



Supporting Online Material for

Global Seabird Response to Forage Fish Depletion—One-Third for the Birds

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This PDF file includes:

Materials and Methods
Figs. S1 to S4
Tables S1 and S2
References (30–138)
Data and codes

Supporting Online Material

Contents

Materials and Methods

1. Data set: times series used and narrative description of seabirds and their prey in the different marine ecosystems (table S1)
2. Statistical methods, threshold determination and model fitting
 - a. Empirical analyses of the dataset: tests of normality and pooling data across ecosystems
 - b. Testing alternative forms of the global (asymptotic) model using parametric models (table S2)

Figures S1-S4

Figure S1: Number of years of observation required for estimating the threshold.

Figure S2: Number of years of observation required to evaluate the maximum observed biomass.

Figure S3: Generalized Additive Mixed Model (GAMM) analysis to account for the 'ecosystem effect' in the relationship between breeding success and prey abundance.

Figure S4: Quantile GAM analysis to account for extreme values of the relationship between breeding success and prey abundance.

Tables S1-S2

Table S1 – Time-series used in the meta-analysis

Table S2 – Parametric models considered for the predator-prey relationship

References and Notes

Data and Codes

1. Data set: narrative description of seabirds and their prey in the different marine ecosystems (table S1)

A total of 19 time series from 7 ecosystems and 14 seabird species was used in the present analysis (table S1). Data are available at the end of the SOM.

Time series were selected based upon the following procedure and criteria during a first workshop held in Sète (France):

1. The time-series was of sufficient duration (> 10 years or “bird years”).
2. The time-series was representative of an ecosystem.
3. The variables were collected using comparable methods resulting in comparable metrics (i.e. breeding success expressed as the number of fledglings per pair and prey abundance estimated using biomass or density)
4. There were reliable data about the populations of the main prey species of the predator concerned and these were collected, independently from seabird data, but at similar spatial and temporal scales.
5. The seabird species involved were known, either directly or indirectly, to depend upon the abundance of low-trophic level species during reproduction. The case of indirect dependence included kleptoparasitic species (such as skuas) and species that feed substantially on discarded fish. In most studies, predation impacted fledging success to some extent. However, in the case of Western Gull (*Larus occidentalis*) studied in the Californian Current, excessive predation was the main factor determining breeding success rather than food, so we excluded this population from the analysis in order to avoid misinterpretation about causal links.

During the second and final workshop held in Cape Town (South Africa) the selected database was analyzed using the different statistical methods presented below.

The following are descriptions of the data sets classified by region:

Gulf of Alaska – Cook Inlet

Alaska’s marine waters support more than 100 million seabirds (30). In the Gulf of Alaska, seabird colony populations have fluctuated widely in recent decades and declined markedly at a few sites (31). The *Exxon Valdez* oil spill (EVOS) of 1989 had an immediate and lingering impact on some species of seabirds (32, 33), adding to other anthropogenic factors influencing populations (e.g., gill-net by-catch, fisheries removals, introduced predators) (30). Variability in the marine environment, however, had an even greater impact on seabird populations in the Gulf of Alaska during the same period. Most notably, a major regime shift occurred in the late 1970s, causing marked changes in oceanography, plankton production, marine fish communities and diets of marine birds and mammals, leading to reproductive failures and population declines at some colonies (33, 34). In particular, populations of small forage fish species, with high energy density, such as capelin (*Mallotus*

villosus) declined precipitously, while populations of forage fish species having lower energy density (0-age class), such as walleye pollock (*Theragra chalcogramma*) and cod (*Gadus macrocephalus*), increased and this change was reflected in the diets of seabirds (33, 35). These population fluctuations of forage fish populations could not be explained by direct effects of fisheries, because most declining forage species such as capelin were never harvested in Alaska, and a few species such as pollock increased for environmental reasons (34, 35).

