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HPAI drives a fourfold increase in adult gannet mortality which requires two decades recovery time

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ABSTRACT

Wildlife disease outbreaks are increasing, representing a growing threat to biodiversity. Despite this, their demographic cost and recover times are poorly quantified. In 2021, HPAI H5Nx viruses entered new wild host groups, infecting colonial seabirds and triggering substantial global die-offs. Here, we estimate annual survival of adult Northern gannets (Morus bassanus) before and after the 2022 outbreak, using longterm (15-year) capture-mark-recapture data from two large UK colonies, and predict post-outbreak time to recovery using a metapopulation state-space model. Adult mortality averaged 6% and 11% (at Bass Rock and Grassholm, respectively) in the 11 years prior to 2022 but increased sharply to ~ 33% and 47% during the HPAI outbreak. Integrating these survival rates into our metapopulation model predicted 26% and 38% decreases in colony size in 2023, and that colonies will only recover to the pre-2022 levels by 2041, 19 years after the outbreak. Monitoring of key life history traits such as adult survival and integrating these estimates into realistically complex population models is paramount to generate robust evidence for seabird conservation planning, management and mitigation for seabirds. Specifically, we recommend revising the global conservation status of Northern gannets in the light of this unprecedented mortality and subsequent population recovery time from a single disease outbreak.

1. Introduction

Wildlife diseases are increasing in frequency and prevalence, with profound conservation implications (Tompkins et al., 2015). Effective management and conservation strategies require a quantitative assessment of the short- and long-term consequences of such infectious diseases, which is often lacking (Fitak et al., 2019). For example, highly pathogenic strains of avian influenza viruses (AIVs) can lead to mass mortality events among domestic and wild bird populations (Hicks et al., 2020), yet while the extent and level of additional mortality can be calculated in domestic stock, they are largely unknown for wild populations (Badia-Boher et al., 2025). This is especially concerning since

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recent outbreaks of high pathogenicity avian influenza (HPAI) clade 2.3.4.4b H5N1 viruses have caused unprecedented levels of wild bird deaths, after spilling over into and infecting a range of novel wild host species including colonial seabirds in 2021–22 (Peacock et al., 2025).

Globally, seabird populations are declining rapidly (Croxall et al., 2012). A recent assessment identified invasive species, fisheries bycatch, hunting, and climate change as the top four threats, with disease ranked only twelfth (Dias et al., 2019). Yet, since most seabirds aggregate at mixed-species breeding colonies, they are potentially highly vulnerable to infection from disease. This became clear in the outbreak of H5N1 HPAI during 2021–23, which killed millions of seabirds across all continents (Animal and Plant Health Agency, 2022; Banyard et al., 2022; FAO, 2025; CDC, 2024). Efforts are underway to develop a mechanistic understanding of the genetic and ecological factors driving the epidemic (Matthiopoulos et al., n.d.), but a key requirement is to quantify the short- and long-term colony-level consequences of this unforeseen mortality on seabirds. This is a challenge because seabird dynamics are complicated by processes of delayed maturity, metapopulation connectivity and density dependence, and seabird counts must often be conducted at inaccessible cliffs and remote islands. Estimates of mortality from the 2021–23 H5N1 outbreak have been derived from widespread testing and carcass counts, colony counts, aerial surveys, ring recoveries, and shore-based counts of passage seabirds (Cunningham et al., 2022; Paradell et al., 2023, Avery-Gomm et al., 2024; Macgregor et al., 2024; Tremlett et al., 2024a; Johnston et al., 2025; Atkinson et al., 2025) but these do not provide information on changes in population size at focal sites, or at the more conservation-relevant scale of the whole metapopulation. Fewer studies have quantified changes to demographic rates (Lewis et al., 2025) crucial for informing population models (O'Hanlon et al., 2023).

One of the most conspicuously impacted species was the northern gannet (*Morus bassanus*, hereafter gannet) in 2022 (Lane et al., 2024; McPhail et al., 2025). As well as anecdotal reports of strikingly high numbers of dead gannets observed across the northeast Atlantic (Paradell et al., 2023; Lane et al., 2024; Tremlett et al., 2024b), at the world's largest gannetry, the Bass Rock in Scotland, it was estimated that around half of the breeding adults perished (Lane et al., 2024). Yet despite gannets being a relatively well studied species across their range, we lack an accurate assessment of how HPAI has affected adult survival at other gannet colonies. Furthermore, for the Bass Rock, a more precise and accurate estimate of adult survival is necessary for a quantitative assessment of how long it might take the population to recover to its pre-outbreak size.

