Population trends of Ospreys *Pandion Haliaetus* in Central Sweden

Dynamics and driving factors

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Population trends of Ospreys Pandion Haliaetus in Central Sweden - dynamics and driving factors

Populationstrender för fiskgjusen i Västra Mälaren

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Abstract

European Ospreys have experienced repeated declines and recoveries throughout modern history. The overall number of breeding Ospreys in this region has increased since 1970 after suffering severe effects from compounds such as DDT and PCB in the decades prior. However, while Sweden can be seen as a stronghold for the European osprey, national population numbers rely heavily on unprecise estimations. This paper explores an osprey population, by analysing and comparing unique time series data on breeding ospreys in Västra Mälaren, Sweden, between two time periods – 1977-1986 and 2005-2011. The number of breeding attempts, successful attempts, number of fledglings and nest trees was analysed using various statistical tools, including general linear models. Furthermore, significant findings were put in comparison to existing literature on reported population changes and their driving factors. Results show a significant decline in the number of breeding attempts (23 %) between the two periods. There was no statistically significant difference in breeding success or number of fledged chicks between the two periods. 71 % of all attempts took place in pine, 25 % in spruce and 4 % in various deciduous trees with no significant difference between the periods. As the osprey mostly breeds in pine, the notably high proportion of nests in spruce may be seen as an indication of a scarcity of suitable nest trees, especially if white-tailed eagles compete for nest trees. Using literature data on adult to juvenile survival rates together with this study’s reproductive data, the study also investigated how much survival rates and proportion of non-breeders need to change to cause the observed decline in number. A three percent decline in adult survival would be enough to reflect the observed population decline in Västra Mälaren. Hence, factors as reduced survival in relation to migration might also be the main driving factor behind the decline. The proven decline of ospreys in the study area contrast national estimates of an increasing or stable population.

Svensk sammanfattning

Fiskgjusen i Europa har genom historien genomgått upprepade perioder av populationsminskning och återhämtning. Det totala antalet häckande fiskgjusar i Europa har ökat sedan 1970-talet, efter att tidigare ha drabbats hårt av miljögifter som DDT och PCB. Sverige kan ses som ett starkt fäste för den europeiska fiskgjusen, men nationella populationsuppskattningar bygger till stor del på osäkra bedömningar. Denna studie undersöker en fiskgjusepopulation genom att analysera och jämföra unika tidsseriedata från Västra Mälaren under två tidsperioder – 1977–1986 och 2005–2011. Antalet häckningsförsök, lyckade häckningar, antal ungar och trädslag för bon analyserades med olika statistiska metoder, bland annat generella linjära modeller (GLM). Signifikanta resultat jämfördes med befintlig litteratur på populationsförändringar och dess bakomliggande faktorer. Resultaten visar en signifikant minskning i antalet häckningsförsök (23 %) mellan de två perioderna. Det fanns ingen statistiskt signifikant skillnad i häckningsframgång eller antal flygga ungar. 71 % av alla häckningsförsök ägde rum i tall, 25 % i gran och 4 % i olika lövträd, utan någon signifikant skillnad mellan perioderna. Eftersom fiskgjusen främst häckar i tall, kan den relativt höga andelen bon i gran eventuellt tolkas som ett tecken på brist gällande lämpliga boträd, speciellt i kombination med konkurrens från havsörn. Med hjälp av litteraturdata om överlevnad hos vuxna och ungfåglar samt denna studies reproduktionsdata, undersöktes även hur förändringar i överlevnad och andel icke häckande individer skulle kunna förklara den observerade nedgången i antalet häckningar. En minskning i vuxna fåglars överlevnad med tre procent skulle vara tillräcklig för att motsvara den observerade populationsminskningen. Faktorer som minskad överlevnad i samband med migration skulle alltså också kunna resultera i en sådan populationsminskning som klarlagts Västra Mälaren. Den påvisade nedgången i studieområdet står i kontrast till nationella uppskattningar som anger att populationen är stabil eller ökande.

Keywords: Osprey, Pandion haliaetus, Population decline, Population dynamics, Data analysis, GLM, Swedish osprey population

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I would like to express my sincere gratitude to Håkan Gilledal for generously sharing the long-term data on osprey breeding in Västra Mälaren, without which this study would not have been possible. I also wish to thank my supervisors, Jonas Knape and Tomas Pärt, for their valuable guidance, encouragement, and insightful feedback throughout the project. Finally, I am grateful to Jan Sondell for taking the time to discuss my findings and his results from "Projekt Fiskgjuse" over the phone.

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1. Introduction

1.1 Background and history

The osprey is, in many ways, one of the most successful raptors. With a wide wingspan, near worldwide distribution and a morphologically, exceptional adaptation to catching fish, the osprey can be viewed as a specialized generalist, bound to thrive across differing coastal and freshwater areas (Saurola 1997; Monti et al. 2015). Ospreys are long-lived (in some cases over 20 years), monogamous and most populations in the northern Hemisphere migrate during winter (Poole 1989; Bierregaard et al. 2014).

However, the populations numbers have fluctuated significantly throughout modern history (Poole 1989). In the early 1800s, many European populations of Osprey were supressed by human persecution. Throughout the 18th- and 19th centuries, osprey populations suffered further declines due to sustained anthropogenic impacts (especially persecution, leading to many populations crashing Schmidt-Rothmund et al. 2014). Situated at the top of the food chain, the osprey is vulnerable to disturbances at lower trophic levels, particularly with regard to fat-soluble contaminants due to its affinity for fish as a food.

During the 1960s and 1970s, many osprey populations suffered dramatic declines, mainly due to the established use of DDT (Spitzer & Poole 1980; Toschik et al. 2006; Monti et al. 2015). Fat-soluble contaminants, such as DDT and PCB, can have severe effects on reproduction and survival for many birds, especially at higher, trophic levels (Padayachee et al. 2023). An establishing of the causal effect between organochlorines and eggshell thinning (Ames 1966; Ratcliffe 1967), played an important role in the banning of DDT in the US and large parts of Europe in the 1970s Bierregaard et al. 2014). In parallel to a political response, the dramatic declines of ospreys (and other species situated at the higher trophic levels) also induced further scientific inquiry. A large portion of the studies focused on exploring effects caused by toxins as well as monitoring population sizes. During this time, many natural osprey populations recovered in size, in addition to several recolonizations through reintroduction programs. As a result of political action and ambitious conservation work including reintroductions, area protection and construction of artificial nests, US and European populations have been increasing since the 1970s (Bierregaard et al. 2014). The number of nesting pairs in the Western Palearctic (northern Africa, Europe and the Middle East) increased from approximately 5.500 pairs in the 1980s to between 9.500 and 11.500 in the early

21st century (Schmidt-Rothmund et al. 2014). Today, the osprey is listed as *Least Concern* (LC), and recognized as increasing, by IUCN global red list (*IUCN* 2021).

1.2 Sweden and Fennoscandia

Scandinavia and Finland hold the largest populations of osprey in Europe, and the largest national population is found in Sweden. Sweden's first nationwide survey of ospreys was performed in 1971, at the peak of chemical contamination, shortly after the 1970 ban on DDT and other organochlorines. The total number of Swedish ospreys was estimated to be about 2100 pairs (Österlöf 1977). The following years, estimates show that the osprey population size experienced a yearly increase of close to 1 % through 1993 (Saurola 1997; Svensson et al. 1999; Ottosson 2012). The results from a nationwide survey done in 2001 reported a number of between 3400 and 3700 breeding pairs (Ryttman 2004), constituting close to 40 % of the total European population (Svensson et al. 1999).

In 2008, the number of nesting Ospreys in Sweden was estimated to 4100 pairs (Ottosson 2012). However, the authors underline that this implied increase is attributed to different estimation approaches and does not state an actual increase from 2001 but rather indicates that the previous assessment was underestimated due to generalization. Thus, the "true number" may very well be found somewhere in between the two. This number, 4100, have been the most used population estimate since, and is still today communicated as the official estimated number of the the Swedish osprey population BirdLife Sverige 2023; SLU Artdatabanken 2025). Thus, while Sweden can be seen as a stronghold for the species, there is a lack of reliable data on Osprey numbers.

In contrast, Finland has a much better understanding of their national population of Ospreys, mainly as a result of a robust, national monitoring program called *Project Pandion* (Saurola 2008). In 2018, the Finnish osprey population was estimated to 1300 pairs (Saurola 2018), following a relatively constant increase from 1982 to 2013 and a stagnation since then. During this period, the breeding success increased considerably, best believed to be attributed to decreased exposure to hydrophilic compounds as well as an increased proportion of artificial nests (Saurola 2008).

1.3 Population dynamics in literature

The early studies on the osprey, mostly regarding its natural history and distribution, was published as early as the beginning of the 19th century. However, up until awareness around the ecological effects of lipophilic toxins, studies on ospreys were rare (Bierregaard et al. 2014). As noted above, several studies were mostly conducted trying to establish the effect of these compounds, especially eggshell thinning. However, there are only a few studies aimed at analysing population dynamics (e.g. survival, breeding, age distribution or dispersal demographically) (Väli et al. 2021). Henny & Wight (1969) conducted studies on population dynamics, focusing on ospreys breeding on the East Coast in the U.S. Further studies on reproduction and survival has been carried out by Spitzer et al (Spitzer & Poole 1980). In Europe, there were similar studies (Eriksson & Wallin 1994a; Ryttman 1994). Nonetheless, more recent demographical studies are rare, and most of the published papers focus on recolonizations and recently established populations. The only study from the 21st century analysing naturally recovered osprey populations was published by Väli et al. (2021), analysing demography in Baltic ospreys. Given the lack of recent research on osprey population dynamics in general, and high reliance on outdated data in Swedish estimates, there is a clear need for an updated examination of the actual status of the Swedish osprey.

1.4 The aim of the study

This paper aims to contribute to knowledge regarding population dynamics in Swedish osprey populations. Håkan Gilledal (2011) has for a long time surveyed breeding ospreys in Lake Malar (henceforth referred to as Västra Mälaren). In a summarizing report of his field work it appears that the population of breeding ospreys declined from 1977-1986 to 2005-2009, contrary to the estimations on the national population from 2008 (Ottosson 2012). The aim of the present study is to further analyse this material.

First, I aim to estimate the change in population size between the two periods mentioned above. Second, I will examine changes in reproductive performance and tree species used for nesting. Third, I explore possible demographic drivers of the observed population change using juvenile to adult survival rates obtained from previous literature and reproductive data from the present study. Finally, I will compare population estimates from other sites to those from the current study area to assess whether similar population trends were evident elsewhere.

2. Materials and Methods

In this chapter, the scope and methods of the field work will be specified. Furthermore, methods used (and not used) for statistical analysis will be motivated. Lastly, the framework of other surveys and population estimates is presented.

2.1 Data

2.1.1 Material

The data used to conduct my analysis is comprised of observations of ospreys in Västra Mälaren (figure 1) between 1971-2019. Observations were mainly made by Håkan Gilledal and Karin Stafström Gilledal. The initial aim of their data collection was to investigate the population size and reproduction as well as ringing fledglings and examine effects caused by environmental toxins. Tony Haglund and Leif Carlsson initiated this project in 1971 which reflected many similar projects sparked by population declines and legitimate cause of concern regarding the ecological effects of DDT and other pesticides (Bierregaard et al. 2014; Odsjö & Sondell 2014). Although the study began in 1971, the survey area and the method of survey had changed by 1977, when Håkan and Karin Gilledal continued to monitor nesting, breeding attempts and the number of fledged chicks, as well as nest tree characteristics, in a more systematic procedure.

The total dataset includes data from 1971-2019. However, the effort has varied over time and the years included in this study are divided into two periods: 1977 & 1979-1986 (period 1) and 2005-2011 (period 2). During these years, the survey method and sample effort is similar and therefore display a high degree of comparability. Nevertheless, as in all ecological studies, minor variation in field work methods occurred over time. This is discussed more in chapter 2.1.2 *Survey Methodology*. The figure below (figure 1) shows the total survey area, divided into three sub-areas. This division will not be used here, since they overlap and a flow of individuals between them is likely.

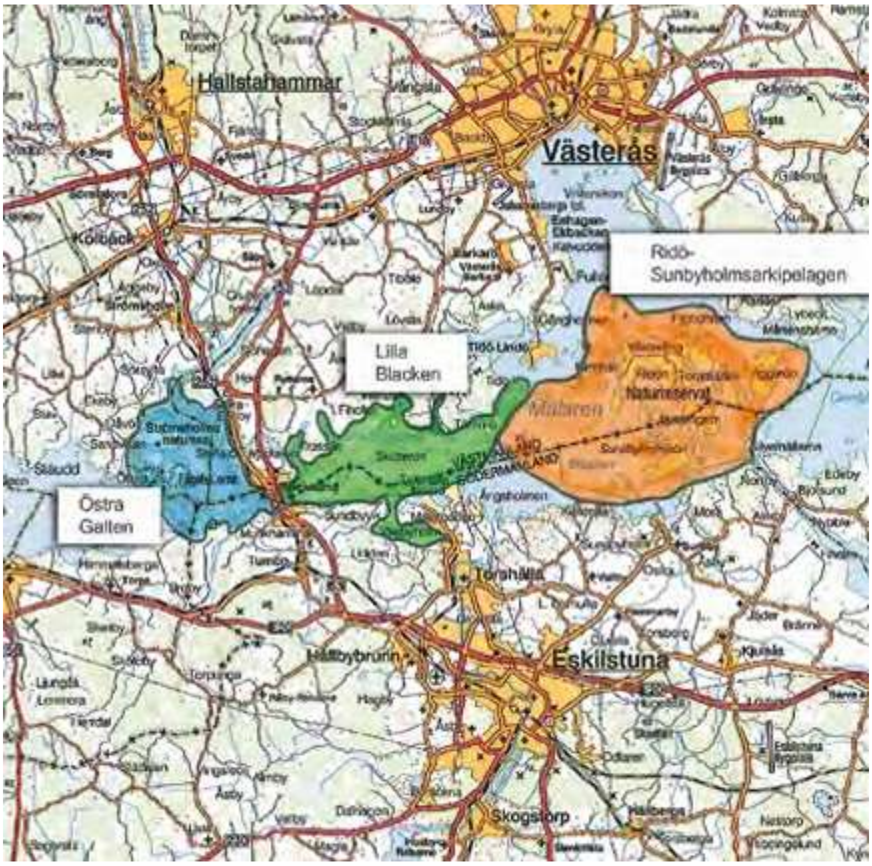

Figure 1. Map and illustration of the survey area and subdivision into the survey regions "Östra Galten, "Lilla Blacken" and "Ridö-Sundbyholmsarkipelagen" (Gilledal 2011).