Ecosystem studies were initiated a few years after the EVOS to assess whether environmental conditions that persisted after the climate-induced regime shift could delay the recovery of seabirds from impacts of the EVOS. In particular, a hypothesis was advanced that food stress brought on by climate change might limit seabird reproductive success. In lower Cook Inlet, Alaska, a natural experiment was devised to examine the response of seabirds to fluctuations in prey density around three neighboring colonies (36) and determine the prey density threshold for breeding success. Historical studies had shown that food supplies and breeding success of common murre (CM, *Uria aalge*) and Black-legged Kittiwakes (BK, *Rissa tridactyla*) were poor at Chisik Island, excellent at Gull Island, and average at the Barren Islands (16). Oceanography, plankton, forage fish ecology and seabird distribution at sea were studied in waters around each colony (e.g., 16, 37–39). Absolute forage fish abundance was measured by echo-integration of the hydroacoustic biomass, after adjusting for catch composition and target strengths of forage species in mid-water trawl catches (16, 40). Seabird foraging behavior, diets, time-budgets, chick growth rates, physiological condition, reproductive success, population trends and adult survival rates were measured concurrently at each of the three colonies (e.g., 16, 37, 41, 42).

These studies revealed that diets of murre and kittiwakes were broadly similar within and among colonies, and reflected the relative abundance of forage species in marine waters around each colony (26, 36, 38–42). Diets of adults were composed largely of oily schooling fishes such as Pacific sand lance (*Ammodytes hexapterus*; CM 47%, BK 51%) and osmerids such as capelin (CM 24%, BK 18%), and to a lesser extent of gadids such as pollock (CM 20%, BK 14%). In contrast to some of the other studies reported below, there were no major changes between years in diet composition or in relative fish community composition around each colony. However, as expected, forage fishes were consistently 1–2 orders of magnitude less abundant around Chisik, and most abundant around Gull Island during each year of study. Seabirds at all colonies responded to variation in prey abundance among years not by switching to alternate prey, but by reducing rates of food delivery to chicks, thereby reducing breeding success (16, 26, 41–42). In general, the response in seabird foraging behaviors and reproductive success to spatio-temporal variability in food supplies was non-linear (16).

Norwegian Sea – Røst

Røst (67°30'N 12°00'E) is an offshore archipelago situated at the south-western tip of the Lofoten Islands in North Norway. Its population of Atlantic puffins (*Fratercula arctica*) is still one of the largest in the world, but decreased from about 1.44 million to 410,000 breeding pairs over the 31-year period 1979–2010 (43–46). As the survival of adult puffins at Røst is not different from that at other European colonies, which have not shown equivalent declines (47), the decrease at Røst (72%) is attributed to the extraordinarily poor breeding success of this colony, which includes 18 years of virtually complete breeding failures since 1975 (20, 44–46). The breeding success has been closely linked to the abundance, quality and timing of first-year herring (*Clupea harengus*) from the Norwegian spring-spawning (NSS) stock, which drift past Røst in summer on their way to their Barents Sea nursery areas (20, 48–50). This herring stock collapsed in the late 1960s due to an extensive and increasing fishery during a period of poor recruitment (51). The stock remained at an extremely low level for two decades before it gradually rebuilt its numbers. The recovery happened as a result of both strict regulations of herring fishing and an improved ocean climate that increased the production of strong year classes and later recruitment to the breeding stock (52). In the only 11 seasons since 1975 with high breeding success (71%–96% of chicks fledged) for the Røst puffins, first-year herring contributed an average of 56% by mass of the chick diet, while non-schooling fish (mainly first-year Gadidae) contributed 25%. In the seasons when breeding failed almost completely (0–8% of chicks fledged), these proportions (when measurable) were reversed (to 27% and 53% of first-year herring and mainly first-year Gadidae, respectively, $n = 12$ years) (44, 46). The availability of first-year herring also explains much of the inter-annual variation in survival of breeding birds (53–55). The 1.5 million pairs of puffins breeding in the western parts of North Norway, where this herring is available in the breeding season, are able to consume 5–15% of a reasonably good herring year-class (56). When converted to newly metamorphosed fish in June–July, this corresponds to 15–45 million metric tons of herring fry. The breeding success of puffins in Røst is a good predictor of NSS herring year-class strength at the age 0 stage (57).