Here, we assess the impact of the 2022 H5N1 outbreak on two large North Atlantic gannetries, Bass Rock and Grassholm, in two stages. First, we use capture-mark-recapture data to estimate apparent annual adult survival before and after 2022. Second, we use a Bayesian state-space metapopulation model based on ~100 years of counts from all northeast Atlantic gannet colonies to forecast longer-term (82 years) colony recovery trajectories for Bass Rock and Grassholm following the outbreak. To estimate the impact on the study colonies, we compare these with colony growth trajectories from a counterfactual scenario of no HPAI outbreak. Finally, we consider the relevance of our findings in terms of monitoring HPAI impacts on seabird populations and conservation interventions for the gannet and other seabird species.

2. Materials and methods

2.1. Estimating adult survival

Fieldwork work took place at Bass Rock, Scotland (56° 07′ N, 02° 64′ W) and Grassholm, Wales (51° 43′ N, 05° 28′ W) during July–August 2010–2024 (Fig. 1) with HPAI H5N1 first confirmed at Bass Rock on 4th June 2022 and at Grassholm on 21st July 2022 (Lane et al., 2024).

Between 2010 and 2023, adult gannets ($n = 949$) were caught at the nest in discrete study areas within the colonies (Bass Rock, $n = 419$; Grassholm $n = 530$), and fitted with a coloured, high-impact acrylic leg-ring, engraved with a unique 4-digit alphanumeric code. Each

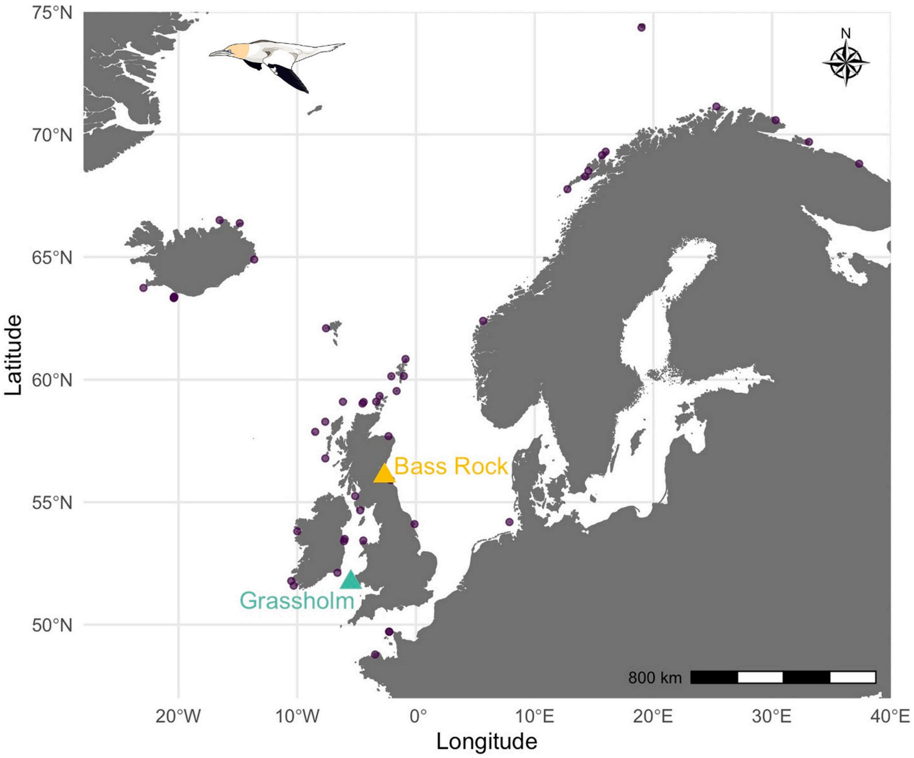

Fig. 1. Locations of the Bass Rock (yellow triangle) and Grassholm (green triangle) gannet colonies within the Northeast Atlantic metapopulation (other colonies indicated by purple circles) at which breeding adult birds were marked with individually identifiable acrylic leg rings between 2010 and 2023, and resighting observations made annually thereafter. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