2.1.2 Survey methodology

Observation of nests and eggs/fledglings was conducted in the first two weeks of May (Gilledal 2011). Known nest sites were visited and observed from a distance with binoculars or monoculars. In addition, a systematic scanning of the coastal areas was conducted to detect any new nests. For the most part, all previously known and new nests were visited in the first two weeks of May. The monitoring of breeding outcome was mainly conducted during the second and third weeks of July.

However, for some years, the first survey was performed at the end of May and beginning of June (2006 & 2009) (Gilledal 2011), which increases the risk of underestimating the number of breeding attempts due to the risk of failed, early attempts. Furthermore, surveying an area of this size always implies a risk of missing breeding events. The main area of concern is missing nest sites difficult to detect from the water. During the years 2004-2005, an extensive survey of the forest areas adjacent to the archipelago was performed by Mats Larshagen and Sveaskog, resulting in the finding of only one osprey nest, active in 2005, that was not included in this material. This suggest that the risk of missing nests further inland is marginal. Moreover, since this risk plausibly remains constant over time, a potential number of missed nests should not affect the comparison between the two time periods to a significant degree.

The criterion for a breeding attempt was considered fulfilled once a bird had been observed sitting calmly for approximately ten minutes in the nest (Gilledal 2011). This definition of a breeding attempt is applied hereafter. An observation spot was located for all nest sites, from which visual observation of hatchlings was conducted with the use of a telescope. The distance from the nest varied from 250 m to 2 km and the observation was mostly done from land, but in some cases from water (Gilledal 2011). Observation of a nest ceased when three chicks were observed - as birthing more than three chicks is extremely rare (Poole 1989; Wahl & Barbraud 2014). However, in some cases, ospreys lay more than three eggs. Over the entire study period, this was observed twice but the actual number of instances with more than three chicks is most probably higher. In some cases, full perception of the entire nest was not possible, especially in those instances where the observation was done from water. Therefore, there is a risk of underestimating the actual number of chicks. However, as this risk is expected to be constant over time, the comparison between the periods should not be affected in a substantial way.

2.2 Analysis methods

In this chapter, the scope and methodology of the data analysis will be motivated.

2.2.1 Data analysis

In order to perform data analysis, the material had to be transferred and compiled to excel and R. When exploring population changes, the crucial question is to see whether these are statistically meaningful or simple display natural variations. Linear models fit well when using count data to estimate population parameters (Morris et al. 1999). For analysis of the number of breeding attempts in the two periods a *general linear model* (GLM) was used. The use of a GLM over a "normal" linear model (OLS) was mainly motivated by the skewed residuals and the fact that the observations are shown as count data (discrete variables and not continuous) (Warton et al. 2016). A negative binomial distribution, commonly used for counts, only functions on overdispersed data (Warton et al. 2016), and was excluded because the data was found to be underdispersed. To account for underdispersion, a *Quasipoisson* family was used. With *Quassipoisson,* the dispersion was adjusted to 0.275.

In the analysis of breeding outcome, e.g. *success* or *failure*, a logistic regression (GLM) was used. It is useful this is useful in modelling this kind of data, since it translate linear inputs into the probability of adopting 0 or 1 (LaValley 2008).

Furthermore, another GLM was used for analysing reproduction numbers (average number of fledged chicks, per total attempt and per successful attempt). A poisson distribution was used since the variation (1.406) is similar to the mean (1.426), a condition required when using this type of model (Warton et al. 2016).

2.2.2 Matrix model

The aim with this part of the analysis was to explore demographical parameters affecting population size. For this, a matrix model is a powerful tool (Leslie 1945). In a case with restricted access to demographical data, a common approach is therefore to supply the model with reference values from previous literature (Morris et al. 1999; Besbeas et al. 2002). Since we do not have demographic data except for reproductive success, we used values of survival and proportion of non-breeding birds (floaters) from literature. Previous research gave values of first year survival ranged from 42 to 65 percent. Adult survival (3 years or higher), varied from 72 to 86 percent. Second year survival rates were consistently high (>80 %) (Henny & Wight 1969; Spitzer & Poole 1980; Eriksson & Wallin 1994b; Ryttman 1994; Wahl & Barbraud 2014; Väli et al. 2021). Second year data, however, must be handled with caution. Since most of these studies are based on ringing data and mark-recapture, together with the fact that most young ospreys stay in their wintering area the first year, fewer dead individuals may be found and survival may be overestimated (Österlöf 1977). The average age of first breeding seem to vary quite a bit between 3-5 years (Väli et al. 2021).

The matrix model used in this study was a 5x5, post-breeding census *Leslie matrix*. As birds are determinate growers with little variation in adult survival and fecundity, this type of model was assessed suitable (Morris et al. 1999). When creating this model, the reproductive values were first added to the matrix model in R. The main goal of this part of the analysis was to explore scenarios of potential drivers of the implied population decline - the reproductive values from period 1 was used as a first step to create a “stable” model (e.g. lambda = 1). Survival rates (1^{st}-, 2^{nd}-, 3^{rd} and 4^{th} year survival and adult survival) and proportion of non-breeders were then varied separately to achieve a decline matching the decline observed in the population between the two periods. Values for reproduction in the model reflects the average number of fledged offspring per breeding attempt. Since this number reflects all chicks, both male and female, it was divided by two, assuming an equal gender composition, which is a method often used (Clutton-

Brock & Sheldon 2010). While it is widely accepted that very few ospreys breed before the age of three, the exact age of first breeding in many populations, including this, is unclear. For this model, I assumed that 50 % of the ospreys breed for the first time at the age of three, 30 % at the age of four and 20 % at the age of five, in line with the method used by Eriksson & Wallin (1994b) and Spitzer & Poole (Spitzer & Poole 1980).

When using reference values, the given aim is for these to reflect the true processes in the studied population. Factors such as environment, geographic location, history and size of the population are all relevant when considering which data to apply (Morris et al. 1999). There are several studies analysing different elements of osprey population dynamics, although most of them focus on newly established or recolonized populations. However, two of the more robust studies, fittingly enough, concern Swedish ospreys (Eriksson & Wallin 1994b; Ryttman 1994). In my model, I initially applied Ryttman's values of annual survival, since these were somewhat higher than those described by Eriksson and Wallin, based on a hypothesis that survival rates were generally lower at that time due to pesticides and hunting. However, the resulting lambda exceeded 1 (corresponding a growing population). Ryttman used the same survival rate for all ospreys 2 years or older. As other studies suggest (Eriksson & Wallin 1994b; Väli et al. 2021), the survival of young adults might be somewhat lower than their older conspecifics. When reducing this marginally the model gave a lambda of approximately 1.001.

2.3 Data from other studies

2.3.1 "Projekt Fiskgjuse"

Föreningen Kvismare fågelstation and *Naturhistoriska riksmuseet* has performed surveys of ospreys in southern and central Sweden every fifth year since 1973 (Odsjö & Sondell 1976). Due to the similarity between "Projekt Fiskgjuse" and this work (geographical location, survey methods etc), a close comparison to these results were extra interesting to investigate. However, some differences in survey methodology are important to underline as these can, if not taken into consideration, cause problems in data analysis as well as incorrect conclusions about the larger population trends of the osprey. The biggest difference in these survey methods concern time of the first survey of nests. The data collected by Håkan Gilledal in Västra Mälaren was retrieved in two visits, the first one in May and the second in the middle of July. The observations constituting the dataset from Projekt Fiskgjuse was also collected in two visits. However, the first visit sometimes took place later in June (Nielsen & Roos 2023). This entails a possible risk of missing early breeding attempts, thereby underestimating total attempts. Nevertheless, as in

Västra Mälaren, this minor uncertainty in data should be rather similar over time. On the other hand, that study provides higher validity for number of eggs and fledglings, as most of the nests were visited by climbing the nest tree.

The survey areas in Projekt Fiskgjuse held a stable population during 1973-2003. However, results show a major decline in 2003-2008 (48 %) in central Sweden and a 38 % decline in southern Sweden during 2008-2013 (Sondell 2013). Driving factors of the declines are not known but the authors discuss competition from newly established white-tailed eagles as well as human presence (outdoor activities and fishing) as potential causes for the sudden population slumps.

2.3.2 Swedish Bird Monitoring

Swedish Bird Monitoring ("Svensk Fågeltaxering") is a citizen science project run by Lunds University, in association with national and regional authorities. The aim is to survey the status and numbers of breeding birds in Sweden, which is mainly performed by volunteers. (Lindström 2024).

2.3.3 Falsterbo Migration counts

Systematic counts of visible, migrating birds have been carried out since the 1940s and standardized counts since 1973. The survey is performed from "Nabben", a land area where a large portion of Sweden's migrating birds passes every year (*Falsterbo Fågelstation* 2025).

3. Results

This section includes results from analysis of population numbers and reproductive performance of the ospreys in Västra Mälaren. A demographical analysis was conducted, as well as a brief analysis of nest trees used. Furthermore, these results are put in comparison with other reports, including “Projekt Fiskgjuse”.

3.1 Data analysis

3.1.1 Summary of data

A comparison of the average number of breeding attempts and fledged chicks per year indicates higher production in period 1. The average number of fledged chicks per year observed reflects a 16 % decline. The only significant discrepancy is in average number of breeding attempts per year (figure 1) marking a decline from 36.3 to 28.

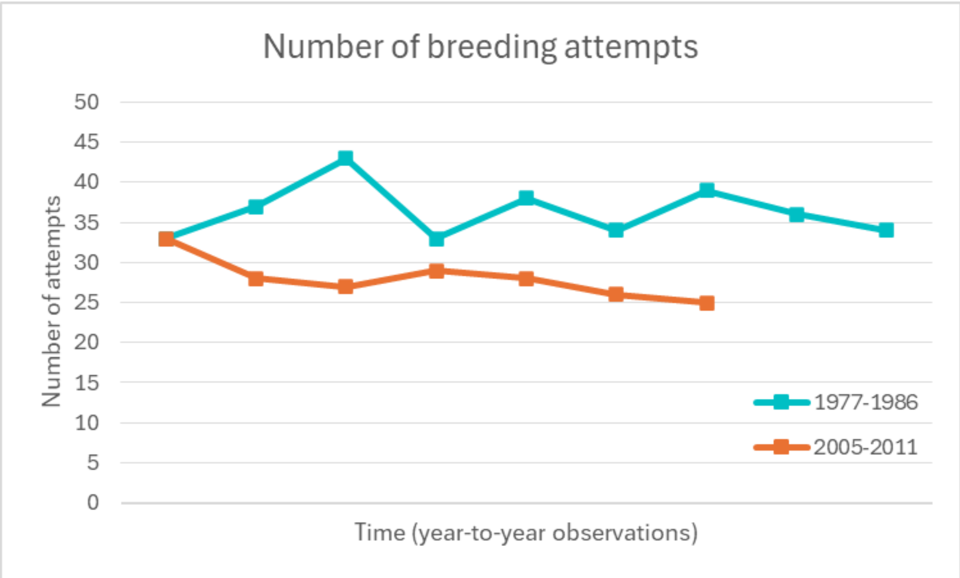

Figure 2. Comparison of number of breeding attempts per year.

Table 1. Summary of total breeding attempts, number of fledged chicks and reproduction number consisted of number of fledged chicks per attempt (successful or not).

Period	Total breeding attempts	Average number of breeding attempts per year	Total fledged chicks	Average number of fledged chicks per year	Average number of fledged chicks per breeding attempt	Average number of fledged chicks per successful attempt
1977-1986	327	36.3	451	50.1	1.38	2.17
2005-2011	196	28	295	42.1	1.51	2.17

When exponentiated, the logarithmic estimated value for reference period 1 is approximately 1.38 with a standard error of around 0.05 (table 5). When exponentiated, the estimated value of period 2 is approximately 1.09, suggesting that the average number of fledged chicks per breeding attempt is 9 % higher in period 2. However, the p-value equals 0.243 and the test is therefore not statistically significant.

3.1.2 General linear models

The GLM, with a quasipoisson response used, to evaluate differences in breeding attempts between the two periods gave an intercept of 3.59, reflecting the estimated logarithm of the average number of breeding attempts per year in the period of reference (1977-1986), as shown in table 2. The natural exponential equals approximately 36.33, reflecting the actual number of breeding attempts. Furthermore, the log scale difference in breeding attempts, -0.26053, reflects the change between the two periods. Since this is a logarithmic value, the actual proportional change in breeding attempts is obtained from the natural exponent (exp(-0,260539)) and equals approximately 0.77, or, equivalently, a 23 % decline. The low p-value of 7.83e-05, show high degree of significance, providing strong support for a decline in breeding attempts, outside of what could be expected by year-to-year variation. 95 % confidence interval give: 33.78 - 38.88 for period 1 and 25.61 – 30.39 for period 2.

Table 2. Summary of GLM of breeding attempts in the two periods. Period 1 (1977-1986) is shown as a reference value.

Coefficients:	Estimate	Std. Error	t value	Pr(>|t|)
Intercept	3.59274	0.02900	123.880	< 2e-16
2005-2011	-0.26053	0.04737	-5.499	7.83e-05

Raw data illustrates a higher proportion of successful breeding attempts compared to failed attempts in period 2, as shown in table 3.

Table 3. Contingency table describing breeding outcome in the two periods.

Period	Successful	Failed	Total	% Success
1977-1986	208	119	327	63.6
2005-2011	136	60	196	69.4

Results from the GLM comparing breeding outcome (binary variable: successful or failed) are shown in table 4. When translated to a proportional value, the estimated intercept is 0.636, compared to 0.694 for period 2. However, the high p-value, indicates that this difference is not proven statistically significant.

Table 4. Summary of GLM on breeding outcome (successful or failed) in the two periods. Period 1 (1977-1986) is shown as a reference value.

