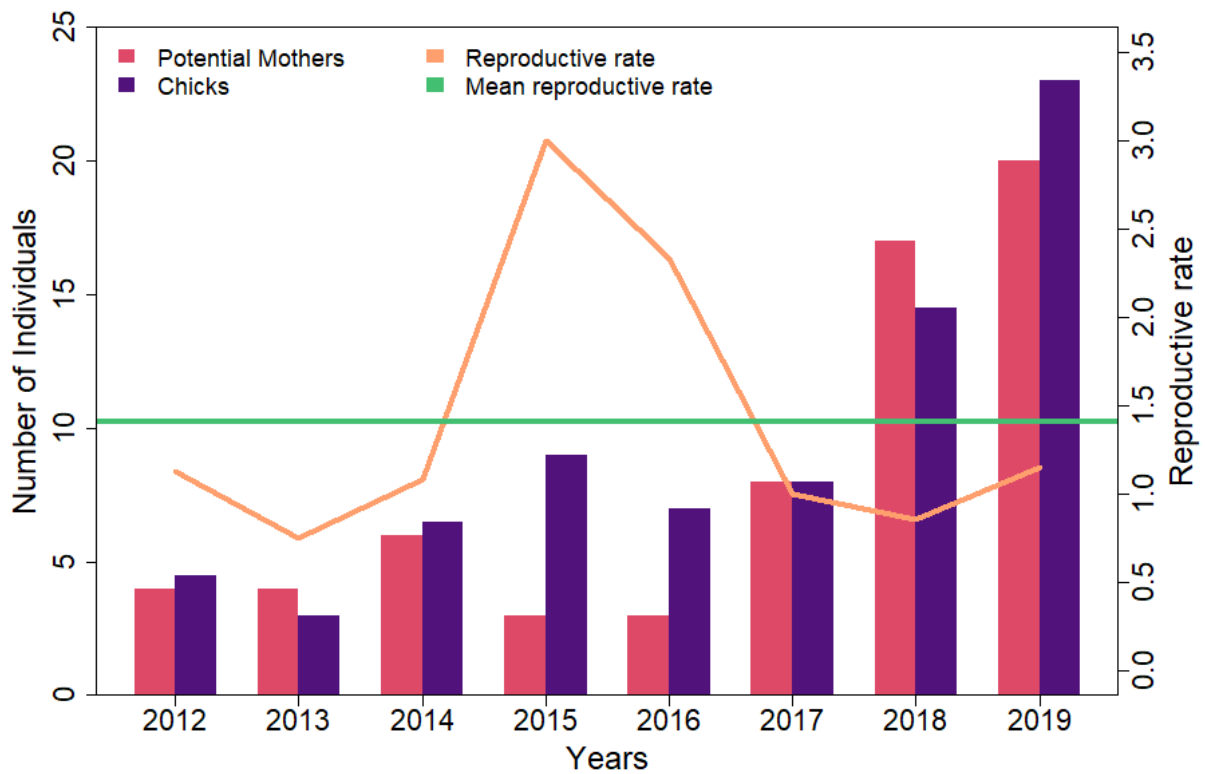
We calculated a baseline reproductive rate of 0.53 (± 0.17) for a total of 37.5 female chicks over 8 years (SUPPLEMENTARY FIG. 3; SUPPLEMENTARY TABLE 1). Then we increased this value by 10%, 25% and 100% (TABLE 1 in the main text).



SUPPLEMENTARY FIG. 3 Number of potential mothers, female chicks and reproductive rate per year from 2012 to 2019 for $RR_{Baseline}$. In addition, the mean reproductive rate across years is plotted.

2.2.2 RR_{Status quo}

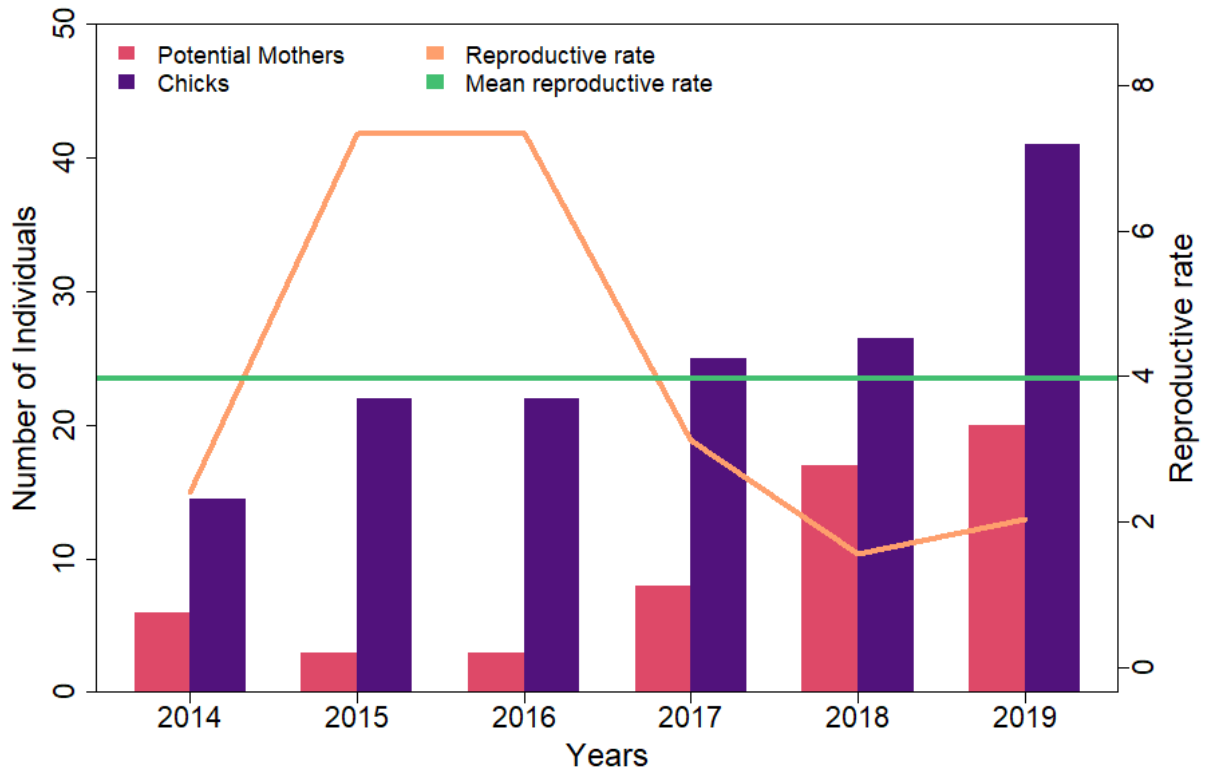
The calculated reproductive rate for this option was 1.41 (± 0.81) for a total of 75.5 chicks over 8 years (SUPPLEMENTARY FIG. 4; SUPPLEMENTARY TABLE 1).