subsequent year (excluding 2020 due to COVID-19 restrictions) during multiple visits throughout July and August, we searched the study areas within each colony for marked birds to generate individual encounter histories for capture-mark-recapture (CMR) analysis; 1 = observed, 0 = not observed. Known nest sites of colour-ringed birds were scanned repeatedly through binoculars from distances of ~5-30 m and ring sequences noted. Attention was focused incrementally on those nest sites where a colour-ringed bird had not yet been observed. Adjacent areas of the colony were also scanned throughout each visit to check for birds that were not at their expected nest sites. Nests abandoned during the 2022 HPAI outbreak created more space for birds to potentially move around, particularly if breeding with a new partner, hence the need to scan adjacent areas of the colony.

We estimated apparent annual survival (ϕ) (probability of true survival and returning to the study area), while controlling for resighting probability (p) using Cormack Jolly Seber Models (CJS) within the RMark package (Laake, 2013) in R version 4.1.1 (R Core Team, 2025). The data for each colony was evaluated for goodness-of-fit (GOF) by U-CARE (Choquet et al., 2009) using R2ucare version 1.0.2 (Gimenez et al., 2018). The CJS model did not fit the data well (Bass Rock, GOF: $\chi^2_{46} = 179.4$, $p \leq 0.001$; Grassholm, GOF: $\chi^2_{67} = 440.9$, $p \leq 0.001$) with evidence for trap happiness (TEST2.CT; Bass Rock, $z = -9.871$, two-sided test, $p < 0.01$ and Grassholm, $z = -16.770$, two-sided test, $p < 0.01$) but not transience (Bass Rock, TEST3.SR; $z = -2.556$, two-sided test, $p = 0.09$; Grassholm, TEST3.SR; $z = 0.194$, two-sided test, $p = 0.103$). We accounted for trap dependence using a two-stage time-since-marking (TSM) structure. Any further heterogeneity was accounted for by using a variance inflation factor ($\hat{c}$) of 1.674, calculated using the CJS model test statistics and degrees of freedom after discarding the TEST2.CT results from both Bass Rock and Grassholm.

The HPAI outbreak and presence of symptomatic birds (Ayuti et al., 2024) at both colonies spanned the re-sighting period in 2022 meaning that any impact of HPAI on survival would be seen in both 2022; birds that died of the virus prior to the re-sighting period, and 2023; birds seen alive in July 2022 but that subsequently died of the virus. To test for the effect of additional mortality above baseline due to HPAI, we allowed survival to vary with a covariate (h) coded according to the proportion of the re-sighting year that HPAI was observed to be affecting birds at the colony; Bass Rock 2022 and 2023 and Grassholm 2023 = 0.167, Grassholm 2022 = 0.08, and both colonies in all other years = 0.

A set of candidate models were specified allowing survival (ϕ) to vary with colony (c), year (t) or remain constant across years (.), and the presence or absence of HPAI (h). *Re*-sighting probability (p) that represents the probability of resighting an individual given that it was alive, was also allowed to vary with colony (c), year (t or .), or with a TSM structure, where resighting probability was constant for the first year after marking but was then allowed to vary (./t) or remain constant but different to the first year (./.). The top two models (cumulative AIC weight = 0.712) included annual variation and colony as factors influencing survival (Table 1). HPAI was included in three of the six top models (Table 1). Annual survival estimates were taken from the top model (ΔQAIC = 2.064 vs the next best model, so model averaging was not performed) with estimates from the top three models provided in Supplementary Table S1. Details of how candidate models were specified can be found in the Supplementary Material.

Table 1
Top six models (ranked by QAICc) for estimating annual survival and resighting probabilities of gannets from Bass Rock and Grassholm between 2010 and 2024. Variance inflation factor ($\hat{c}$) = 1.67. Effects fitted to survival (ϕ) and re-sighting probabilities (p) (t: time; c: colony; h: presence of HPAI) with a two-stage time-since-marking (TSM) structure applied to p to account for the trap dependence (first year after marking; constant: .; second and additional years; . or t). QAICc: Akaike Information Criterion for small samples. ΔAICc: difference in AICc between model in question and best model. Num. Par.: number of parameters.