Coefficients:	Estimate	Std. Error	z value	Pr(>|t|)
Intercept	0.5584	0.1149	4.858	1.18e-06
2005-2011	0.2599	0.1930	1.347	0.178

Table 5. Response from GLM model using a Poisson distribution comparing average number of fledged chicks of successful attempts between the two periods.

Period	Estimate	Std. Error	z value	Pr(>|z|)
Intercept	0.32151	0.04709	6.828	8.62e-12
2005-2011	0.08735	0.07488	1.167	0.243

In summary, general linear models showed a significant decline in number breeding attempts between the two periods, which should be viewed as the main takeaway from this part of the analysis. A subsequent decrease in chicks per year was therefore expected. From this stated decline, tests on parameters possibly affecting the number of attempts were performed in an attempt of finding parameters affecting number of attempts.

3.1.3 Nest trees

Several tree species were used for nests. Nests in scots pine accounted for 71 % of all attempts. Almost 25 % were in spruce and just 4.4 % in different species of deciduous trees. Since most nests are used multiple times, this variable shows dependency. Therefore, any statistical tests such as G-test or chi^2-test, would not be suitable, since these require independent variables.

Table 6. Breeding attempts in different tree species. Note that several nests are counted multiple times, since the osprey usually return to their former nest site if possible.

Substrate	Pine	Spruce	Deciduous
Frequency	371	129	23
Proportion	70.9 %	24.7 %	4.4 %

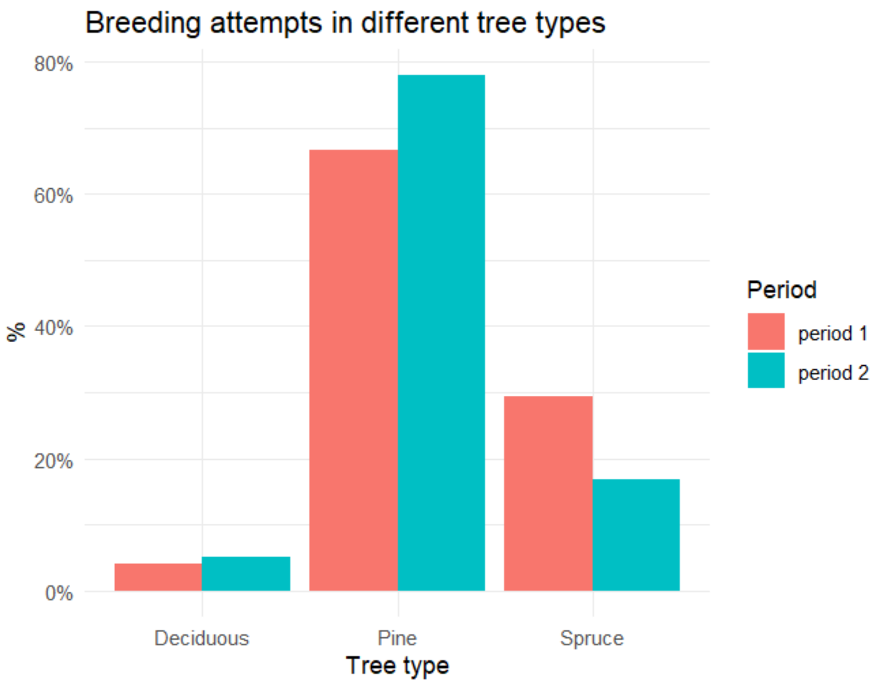

Figure 3. Breeding attempts in different tree types/species.

The number of unique nest trees in each period are summarized in table 7. A Fisher exact test gave a p-value of 0.2372 (not significant). The average number of years a nest tree is being used is 3.53 years. A total of 13 nest trees (out of 161 in total) were used in both period 1 and 2.

Table 7. Unique nest trees described as proportion of total nest trees used.

Tree species (Proportion of total trees)	Period 1	Period 2	Both periods
Pine	0.64	0.77	0.69
Spruce	0.28	0.17	0.24
Deciduous trees	0.08	0.06	0.07
Total	**1.00**	**1.00**	**1.00**

3.1.4 Life cycle analysis

The life-cycle graph behind the Leslie model, illustrating assumed flows of individuals between age classes, is shown in figure 3. As with most large raptors, it reflects rather consistent adult survival rate, also visualized in figure A4. Note that this does not reflect the studied population but instead what is being stated in previous research. Nevertheless, it visualizes a life cycle possible for ospreys.

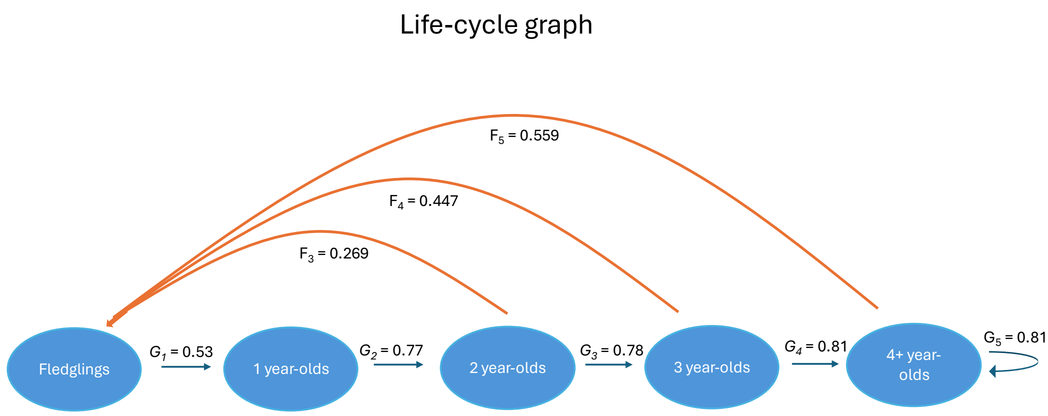

Figure 4. Age-structured life cycle graph reflecting the Leslie Matrix and the flow of individuals from one age class to another, using this studies values of reproductive performance together with values on survival and proportion of breeders from literature. G_x = proportion of individuals, F_x = Number of female offspring per female and year.

A sensitivity analysis of the Leslie matrix model, suggest that changes in adult survival have the biggest overall effect on population growth rate, illustrated in figure 4 and figure A1. This was not surprising, since it reflects what is expected from a long-lived individual reproducing at a constant rate. When adjusting the reproductive value from what was observed in period 1 to 2 (from 0.755 to 0.69), parameter adjustments were tested to replicate the population decline between the two periods. An adjustment in 1st year survival from 0.53 to ~0.44 was required to reach λ = 0.9896 (reflecting a 23 % decline over 25 years). In contrast, only a drop from 0.81 to 0.78 in adult survival was required to reach λ = 0.9896. Similarly, if changes in the proportion of reproducing individuals had caused the decline, it would, for example, require that no 3-year-olds and just over 40 % of the 4-year-olds managed to reproduce compared to what I assumed from the beginning (that 50 % of 3-year-olds, 80 % of four-year-olds reproduce).

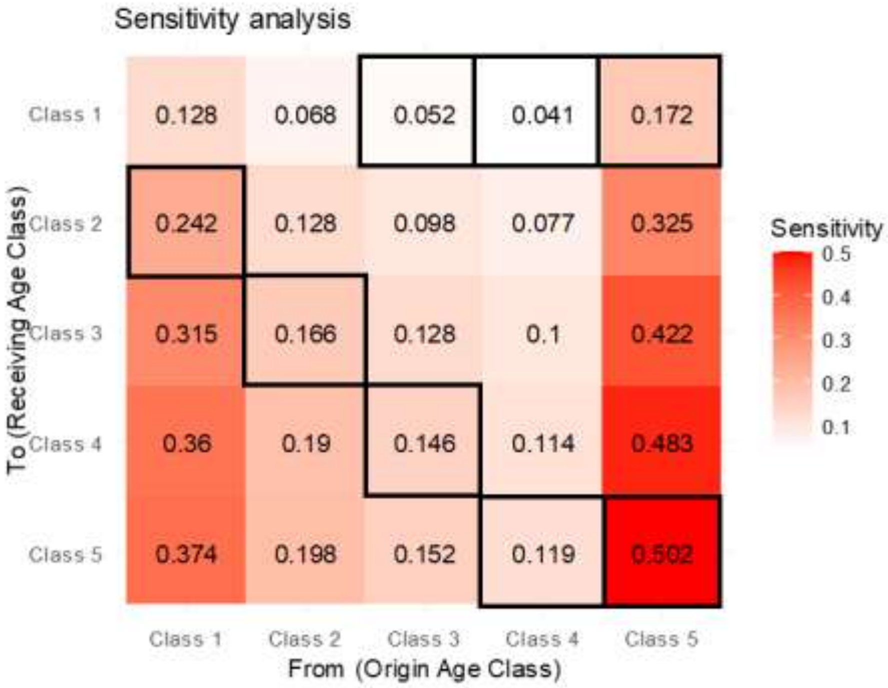

Figure 5. Heatmap illustrating output (absolute contribution of each transition to λ) from Sensitivity()-function in R. Notice that most of these cell's equal zero "in reality". For example, the chance of an individual going from the age 4 to 2 is in fact zero.

3.2 Other surveys

3.2.1 Projekt Fiskgjuse

The survey of breeding ospreys in lake "Båven" reveals a major decline in the number of breeding attempts between 1978-1988 and 2003-2013, as shown in table 8 and figure 5. The drop from 28.33 to 17.33 marks a notable 39 % decline in the average breeding attempts per year. The decreased number of attempts in the forested area of Stora Mellösa was even bigger (50 %) between the periods (13.33 to 6.67). Attempts in "Helgasjön" also dropped but to the lesser extent of about 11 %. The observed lakes in southern Sweden showed a similar trend,

where the average yearly breeding attempts in "Åsnen" dropped from 42 to 33.67 per year (~20 %) and "Sottern" from 8.33 to 6 (~ 28 %). A similar pattern in average number of fledged chicks could not be recognized. The biggest declines in central Sweden were recorded between 2003-2008, while a similar trend was observed in southern Sweden between 2008-2013 (figure 5).

Table 8. Summary of breeding data from "Projekt Fiskgjuse" (Sondell 2013), an osprey monitoring project run by Kvismare fågelstation and Naturhistoriska riksmuseet. Notice that both average number of eggs and fledged chicks are combined for "Båven" and "Sottern" and "Stora Mellösa" and "Asker". Regions in bold type are total averages of the areas above.

Region:	Period	Average number breeding attempts	Average number of eggs (& small nestlings)	Average number of fledged chicks
Åsnen	1978-1988	42.00	2.55	1.63
Åsnen	2003-2013	33.67	2.65	1.65
Helgasjön	1978-1988	12.33	2.66	1.73
Helgasjön	2003-2013	11.00	2.78	1.76
Central Sweden	**1978-1988**	**18.33**	**2.67**	**1.75**
Central Sweden	**2003-2013**	**11.67**	**2.57**	**1.51**
Båven	1978-1988	28.33	*2.63*	*1.75*
Båven	2003-2013	17.33	*2.57*	*1.51*
Sottern	1978-1988	8.33	-"-	-"-
Sottern	2003-2013	6.00	-"-	-"-
Stora Mellösa	1978-1988	13.33	*2.50*	*1.72*
Stora Mellösa	2003-2013	6.67	*2.74*	*1.47*
Asker	1978-1988	2.33	-"-	-"-
Asker	2003-2013	0	-"-	-"-
Southern Sweden	**1978-1988**	**13.08**	**2.61**	**1.61**
Southern Sweden	**2003-2013**	**7.5**	**2.73**	**1.63**

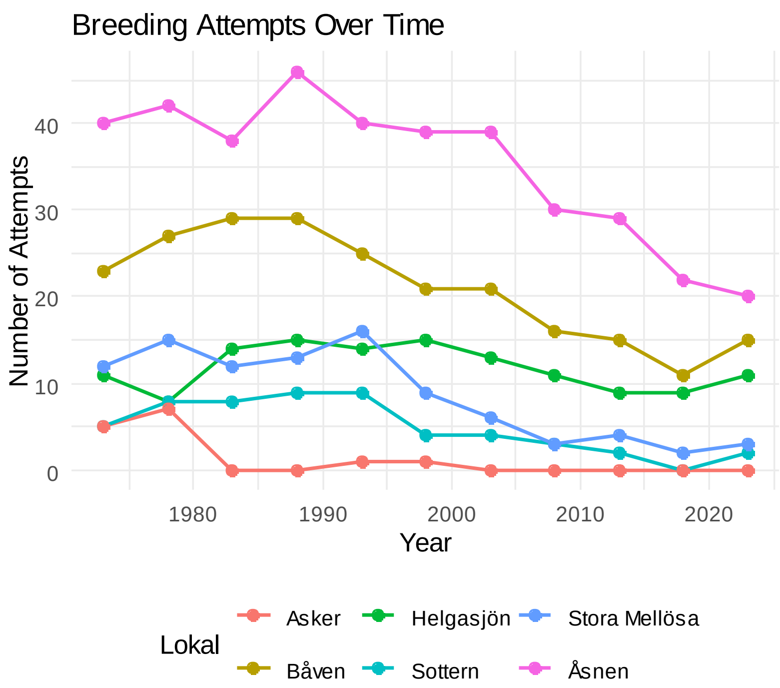

Figure 6. Observed breeding attempts (every fifth year) in the six survey areas in "Projekt Fiskgjuse".

The observed decline in Västra Mälaren in relation to what has been observed in the survey areas of "Projekt Fiskgjuse", as displayed in figure 6. Many areas show a similar decrease in the number of breeding attempts.