SUPPLEMENTARY FIG. 4 Number of potential mothers, female chicks and reproductive rate per year from 2012 to 2019 for RR_{Status quo}. In addition, the mean reproductive rate across years is plotted.

2.2.3 RR_{All chicks}

The highest value for the reproductive rate was 3.97 (± 2.66) for a total of 151 chicks over 6 years (SUPPLEMENTARY FIG. 5; SUPPLEMENTARY TABLE 1).



SUPPLEMENTARY FIG. 5 Number of potential mothers, female chicks and reproductive rate per year from 2014 to 2019 for $RR_{All\ chicks}$. In addition, the mean reproductive rate across years is plotted.

The explained values for $RR_{Baseline}$, $RR_{Status\ quo}$ and $RR_{All\ chicks}$ were used for the simulations with *NetLogo* and the *BehaviorSpace* tool (TABLE 1 in the main text).

SUPPLEMENTARY TABLE 1 Counted female chicks of biological parents (BPs) and potential mothers (raising types BP and FP (foster parent raised)) and the calculated reproductive rate per year for RR_{Baseline} , $RR_{\text{Status quo}}$ and $RR_{\text{All chicks}}$. In the number of chicks per year, half of the chicks of unknown sex were integrated, i.e. we used the sex-ratio of 1:1 to assign the chicks either to female or male. Thus, in some years this resulted in 0.5 chicks. For $RR_{\text{Status quo}}$ we included the chicks of BP females in the population and the temporarily added females as considered female chicks. For $RR_{\text{All chicks}}$ we included the chicks of BP females in the population and the FP raised chicks per year as considered female chicks. The mean annual RR_{Baseline} is 0.53 ± 0.17 SD across the years 2012–2019. The mean annual $RR_{\text{Status quo}}$ is 1.41 ± 0.81 across the years 2012–2019. The mean annual $RR_{\text{All chicks}}$ is 3.97 ± 2.66 across the years 2014–2019.

Category/year	2012	2013	2014	2015	2016	2017	2018	2019
Potential mothers (BP, FP)	4	4	6	3	3	8	17	20
Considered female chicks for RR_{Baseline} (BP)	2.50	3.00	3.50	1.00	1.00	3.00	9.50	14.00
Resulting RR_{Baseline}	0.63	0.75	0.58	0.33	0.33	0.38	0.56	0.70
Considered female chicks for $RR_{\text{Status quo}}$ (BP)	4.50	3.00	6.50	9.00	7.00	8.00	14.50	23.00
Resulting $RR_{\text{Status quo}}$	1.13	0.75	1.08	3.00	2.33	1.00	0.85	1.15
Considered female chicks for $RR_{\text{All chicks}}$ (BP, FP)			14.50	22.00	22.00	25.00	26.50	41.00
Resulting $RR_{\text{All chicks}}$			2.42	7.33	7.33	3.13	1.56	2.05

2.2.4 Reproductive rate per raising type

We calculated a reproductive rate for FP NBI (RR_{FP}) of $0.56 (\pm 0.14)$ for a total of 24 potential mothers and 30 female fledglings over 8 years (SUPPLEMENTARY TABLE 2). Additionally, we calculated a reproductive rate for BP NBI (RR_{BP}) of $0.34 (\pm 0.31)$ for a total of 7 potential mothers and 5.5 female fledglings over 3 years (SUPPLEMENTARY TABLE 2).

SUPPLEMENTARY TABLE 2 Counted female chicks of biological parents (BPs) and potential mothers and the calculated reproductive rate per year for biological parent raised NBI (BP) and foster parent raised NBI (FP). In the number of female chicks per year, half of the chicks of unknown sex were integrated, i.e. we used the sex-ratio of 1:1 to assign the chicks either to female or male, Thus in some years this resulted in 0.5 chicks. The mean annual reproductive rate of FP NBI is 0.56 ± 0.14 SD across the years 2012–2019 with a total of 24 potential mothers and 30 female fledglings. The mean annual reproductive rate of BP NBI is 0.34 ± 0.31 SD across the years 2017–2019 with a total of 7 potential mothers and 5.5 female fledglings.

Category/year	2012	2013	2014	2015	2016	2017	2018	2019
Potential mothers FP	4	4	6	3	2	4	11	15
Female chicks (only BP) FP mothers	2.00	2.00	3.00	1.00	1.00	3.00	7.00	11.00
Resulting RR_{FP}	0.50	0.50	0.50	0.33	0.50	0.75	0.64	0.73
Potential mothers BP						4	6	5
Female chicks (only BP) BP mothers						0	2.50	3.00

Resulting RR_{BP}	0	0.42	0.60
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2.2.5 Reproductive rate per colony

We calculated a reproductive rate for the colony in Burghausen (RR_B) of $0.59 (\pm 0.40)$ for a total of 13 potential mothers and 22.5 female fledglings over 8 years (SUPPLEMENTARY TABLE 3). Additionally, we calculated a reproductive rate for the colony in Kuchl (RR_K) of $0.42 (\pm 0.26)$ for a total of 12 potential mothers and 15 female fledglings over 6 years (SUPPLEMENTARY TABLE 3).