More than 90% of the black-legged kittiwakes (*Rissa tridactyla*) in Røst, the second-most numerous seabird in the archipelago, breed in a colony that decreased from about 25,000 pairs to 7,500 pairs over the same 31-year period (44, 46). Since 2007, based on regurgitations collected annually from black-legged kittiwake chicks and adults, first-year herring was a regular but small component of the kittiwake diet (45). In all these years kittiwake breeding success was very poor, although the data are insufficient to indicate the normal diet composition. Until the mid 1990s, however, breeding success of the Røst kittiwakes correlated well with the abundance of young herring (58), but this relationship was later affected by extensive harassment and predation of kittiwake chicks from a booming population of non-breeding white-tailed eagles (*Haliaeetus albicilla*) summering in the area (59).

Breeding numbers and reproductive success of kittiwakes and puffins were monitored annually in study plots, and food loads of adult puffins were

collected regularly throughout the chick period using mist nets (43, 60). Annual estimates of first-year abundance and spawning stock biomass of NSS herring were provided by ICES (61). No sufficiently long-term data exists on the breeding success of other seabirds feeding on this food source.

North Sea – Shetland

Shetland is an archipelago in the northwest corner of the North Sea, strongly influenced by inflowing North Atlantic water. Most islands are bounded by sea cliffs and provide ideal nesting habitat for many seabird species (62). Seas around Shetland hold stocks of lesser sandeels *Ammodytes marinus* and adult herring *Clupea harengus* (but no juveniles), and are visited seasonally by adult mackerel *Scomber scombrus* (63). Since only northern gannets *Morus bassanus*, great black-backed gulls *Larus marinus* and great skuas *Stercorarius skua* are large enough to swallow adult herring and mackerel (64), most seabirds in Shetland feed predominantly on sandeels while breeding (22, 65). *Larus* gulls, great skuas, gannets and fulmars *Fulmarus glacialis*, also scavenge on trawl fishery offal and discards (64, 66, 67), but even in those species, sandeels represent most of the diet in years when sandeel abundance is high (66, 68–70). Due to the lack of alternative small pelagic fish species at Shetland, most small seabirds (including Arctic skuas *Stercorarius parasiticus* and kittiwakes *Rissa tridactyla*) have little opportunity for prey switching when sandeels are scarce, but either increase effort searching for sandeels (71–73) or abandon breeding (62, 74).

Seabird consumption and diet composition data (75) refer to the period when the Shetland sandeel stock was large (ca. 120,000 tonnes) in the late 1970s and early 1980s. When the sandeel stock collapsed in the late 1980s, some seabirds switched diet (sandeels almost disappeared from diet of northern fulmars, northern gannets, great black-backed gulls, great skuas and herring gulls), and all except northern gannet declined in breeding numbers.

The Shetland stock of sandeels is considered to be quite distinct from others in the North Sea, with independent dynamics (76–78). Shetland sandeel stock biomass was assessed by Virtual Population Analysis (VPA) during the period when there was a sandeel fishery at Shetland and by research trawl surveys after the fishery closed (22, 78). Seabird breeding success at Foula was monitored by RWF and colleagues from the early 1970s, under contract to Shetland Oil Terminal Environmental Advisory Group (SOTEAG), following standard methods used for UK seabirds, as established by Walsh et al. (79). Seabird breeding success at many other Shetland colonies was monitored since 1986 by the national seabird monitoring program coordinated by the Joint Nature Conservation Committee (JNCC) as reported in their annual reports (80). We therefore included in the analysis all seabird species from Foula for which there was a time series of breeding success data matching that of the Shetland sandeel stock. This included species that feed by scavenging on fishery discards as well as on sandeels, since in years of sandeel abundance these birds feed predominantly on sandeels, and mainly switch to discards when preferred small pelagic fish are scarce (66, 68–70).

Shetland sandeel stock biomass was high in the 1970s when a fishery on sandeels began for the first time, and declined rapidly during the 1980s as large catches of sandeels were taken (22). The fishery was closed in 1990 due to low stock biomass and associated concerns about seabird breeding failures, and although sandeel recruitment was good in 1991 immediately following closure, the stock biomass showed only partial recovery. Stock biomass fell again very rapidly after 2000. Causes of stock decline are not fully understood (22, 75-78), but may relate to a combination of sequential fishery exploitation of stocks on local sandbanks, effects of increasing sea temperatures, changes in currents, and (especially since 2000) impacts of predation by an increasing stock of adult herring (81).