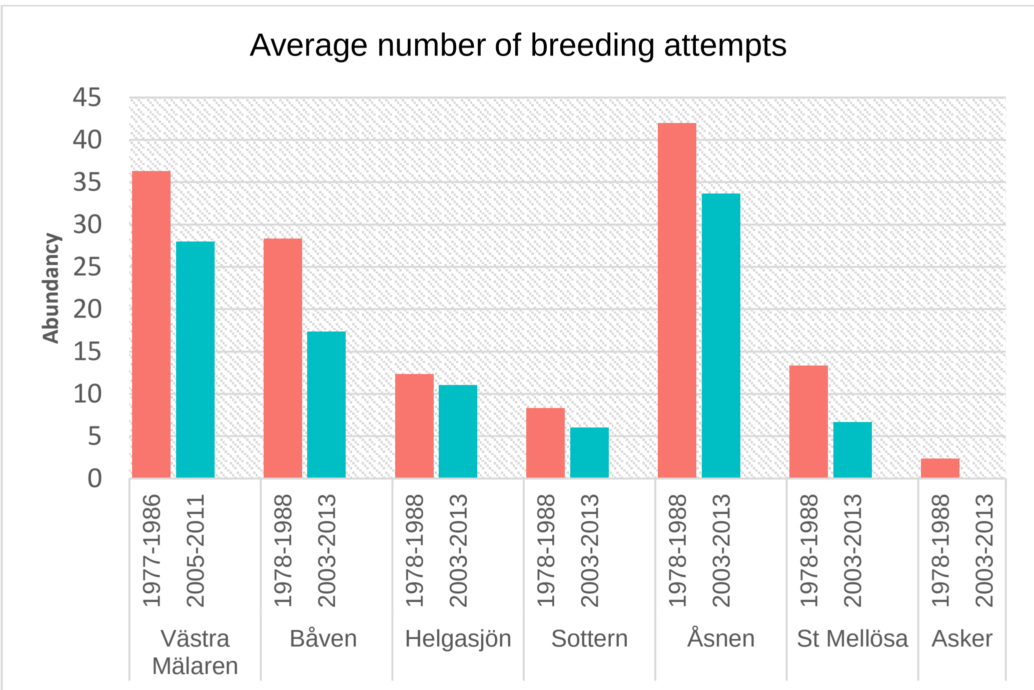

Figure 7. Grouped bar chart showing discrepancy in number of breeding attempts over time in Västra Mälaren and areas surveyed in Projekt Fiskgjuse (same data as table 7).

3.2.2 Atlas surveys in Skåne (74-84 & 03-09) & Närke 74-84 & 05-15)

Atlas inventories were carried out in Skåne in two comparable periods (1974-1984 and 2003-2009). In this survey, they confirmed an earlier indication of a large increase in the number of breeding osprey pairs. The number of atlas grids (5x5 km) with a confirmed breeding attempt increased from 23-46 squares, marking a 96 % increase (Bengtsson & Green 2013). A similar study was conducted in Närke during 1974-1984 and 2005-2015. Between these two periods, the number of grids in which a breeding occurred increased with 9 % together with a slight dispersal increase (Lindqvist et al. 2020).

3.2.3 Swedish Bird Monitoring

In the following figures, all diagrams contain information about the sample. This is displayed after the name of the species, in a parenthesis, where the first number show average number of observations, the second number show number of routes surveyed, the third number show the calculated trend over time (1998-2024) and lastly if this trend is significant or not. "NS" means "not significant" (0.05<p) and *, ** and *** refers to the degree of significance (p<0.05, p<0.01, 0<0.001). The number of birds observed in the first year is used for reference and holds a value of 1. Following amounts of observations are put in proportion to this.

The trend for Swedish ospreys retrieved from *fixed routes* is visualized in figure 7. It holds an average of 35 observations per year over 267 routes. Since the start of the surveys, in 1998, the trend appears quite stable (-0.1 % per year). However, this estimate is not significant. *Summer point counts* show an average of 32 observations per year over 388 routes. The trend is 0.9 % population increase per year (not significant).

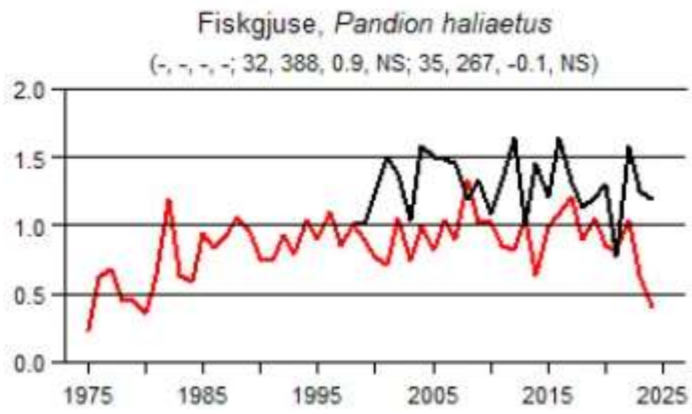

Figure 8. Trend diagram showing observations from "Summer point counts" and "Fixed routes". No significant trends. Figure retrieved from https://www.fageltaxering.lu.se/resultat/populationstrender-enskilda-arter.

The Swedish waterfowl count from May include more observations (an average of 78 observations over 209 routes), than fixed routes and summer point counts (figure 8). The estimated trend is found significant (**). Note that these counts were initiated 2015.

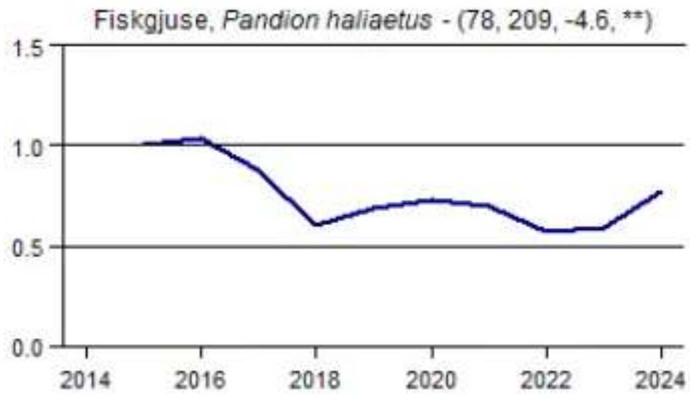

Figure 9. The Swedish waterfowl count (Svenska sjöfågelrutterna) in May. Note that these surveyes were initiated in 2015. Significant trend. Figure retrieved from https://www.fageltaxering.lu.se/resultat/populationstrender-enskilda-arter.

The *Archipelago squares* survey depicts high variability, presumably explained by the low number of observations (average of 9). The trend estimate of -8.8 % per year (not significant) is therefore regarded as highly uncertain.

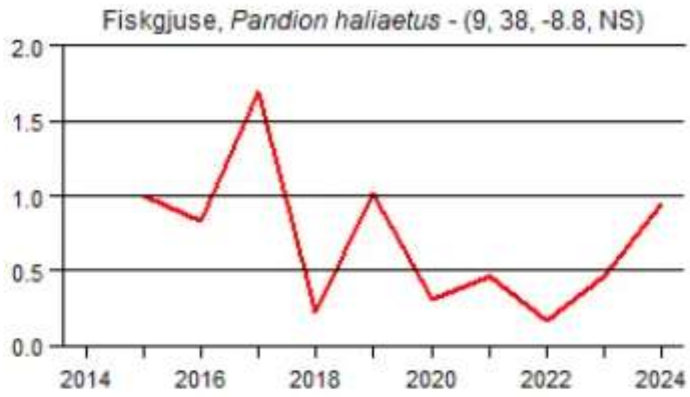

Figure 10. Archipelago squares (Kustfågelrutorna). Not significant. Figure retrieved from https://www.fageltaxering.lu.se/resultat/populationstrender-enskilda-arter.

3.2.4 Falsterbo fågelstation

The observations from "Nabben" of migrating birds are shown in figure 10. A generalized linear model (GLM) with a quasipoisson distribution was fitted to assess temporal trends in osprey observations. The model indicated a negative relationship between year and abundance (estimate = -0,00979 (log)), suggesting an average annual decrease of approximately 0.98 % in the number of observations. However, this trend was not statistically significant (p = 0.18).

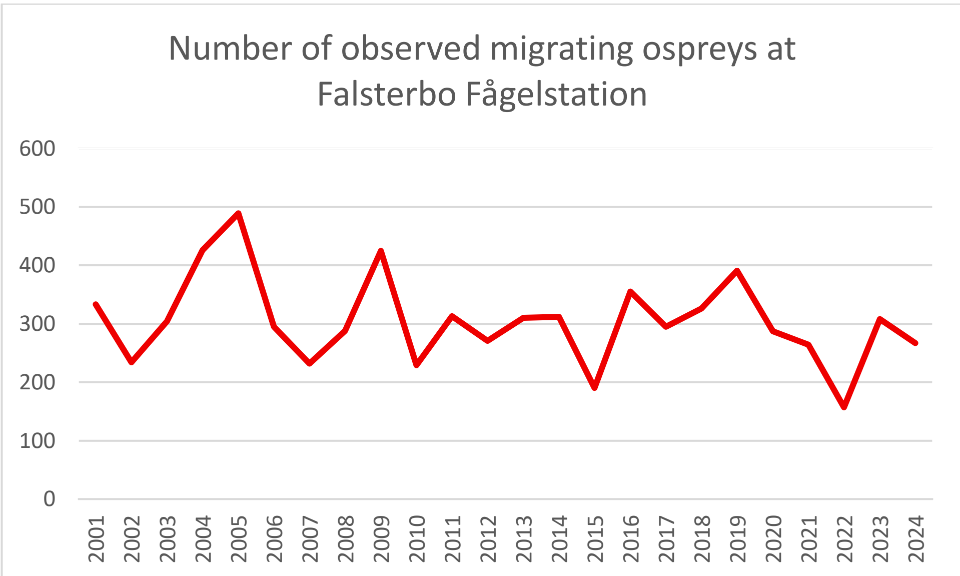

Figure 11. Total counts of observed, migrating birds during 11/8 - 10/11 during 2001-2024 at "Nabben", Falsterbo.

4. Discussion

Results from Västra Mälaren showed a 23 % decline in breeding attempts between the two periods but no clear changes in reproductive performance. Population modelling suggest that the present decline could be driven by relatively small changes in adult survival. Furthermore, it is possible that declines could be driven by habitat deterioration.

In the following section, potential drivers of the population decrease—including reproductive performance, adult survival, and habitat loss or degradation—are discussed. Finally, I consider whether current national population estimates should be revised in light of the evidence presented in this study.

Change in population numbers

As results suggests (table 1), the number of breeding attempts observed in the study area declined with approximately 23 % over the 25 years between period 1 and 2. There is no reason to believe that this decline is a result of changed effort or a changed cryptic behaviour as the people conducting the survey have very good knowledge of the surroundings and would most likely notice nearby establishments. Furthermore, a new, substantial establishment elsewhere would surely be noticed in some way, since the osprey and its nest is easily recognizable and is a bird of general interest.

There are several other studies also displaying local and regional declines in population numbers. The lake and forest areas surveyed in *Projekt Fiskgjuse* show a similar trend in reduced breeding attempts as observed in Västra Mälaren. In all areas combined, a decline of around 40 % was observed (compared to 23 % in Västra Mälaren) between the two periods. When only lakes were included, the observed decline was 27 %, notably similar to Västra Mälaren. The number of attempts decreased in all areas but to different extents (11 – 50 %). In the areas around Båven and Sottern (central Sweden), the biggest decline was observed between 2003-2008, while a similar trend was shown in southern Sweden between 2008-2013. To my knowledge, these two datasets are unique regarding preciseness and longevity. Both studies are carried out in a scientific manner with high validity and reliability as a result.

Results from *Projekt Fiskgjuse* and this study, are contrary to what is given by national estimates during the same period. It is generally assumed that the Swedish osprey population increased at a rather constant rate of about 1 % from the 1970s to the early 2000s, after which it is believed to have stabilized. These estimates are mostly based on passage counts and migration passages. Over an extended period, such counts can give useful insight into large trends. However, the quality and adequacy of these counts differs among bird species. For the osprey, these counts show low sample size and high variation. Furthermore, the validity can be questioned. Migrating ospreys show a latitudinal spread and often use thermal uplift, enabling them to fly over several hundred kilometres of open water if necessary (Österlöf 1977; Duriez et al. 2018). In addition, it is reasonable to assume that several ospreys from neighbouring countries also pass the south of Sweden. Therefore, I argue that the findings in this study, and results from "Projekt Fiskgjuse", should induce questions about how well previous estimates reflects the "real" state of the osprey and urge the need for further monitoring.

Demography

The observed number of fledged chicks per breeding attempt was higher in period 2 than 1, but differences in breeding success and fledged young per successful attempt was not found significant between the two periods.

Analysis through matrix models indicate adult survival to be the most impactful on total population size. The model relies on a fixed assumption on the age of first-time breeders. This is a rough estimate, considering the lack of information of non-reproducing individuals in this specific population and scarce literature on the subject. The observed change in breeding attempts could in theory be explained by a higher age of first reproduction (e.g. larger proportion of non-reproducing floaters). As the results suggest, a scenario in which no three-year-olds and less than half of the four-year-olds reproduce, results in a similar decline as what has been observed. This is in no way inconceivable, since average age of first breeding seems to vary quite a bit between 3-5 years (Väli et al. 2021).

During migration, Swedish ospreys are found widely spread in time and space (Österlöf 1977) and mortality rates are higher during migration than in stationary periods. Spatiotemporal patterns show that deaths during spring take place crossing the Sahara desert, while deaths during autumn occur in Europe (Klaassen et al. 2014). Swedish ospreys mostly winter on the African West coast, north of the equator (Österlöf 1977). It is common for 1-year-olds and some 2-year-olds to stay the following season in their wintering grounds. There is not much data on the Scandinavian Ospreys in Africa. Therefore, reduced survival in their wintering areas is difficult to uncover. However, a study on mortality patterns in migratory birds concluded that Swedish Ospreys show up to six times higher mortality rates in spring migration compared to stationary periods (Klaassen et al. 2014) as more than half of the recorded deaths occurred during migration.

In a population like the one assumed in the matrix models, a decreased adult survival rate of mere 3 percent would make up for the observed decline in breeding individuals, making reduced survival in relation to migration a plausible driver of the population decline. To prove this empirically, would require an extensive number of ringed birds continuously observed and individually identified.

Habitat change as a driver of population change

Loss of, or deterioration of habitat can lead to population declines (Poole 1989; Ewins 1997; Saurola 1997; Schmidt-Rothmund et al. 2014), including loss of potential nesting trees, reduced abundance of fish, loss of habitat to due to agriculture and shoreline development, human disturbance during breeding and interspecific competition.