SUPPLEMENTARY TABLE 3 Counted female chicks of biological parents (BPs) and potential mothers and the calculated reproductive rate per year for the NBI colonies in Burghausen (B) and Kuchl (K). In the number of female chicks per year, half of the chicks of unknown sex were integrated, i.e. we used the sex-ratio of 1:1 to assign the chicks either to female or male. Thus in some years this resulted in 0.5 chicks. The mean annual reproductive rate of the colony in Burghausen is 0.59 ± 0.40 SD across the years 2012–2019 with a total of 13 potential mothers and 22.5 female fledglings. The mean annual reproductive rate of the colony in Kuchl is 0.42 ± 0.26 SD across the years 2014–2019 with a total of 12 potential mothers and 15 female fledglings.

Category/year	2012	2013	2014	2015	2016	2017	2018	2019
Potential mothers B	4	4	3	0	1	5	6	6
Female chicks (only BP) B	2.50	3.00	2.50	0	0	3.00	4.50	7.00
Resulting RR_B	0.63	0.75	0.83	0	0	0.60	0.75	1.17
Potential mothers K			3	3	2	3	9	9
Female chicks (only BP) K			1.00	1.00	1.00	0	5.00	7.00
Resulting RR_K			0.33	0.33	0.50	0	0.56	0.78

TRACE document

This is a TRACE document (“TRAnsparent and Comprehensive model Evaludation”) which provides supporting evidence that our model presented in this article was thoughtfully designed, correctly implemented, thoroughly tested, well understood, and appropriately used for its intended purpose. The rationale of this document follows:

Schmolke A, Thorbek P, DeAngelis DL, Grimm V. 2010. Ecological modelling supporting environmental decision making: a strategy for the future. *Trends in Ecology and Evolution* 25: 479-486.

and uses the updated standard terminology and document structure in:

Grimm V, Augusiak J, Focks A, Frank B, Gabsi F, Johnston ASA, Kułakowska K, Liu C, Martin BT, Meli M, Radchuk V, Schmolke A, Thorbek P, Railsback SF. 2014. Towards better modelling and decision support: documenting model development, testing, and analysis using TRACE. *Ecological Modelling* 280: 129-139.

and

Augusiak J, Van den Brink PJ, Grimm V. 2014. Merging validation and evaluation of ecological models to ‘evaludation’: a review of terminology and a practical approach. *Ecological Modelling* 280: 117-128.

3.1 Model description

Summary: The purpose of the model is to investigate the population viability of the reintroduced Northern Bald Ibis (NBI) population. We tested how the demographic effects of survival and reproduction probabilities for the four different stages, as analysed from field data, changed the model predictions about the population viability. Only females are considered in the model.

3.1.1 Purpose

The purpose of the model is to investigate if the reintroduced NBI population is viable. We tested how different survival probabilities and reproduction probabilities changed the model predictions.

3.1.2 Entities, state variables, and scales

The model entities are female individuals in four different stages (SUPPLEMENTARY TABLE 3.4). All individuals are described by constant state variables, Raising type (raising type in Stage 1), and their age (Years of life). One step in the simulation corresponds to one year. Each run takes 50 years, and we did 100 repetitions per run. Space is not considered.

3.1.3 Process overview and scheduling

At each time step, a year, the entities, female NBI, go through the processes in the following order: *breeding*, *death* and *aging*.

Breeding: Only the adults, NBI in stage 4, can reproduce at the beginning of each time step and produce female chicks. For the simulation of the baseline scenario, we included the standard deviation across years, so the reproductive rate varies in each time step, i. e. year, adding environmental variability such as good or bad years to the simulations.

Death: For every stage there is a certain mortality probability, the opposite of our calculated survival probabilities and their improvements (SUPPLEMENTARY TABLE 3.5). We included the standard deviation only for the simulation of the baseline scenario, described under 3.1.7.2.2 `death_juveniles`, `death_one_year_olds`, `death_two_year_olds`, `death_adults`.

Aging: The state variable age will be updated during the *aging* process synchronously for all individuals at the end of each time step. All individuals who reach the age of 25 years will be removed ('die') as this is the maximum lifespan of an NBI (Bowden, 2015).

SUPPLEMENTARY TABLE 3.4 Entities, their corresponding state variables and possible status or units. In brackets: Notation in the NetLogo Code.

Entity (code notation)	State variable (code notation)	Status/Units
Stage 1 Juveniles: Fledgling and first-time migrator, either with foster parents or biological parents For BP: first-time migration back to breeding area alone in spring (Number_Juveniles)	Age (age) Raising type (raising)	Numeric (years) FP (foster parent raised), BP (biological parent raised)
Stage 2 1-Year-Old : for BP: experienced migrator; for FP: in wintering grounds (Number_Subadults_Age1)	Age (age) Raising type (raising)	Numeric (years) FP (foster parent raised), BP (biological parent raised)
Stage 3 2-Year-Old: for BP: experienced migrator; for FP: in wintering grounds and first-time migration back to breeding area alone (Number_Subadults_Age2)	Age (age) Raising type (raising)	Numeric (years) FP (foster parent raised), BP (biological parent raised)
Stage 4 Adults: reproductive age class and experienced migrator (Number_Adults)	Age (age) Raising type (raising)	Numeric (years) FP (foster parent raised), BP (biological parent raised)

3.1.4 Design concepts

Basic principles. The model is based on the demographic effects of mortality and reproduction probabilities for different stages as analysed from field data.

Emergence. The population trajectories emerge from the underlying processes of mortality and reproduction and may vary because of different survival and reproduction probabilities. Even with the same probabilities different results are possible due to environmental stochasticity.

Sensing. NA

Interaction. There are no interactions between agents. Only females are considered

Stochasticity. We have stochasticity in the birth and death processes. We took a random number for each individual and compared it to the number of the death probability for the respective stage of the individual. If the random was number smaller, the agent died. And we took a random number for each individual in stage 4 and compared it with the value for the reproduction. If the random number was smaller, the agent reproduced. And only for the simulation of the baseline scenario did we additionally implement the standard deviation for the survival and reproduction probabilities. Thus, the survival and reproduction probabilities changed at each time step and were within one standard deviation. Then we proceeded as described above.