Rank	Model	QAICc	ΔQAICc	AICc Weight	Num. Par.	QDeviance
1	$\phi\ (t + c)\ p\ (./. + c)$	4468.55	0	0.525	18	1369.04
2	$\phi\ (t + c)\ p\ (./t + c)$	4470.62	2.064	0.188	18	1371.11
3	$\phi\ (t + c + h)\ p\ (./. + c)$	4471.32	2.764	0.132	20	1367.77
4	$\phi\ (t + c)\ p\ (c)$	4472.13	3.576	0.088	17	1374.64
5	$\phi\ (t + c + h)\ p\ (./t + c)$	4473.37	4.821	0.047	20	1369.83
6	$\phi\ (t + c + h)\ p\ (c)$	4474.95	6.391	0.021	19	1373.42

2.2. Predicting the long-term impact of HPAI

Using these adult survival estimates, we predicted the short-term demographic impact of the HPAI outbreak (i.e. reduction of colony size in the following year) and the longer-term recovery of the two study colonies, based on the most accurate metapopulation model currently available for the Northeast Atlantic gannet metapopulation (Jeglinski et al., 2023, 2024). This mechanistic Bayesian state-space model is fitted to a 116-year time series of discontinuous colony counts and fecundity data for all 53 gannet colonies, as well as hind- and forecast climate data from the latest version of the Coupled Model Intercomparison Project Phase 6 (CMIP6, supporting_information1) (Eyring et al., 2016; C3S & CDS, 2021) based on the HadGEM3.1-MM model (Ridley et al., 2019). The model is described in detail in Jeglinski et al. (2023, 2024), but briefly it includes connectivity between colonies driven by attraction to conspecifics and density-dependent colony growth dynamics, by estimating terrestrial and marine carrying capacities, the latter driven by mechanistic links between sea-surface temperature and recruitment. The demographic impact of climate change is represented by links between air temperature and rainfall, with fecundity. In the absence of HPAI, the baseline (i.e. the intercept of the linear predictor) of adult survival (s_a) is based on survival estimates from Wanless et al. (2006) and therefore has a rescaled beta prior with a mean of 0.918 and a range of 0.872–0.964. We translated the mechanistic equations of the metapopulation model (implemented in JAGS, Plummer, 2003) into a simulation model in R to estimate 1) the population-level impact of HPAI-related decrease in adult survival at Bass Rock and Grassholm, and 2) the time to recovery by comparing the population trajectories under the HPAI outbreak with a theoretical baseline that assumes no additional disease-related mortality. For this purpose, we supplied to the simulation model posterior population estimates for all 46 extant colonies in AOS (apparently occupied sites), posterior estimates of all required demographic parameter values (e.g. survival, fecundity) for the first five years of the forecast time series (2018–2022), and realistic climate change forecast scenarios (SSP5), estimating air temperature exceeding 4 °C by the end of the century (for details see Jeglinski et al., 2024).

To estimate the population-level impact of HPAI-related increases in adult mortality, we adjusted survival in 2022 using colony-specific estimates. For Bass Rock and Grassholm, we used the mean of the two respective survival estimates from the years HPAI affected birds at each colony, as derived from the survival modelling above. Since there are no colony-specific survival estimates available for other gannet colonies, we assigned the survival rates for 43 of the 44 additional colonies in the simulation model randomly by drawing from a uniform distribution bound by the lowest (0.46) and highest (0.74) confidence bands estimated for both Bass Rock and Grassholm (see results of survival analysis below). For the small colony Bjørnøya, the only colony that has not been impacted by HPAI (Lane et al., 2024), we supplied the baseline survival rate (see above).

To generate a theoretical baseline (a counterfactual colony trajectory in the absence of HPAI), we ran the simulation model without the survival reductions and extracted the projections for Bass Rock and

Grassholm. We ran the simulation model for 100 replicates, in each replicate using a different parameter value randomly drawn from the posterior distribution for 82 years (i.e., from 2018 until 2100). This allowed us to estimate mean colony size reductions and credible intervals in 2023, a year after the outbreak, and forecast subsequent colony trajectories. Importantly, our approach estimates the demographic impact of HPAI for Bass Rock and Grassholm whilst controlling for density-dependence and connectivity in the metapopulation they are part of (Jeglinski et al., 2023; Jeglinski et al., 2024).