Nest sites and nest trees

Concerning nest sites, multiple reports suggest that availability of nest sites can limit breeding densities (Poole 1989; Newton 2010) as breeding ospreys defend their nest sites (Poole 1989). As the osprey is an obligate fish eater, proximity to water and exposure in all directions is crucial for foraging purposes (Lohmus 2001; Canal et al. 2018). Therefore, they are typically situated at the very top of a tree, with no branches extending above the nest rim. Moreover, tree species seem to be an important factor, since most European ospreys breed in scots pines (Saurola 1997; Canal et al. 2018). Saurola reports that 88 % of the natural nests in Finland were placed in scots pines. Reasonably, a similar number should apply to the Swedish population. However, over the entire study period the total proportion of nests in scots pine was ~71 %, notably lower than that reported by Saurola (1997). Surprisingly, about one fourth of the attempts took place in Norwegian spruce. The high degree of breeding attempts in spruce may indicate a limited number of nest trees but since no further analysis was made, this remains a speculation. For example, an abundance of exceptionally large spruce trees, suitable for an osprey nest, could also explain this divergent distribution.

Land use such as forestry, agriculture, and shoreline development can all lead to population declines as these can reduce satisfactory foraging grounds and nest habitats. In “Västergötland” a breeding population increased from 1 to 20 pairs during a 15-year period following the construction of artificial nests (Svensson et al. 1999) and in Finland the proportion of artificial nests in relation to total nests increased from 15 to 45 % during 1972-2016 (Saurola 2018). Saurola further concludes that ospreys have returned to their original nest sites (e.g. shorelines) from peat bogs and forests, in comparable rates to which artificial nests have been constructed. These findings are interesting, as this implies that an inland refuge is more closely related to finding decent nesting substrate rather than, for example, a foraging strategy in a degraded or fragmented landscape presence of for example white-tailed eagle. Additionally, a possible implication of this finding is that lack of decent nesting substrates in some cases overlook human disturbances such as outdoor life, boat traffic and other human activities.

White-tailed eagle

Since the 1980s, the Swedish population of white-tailed eagle has increased and show strong, significant increases over the past 20 years (BirdLife Sverige 2021). In the studied lakes and areas of this project and in "Projekt Fiskgjuse", the increase of white-tailed eagle has partly correlated to local declines in the number breeding ospreys, which has led ornithologists to attribute declines in osprey to interspecific competition and interaction white the white-tailed eagle (Gilledal 2011; Sondell 2013). As *kleptoparasitism* (stealing or forcing an individual to drop its prey) has been observed between the species, this has been suggested as the main cause for local declines. Repeated cases of this type of "robbery" would surely impact breeding success negatively. Furthermore, with limited nest sites, a battle for few, decent nest trees would surely by won by the bigger white-tailed eagle, causing ospreys to move. However, more research is required on the osprey-eagle interaction to make any certain statement since there is not much literature supporting this theory. A study on this in Lithuania by Treinys et al. (2011) found that a recovering population of white-tailed eagle may limit osprey population numbers due to *niche overlap* (competition of nesting habitat resulting in relocation or reduced density of the subdominant species). However, these results were ambiguous and cannot confirm this relationship by themselves.

On the other hand, *bald eagle* recoveries in North America have been shown to limit osprey numbers. In a study by Cruz et al (2019), they explored how bottom-up vs top-down effects might limit breeding osprey populations. The study, carried out in 1973 to 2012, showed that top-down effects like recovering bald eagle populations were the main factors affecting osprey nesting demography (reduced persistence and success). Further, the authors discuss kleptoparasitism as another possible contributing factor.

Human activities

Anthropogenic disturbances have been found to have a negative effect on breeding performance and overall population size (Poole 1989; Coetzee et al. 2014; Canal et al. 2018). Evidently, shooting and pesticides have impacted osprey populations in a severe manner, but lighter" disturbances such as outdoor life, boat traffic etc. also affect the ospreys breeding performance (Canal et al. 2018). As the survey area is well visited with lots of outdoor life, this may serve as a threat to some ospreys.

5. Conclusions

This study provides clear evidence that the breeding population of ospreys in Västra Mälaren has suffered substantial declines between 1977-1986 and 2005-2011. While the exact demographic drivers cannot be determined, changes in adult survival and an increased proportion of non-breeding individuals are two feasible demographical explanations. In a similar manner, external driving factors are difficult to establish. However, scarcity of nest sites and human disturbance have been found driving declines elsewhere. While the relation between abundance of nesting substrate and population change is well-established in other populations (especially Finland), further similar studies are encouraged for the Swedish ospreys. Nevertheless, this issue is relevant from a conservation perspective, and initiatives aimed at protecting natural nesting trees as well as constructing artificial nesting structures should be viewed as relevant conservation efforts.

This paper highlights the need for more precise, up-to-date estimations for the status of the Swedish population of ospreys. While numerous reports, including the present one, document local and regional declines, the prevailing consensus - dependent on rough estimates from almost 20 years ago - presume a stable population. As these national estimates serve as a basis for policy making and conservation strategies, a false sense of optimism may be detrimental for a long-lived species, sensitive to human activities and environmental change.

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Appendix 1

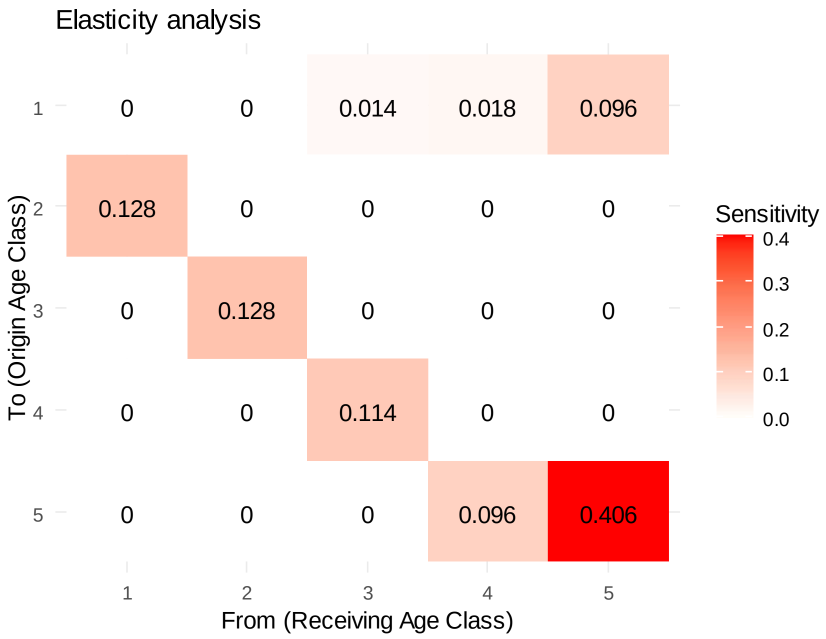

Figure A1. Heatmap illustrating output from Elasticity()-function in R. Elasticity relates to sensitivity but is weighted by the transition elements, e.g. the proportional effect on λ.

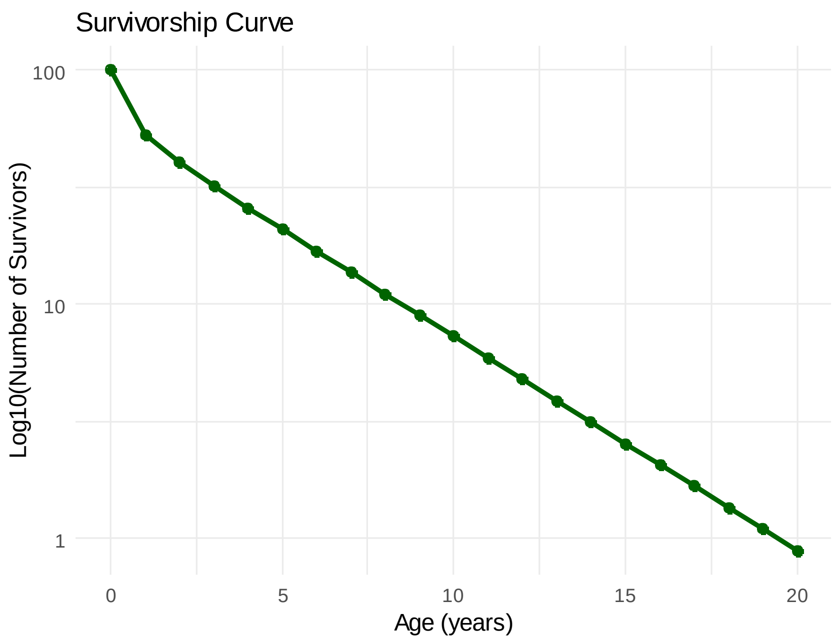

Figure A2. Logarithmic survivorship curve visualizing each individual surviving to the next age class in a starting cohort of 100 individuals. A display of a typical "type II"-species, meaning that the drop-off in individuals surviving is rather consistent.

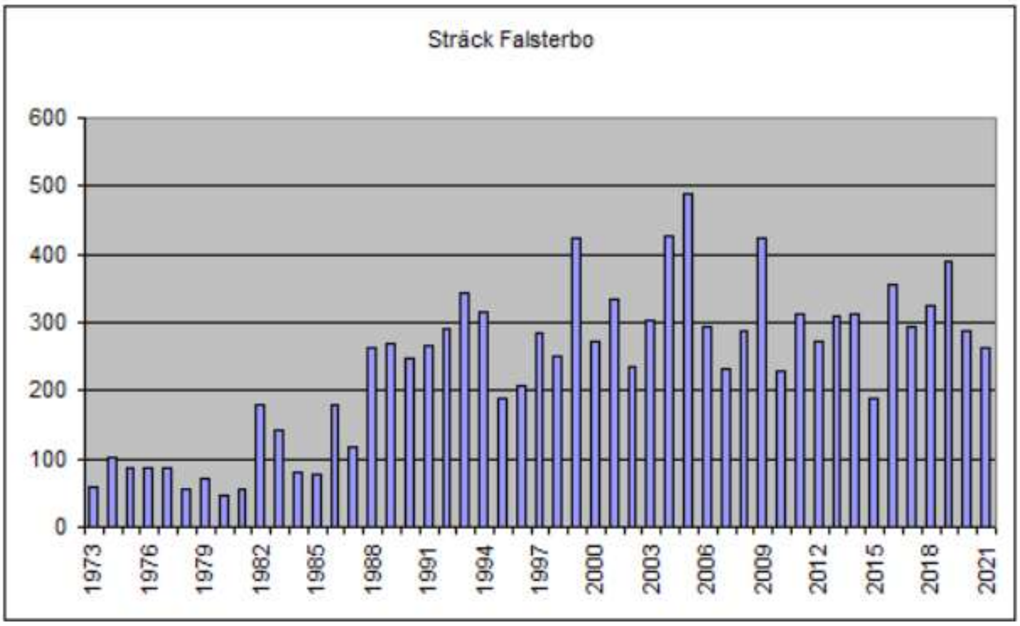

Figure A3. Osprey observations at Nabben, Falsterbo 1973-2021.