Collectives. The individuals are assigned to 2 different raising types and 3 different colonies (SUPPLEMENTARY TABLE 3.4). In this model, for the simulation for H1, the different groups have no effects on survival and reproduction. But for H2 and H3 we calculated different survival and reproduction probabilities depending on the raising type (H2) or the colony (H3), as explained in the main text.

Observation. Number of individuals, individuals per raising type, individuals per stage. All numbers were gathered at each time step. Please note that we only modelled the female part of the population.

3.1.5 Initialization

The values for the female start population at time $t = 0$ are 37 juveniles, 11 One-Year-Old NBI, 8 Two-Year-Old NBI and 18 adults. The values for the start population were taken from the field data from the Waldrappteam.

SUPPLEMENTARY TABLE 3.5 Parameters used for the individual-based model in NetLogo. Parameters are described with their definition, baseline value in the simulation (baseline scenario), other possible values (in different combinations in the other scenarios) and unit. In brackets in the column default value: standard deviation (SD).

Name	Definition	Baseline value (\pm SD)	Other possible values	Unit
Number_Juveniles	Number of female individuals in Stage 1	37	-	Number
Number_Subadults_Age1	Number of female individuals in Stage 2	11	-	Number
Number_Subadults_Age2	Number of female individuals in Stage 3	8	-	Number
Number_Adults	Number of female individuals in Stage 4	18	-	Number
Mortality_Juveniles	Mortality probability of individuals in Stage 1 (s1)	0.36 (\pm 0.36)	0.20, 0.30	
Mortality_Subadults_Age1	Mortality probability of individuals in Stage 2 (s2)	0.26 (\pm 0.35)	0.08, 0.19	
Mortality_Subadults_Age2	Mortality probability of individuals in Stage 3 (s3)	0.31 (\pm 0.35)	0.14, 0.24	
Mortality_Adults	Mortality probability of individuals in Stage 4 (s4)	0.22 (\pm 0.14)	0.02, 0.14	
Repro_Rate	Probability to hatch a chick	0.53(\pm 0.17)	0.58, 0.66, 1.06, 1.41, 3.97	

3.1.6 Input data

The model does not use input data.

3.1.7 Sub models

There are three main sub models (*breeding, death, aging*) and for the baseline scenario there are six submodels (*breeding_sd, death_juveniles, death_one_year_olds, death_two_year_olds, death_adults, aging*).

3.1.7.1 Baseline values and Improvements

For these scenarios, which were simulated with the baseline values and the improved values for reproduction and survival, we only simulated the mean reproductive rate and survival values without including the standard deviation.

3.1.7.1.1 Breeding

How many chicks a female hatches is defined through the reproductive rate, i. e. the number of fledged chicks per female. As potential mothers only individuals in Stage 4 count, because only these reached sexual maturity.

Is the reproductive rate < 1 , a random number between 0-1 is drawn. If this value is smaller than the reproductive rate the female hatches a chick otherwise not. Is the reproductive rate between 1 and 2 a random number between 1 and 2 is drawn. Is the value smaller than the reproductive rate the female hatches 2 chicks otherwise 1. Is the reproductive rate between 2 and 3 a random number between 2 and 3 is drawn. Is the value smaller than the reproductive rate the female hatches 3 chicks otherwise 2. Is the reproductive rate between 3 and 4 a random number between 3 and 4 is drawn. Is the value smaller than the reproductive rate the female hatches 4 chicks otherwise 3.

All born chicks have the raising type “BP”.

3.1.7.1.2 Death

For each stage there is a unique mortality probability (Mortality_Juveniles, Mortality_Subadults_Age1, Mortality_Subadults_Age2, Mortality_Adults). Each stage is defined through the age, and for each individual in one of the stages a random number between 0 and 1 is drawn. Is this number smaller than the respective mortality probability the individual dies.

3.1.7.1.3 Aging

At the end of each time step the individuals age one year. Individuals from stage 1, 2 or 3 reach the next stage. Individuals in stage 4 remain in this stage until the end of their life, but their age status is updated. Chicks are in the first stage. Individuals older than 25 years will die.

3.1.7.2 Baseline scenario

For this scenario, which was simulated only with the baseline values for reproduction and survival, we included the standard deviation. Every year a new survival and reproduction probability was set for each individual. This corresponds to demographic stochasticity.

3.1.7.2.1 Breeding_sd

Only females in stage 4 were included. We bounded the reproductive rates within their standard deviations as follows: A counter variable will be set to 0. While this counter variable is 0, a random number will be drawn from a normal distribution with mean = reproductive rate ± 1 SD (step_repro; SUPPLEMENTARY TABLE 3.5). Is this value <1 or >0 , the counter variable will be set to 1 and the while loop ends. Then a random number between 0 and 1 will be drawn. Please note that for the baseline scenario the reproductive rates were <1 (see chapter 3.1.7.1.1 Breeding). Is this number smaller than step_repro the female hatches a chick, otherwise not. The step_repro will be drawn each time step for each individual. The raising type is again set to "BP".

3.1.7.2.2 death_juveniles, death_one_year_olds, death_two_year_olds, death_adults

We bounded the mortality probabilities within their standard deviations in the following way: A counter variable will be set to 0. While this counter variable is 0, a random number will be drawn from a normal distribution with mean as given by the average mortality probability for each stage ± 1 SD (step_mortality). Is this value <1 or >0 the counter variable will be set to 1 and the while loop ends. Then a random number between 1 and 0 will be drawn. Is this number smaller than the step_mortality of the stage, the individual dies. The step_mortality will be drawn each time step for each individual in the respective stage accounting for demographic stochasticity.

3.2 Model analysis

Summary: We analysed the model in two ways: (I) management improvement scenarios and (II) stochastic event and juvenile supplement sub-scenarios.