3. Results

3.1. Impact of HPAI on adult survival

Of 419 individually marked birds at Bass Rock and 530 at Grassholm, 403 (96%) and 426 (80%) were seen again, respectively. At Bass Rock, of the 370 birds marked prior to 2021, 220 (60%) were seen in 2021, and 158 (43%) were seen after 2022. At Grassholm, of the 462 birds marked prior to 2021, 156 (34%) were seen in 2021, and 67 (15%) were seen after 2022.

All three top-ranked models indicated that adult survival differed between colonies, and over time. The effect of HPAI was included in the third ranked model, although confounded by the effect of year (Table 1).

Prior to the HPAI outbreak, adult survival averaged 0.938 (95% CI: 0.855–0.989) at Bass Rock, and 0.893 (95% CI: 0.767–0.980) at Grassholm (Fig. 2) but between 2021 and 2022 it dropped to 0.692 (95% CI: 0.636–0.742) at Bass Rock and 0.553 (95% CI: 0.491–0.613) at Grassholm, and between 2022 and 2023 to 0.674 (95% CI: 0.612–0.731) and 0.533 (95% CI: 0.464–0.601) (Fig. 2).

Resighting probability in the first year after marking was 0.850 (0.823–0.874) at Bass Rock and 0.739 (95% CI: 0.702–0.774) at Grassholm, declining to 0.809 (95% CI: 0.788–0.827) at Bass Rock and 0.678 (95% CI: 0.654–0.702) at Grassholm for all subsequent years.

3.2. Demographic consequence of HPAI-related mortality

Increased adult gannet mortality was estimated to reduce colony size by 25.9% at Bass Rock and 38.4% at Grassholm compared to a theoretical non-HPAI outbreak scenario (Fig. 3A). For both colonies, the reduction in size broadly agreed with published colony count data from drone surveys in 2023 (Harris et al., 2023; Morgan et al., 2023), with a closer coherence for the Bass Rock (projected size = 99% of count; count = 51,844 AOS, 27th June, projected colony size = 51,512, lower CI = 40,252, upper CI = 66,468), and a lower count compared to colony size estimate for Grassholm (projected size = 127% of count; count = 16,482 AOS, 20th June, projected population = 20,928 (lower CI = 16,161, upper CI = 30,513). In 2024, there was less coherence between the count and projected colony size at Bass Rock (count = 46,045 AOS, 29th July, projected colony size = 60,306, lower CI = 50,447, upper CI = 80,239), than at Grassholm (count = 19,199 AOS, 20th June, projected colony size = 25,368, lower CI = 20,137, upper CI = 37,066).

Projections of colony growth suggested long recovery times to the counterfactual ‘baseline’ colony sizes (Fig. 3A & B). For Grassholm, the residuals between HPAI outbreak and baseline scenario became positive for the first time in 2041, nearly two decades after the HPAI outbreak (Fig. 3B). For the Bass Rock, the recovery trajectory was less monotonic - residuals became 0 for the first time in 2027, but decreased again in subsequent years, with small residuals undulating around 0 for the first time in 2040.