Table 6. Number of unique nest trees

	Period 1	Period 2
Spruce	27	11
Pine	62	49
Decidious trees	8	4

```
data <- read_excel("osprey.xlsx")
view(data)
library(tidyverse)
library(dplyr)
#radera kolumner skapade i excel
data <- data %>%
   select(-`Häckning (Y/N)`, -Häckningsutfall, -`Antal ungar`)
view(data)

#skapa ny kolumn för påbörjade häckningar
data <- data %>%
  mutate(breeding_all = if_else(kod == "HMi" | str_detect(kod, "HL"), 1, 0))
view(data)

#skapa ny kolumn för häckningsstatus
data <- data %>%
  mutate(
    breeding_status = case_when(
      str_detect(kod, "HL") ~ "Lyckad",
      kod == "HMi" ~ "Misslyckad",
      TRUE ~ "Ingen häckning"))
view(data)

#städa data
data <- data %>%
  mutate(kod = if_else(kod == "Hl 3 (3)", "HL 3 (3)", kod))
view(data)

#påbörjade häckningar år-för-år
breeding_all_yearly <- data %>%
  group_by(år) %>%
  summarise(breeding_amount = sum(breeding_all, na.rm = TRUE))
view(häckn)
rm(häckningar_per_år)

#häckningsstatus år-för-år
breeding_status_yearly <- data %>%
  group_by(år, breeding_status) %>%
  summarise(antal = n(), .groups = "drop")
view(breeding_status_yearly)

#en plot över häckningsstatus över tid
ggplot(breeding_status_yearly, aes(x = år, y = antal, color = breeding_status)) +
  geom_line(size = 1.2) +
  geom_point() +
  labs(
    title = "Breeding status over time",
    x = "Year",
    y = "Number of observations",
    color = "Status"
  ) +
  theme_minimal()

#häckningsstatus ytterligare kolumn för proportioner
breeding_status_yearly <- data %>%
  group_by(år, breeding_status) %>%
  summarise(count = n(), .groups = "drop") %>%
  group_by(år) %>%
  mutate(
    total = sum(count),
    proportion = count / total
  ) %>%
  ungroup()
View(breeding_all_yearly)
View(breeding_status_yearly)

library(tidyverse)

data <- data %>%
  rename(
    year = år,
    nest_id = bo,
```

```
    region = delområde,
    tree_species = trädslag,
    code = kod)
# Egen tidsserie För perioden 1977-1986
tidsserie1 <- data %>%
  filter(year >= 1977 & year <= 1986)

# Egen tidsserie För perioden 2005-2011
tidsserie2 <- data %>%
  filter(year >= 2005 & year <= 2011)

#byta namn till engelska
period1 <- tidsserie1
period2 <- tidsserie2
rm(tidsserie1)
rm(tidsserie2)

mean_period1 <- period1 %>%
  summarise(avg_breeding = mean(breeding_all, na.rm = TRUE))
mean_period2 <- period2 %>%
  summarise(avg_breeding = mean(breeding_all, na.rm = TRUE))
rm(mean_period1, mean_period2)


#Genomsnittligt antal påbörjade häckningar per år (36.3 & 28)
sum(period1$breeding_all, na.rm = TRUE)
sum(period2$breeding_all, na.rm = TRUE)
327/9
196/7


#Ändra namn till engelska
data <- data %>%
  mutate(breeding_status = case_when(
    breeding_status == "Lyckad" ~ "Successful",
    breeding_status == "Misslyckad" ~ "Failed",
    breeding_status == "Ingen häckning" ~ "None",
    TRUE ~ breeding_status  # behåll andra värden som de är (om det skulle
finnas)
  ))
data <- period1  %>%
  mutate(breeding_status = case_when(
    breeding_status == "Lyckad" ~ "Successful",
    breeding_status == "Misslyckad" ~ "Failed",
    breeding_status == "Ingen häckning" ~ "None",
    TRUE ~ breeding_status  # behåll andra värden som de är (om det skulle
finnas)
  ))


#Rätta till fel från ovanstående formel och ändra namn igen
data <- bind_rows(period1, period2)
data <- data %>%
  mutate(breeding_status = case_when(
    breeding_status == "Lyckad" ~ "Successful",
    breeding_status == "Misslyckad" ~ "Failed",
    breeding_status == "Ingen häckning" ~ "None",
    TRUE ~ breeding_status  # behåll andra värden som de är (om det skulle
finnas)
  ))
period1 <- period1 %>%
  mutate(breeding_status = case_when(
    breeding_status == "Lyckad" ~ "Successful",
    breeding_status == "Misslyckad" ~ "Failed",
    breeding_status == "Ingen häckning" ~ "None",
    TRUE ~ breeding_status  # behåll andra värden som de är (om det skulle
finnas)
  ))
period2 <- period2 %>%
  mutate(breeding_status = case_when(
    breeding_status == "Lyckad" ~ "Successful",
    breeding_status == "Misslyckad" ~ "Failed",
    breeding_status == "Ingen häckning" ~ "None",
```

```
    TRUE ~ breeding_status  # behåll andra värden som de är (om det skulle
finnas)
  ))

#Backup
data_full_backup <- data
period1_full_backup <- period1
period2_full_backup <- period2

#Genomsnittligt antal lyckade häckningar per år
period1 %>%
  count(breeding_status)
period2 %>%
  count(breeding_status)

# Summering för period 1
summary_period1 <- period1 %>%
  count(breeding_status) %>%
  mutate(
    period = "1977-1986",
    proportion = n / sum(n))

# Summering för period 2
summary_period2 <- period2 %>%
  count(breeding_status) %>%
  mutate(
    period = "2005-2011",
    proportion = n / sum(n))

#Slå ihop ovanstående
breeding_summary_all <- bind_rows(summary_period1, summary_period2)

#Visualisera i plot
ggplot(breeding_summary_all, aes(x = breeding_status, y = proportion, fill =
period)) +
  geom_col(position = position_dodge(width = 0.8)) +
  geom_text(aes(label = scales::percent(proportion, accuracy = 1)),
            position = position_dodge(width = 0.8),
            vjust = -0.5, size = 4) +
  scale_y_continuous(labels = scales::percent_format(), limits = c(0, 1)) +
  labs(
    title = "Comparison of breeding outcomes",
    x = "Breeding status",
    y = "Proportion",
    fill = "Period"
  ) +
  theme_minimal()
#Ovanstående blir missvisande då det räknar på antalet observationer ist för år

#Ny beräkning där genomsnitt beräknas på antal år

# Antal år per period
n_years_period1 <- 9
n_years_period2 <- 7

#Byta namn
data <- data %>%
  mutate(region = case_when(
    region == "Ridö-Sundbyholmsarkipelagen (RS)" ~ "RS",
    region == "Östra Galten (ÖG)" ~ "ÖG",
    region == "Lilla Blacken-området (LB)" ~ "LB",
    TRUE ~ region  # behåll övriga värden orörda
    ))
period1 <- period1 %>%
  mutate(region = case_when(
    region == "Ridö-Sundbyholmsarkipelagen (RS)" ~ "RS",
    region == "Östra Galten (ÖG)" ~ "ÖG",
    region == "Lilla Blacken-området (LB)" ~ "LB",
    TRUE ~ region  # behåll övriga värden orörda
  ))
period2 <- period2 %>%
  mutate(region = case_when(
    region == "Ridö-Sundbyholmsarkipelagen (RS)" ~ "RS",
    region == "Östra Galten (ÖG)" ~ "ÖG",
```

```
    region == "Lilla Blacken-området (LB)" ~ "LB",
    TRUE ~ region  # behåll övriga värden orörda
  ))

#Skapa dataset för delområden
unique(data$region)
data_RS <- data %>% filter(region == "RS")
data_LB <- data %>% filter(region == "LB")
data_OG <- data %>% filter(region == "ÖG")

# RS
rs_period1 <- data %>% filter(region == "RS", year >= 1977, year <= 1986)
rs_period2 <- data %>% filter(region == "RS", year >= 2005, year <= 2011)

# LB
lb_period1 <- data %>% filter(region == "LB", year >= 1977, year <= 1986)
lb_period2 <- data %>% filter(region == "LB", year >= 2005, year <= 2011)

# ÖG
og_period1 <- data %>% filter(region == "ÖG", year >= 1977, year <= 1986)
og_period2 <- data %>% filter(region == "ÖG", year >= 2005, year <= 2011)

library(tidyverse)
library(stringr)

#backup
data_full_backup <- data

#Rensa data ytterligare, omvandlade 1 "HL m 1" till HL 1 och 1 "HL m 2" till HL 2
clean_code <- function(df) {
  df %>%
    mutate(code = str_replace(code, "^(HL [1234]) \\(.*\\)", "\\1"))
}

clean_code <- function(df) {
  df %>%
    mutate(code = case_when(
      code == "HL m 1" ~ "HL 1",
      code == "HL m 2" ~ "HL 2",
      TRUE ~ code
    )) %>%
    mutate(code = str_replace(code, "^(HL [1234]) \\(.*\\)", "\\1"))
}
rm(clean_kod)


data <- clean_code(data)
period1 <- clean_code(period1)
period2 <- clean_code(period2)
data_LB <- clean_code(data_LB)
data_OG <- clean_code(data_OG)
data_RS <- clean_code(data_RS)
lb_period1 <- clean_code(lb_period1)
lb_period2 <- clean_code(lb_period2)
og_period1 <- clean_code(og_period1)
og_period2 <- clean_code(lb_period2)
rs_period1 <- clean_code(rs_period1)
rs_period2 <- clean_code(lb_period2)

#addera kolumn för flygga ungar
add_fledged_chicks <- function(df) {
  df %>%
    mutate(fledged_chicks = case_when(
      code == "HL 1" ~ 1,
      code == "HL 2" ~ 2,
      code == "HL 3" ~ 3,
      code == "HL 4" ~ 4,
      code == "HMi"  ~ 0,
      TRUE ~ NA_real_
    ))
}

data <- add_fledged_chicks(data)
period1 <- add_fledged_chicks(period1)
```

```
period2 <- add_fledged_chicks(period2)

data_LB <- add_fledged_chicks(data_LB)
data_OG <- add_fledged_chicks(data_OG)
data_RS <- add_fledged_chicks(data_RS)

lb_period1 <- add_fledged_chicks(lb_period1)
lb_period2 <- add_fledged_chicks(lb_period2)
og_period1 <- add_fledged_chicks(og_period1)
og_period2 <- add_fledged_chicks(og_period2)
rs_period1 <- add_fledged_chicks(rs_period1)
rs_period2 <- add_fledged_chicks(rs_period2)

#Ny backup för rensad data
data_clean_backup <- data

#rensa och fyll i i breeding_summary_all
breeding_summary_all <- breeding_summary_all %>%
  select(-proportion)

breeding_summary_all <- breeding_summary_all %>%
  mutate(n_per_year = case_when(
    period == "1977-1986" ~ n / 9,
    period == "2005-2011" ~ n / 7,
    TRUE ~ NA_real_
  ))

#diagram över häckningsutfall (successful 23.1 -> 19.4, Failed 13.2 -> 8.6)
ggplot(breeding_summary_all, aes(x = breeding_status, y = n_per_year, fill =
period)) +
  geom_col(position = position_dodge(width = 0.8)) +
  geom_text(aes(label = round(n_per_year, 1)),
            position = position_dodge(width = 0.8),
            vjust = -0.5, size = 4) +
  labs(
    title = "Average number of breeding outcomes per year",
    x = "Breeding status",
    y = "Average count per year",
    fill = "Period"
  ) +
  theme_minimal()
library(tidyverse)
#reproduktionstal(?) för period 1
repro_period1 <- period1 %>%
  filter(!is.na(fledged_chicks)) %>%
  summarise(
    fledged_total = sum(fledged_chicks, na.rm = TRUE),
    breeding_attempts = n(),
    fledged_per_year = fledged_total / 9,
    attempts_per_year = breeding_attempts / 9,
    reproduction_rate = fledged_per_year / attempts_per_year
  )
#reproduktionstal(?) för period 2
repro_period2 <- period2 %>%
  filter(!is.na(fledged_chicks)) %>%
  summarise(
    fledged_total = sum(fledged_chicks, na.rm = TRUE),
    breeding_attempts = n(),
    fledged_per_year = fledged_total / 7,
    attempts_per_year = breeding_attempts / 7,
    reproduction_rate = fledged_per_year / attempts_per_year
  )
sum(period1$fledged_chicks, na.rm = TRUE)

library(tidyverse)
library(MASS)
library(dplyr)
#Grundläggande statistiska mått för period 1
period1_summary <- period1 %>%
  group_by(year) %>%
  summarise(
    n_attempts = sum(breeding_all, na.rm = TRUE),
    n_success = sum(breeding_status == "Successful", na.rm = TRUE)
  ) %>%
```

```
  summarise(
    mean_per_year = mean(n_attempts),
    var_per_year = var(n_attempts),
    sd_per_year = sd(n_attempts),
    total_attempts = sum(n_attempts),
    total_success = sum(n_success),
    years = 9,
    proportion_successful = total_success / total_attempts
  ) %>%
  mutate(period = "1977-1986")

#Grundläggande statistiska mått för period 2
period2_summary <- period2 %>%
  group_by(year) %>%
  summarise(
    n_attempts = sum(breeding_all, na.rm = TRUE),
    n_success = sum(breeding_status == "Successful", na.rm = TRUE)
  ) %>%
  summarise(
    mean_per_year = mean(n_attempts),
    var_per_year = var(n_attempts),
    sd_per_year = sd(n_attempts),
    total_attempts = sum(n_attempts),
    total_success = sum(n_success),
    years = 7,
    proportion_successful = total_success / total_attempts
  ) %>%
  mutate(period = "2005-2011")

#Modellering
library(tidyverse)
library(dplyr)
library(MASS)

# Summera per år för varje period
period1_per_year <- period1 %>%
  group_by(year) %>%
  summarise(
    n_attempts = sum(breeding_all, na.rm = TRUE),
    period = "1977-1986"
  )

period2_per_year <- period2 %>%
  group_by(year) %>%
  summarise(
    n_attempts = sum(breeding_all, na.rm = TRUE),
    period = "2005-2011"
  )
attempts_per_year_combined <- bind_rows(period1_per_year, period2_per_year)

#GLM med neg.bin.fördelning för antal häckningar/år i period 1 & 2
#MISSLYCKADES med neg bin.fördelning pga underdispersion
glm_nb_model <- glm.nb(n_attempts ~ period, data = attempts_per_year_combined)

#GLM med poisson
glm_poisson <- glm(n_attempts ~ period, family = poisson, data =
attempts_per_year_combined)

#GLM med quasipoisson
glm_quasipoisson <- glm(n_attempts ~ period, family = quasipoisson, data =
attempts_per_year_combined)
glm_poisson
glm_quasipoisson
summary(glm_poisson)

summary(glm_quasipoisson)

exp(coef(glm_quasipoisson))
confint(glm_quasipoisson)
exp(3.59274)

library(tidyverse)
library(MASS)
library(dplyr)
```

```
summary(glm_quasipoisson)

#Undersöka häckningsframgång med binomial GLM
#Utgår endast från påbörjad häckningsförsök, kan man modellera
#"floaters" för att få totala odds för lyckad häckning?
breeding_status_bin <- data %>%
  filter(breeding_status %in% c("Successful", "Failed"))

breeding_status_bin <- breeding_status_bin %>%