California Current – Southeast Farallon Island

The California Current Ecosystem (CCE) is one of 4 highly productive eastern boundary current systems in the world. Exceptional, yet variable productivity of forage fish arises from transport of sub-arctic water from the north via the California Current, transport of sub-tropical waters from the south relative to El Niño/La Niña events and regional wind-driven coastal upwelling (vertical transport) currents that supply nutrients to the light-penetrating upper ocean, thereby stimulating photosynthesis and food web development (82). Inter-annual and inter-decadal variability in forage fish have been related to water temperature, upwelling indices, and large-scale climatic factors such as the Southern Oscillation Index (SOI) and the Pacific Decadal Oscillation Index (PDO). Generally speaking, when upwelling and southward transport are strong, waters are colder and primary productivity is higher, with corresponding effects at higher trophic levels.

In the CCE, the upper trophic level predator community includes ~2–7M individuals of ~100 seabird species (83), though recent population declines of dominant species (e.g., shearwaters) have been documented (84, 85). Seabird prey in this ecosystem consists largely of forage fish, including age-0 predatory fish, such as hake (*Merluccius productus*) and rockfishes (*Sebastes* spp.), and coastal pelagic species such as northern anchovy (*Engraulis mordax*) and Pacific sardine (*Sardinops sagax*). Market squid (*Loligo opalescens*) and mesozooplankton, primarily euphausiid crustaceans, also are important diet items (86, 87). Roth et al. (88) provide estimates of consumption (MT) of various prey species by common murre (*Uria aalge*) in the central-northern portion of the CCE.

To study the reproductive success of seabirds, focal breeding pairs were sampled throughout each nesting season by PRBO Conservation Science at Southeast Farallon Island, Farallon National Wildlife Refuge (37°42'N, 123°W) (89, 90). The species monitored were western gull (*Larus occidentalis*), Brandt's cormorant (*Phalacrocorax penicillatus*), common murre, pigeon guillemot (*Cephus columba*), pelagic cormorant (*Phalacrocorax pelagicus*), Cassin's auklet (*Ptychoramphus aleuticus*), ashly storm-petrel (*Oceanodroma homochroa*) and rhinoceros auklet (*Cerorhinca monocerata*). For each species, individual nest sites were monitored (n=15–500 nests per species per year) at 1–7 day intervals for breeding activity. Reproductive performance

was defined as the number of offspring departing the colony per breeding pair per year (or “jumping” for murre) (90). As Cassin’s auklet and ashby storm-petrel are planktivorous (91, 92), and limited spatially and temporally congruent data about plankton (krill) population abundance was available (2002-2008), they have not been included in this analysis. Western gull breeding success has largely been determined by predation (93), so similarly they have not been included in the analysis. The breeding success of Brandt’s cormorant is now largely determined by the abundance of northern anchovy (*Engraulis mordax*) for which we did not have a time series on prey abundance. The breeding success of Pelagic cormorant is driven largely by the abundance of benthic, neritic prey, another prey group for which there was no data. Thus, we selected for our analysis Common murre, Rhinoceros Auklet and Pigeon Guillemot, 3 species for which we had appropriately sampled prey data.

The availability of juvenile rockfish is the single most important determinant of seabird breeding success at Southeast Farallon Island, at least through the period in which we have overlapping time series of seabird breeding success and independent measures of prey availability, 1983–2007. There is substantial inter-annual variability in the consumption of juvenile rockfish. For the period 1975–2007, juvenile rockfish comprised from 1% to 94% (mean=43%) of the offspring diet of murre. For the period 1989–2006, juvenile rockfish comprised 1% to 56% (mean=20%) of the chick diet for guillemots, and for the period 1987–2007, juvenile rockfish comprised 0% to 59% (mean=16%) of the diet for rhinoceros auklet young.