For the management improvement scenarios, we tested the different combinations of the parameters for survival (s1-s4) and reproductive rate (RR; calculations are described in the main text).

3.2.1 Management improvement scenarios

The first model analysis is the management improvement scenarios. Here we performed local and global sensitivity analyses. At first, we tested different sets, the scenarios, of the parameters for survival (s1-s4) and reproductive rate (RR) (calculations are described in the main text and SUPPLEMENTARY MATERIAL 2). Here either one of the parameters (local sensitivity analysis) or more were changed (global sensitivity analysis). For both ways we analysed the population trajectories on the basis of the number of individuals per scenario and per time step (year). Furthermore, we calculated the extinction probability as the number of runs of 100 repetitions per scenario where the population died out (0 individuals), and lambda, the intrinsic growth rate of the population. Scenarios where $\lambda > 1$, which

means population growth, and extinction probability $\leq 5\%$ were chosen for more detailed analyses. We used a 5% limit as this is a commonly used limit for extinction probability of the MVP (Flather et al., 2011). The distribution of the input parameters of mortality and reproduction probabilities in scenarios where $\lambda > 1$ and extinction probability $\leq 5\%$ was analysed. In addition, we set up a generalized linear model (glm) to rank the effects of survival and reproduction probabilities on λ (see also SUPPLEMENTARY MATERIAL 5). Beside this we chose scenarios of special interest for closer examination. These are: baseline, juvenile survival (s1) improved by 10% and 25%; adult survival (s4) improved by 10% and 25%; reproductive rate (RR) improved by 10%, 25%, 100%; 10% and 25% improved survival for all stages, 10% and 25% improved survival for all stages and for reproductive rate, “status quo” and “all chicks”.

3.2.2 Stochastic event and juvenile supplement sub-scenarios

The second analysis dealt with the topics stochastic events and supplementation of FP juveniles. Stochastic events can be e. g. droughts or storms. We chose from the scenarios of special interest, the scenarios where $\lambda > 1$ and extinction probability $\leq 5\%$. For the supplements we assumed 15 or 30 juveniles were added per year for the duration of 4 or 7 years. The stochastic events were modelled with frequencies between 5 and 20% (5, 10, 15, 20). This corresponds to a mean frequency of every 20 years to every 5 years, respectively. The severity of the stochastic events was assumed to be between 5 to 25% (5, 10, 15, 20, 25) additional mortality per stochastic event. This resulted in 80 combinations of these values, the sub-scenarios, per scenario. We calculated λ , the intrinsic growth rate of the population, and extinction probability, number of runs of 100 repetitions per case where the population died out (0 individuals) and analysed the distribution between the mortality rates per stage and the reproductive rate. Additionally, we set up a GLMs (see main text). λ was the response variable, and the predictor variables were formed by the survival probabilities per stage (s1-s4), the reproductive rate (RR) and the stochastic event frequency and severity. Besides, we looked how often each combination of stochastic event frequency (5-20%) and severity (5-25%) and each combination of numbers of supplements (15 or 30) and time (4 or 7 years) were used. This is also a global sensitivity analysis where several parameters were changed simultaneously.

3.3 References

- BOWDEN, C.G.R. (2015) International Single Species Action Plan for the Conservation of the Northern Bald Ibis (*Geronticus eremita*). *AEWA Technical Series No. 55*, 55.
- FLATHER, C.H., HAYWARD, G.D., BEISSINGER, S.R. & STEPHENS, P.A. (2011) Minimum viable populations : is there a ‘ magic number ’ for conservation practitioners ? *Trends in Ecology and Evolution*, 26, 307–316. Elsevier Ltd.

SUPPLEMENTARY MATERIAL 4 Data and code availability.

The data and the code for the analysis in *R* and the simulations in *NetLogo* can be found on:

Zenodo: <https://doi.org/10.5281/zenodo.6790671>

CoMSES: <https://www.comses.net/codebases/f021a012-1507-417f-88ad-d181914219d1/releases/1.0.0/>

GitHub: https://github.com/EcoDynIZW/Drenske_2022_Oryx

5.1 Equations for the number of scenarios in *NetLogo*

5.1.1 Management improvement scenarios

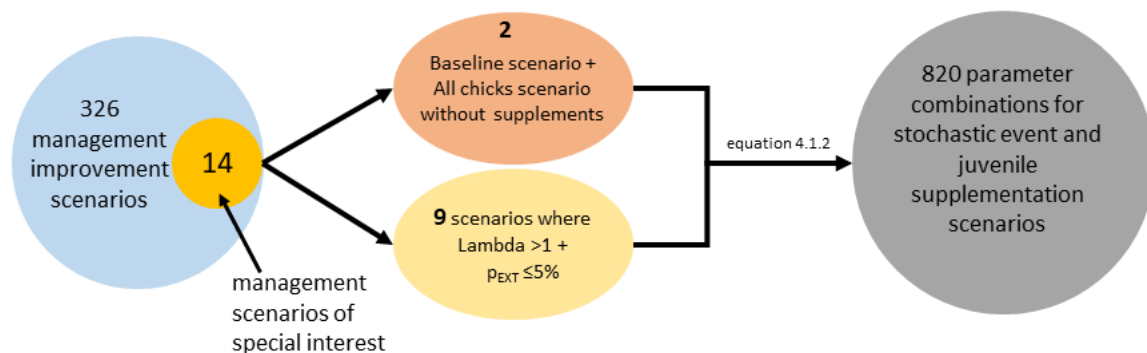
No. Scenarios = 3 possible values for s_1 * 3 possible values for s_2 * 3 possible values for s_3 * 3 possible values for s_4 * 4 possible values for RR + “Status quo”-Scenario + “All chicks”-Scenario = 326 (4),

where s_1 = juveniles with their first migration to the wintering grounds, s_2 = 1-year-old NBI that stay in the wintering grounds, s_3 = 2-year-old birds with the first independent migration back to the breeding area, s_4 = reproductive adults, RR = RR_{Baseline} and the improvements.