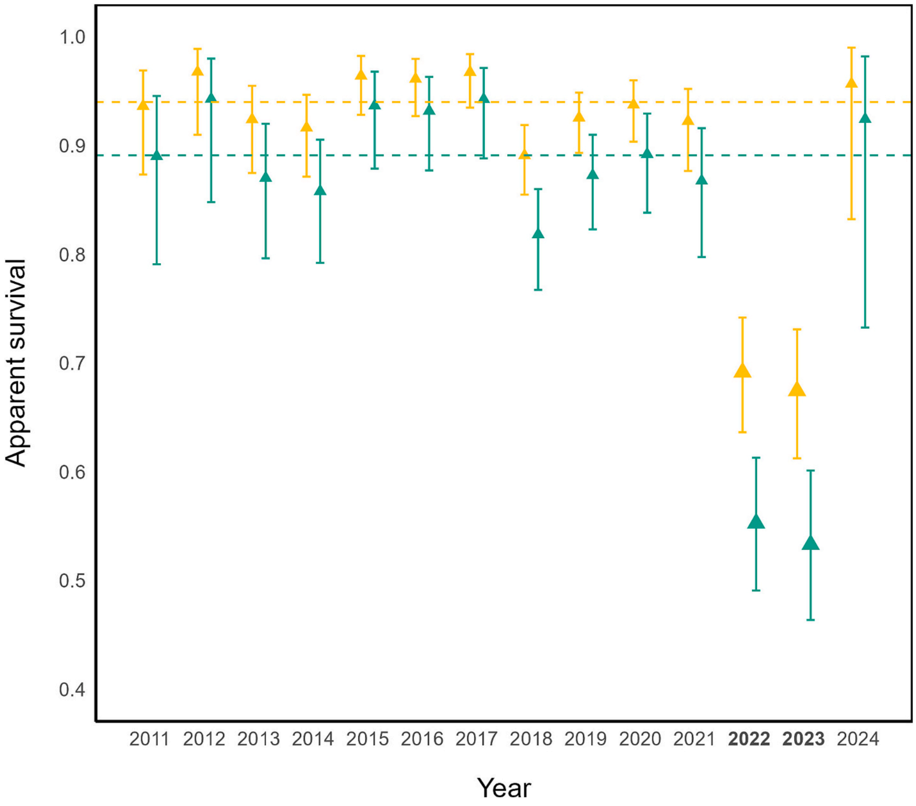

Fig. 2. Annual survival estimates with 95% confidence intervals for adult gannets from Bass Rock (yellow), and Grassholm (green) between 2010 and 2024, taken from the best fitting model in Table 1 above. Years correspond to the annual survival rate estimated for the interval from the previous year to that year (e.g. the value plotted for 2011 represents survival from 2010 to 2011). Years highlighted in bold are years where survival estimates were impacted by the 2022 HPAIV outbreak. Dashed lines represent mean survival between 2010 and 2021 (prior to the HPAIV outbreak). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Fig. 3. **(A)**: Estimated impact of reduced adult survival in 2022 on colony growth trajectories for the Bass Rock and Grassholm gannet colonies (orange line) compared to a theoretical baseline scenario without an outbreak (grey line) until the year 2045. Blue dots represent drone-based count data; Bass Rock 2023 and 2024 (Harris et al., 2023, Burton et al., 2024), Grassholm 2023 and 2024 (Morgan et al., 2023; Morgan and Stephens, 2024). **(B)** The residual between the baseline and HPAI scenarios highlights the scale of the impact and the long recovery times for both colonies. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

4. Discussion

The 2021–22 H5N1 panzootic increased adult gannet mortality by a factor of ~6 and ~ 4 at two of the largest colonies in the world (Bass Rock and Grassholm). Seabird populations are ordinarily characterised by low mortality, particularly among adults (Hamer et al., 2002). Since adult breeders form the vital part of seabird populations driving population growth these mortality increases will have a profound negative impact on their overall population size and future sustainability.

While the unprecedented level of wild bird mortality due to HPAI – across species, individuals, and geographic extent – was already evident (Adlhoch et al., 2022; Renaud et al., 2023; Kuiken et al., 2025), our study is the first to provide robust estimates of adult survival in a seabird species. Moreover, by using a CMR framework, we were thereby able to account for the well-known limitations of imperfect detection to produce less biased, more precise estimates of demographic rates. Although the best-fitting model did not include HPAIV because its effect was confounded with year, the results clearly indicate that survival estimates during the two years coinciding with the outbreak were substantially lower, with non-overlapping confidence intervals (Fig. 2).