Juvenile rockfish relative abundance was estimated from annual trawl surveys conducted by the National Marine Fisheries Service (NMFS) in May and early June from 1983 to 2007 (94), in the region of central California that closely approximates the foraging range of the seabird species studied (24). Pelagic juvenile rockfish experience high mortality from predation so abundance was calculated after the raw catch had been adjusted to a standard age of 100 days (95). To develop an annual index of age-0 abundance, we used tow-specific catch rate and a delta-general linear model (GLM) approach (24).

The relationship between juvenile rockfish in the offspring diet of murre, guillemots and rhinoceros auklets relative to the estimated abundance of these forage fish in the environment based on the NMFS surveys (87, 93, 96) is asymptotic (87). There was substantial inter-annual variation in the covariance of rockfish abundance and seabird consumption (96). Amongst murre, 81% of the variation in juvenile rockfish in the diet was explained by juvenile rockfish relative abundance in the environment (96). Declines in predation of juvenile rockfish by the birds as well as abundance in the environment (87, 90) were related to upwelling and other oceanographic factors as well as fishing (24). Rockfish fisheries in the region targeted adults, so the link to the abundance of juveniles (age-0) which constitutes the seabird’s diet is difficult to assess. However, across this assemblage, there have been substantial declines in rockfish populations (24). One of the primary species preyed on by seabirds, the shortbelly rockfish (*Sebastes jordanii*), is not fished directly, although it may be by-caught in other fisheries.

Benguela Current – Lambert’s Bay, Malgas Island, Robben Island

The Benguela ecosystem off south-western Africa is one of the world's four major eastern-boundary-current upwelling ecosystems. It supports high biomasses of anchovy *Engraulis encrasicolus* and sardine *Sardinops sagax*, which are the main prey of a wide spectrum of predators and are also exploited by purse-seine fisheries (97). Amongst the predators that feed mainly on anchovy and sardine are four seabirds: African penguin *Spheniscus demersus*, Cape gannet *Morus capensis*, Cape cormorant *Phalacrocorax capensis* and swift (or crested) tern *Thalasseus bergii* (98, 99). The first three of these seabirds are endemic to southern Africa, as also is the nominate race of swift tern (100). The other main eastern-boundary-current upwelling ecosystem of the southern hemisphere is the Humboldt system off western South America (101). In that system, anchovy *Engraulis ringens* and sardine again are the dominant forage fishes and it also has an endemic penguin, sulid, cormorant and tern that subsist mainly on these two prey species (100). In the Benguela ecosystem, there have been large fluctuations in the abundances of both anchovy and sardine (102), as well as shifts in their distributions (103, 104), which provide opportunity to investigate relationships between the population sizes and demographic parameters of predators, or their diet, and the abundance or availability of their prey. For example, numbers of African penguins and Cape gannets breeding in Namibia were significantly correlated with the biomass of small epipelagic fish, mostly sardine, off that country (99). Off South Africa, in the 2000s, a large increase in the number of swift terns breeding coincided with an increased abundance of anchovy and sardine (105). At Robben Island, South Africa, the breeding success of African penguins was significantly correlated with the combined biomass of anchovy and sardine (106). Off South Africa's Western Cape, from 1984–1993 the contribution of anchovy to the diet of Cape gannets was significantly related to the biomass of anchovy (107). The causes of the large fluctuations in the abundance and distribution of anchovy and sardine in the Benguela ecosystem are not fully understood but are thought to have been influenced by both environmental factors and fishing, with some major collapses of stocks attributed to over-exploitation (108).

For African penguins at Robben Island we used information on breeding success (chicks fledged per pair) and prey abundance for 1989–2004 published by Crawford et al. (106). For Cape gannets at Lambert’s Bay and Malgas Islands, we used information on breeding success from Adams et al. (107), and unpublished records of Department of Environmental Affairs, South Africa and annual estimates of the spawner biomass of anchovy and sardine (combined) found west of Cape Agulhas (kindly provided by J Coetzee of Department of Agriculture, Fisheries and Forestry, see also 102). Most Cape gannets breeding at Lambert’s Bay and Malgas Island feed west of Cape Agulhas. When breeding, African penguins and Cape gannets at these localities feed mainly on anchovy and sardine; outside the breeding season Cape gannets may scavenge substantial quantities of hakes *Merluccius* spp. that have been discarded by trawlers (108).