5.1.2 Stochastic event and juvenile supplementation scenarios

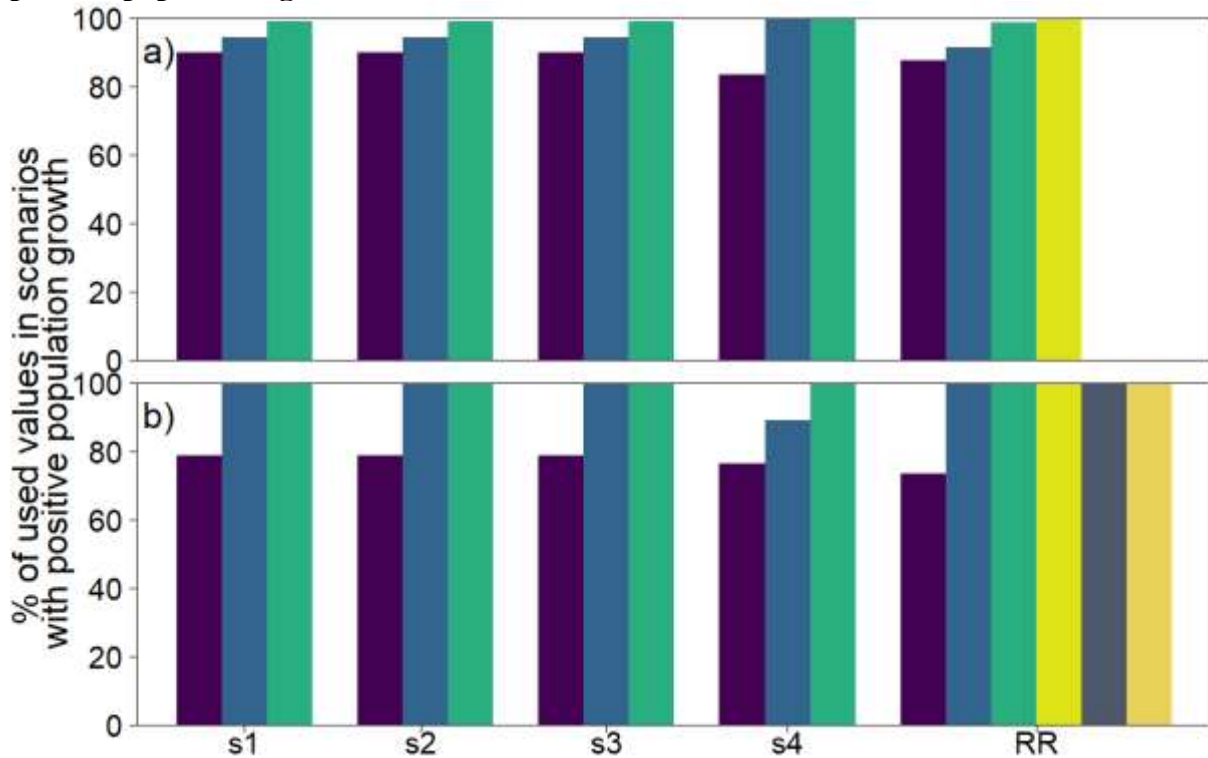
No. cases = $1a * 4 \text{ freq} * 5 \text{ severity} + 10 \text{ sc} * 4 \text{ freq} * 5 \text{ severity} * 2 \text{ supplements} * 2 \text{ time} = 820$ (5),

where a = all chicks scenario, freq = possible values for stochastic event frequency, severity = possible values for stochastic event severity, sc = Baseline scenario and 9 out of 14 scenarios of special interest where $\lambda > 1$ and extinction probability $\leq 5\%$, supplements = possible values for number of supplements, time = possible durations of supplementing individuals. All possible combinations were tested.



SUPPLEMENTARY FIG. 6 Scheme for the calculation of the number of parameter combinations for the stochastic event and juvenile supplementation scenarios.

5.2 Percentage distribution of values for survival and reproduction in scenarios with positive population growth



SUPPLEMENTARY FIG. 7 a) Percentage of values of survival (s1-s4) and reproduction probabilities (RR) occurring in 308 out of 326 management improvement scenarios where $\lambda > 1$ and extinction probability $P_{EXT_50} \leq 5\%$. The scenarios 'status quo' and 'all chicks' were not considered. b) Percentage of values of survival (s1-s4) and reproduction probabilities (RR) in the 714 stochastic event and supplement sub-scenarios where $\lambda > 1$ and extinction probability $P_{EXT_50} \leq 5\%$. The scenarios 'status quo' and 'all chicks' were considered. Purple: Baseline value. Blue: Baseline value increased by 10%. Green: Baseline value increased by 25%. Yellow: Baseline value increased by 100%. Grey blue: 'Status quo' value. Dark yellow: 'All chicks' value.

SUPPLEMENTARY MATERIAL 6 Description of the generalized linear models (GLMs)

6.1 Management improvement scenarios

We tested how lambda was influenced by the survival of juvenile NBI (s1), 1-year old NBI (s2), 2-years old NBI (s3), adult NBI (s4) and the reproductive rate (RR). In this analysis, we have taken into account the mean values of 100 runs per scenario for all 326 scenarios (N = 326). The model was formulated as generalized linear model with gamma error distribution and identity link function in R-Studio. Additionally, we formulated a general additive linear model. The formulas as R code were as follows, where k is the number of smoothing splines:

$$glm \quad \text{Lambda} \sim (s1 + s2 + s3 + s4) * RR \quad (6)$$

$$gam \quad \text{Lambda} \sim s(s1, k = 3) + s(s2, k = 3) + s(s3, k = 3) + s(s4, k = 3) + s(RR, k = 3) \quad (7)$$