Using these reduced survival estimates in our metapopulation projection produced two major findings. First, we estimated that the reductions in survival at Bass Rock and Grassholm in 2022 lead to colony size declines of ~26% and ~ 38% in 2023, the year after the outbreak (Fig. 3), comparable to the estimates from drone surveys (Harris et al., 2023; Morgan et al., 2023) and Bayesian metapopulation modelling (Matthiopoulos et al., n.d.). Second, we predict these colonies are unlikely to regain population sizes anticipated in the absence of the H5N1 outbreak until around 2040. While these findings suggest that the time to recovery is likely to require almost two decades for both colonies, we caution that these are probably underestimates of the true impact of HPAI. In our simulation model, we modulated only adult survival, based on the insights from our mark recapture modelling, whilst priors for the other demographic rates remained unchanged. Other relevant demographic rates, such as immature and juvenile survival may also have been reduced by the HPAI outbreak which would lead to additional decreases in colony size and increases in recovery times (Jenouvrier et al., 2018). Fecundity responses to the outbreak remain unclear: it declined the year following the outbreak at one of our study colonies (Lewis et al., 2025) but increased at another colony (Ponchon et al., 2026). The discrepancy between our modelled colony size estimates and the count data from aerial survey data (Fig. 3A & B) may, to some degree, be explained by such additional, currently unquantified reductions in demographic rates. Calculating survival rates of juvenile and immature seabirds that spend their first few years at sea is challenging (Horswill et al., 2018), and while a range of plausible reductions in survival could be simulated and scenarios compared, it would remain unclear which one would be most likely.

We also note that compensatory demographic effects could buffer the estimated impact of the HPAI outbreak and colony size recovery. Beside breeders, seabird populations also include a pool of non-breeding adult known as 'floaters' (Ainley et al., 2024) which may be able to buffer increased adult mortality via increased recruitment (Votier et al., 2008). Equally, immature birds yet to reach adulthood, could recruit earlier into vacant sites and bolster the breeding population as has happened at three gannetries in the Northwest Atlantic in 2023, following the HPAI outbreak (Sceviour et al., 2024). Nevertheless, despite detailed observations the number of immature gannets at Bass Rock and Grassholm suggest only limited compensatory recruitment by immatures. For example, we only noted a single four-year old immature rearing a chick at Bass Rock and there was no rapid increase in population estimates from drone surveys (Fig. 3A & B; with Bass Rock counts declining by 11% between 2023 and 2024.

4.1. Impact assessment

Following the HPAI outbreak, the Bass Rock gannet breeding population declined by 43% (from ~81,000 AOSs in 2021 (Harris et al., 2023) to ~46,045 in 2024 (Burton et al., 2024)), compared with a 27% decrease in adult survival while the Grassholm population declined from by 47% (from ~36,011 in 2015 to ~19,199 in 2024 (Morgan and Stephens, 2024)), compared with a 36% decrease in adult survival. The discrepancies between drone counts and survival estimates may reflect difficulties differentiating between breeders and non-breeders from digital images and drone counts representing a narrow (1–2 day) snapshot. Alternatively, differences may relate to inter-colony heterogeneity in transmission rates (Matthiopoulos et al., n.d.) generating mortality differences between our CMR sites and the colony as a whole.

Individual and population level immunity to HPAI is currently not well understood, however serological analysis has shown both adult and juvenile gannets can survive HPAI infection (Gremillet et al., 2023; Lane et al., 2024). Persistence of H5 antibodies has been found in gannets a year following the 2022 outbreak, but prevalence within the population and understanding of long-term persistence is still unclear (McLaughlin et al., 2025; Ponchon et al., 2026). Immunity within the population would allow population recovery but the rates will depend on the extent of immunity, viral circulation, virus evolution and interspecific spillovers (Bichet et al., 2021; Charostad et al., 2023; Wight et al., 2024).

Our results demonstrate the value of long-term ring resighting data sets for assessing impact of disease outbreaks and the need for integrated approaches for monitoring and impact assessment (Clutton-Brock and Sheldon, 2010). We advocate establishing new colour ringing and resighting schemes for species and sites where it is practicable to do so, while also focussing on marking juvenile birds to better understand recruitment and buffering capacity (O'Hanlon et al., 2023). For sites where ring-resighting is impractical, alternatives such as camera traps, biotelemetry systems, Passive Integrated Transponder (or PIT) tags and digitally coded transmitters, may provide an effective alternative (Frederiksen et al., 2025). Additional information such as impacts on fecundity and foraging behaviour also warrant further examination.