New Zealand – Kaikoura Peninsula

The coastal water off Kaikoura on the east coast of New Zealand is a highly productive system (109) that supports a variety of sea birds and marine mammals (110). The hydrology is relatively complex as it is a region of interaction of warm northern water from the East Cape Current and cooler southern water of the Southland Current (111, 112). The continental shelf off the coast is relatively narrow and incursions of warm or cold water have a major impact on the productivity of the region (109).

The Kaikoura Peninsula is home to the third largest breeding population of red-billed gulls (*Larus novaehollandiae scopulinus*). Adults can often sustain themselves on alternative foods such as earthworms, small fish, garbage and kelp flies (23), but they are dependent upon an abundant and regular supply of *Nyctiphanes australis* (krill), their preferred food for successful breeding.

The availability of krill varies annually in response to changes in climate and oceanography. Prior to the gulls' breeding season, the critical period for growth and productivity of krill is winter-early spring when egg formation occurs. Nitrogen enrichment in the coastal water at this time is greatest when there is no influx of warm offshore water (23, 106). During the breeding season the relative availability of krill was correlated positively with the Southern Oscillation Index and the frequency of occurrence of NE winds which induce upwelling (23). Incursions of warm oceanic water, often induced by westerly winds, which are characteristic of El Niño years, were associated with reduced euphausiid availability and reduced breeding success. Strong incursions sometimes displaced the coastal water column with lower nutrient water, and less dramatic incursions resulted in warm water overlying the colder water, preventing the migration of euphausiids to the surface (23, 109, 112).

The reproductive success of the red-billed gull has been monitored at Kaikoura for the past 47 years and the abundance of euphausiids available to the birds was determined for 35 years during the period (1975–2010). Between 1993 and 2003, the population declined by 51% (85). The availability of *N. australis* to the red-billed gull was assessed by calculating the proportion of breeders and non-breeders which regurgitated the euphausiid when captured (23). Between 1975 and 2010, 62% of 7215 adult red-billed gulls regurgitated *N. australis* during the breeding season. The contribution of *N. australis* to the diet reached up to 84% (23). The relationships between food availability and the number of pairs that bred, laying date, clutch size, fledging success and age of first breeding were different before and after the population decline (23). The underlying cause appears to have been a compensatory density-dependent mechanism that reduced interspecific competition for food. The index of availability measures the frequency the bird obtained euphausiids. When the population declined by 51% after 1993 from 19,000 to 9,000 individuals, competition for food at the irregular surface forming swarms lessened and consequently the food index changed and was

not comparable to the index when the population was stable at the higher level. The data set therefore needed to be partitioned into pre- and post-decline phases (23). The analysis of the impact of food on breeding success in the present paper was restricted to the pre-period from 1975 to 1994 when the population was stable. The prey availability index was calculated from different red-billed gulls than the individually colour-marked birds that were studied to ascertain the reproductive performance; so these can be considered as two independent data sets.

Scotia Sea – Bird Island

The Scotia Sea is part of the Southern Ocean and is bounded in the west by Drake Passage, while to the south, east and north, it is surrounded by the Scotia Arc. The oceanographic regime is dominated by the easterly flow through Drake Passage of the Antarctic Circumpolar Current (ACC) and by northerly outflows from the Weddell Sea. To the east of Drake Passage the ACC is deflected northwards by the Scotia Arc, which brings high nutrient waters north and eastwards into areas of high natural iron concentration, making it one of the more productive regions of the Southern Ocean (113). The northward flowing currents also transport Antarctic krill (*Euphausia superba*) from ice dominated areas in the south into the region around the Island of South Georgia, in a process that is considered to be crucial in maintaining the local krill population (114–116). The high production and northward dispersal generate a high biomass of krill around the island, where it is the prey for many upper-trophic level predators. Climate related fluctuations in oceanic and sea ice conditions across the Scotia Sea affect krill recruitment and dispersal generating large inter-annual variations in krill biomass around South Georgia (113, 116, 117–119). A series of acoustic estimates of krill biomass was maintained at South Georgia for over 20 years and provided an annual index of krill availability (113, 119).