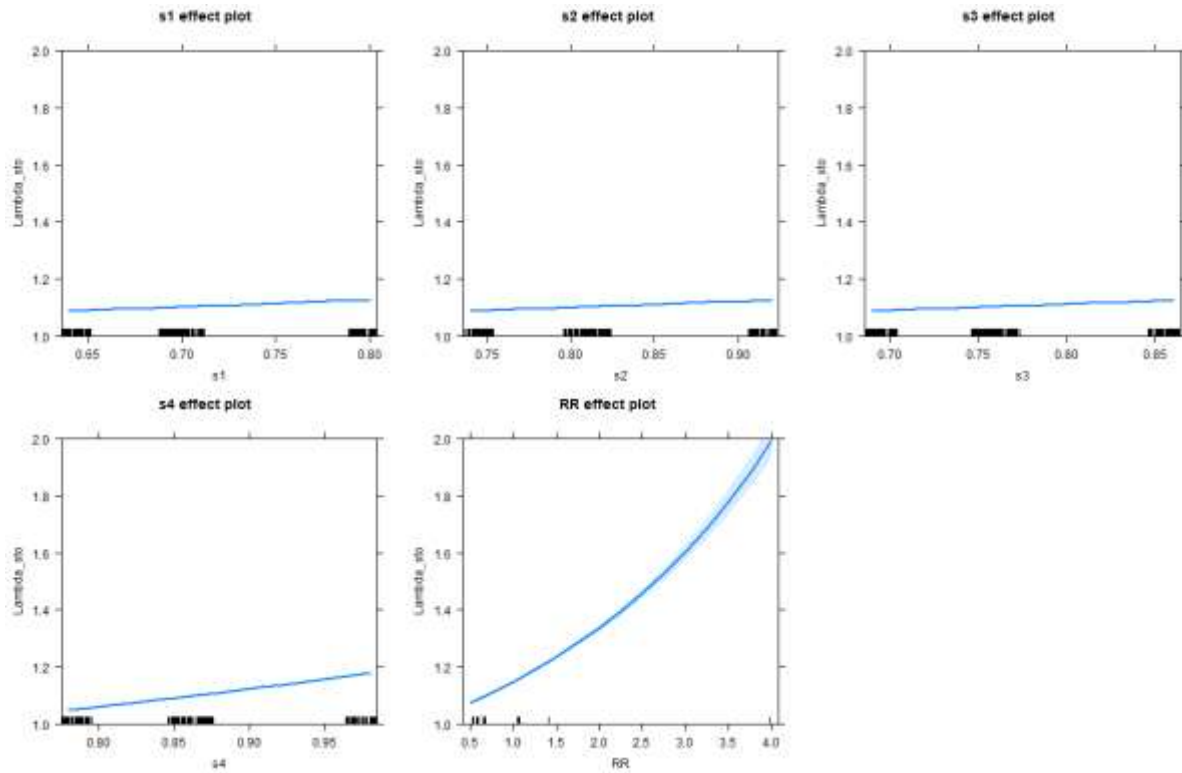
All explanatory variables had a significant effect on lambda, but s4 had the strongest effect (SUPPLEMENTARY TABLE 6; SUPPLEMENTARY TABLE 5). The effect plots of the glm and perspective plots of the gam of the explanatory variables confirm this result (SUPPLEMENTARY FIG. 8; SUPPLEMENTARY FIG. 9). The effect plots were made with the *ggeffects* package in R (Lüdtke, 2018). R² is 0.97 and the effect size for a significance level of 0.05, a N of 326 and a power of 0.8 is 0.20. To calculate the effect size, we used the *pwr* package in R (Champely, 2020).

SUPPLEMENTARY TABLE 6 Summary of the results of the glm model and the effects of the explanatory variables s1 (juvenile survival), s2 (survival 1 year old NBI), s3 (survival 2 years old NBI), s4 (adult survival) and RR (reproductive rate) on lambda. t value = value of the test statistic.

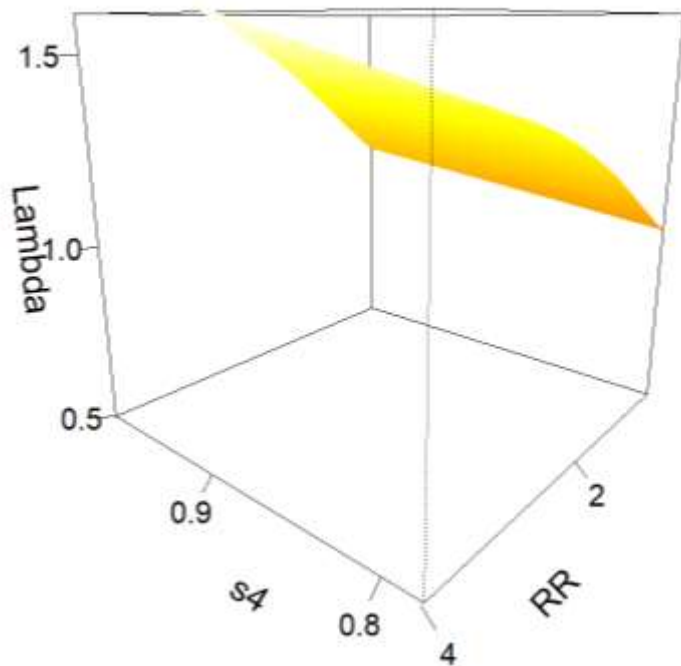
Explanatory variable	Estimate (± SE)	t value	p value
s1	-0.20 (± 0.01)	-15.59	<0.0001***
s2	-0.17 (± 0.01)	-14.99	<0.0001***
s3	-0.18 (± 0.01)	-15.06	<0.0001***
s4	-0.52 (± 0.01)	-51.15	<0.0001***
RR	-0.12 (± 0.00)	-49.43	<0.0001***

SUPPLEMENTARY TABLE 7 Summary of the results of the ANOVA of the glm model and the effects of the explanatory variables s1 (juvenile survival), s2 (survival 1 year old NBI), s3 (survival 2 years old NBI), s4 (adult survival) and RR (reproductive rate) on lambda. Df = degrees of freedom.