  mutate(success = ifelse(breeding_status == "Successful", 1, 0))

breeding_status_bin <- breeding_status_bin %>%
  mutate(period = case_when(
    year >= 1977 & year <= 1986 ~ "period 1",
    year >= 2005 & year <= 2011 ~ "period 2",
    TRUE ~ NA_character_))

success_attempts <- glm(success ~ period, family = binomial, data =
breeding_status_bin)
summary(success_attempts)
rm(success_total)


exp(coef(success_total))
exp(confint(success_total))
library(tidyverse)
library(dplyr)
#kontingenstabell
korstabell_utfall <- table(breeding_status_bin$period,
breeding_status_bin$breeding_status)
chisq.test(korstabell_utfall)
sum(data$breeding_all)
119+208+60+136


breeding_status_bin %>%
  group_by(period) %>%
  summarise(
    total = n(),
    successful = sum(success),
    proportion = mean(success))

#Första försök på reproduktionstal
library(tidyverse)
data %>%
  filter(!is.na(fledged_chicks)) %>%
  summarise(
    total_fledged = sum(fledged_chicks),
    n_attempts = n(),
    reproduction_rate = total_fledged / n_attempts)

data <- data %>%
  mutate(period = case_when(
    year >= 1977 & year <= 1986 ~ "period 1",
    year >= 2005 & year <= 2011 ~ "period 2",
    TRUE ~ NA_character_  # Sätter NA för år utanför dessa intervall
  ))

data <- data %>%
  mutate(period = factor(period, levels = c("period 1", "period 2")))

data %>%
  filter(!is.na(fledged_chicks)) %>%
  group_by(period) %>%
  summarise(
    total_fledged = sum(fledged_chicks),
    n_attempts = n(),
    reproduction_rate = total_fledged / n_attempts)
327/9
196/7
451/9
295/7
#Det ovan står som table 4 i word
```

```
#Testa om normalfördelat: svar: nej.
library(ggplot2)
ggplot(data, aes(x = fledged_chicks)) +
  geom_histogram(binwidth = 1) +
  facet_wrap(~period)

wilcox.test(fledged_chicks ~ period, data = data, subset =
!is.na(fledged_chicks))
library(tidyverse)
#Modellera reproduktionstal
glm_repro_poisson <- glm(fledged_chicks ~ period, family = poisson, data = data,
subset = !is.na(fledged_chicks))
#Kontrollera dispersion: var = 1.406, mean = 1.426 -> Poisson ok?
var(data$fledged_chicks, na.rm = TRUE)
mean(data$fledged_chicks, na.rm = TRUE)

summary(glm_repro_poisson)
exp(0.32151)
exp(0.08735)

#Fördelning av boträd i perioderna
library(dplyr)
library(tidyverse)
library(ggplot2)

data %>%
  count(period, tree_species) %>%
  tidyr::pivot_wider(names_from = period, values_from = n, values_fill = 0)

#Kategorisera trädslag
data <- data %>%
  mutate(tree_category = case_when(
    tree_species %in% c("Al", "Asp", "Ek", "Lind", "Trätorn", "Björk") ~
"Lövträd",
    tree_species %in% c("Tall", "Gran") ~ tree_species,
    TRUE ~ "Annat"))
library(tidyr)
data %>%
  count(period, tree_category) %>%
  pivot_wider(names_from = period, values_from = n, values_fill = 0)
sum(data$breeding_all) #Blev fel då alla obs visades, nytt försök nedan

totalattempts <- breeding_status_bin %>%
  mutate(tree_category = case_when(
    tree_species %in% c("Al", "Asp", "Ek", "Lind", "Trätorn", "Björk") ~
"Lövträd",
    tree_species %in% c("Tall", "Gran") ~ tree_species,
    TRUE ~ "Annat"))

totalattempts %>%
  count(period, tree_category) %>%
  pivot_wider(names_from = period, values_from = n, values_fill = 0)

totalattempts %>%
  group_by(period, tree_category) %>%
  summarise(n = n(), .groups = "drop") %>%
  group_by(period) %>%
  mutate(proportion = round(n / sum(n) * 100, 1))
#Allt ovan missvisande p.g.a. skillnad i antal år

#Nytt försök med andel
totalattempts %>%
  group_by(period, tree_category) %>%
  summarise(n = n(), .groups = "drop") %>%
  group_by(period) %>%
  mutate(proportion = round(n / sum(n) * 100, 1)) %>%
  arrange(period, desc(proportion))

totalattempts %>%
  group_by(period, tree_category) %>%
  summarise(n = n(), .groups = "drop") %>%
  group_by(period) %>%
  mutate(prop = n / sum(n)) %>%
  ggplot(aes(x = tree_category, y = prop, fill = period)) +
```

```r
  geom_col(position = "dodge") +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(
    title = "Proportion of breeding attempts in different tree species",
    x = "Tree species", y = "(%)",
    fill = "Period"
  ) +
  theme_minimal()

totalattempts %>%
  group_by(period, tree_category) %>%
  summarise(n = n(), .groups = "drop") %>%
  group_by(period) %>%
  mutate(
    prop = n / sum(n),
    tree_category_eng = recode(tree_category,
                               "Gran" = "Spruce",
                               "Tall" = "Pine",
                               "Lövträd" = "Deciduous"
    )
  ) %>%
  ggplot(aes(x = tree_category_eng, y = prop, fill = period)) +
  geom_col(position = "dodge") +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(
    title = "Breeding attempts in different tree types",
    x = "Tree type", y = "%",
    fill = "Period"
  ) +
  theme_minimal()

#Testa statistiskt
#Chi2-test
table_treetype <- table(totalattempts$tree_category, totalattempts$period)
table_treetype
table(tree_summary_unique)
# Chi2-test
chisq.test(table_treetype)
chisq.test(table_treetype)$stdres

#Fisher exact
fisher.test(table_treetype)

#Andelar
library(tidyverse)
library(dplyr)
totalattempts %>%
  group_by(period, tree_category) %>%
  summarise(n = n(), .groups = "drop") %>%
  group_by(period) %>%
  mutate(proportion = round(n / sum(n) * 100, 1)) %>%
  arrange(period, desc(proportion))

#G-test
install.packages("devtools")
library(devtools)

exp(-0.26053)

#Prova fisher.test här!!!

table(data$tree_category)
table(data$tree_species)

#Antal ungar per lyckad häckning, 2.17 på båda
library(tidyverse)
library(dplyr)

data %>% filter(breeding_status == "Successful",
!is.na(fledged_chicks)) %>%
  group_by(period) %>%
  summarise(total_fledged = sum(fledged_chicks),
  successful_attempts = n(),
  reproduction_per_successful = (total_fledged/successful_attempts))
```

```
#Testar om det skiljer sig på senare decimaler
451/208
295/136

#Testa trädslag baserat på unika träd

tree_summary_unique <- totalattempts %>%
  distinct(nest_id, period, tree_category)

# Skapa kontingenstabell
table_tree_unique <- table(tree_summary_unique$tree_category,
tree_summary_unique$period)
table_tree_unique
# Chi2-test
chisq.test(table_tree_unique)

#Fisher exact test
fisher.test(table_tree_unique)

#G-test
install.packages("DescTools")
library(DescTools)
GTest(table_tree_unique)
GTest(table_treetype)

#Antal år ett boträd nyttjas
nest_usage <- data %>%
  filter(breeding_all == 1) %>%
  group_by(nest_id) %>%
  summarise(years_used = n())
summary(nest_usage)
mean(nest_usage$years_used)

#Antal år ett boträd nyttjas uppdelat på perioderna -> i snitt 3.534
nest_usage_by_period <- data %>%
  filter(breeding_all == 1) %>%
  group_by(nest_id, period) %>%
  summarise(years_used = n(), .groups = "drop")

table_nest_per_period <- nest_usage_by_period %>%
  group_by(period) %>%
  summarise(mean_years_used = mean(years_used),
            median_years_used = median(years_used),
            sd_years_used = sd(years_used),
            n = n())
#Wilcoxon test -> ej signifikant skillnad, periodvis uppdelning
#inte lönt att visa alltså.
wilcox.test(years_used ~ period, data = nest_usage_by_period)

#Test av hur många bon som häckats i under båda perioderna -> 13st
used_in_both_periods <- data %>%
  filter(breeding_all == 1) %>%
  distinct(nest_id, period) %>%
  group_by(nest_id) %>%
  summarise(n_periods = n()) %>%
  filter(n_periods == 2)
nrow(used_in_both_periods)
used_in_both_periods$nest_id

#Ett försök till att analysera konsekutiva år ett bo används men
#lämnar det tills vidare
streak_data <- data %>%
  filter(breeding_all == 1) %>%
  select(nest_id, year, breeding_status)

library(tidyr)
streak_data <- streak_data %>%
  arrange(nest_id, year) %>%
  group_by(nest_id) %>%
  mutate(
    year_diff = year - lag(year),
    new_streak = ifelse(is.na(year_diff) | year_diff != 1, 1, 0),
    streak_id = cumsum(new_streak),
```

```
    streak_length = ave(year, nest_id, streak_id, FUN = length),
    years_into_streak = sequence(rle(new_streak)$lengths)
  ) %>%
  ungroup()

#Lägga in data från projekt fiskgjuse. Tar bara med sjöar samt jmf-bara år
library(tibble)

projektfiskgjuse <- tribble(
  ~ area,          ~ year, ~ period,    ~ active_nests, ~ n_eggs,  ~
n_fledged_chicks,
  "Åsnen",          1978, "period 1",  42,            2.4,      1.56,
  "Helgasjön",      1978, "period 1",  8,             2.25,     1.63,
  "Båven",          1978, "period 1",  27,            2.61,     1.5,
  "Sottern",        1978, "period 1",  8,             2.41,     1.5,
  "Åsnen",          1983, "period 1",  38,            2.54,     1.49,
  "Helgasjön",      1983, "period 1",  14,            3,        1.57,
  "Båven",          1983, "period 1",  29,            2.91,     1.79,
  "Sottern",        1983, "period 1",  8,             2.91,     1.79,
  "Åsnen",          1988, "period 1",  46,            2.7,      1.85,
  "Helgasjön",      1988, "period 1",  15,            2.73,     2,
  "Båven",          1988, "period 1",  29,            2.57,     1.97,
  "Sottern",        1988, "period 1",  9,             2.57,     1.97,
  "Åsnen",          2003, "period 2",  40,            2.76,     1.62,
  "Helgasjön",      2003, "period 2",  13,            2.54,     1.54,
  "Båven",          2003, "period 2",  21,            2.5,      1.31,
  "Sottern",        2003, "period 2",  11,            2.5,      1.31,
  "Åsnen",          2008, "period 2",  39,            2.62,     1.65,
  "Helgasjön",      2008, "period 2",  11,            2.91,     1.73,
  "Båven",          2008, "period 2",  16,            2.6,      1.85,
  "Sottern",        2008, "period 2",  4,             2.6,      1.85,
  "Åsnen",          2013, "period 2",  22,            2.58,     1.67,
  "Helgasjön",      2013, "period 2",  9,             2.89,     2,
  "Båven",          2013, "period 2",  15,            2.6,      1.38,
  "Sottern",        2013, "period 2",  3,             2.6,      1.38,
)

library(tidyverse)
library(dplyr)

#Sammanfattande tabell för projektfiskgjuse
refdata_summary_period <- projektfiskgjuse %>%
  group_by(period) %>%
  summarise(
    mean_active_nests = mean(active_nests, na.rm = TRUE),
    mean_eggs = mean(n_eggs, na.rm = TRUE),
    mean_fledged_chicks = mean(n_fledged_chicks, na.rm = TRUE)
  )

refdata_summary_total <- projektfiskgjuse %>%
  summarise(
    period = "Total",
    mean_active_nests = mean(active_nests, na.rm = TRUE),
    mean_eggs = mean(n_eggs, na.rm = TRUE),
    mean_fledged_chicks = mean(n_fledged_chicks, na.rm = TRUE)
  )

# Kombinera period + total
refdata_summary_combined <- bind_rows(refdata_summary_period,
refdata_summary_total)

#Lägga till kolumn för region i projektfiskgjuse
projektfiskgjuse <- projektfiskgjuse %>%
  mutate(region = case_when(
    area %in% c("Åsnen", "Helgasjön") ~ "Södra Sverige",
    area %in% c("Båven", "Sottern")   ~ "Mellansverige",
    TRUE                              ~ NA_character_
  ))

refdata_summary_region <- projektfiskgjuse %>%
  group_by(region, period) %>%
  summarise(
    mean_active_nests = mean(active_nests, na.rm = TRUE),
    mean_eggs = mean(n_eggs, na.rm = TRUE),
```

```
    mean_fledged_chicks = mean(n_fledged_chicks, na.rm = TRUE),
    .groups = "drop"
  )


exp(-0.26053)

library(tidyverse)
library(dplyr)
library(readxl)

read.csv(Home/R/lifetablegjusar.csv)
view(lifetablegjusar)

library(tidyverse)
library(dplyr)

log(0.582)/5.34

library(tidyverse)
library(dplyr)

summary_by_period <- projektfiskgjuse %>%
  group_by(period) %>%
  summarise(
    mean_active_nests = mean(active_nests, na.rm = TRUE),
    mean_eggs = mean(n_eggs, na.rm = TRUE),
    mean_fledged_chicks = mean(n_fledged_chicks, na.rm = TRUE)
  )

summary_by_area_period <- projektfiskgjuse %>%
  group_by(area, period) %>%
  summarise(
    mean_active_nests = mean(active_nests, na.rm = TRUE),
    mean_eggs = mean(n_eggs, na.rm = TRUE),
    mean_fledged_chicks = mean(n_fledged_chicks, na.rm = TRUE),
    .groups = "drop"
  )

#Avg chicks per total attempt -> 1.43
data %>%
  filter(!is.na(fledged_chicks)) %>%
  summarise(
    total_fledged = sum(fledged_chicks),
    n_attempts = n(),
    reproduction_rate = total_fledged / n_attempts)

1.43/2

#Matrismodell

#Läs in excelfil
library(readxl)

input_matrismodell <- read_excel("R/InputMatrismodell.xlsx", sheet = "Blad1")
names(input_matrismodell) <- c("x", "bx", "gx")
view(input_matrismodell)
rm(input_matrismodell)

input_matrismodell <- input_matrismodell[-c(6), ]

#Matrismodell. 5 åldersklasser,
#Repro. första gången 3 år=50%, 4 år=30%, 5 år=20%
#(0.69 honlig avkomma,baserat avg flygga ungar/försök i period 1)

#ANALYS: Generell påverkan på lambda
#G1: 0.53 -> 0.482 ger motsvarande lambda(0.9896...)
#G2: 0.77 -> 0.70 ger motsvarande lambda(0.9896...)
#G3: 0.78 -> 0.71 ger motsvarande lambda (0.9896...)
#G4: 0.81 -> 0.73 ger motsvarande lambda (0.9896...)
#G5: 0.81 -> 0.791 ger motsvarande lambda (0.9896...)