4.2. Conservation implications

Our results revealed unprecedentedly high HPAI-related adult mortality at two of the largest gannetries - levels which have led to the breeding population declining by about a half and an impact that will take almost two decades to recover from, even when considering the potential for metapopulation-level buffering. We highlight again that the estimated recovery time here is likely a best-case scenario. The recovery of the gannet colonies may additionally be impeded by factors such as increased levels anthropogenic activity at sea, e.g. fishing and bycatch, offshore windfarm installations, marine traffic and pollution, and by climate change related factors such as extreme storms or marine and terrestrial heat waves. We therefore recommend a precautionary approach to re-evaluation of the global conservation status of the gannet, currently classed as a species of Least Concern (Stanbury et al., 2024) and further modelling projections to estimate the impact of additional extreme and catastrophic events on this species.

Opportunities for direct infectious disease interventions are however likely to be limited. Vaccines may provide one possible safeguard against future outbreaks. For example, avian cholera outbreaks (a contagious bacterial disease) in the Southern Indian Ocean have severely impacted seabird chick survival, but a vaccine administered to Indian yellow-nosed albatross (*Thalassarche carteri*) chicks, has increased fledging success from 14% to 46% (Bourret et al., 2018). More recently, there have also been some promising field trails of an H5 HP vaccine in wild king penguins in the sub-Antarctic (Lejeune et al., 2026). Nevertheless, given the financial and logistical challenges of developing a vaccine, the size and distribution of the gannet metapopulation (Jeglinski et al., 2023), and the poorly understood transmission routes within the global seabird community (Gorta et al., 2024), such a vaccination programme seems unfeasible. Other more manageable measures such as the removal of infected carcasses could mitigate potential spread (Knief et al., 2024; Ewing and Bouwhuis, 2025; Gold et al., 2026). This may be most effective where scavenging and kleptoparasitic species like gulls and skuas are a significant driver of disease spread, which is likely the case across the gannet metapopulation (Matthiopoulos et al., n.d.).

Conservation efforts may therefore be best focussed on maintaining favourable population status via other interventions. There are several methods which could aid population recovery for a range of seabird species including bycatch mitigation (Votier, 2023), invasive species removal (Dias et al., 2019) and strategic fisheries management (Searle et al., 2023). The benefits of such interventions are unknown for gannets, but this is a species with a high bycatch risk (e.g. ~18,000 are estimated to be bycaught annually in European waters, Ramírez et al., 2024) and strong reliance on discarded fisheries waste and slippage (Votier et al., 2013) indicating that implementation of more sustainable fishing practices may be beneficial. Moreover, while invasive species do not appear to be a current threat to gannets, maintaining effective biosecurity is desirable. Climate change may impact gannets indirectly via changes in marine environmental conditions (Jeglinski et al., 2024) or directly in terms of heat stress (Navarro et al., 2018), providing further incentive to reduce our reliance on burning fossil fuels (although the plight of gannets is, regrettably, unlikely to tip global attitudes towards the climate crisis).

CRediT authorship contribution statement

Jude V. Lane: Writing – review & editing, Writing – original draft, Visualization, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Jason Matthiopoulos:** Writing – review & editing, Writing – original draft, Methodology, Funding acquisition. **David Astins:** Writing – review & editing, Investigation. **Ian Cleasby:** Writing – review & editing, Investigation. **Keith C. Hamer:** Writing – review & editing, Investigation, Funding acquisition. **Kirsty A. Franklin:** Writing – review & editing, Investigation. **Ruth Jeavons:** Writing – review & editing, Investigation. **Liam P. Langley:** Writing – review & editing, Investigation. **Aly McCluskie:** Writing – review & editing, Funding acquisition. **Greg Morgan:** Writing – review & editing, Investigation. **Lisa Morgan:** Writing – review & editing, Investigation. **Christopher J. Pollock:**

Writing – review & editing, Investigation. **Maggie Sheddan:** Writing – review & editing, Investigation. **Claudia Tapia-Harris:** Writing – review & editing, Investigation. **Lucy J. Wright:** Writing – review & editing, Supervision. **Steve Votier:** Writing – review & editing, Writing – original draft, Project administration, Methodology, Funding acquisition, Conceptualization. **Jana W.E. Jeglinski:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Funding acquisition, Formal analysis, Conceptualization.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.biocon.2026.111887.

Data availability

The authors do not have permission to share data.

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