Explanatory variable	Deviance	Residual Deviance	Df	Residual Df	p value
s1	0.05	1.45	1	324	<0.0001***
s2	0.05	1.41	1	323	<0.0001***
s3	0.05	1.36	1	322	<0.0001***
s4	0.68	0.68	1	321	<0.0001***
RR	0.58	0.10	1	320	<0.0001***



SUPPLEMENTARY FIG. 8 Plots of the effects of each explanatory variable of the GLM for the management improvement scenarios on the extinction probability. The explanatory variables are: s1 (juvenile survival), s2 (survival 1 year old NBI), s3 (survival 2 years old NBI), s4 (adult survival) and RR (reproductive rate). Solid line: mean effect. Blue area: confidence interval. Please consider the different x-axis and y-axis ranges.



SUPPLEMENTARY FIG. 9 Perspective plot of the explanatory variables of a GAM for the management improvement scenarios. Plot of the effects of s4 (adult mortality) and RR (reproductive rate) on lambda. The effect plots are based on a GAM and not a GLM. However, this does not change the significance.

SUPPLEMENTARY MATERIAL REFERENCES

- BIRDLIFE INTERNATIONAL (2017) *Geronticus eremita*. *The IUCN Red List of Threatened Species 2017*.
- BIRDLIFE INTERNATIONAL (2018) *Geronticus eremita*. In *The IUCN Red List of Threatened Species 2018* p. .
- BÖHM, C., BOWDEN, C.G.R., SEDDON, P.J., HATIPOĞLU, T., OUBROU, W., EL BEKKAY, M., ET AL. (2020) The northern bald ibis *Geronticus eremita*: history, current status and future perspectives. *Oryx*, 55, 934–946.
- BÖHM, C. & PEGORARO, K. (2011) *Der Waldrapp Geronticus eremita: Ein Glatzkopf in Turbulenzen*, 1st edition. VerlagsKG Wolf, Neue Brehm-Bücherei, Bd. 659, Magdeburg, Germany.
- BOWDEN, C.G.R. (2015) International Single Species Action Plan for the Conservation of the Northern Bald Ibis (*Geronticus eremita*). *AEWA Technical Series No. 55*, 55.
- BOWDEN, C.G.R., AGHNAJ, A., SMITH, K.W. & RIBI, M. (2003) The status and recent breeding performance of the critically endangered Northern Bald Ibis *Geronticus eremita* population on the Atlantic coast of Morocco. *Ibis*, 145, 419–431.
- BOWDEN, C.G.R., SMITH, K.W., EL BEKKAY, M., OUBROU, W., AGHNAJ, A. & JIMENEZ-ARRESTO, M. (2008) Contribution of research to conservation action for the Northern Bald Ibis *Geronticus eremita* in Morocco. *Bird Conservation International*, 18, S74–S90. Cambridge University Press.
- CHAMPELY, S. (2020) pwr: Basic Functions for Power Analysis v1.3-0. <https://cran.r-project.org/package=pwr>.
- FRITZ, J., KRAMER, R., HOFFMANN, W., TROBE, D. & UNSÖLD, M. (2017) Back into the wild: establishing a migratory Northern bald ibis *Geronticus eremita* population in Europe. *International Zoo Yearbook*, 51, 107–123.
- FRITZ, J. & UNSÖLD, M. (2015) Internationaler Artenschutz im Kontext der IUCN Reintroduction Guidelines: Argumente zur Wiederansiedlung des Waldrapps *Geronticus eremita* in Europa. *Vogelwarte*, 53, 157–168.
- FRITZ, J., UNSÖLD, M. & VÖLKL, B. (2019) Back into European Wildlife: the reintroduction of the northern bald ibis (*Geronticus eremita*). In *Scientific Foundations of Zoos and Aquariums: their Role in Conservation and Research* (eds A.B. Kaufman, M.J. Bashaw & T.L. Maple), pp. 339–366, 1st edition. Cambridge University Press, Cambridge, UK.
- LÓPEZ, J.M. & QUEVEDO, M.A. (2016) Northern Bald Ibis Reintroduction program in Andalusia. In *Proceedings of 4th International Advisory Group for the Northern Bald Ibis (IAGNBI) meeting Seekirchen, Austria* (eds C. Böhm & C.G.R. Bowden), pp. 57–67. RSPB, The Lodge, Sandy, Bedfordshire, UK and Alpenzoo Innsbruck-Tirol, Austria.
- LÜDECKE, D. (2018) ggeffects: Tidy Data Frames of Marginal Effects from Regression Models. *Journal of Open Source Software*, 3, 772.

- SCHENKER, A. (1977) Das ehemalige Verbreitungsgebiet des Waldtrapps *Geronticus eremita* in Europa. *Der Ornithologische Beobachter*, 74, 13–30.
- SCHENKER, A., CAHENZLI, F., GUTBROD, K.G., THEVENOT, M. & ERHARDT, A. (2020) The Northern Bald Ibis *Geronticus eremita* in Morocco since 1900: Analysis of ecological requirements. *Bird Conservation International*, 30, 117–138.
- SERRA, G. (2015) The Northern Bald Ibis is extinct in the Middle East - but we can't blame it on IS. *Ecologist*.
- UNSÖLD, M. & FRITZ, J. (2011) Der Waldtrapp-ein Vogel zwischen Ausrottung und Wiederkehr. *Wildbiologie 2: 1-16.*, 2, 1–16.
- WIRTZ, S., BÖHM, C., FRITZ, J., KOTRSCHAL, K., VEITH, M. & HOCHKIRCH, A. (2018) Optimizing the genetic management of reintroduction projects: genetic population structure of the captive Northern Bald Ibis population. *Conservation Genetics*, 19, 853–864.
- YENÍYURT, C., OPPEL, S., İSFENDİYAROĞLU, S., ÖZKINACI, G., ERKOL, I.L. & BOWDEN, C.G.R. (2017) Influence of feeding ecology on breeding success of a semi-wild population of the critically endangered Northern Bald Ibis *Geronticus eremita* in southern Turkey. *Bird Conservation International*, 27, 537–549.