

# How to run the model

## „Survival analysis and Population viability analysis of the Northern Bald Ibis“

This is the full repository to run the survival analysis (in R) and run the population viability model and its analysis (NetLogo + R) of the Northern Bald Ibis (NBI; *Geronticus eremita*) presented in the study “On the road to self-sustainability: Reintroduced migratory European Northern Bald Ibises (*Geronticus eremita*) still need management interventions for population viability” by Sinah Drenske, Viktoriia Radchuk, Cédric Scherer, Corinna Esterer, Ingo Kowarik, Johannes Fritz and Stephanie Kramer-Schadt accepted by Oryx (not published yet).

## Directories

- data
  - Text file referring to the GitHub repository
- docs
  - This file
  - The TRACE file (but we left out some chapters)
- Code
  - R Project file
  - R
    - R Markdown files
  - model
    - The NetLogo models that were used for the PVA
- results
  - Text file referring to the GitHub repository

## Workflow

To carry out the analysis, first open the R project "Drenske\_2022\_Oryx". Here you first open the R script “01\_Demography\_data\_preparation” and start with the data exploration and the survival analysis in scripts 01- 05b. Then you use the NetLogo models (folder model) for the PVA. Then you analyse the results for the PVA model in R again with the scripts 06a-08 are edited. Script 09 is only used to create the html reports of the Markdown files.

All further explanations can be found in the respective scripts and in the TRACE document.