#G4 & G5: -> 0.81 -> 0.795 ger motsvarande lambda(0.9896...)

#ANALYS: Reprotal från period 2 (0.755): vilken överlevnad kompenserar?
```

```
#G1: 0.53 -> 0.441 ger motsvarande lambda(0.9896...)
#G2: 0.77 ->  0.641 ger motsvarande lambda (0.9896...)
#G3: 0.78 -> 0.649 ger motsvarande lambda (0.9896...)
#G4: 0.81 -> 0.658 ger motsvarande lambda (0.9896...)
#G5: 0.81 -> 0.771 ger motsvarande lambda (0.9896...)
#G4 & G5: 0.81 -> 0.779 ger motsvarande lambda (0.9896...)

#ANALYS: Reprotal från period 2 (0.755): vilken andel floaters kompenserar?
#Inga 3-åringar och 42 % av 4-åringarna reproducerar sig ger 0.9896.
G1 <- 0.53
G2 <- 0.77
G3 <- 0.78
G4 <- 0.81
G5 <- 0.81

F3 <- 0.755*0*G3
F4 <- 0.755*0.42*G4
F5 <- 0.755*G5

A = rbind(c(0, 0, F3, F4, F5),
          c(G1, 0, 0, 0, 0),
          c(0, G2, 0, 0, 0),
          c(0, 0, G3, 0, 0),
          c(0, 0, 0, G4, G5))

sensitivity(A)

#Beräkna Lambda -> 1.001348.
#I min population -> 0.9896692
eigen_A <- eigen(A)
lambda <- max(Re(eigen_A$values))
lambda

#Testar matrisen
library(dplyr)
library(tidyverse)


#Få fram ålderstruktur
stable_structure <- Re(eigen_A$vectors[, 1])
stable_structure <- stable_structure / sum(stable_structure)  # normalisera till
andel
stable_structure

0.9896^25
(28/36.33)^(1/25)

#Känslighetsanalys
install.packages("popbio")
library(popbio)

sensitivity_analysis <- sensitivity(A)
elasticity_analysis <- elasticity(A)
sensitivity_analysis
elasticity_analysis

library(ggplot2)
install.packages("reshape2")
library(reshape2)
library(ggplot2)
library(tidyverse)
library(popbio)
#Visualisera sensitivityanalys -> Värmekarta
#Matris över sensitivity

#Skapa känslighetsmatris
sensitivity_matrix <- matrix(c(
  0.1280318, 0.06776552, 0.05210922, 0.04059049, 0.1718249,
  0.2418950, 0.12803179, 0.09845179, 0.07668905, 0.3246348,
  0.3145727, 0.16649914, 0.12803179, 0.09973039, 0.4221719,
  0.3596709, 0.19036902, 0.14638686, 0.11402807, 0.4826958,
  0.3739630, 0.19793365, 0.15220379, 0.11855917, 0.5018766
), nrow = 5, byrow = TRUE)
```

```
#Värmekarta känslighetsanalys
ggplot(df, aes(x = To, y = From, fill = Sensitivity)) +
  geom_tile() +
  geom_text(aes(label = round(Sensitivity, 3)), color = "black") +
  scale_fill_gradient(low = "white", high = "red") +
  scale_x_discrete(labels = rev(levels(df$To))) +
  scale_y_discrete(labels = rev(levels(df$From))) +
  theme_minimal() +
  labs(title = "Sensitivity analysis",
       x = "From (Origin Age Class)",
       y = "To (Receiving Age Class)")

#Värmekarta elasticitet
elasticity_matrix <- matrix(c(
  0.0000000, 0.0000000, 0.01400372, 0.01812439, 0.09590368,
  0.1280318, 0.0000000, 0.00000000, 0.00000000, 0.00000000,
  0.0000000, 0.1280318, 0.00000000, 0.00000000, 0.00000000,
  0.0000000, 0.0000000, 0.11402807, 0.00000000, 0.00000000,
  0.0000000, 0.0000000, 0.00000000, 0.09590368, 0.40597288),
  nrow = 5, byrow = TRUE)

# Omforma till dataframe i long format
df <- melt(elasticity_matrix)
colnames(df) <- c("From", "To", "Sensitivity")

# Konvertera till faktorer för att få rätt ordning
df$From <- factor(df$From)
df$To <- factor(df$To)

# Rita värmekartan
ggplot(df, aes(x = To, y = From, fill = Sensitivity)) +
  geom_tile() +
  geom_text(aes(label = round(Sensitivity, 3)), color = "black") +
  scale_fill_gradient(low = "white", high = "red") +
  scale_y_discrete(limits = rev(levels(df$From))) +  # Vänd endast y-axeln
  theme_minimal() +
  labs(title = "Elasticity analysis",
       x = "From (Receiving Age Class)",
       y = "To (Origin Age Class)")

#


library(reshape2)
library(ggplot2)
library(tidyverse)
library(popbio)

#Plotta stable age structure
df <- data.frame(
  AgeClass = factor(paste("Class", 1:length(stable_structure))),
  Proportion = stable_structure
)

# Rita stapeldiagram
library(ggplot2)

ggplot(data = df, aes(x = AgeClass, y = Proportion)) +
  geom_col(fill = "steelblue") +
  labs(title = "Stable Age Distribution",
       x = "Age Class",
       y = "Proportion") +
  theme_minimal()

#Survivorship curve

# Skapa vektor med överlevnadssannolikheter upp till 18 års ålder
g <- c(0.53, 0.77, 0.78, rep(0.81, 17))

# Initiera vektor för antal överlevande
S <- numeric(length(g) + 1)
S[1] <- 100  # Startpopulation

# Beräkna överlevande för varje ålder
```

```
for (i in 2:length(S)) {
  S[i] <- S[i-1] * g[i-1]
}

# Gör data.frame
df <- data.frame(
  Age = 0:20,
  Survivors = S
)

# Rita kurvan med logaritmisk skala

ggplot(df, aes(x = Age, y = Survivors)) +
  geom_line(size = 1.2, color = "darkgreen") +
  geom_point(size = 2, color = "darkgreen") +
  scale_y_log10() +
  labs(title = "Survivorship Curve",
       x = "Age (years)",
       y = "Log10(Number of Survivors)") +
  theme_minimal()

A
sensitivity_matrix

install.packages("forcats")
library(forcats)
library(reshape2)
library(ggplot2)
library(tidyverse)
library(popbio)
library(dplyr)

sensitivity_analysis

data
#Matris för fledged chicks per year
fledged_summary <- data %>%
  filter(!is.na(fledged_chicks)) %>%
  group_by(year) %>%
  summarise(
    mean_fledged = mean(fledged_chicks, na.rm = TRUE))

# Slå ihop attempts och fledged per year
combined_plot_data <- full_join(
  attempts_per_year_combined %>% select(year, n_attempts),
  fledged_summary %>% select(year, mean_fledged),
  by = "year")
combined_plot_data

#Plotta OBS misslyckat pga olika skalor
ggplot(combined_plot_data, aes(x = year)) +
  geom_line(aes(y = n_attempts, color = "Breeding Attempts"), size = 1.2) +
  geom_line(aes(y = mean_fledged, color = "Fledged Chicks (avg)"), size = 1.2,
linetype = "dashed") +
  scale_color_manual(values = c("Breeding Attempts" = "blue", "Fledged Chicks
(avg)" = "darkgreen")) +
  labs(
    title = "Yearly Trends: Breeding Attempts and Fledged Chicks",
    x = "Year",
    y = "Count / Average",
    color = "Legend"
  ) +
  theme_minimal()

#Separata plots
ggplot(attempts_per_year_combined, aes(x = year, y = n_attempts)) +
  # Skuggad bakgrund för perioden utan data
  annotate("rect", xmin = 1987, xmax = 2004, ymin = 0, ymax = 50, alpha = 0.2,
fill = "gray") +
  geom_line(color = "blue", size = 1.2) +
  geom_point(color = "blue", size = 2) +
  scale_y_continuous(limits = c(0, 50)) +
  labs(
    title = "Breeding Attempts per Year",
```

```
    x = "Year",
    y = "Number of Attempts"
  ) +
  theme_minimal()

#Ny tabell med NA-värden för åren emellan perioderna
# Skapa en full årsföljd
all_years <- tibble(year = 1971:2018)

# Fyll ut n_attempts per år, sätt NA för saknade år
attempts_complete <- all_years %>%
  left_join(attempts_per_year_combined, by = "year")

# Fyll ut fledged_chicks per år, sätt NA för saknade år
fledged_complete <- all_years %>%
  left_join(fledged_summary, by = "year")

attempts_complete
fledged_complete

ggplot(attempts_complete, aes(x = year, y = n_attempts)) +
  geom_line(color = "blue", size = 1.2, na.rm = FALSE) +
  geom_point(data = attempts_complete %>% filter(!is.na(n_attempts)),
             aes(x = year, y = n_attempts), color = "blue", size = 2) +
  scale_y_continuous(limits = c(0, 50)) +
  labs(
    title = "Breeding Attempts per Year",
    x = "Year",
    y = "Number of Attempts"
  ) +
  theme_minimal()

#Nytt försök med relativa år
library(tibble)

attempts_manual <- tibble(
  time = c(1, 3, 4, 5, 6, 7, 8, 9, 10),
  attempts_p1 = c(33, 37, 43, 33, 38, 34, 39, 36, 34),
  attempts_p2 = c(NA, NA, 33, 28, 27, 29, 28, 26, 25)
  )
attempts_manual

#Ny plot, absoluta tidssteg
ggplot(attempts_manual, aes(x = time)) +
  geom_line(aes(y = attempts_p1, color = "Period 1"), size = 1.2) +
  geom_line(aes(y = attempts_p2, color = "Period 2"), size = 1.2) +
  labs(
    title = "Breeding Attempts per Period",
    x = "Time",
    y = "Number of Attempts",
    color = "Period"
  ) +
  scale_y_continuous(limits = c(10, 50)) +
  theme_minimal() +
  theme(
    axis.text.x = element_blank()  # ← tar bort etiketterna
  )


library(forcats)
library(reshape2)
library(ggplot2)
library(tidyverse)
library(popbio)
library(dplyr)

#Totalt antal flygga år för år
fledged_totals <- data %>%
  filter(!is.na(fledged_chicks)) %>%
  group_by(year) %>%
  summarise(
    fledged_total = sum(fledged_chicks),
    .groups = "drop")
fledged_totals
```

```
#Lägg till period
fledged_totals <- fledged_totals %>%
  mutate(
    period = case_when(
      year >= 1977 & year <= 1986 ~ "Period 1",
      year >= 2005 & year <= 2011 ~ "Period 2",
      TRUE ~ NA_character_  ))
fledged_totals

#T-test
t.test(fledged_total ~ period, data = fledged_totals)
wilcox.test(fledged_total ~ period, data = fledged_totals)

#Nest trees hela perioden
as.data.frame(table(data$tree_category))
prop.table(table(data$tree_category)) * 100

#Endast där häckning påbörjats
table(data$tree_category[data$breeding_all == 1])
prop.table(table(data$tree_category[data$breeding_all == 1])) * 100

70.9+24.7+4.4

#Diagram för projektfiskgjuse
library(forcats)
library(reshape2)
library(ggplot2)
library(tidyverse)
library(popbio)
library(dplyr)

# Lista över lokaler som ska med
valda_lokaler <- c("Åsnen", "Helgasjön", "Båven", "Sottern", "Stora Mellösa",
"Asker")

#Ändra felaktiga värden för Asker
projektfiskgjuse_active_nests[7, 9:12] <- 0

# Filtrera rader för dessa lokaler
data_filtered <-
projektfiskgjuse_active_nests[projektfiskgjuse_active_nests$Lokal %in%
valda_lokaler, ]

# Omvandla till långt format
data_long <- melt(data_filtered, id.vars = "Lokal", variable.name = "År",
value.name = "Häckningar")
data_long$År <- as.numeric(as.character(data_long$År))  # Omvandla år till
numeriskt
data_long

#Plotta
ggplot(data_long, aes(x = År, y = Häckningar, color = Lokal)) +
  geom_line(size = 0.8) +
  geom_point(size = 2) +
  theme_minimal() +
  labs(title = "Breeding Attempts Over Time",
       x = "Year",
       y = "Number of Attempts",
       color = "Lokal") +
  theme(legend.position = "bottom")

6.67/13.33
#Stapeldiagram häckningsförsök
library(ggplot2)

ggplot(parvisdecline, aes(x = Area, y = Attempts, fill = Period)) +
  geom_bar(stat = "identity", position = position_dodge(width = 0.8)) +
  scale_y_continuous(limits = c(0, 50)) +
  labs(title = "Häckningsförsök per område och period",
       x = "Område",
       y = "Antal häckningsförsök",
       fill = "Period") +
  theme_minimal() +
```

```
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

library(ggplot2)

# Skapa en kombinerad etikett för x-axeln: t.ex. "Åsnen\n1977-1986"
parvisdecline$label <- paste(parvisdecline$Area, parvisdecline$Period, sep =
"\n")

parvisdecline$label <- NULL
parvisdecline

(22.33/27.17 + 11.67/18.33)/2
projektfiskgjuse
projektfiskgjuse_active_nests

(28.33+8.33+13.33+2.33)/4
(17.33+6.00+6.67)/4
(11.67+7.5)/(18.33+13.08)

plogis(0.5584)
plogis(0.2599+0.5584)

glm_poisson
glm_quasipoisson
glm_poisson
glm_repro_poisson

27+11+8+4+62+49
27+8+62
27/97
8/97
62/97
11+4+49
11/64
4/64
49/64

7.83*10^-5

summary(tree_summary_unique)
table(tree_summary_unique)
tree_summary_unique

library(dplyr)

tree_summary_unique %>%
  count(tree_category) %>%
  arrange(desc(n))
111+38+12
111/161
38/161
12/161

tree_summary_unique %>%
  count(period, tree_category) %>%
  arrange(period, desc(n))

bon_mat <- matrix(c(62, 27, 8, 49, 11, 4),
                  nrow = 3,
                  byrow = FALSE)
rownames(bon_mat) <- c("Tall", "Gran", "Lövträd")
colnames(bon_mat) <- c("Period1", "Period2")
bon_mat
fisher.test(bon_mat)
chisq.test(bon_mat)

Falsterbo
summary(Falsterbo$Abundance)
var(Falsterbo$Abundance)

glm_falsterbo <- glm(Abundance ~ Year, data = Falsterbo, family = quasipoisson)
glm_falsterbo
summary(glm_falsterbo)
exp(-0.009792)
```

```
data

# Filtrera perioderna
period1 <- attempts_per_year_combined[attempts_per_year_combined$period == "1977-
1986", ]
period2 <- attempts_per_year_combined[attempts_per_year_combined$period == "2005-
2011", ]
unique(attempts_per_year_combined$period)
period1 <- subset(attempts_per_year_combined, period == "1977-1986")
period2 <- subset(attempts_per_year_combined, period == "2005-2011")

get_ci <- function(values) {
  m <- mean(values)
  s <- sd(values)
  n <- length(values)
  error <- qt(0.975, df = n - 1) * s / sqrt(n)
  return(c(mean = m, lower = m - error, upper = m + error))
}

# Räkna ut CI för varje period baserat på n_attempts
ci1 <- get_ci(period1$n_attempts)
ci2 <- get_ci(period2$n_attempts)

# Skriv ut resultaten
cat("1977-1986: Mean =", round(ci1["mean"], 1),
    "CI =", round(ci1["lower"], 2), "-", round(ci1["upper"], 2), "\n")
cat("2005-2011: Mean =", round(ci2["mean"], 1),
    "CI =", round(ci2["lower"], 2), "-", round(ci2["upper"], 2), "\n")
```

Publishing and archiving

☒ YES, I, Patrik Lundin, have read and agree to the agreement for publication and the personal data processing that takes place in connection with this

☐ NO, I/we do not give my/our permission to publish the full text of this work. However, the work will be uploaded for archiving and the metadata and summary will be visible and searchable.