Seabirds and seals that breed at South Georgia are important predators of krill and their responses to changes in prey abundance have been used to monitor the ecosystem (29, 118, 120). Two or three times in a decade krill abundance has been very low and the foraging and breeding performance of a range of predators has been affected (113, 117, 118, 121). The response of particular species to variations in food availability has depended on the magnitude of the variation and the flexibility of their feeding, foraging and breeding strategies (121). The quantitative responses of predators to changes in krill abundance depend upon the characteristics of the variable being measured. Those involving population changes had greatest buffering and lowest variance compared with those associated with breeding behaviour (122). Those with highest variance were most sensitive to inter-annual variation in indices of krill abundance, and breeding behaviour and diet during the breeding season showed non-linear functional relationships between independently-collected krill density estimates (19). Behavioural and short term responses can, therefore, allow buffering of life history responses to variation, which can mask population responses to change in food availability (123, 124). In years of low krill availability the fish component in particular tends to increase, but this is set against a decrease in overall breeding

success (125). The gentoo penguin (*Pygoscelis papua*) is one of the species monitored at South Georgia and its breeding success was significantly reduced in periods of low krill availability (118, 121). The measured responses to inter-annual changes in food availability at South Georgia occurred within a context of significant decadal change in the Scotia Sea ecosystem and in the dynamics of predator populations across the Southern Ocean (126).

The major fluctuations in krill abundance around South Georgia have been related to Southern Hemisphere scale atmospheric fluctuations that affected Scotia Sea oceanic and sea ice conditions, which in turn directly impact the krill population dynamics. The fishery for krill in the Southern Ocean is currently operating at a lower level than during the 1980s and 1990s and even peak catches were far below the current maximum allowable catch levels (127). The fishery around South Georgia operated mainly during winter months, outside the main breeding season for most predators. There has been a rapid increase over the last few years in overall krill catch levels from the fishery, which reflects changes in gear and the development of new krill-based products. This rapid expansion is causing concern, although current catches are still well below the peak catches previously recorded. In addition to Gentoo penguins, a range of other species at South Georgia depends on krill as a major component of the diet (121) including Macaroni penguins, fur seals and black-browed and grey-headed albatrosses. These species show different levels of dependence on krill in their diets and in their responses to changes in availability (21, 121, 128), and may be affected differently by a future intensification of the krill fishery.

2. Statistical methods, threshold determination and model fitting

The data analysis was designed to optimize across the constraints presented by the data. We made no *a priori* assumptions about the distribution of the data or about the form of any functional relationships between seabird breeding success and prey availability. We used generalized additive models (GAMs) to explore the shape (also described as “form” in the main text) of the functional relationships. GAMs are similar to generalized linear models in that they relate a single dependent variable to one or more independent variables but they also have the property of exploring non-linearity in the relationships using smoothers with no *a priori* assumption on the shape of the relationship. We then applied a parametric approach using model selection criteria (AIC) across a range of deterministic models to verify and reinforce the results revealed by the GAM. All the statistical methods were assessed using a hierarchical modeling framework to account for the repetition of the same relationship in each ecosystem. All the R-codes that were used are available at the end of the SOM.

a) Empirical analyses of the dataset: tests of normality and pooling data across ecosystems

To enable comparison of the data between ecosystems and species groups, we first normalized each time series by subtracting the mean and dividing by the standard deviation for each time series. The Shapiro test for normality was applied to each time-series of prey abundance and seabird breeding success to investigate if the data were normally distributed. Sixteen of 19 (table S1), prey abundance time-series and 12 seabird series were normally distributed. We also ensured that the normalization did not affect the shape of the relationship between breeding success and prey abundance, especially for non-normally distributed data. Consequently, we used a non-parametric approach, generalized additive models (GAM) fitted to the pooled normalized data to explore the functional form of the relationship between seabird breeding success and the abundance of forage fish (Fig. 2A). *R* package “gam” was used (129).

Identification of a threshold from non-parametric GAM analysis

To identify and quantify a threshold in the functional relationship between prey abundance and breeding success of predators, a change-point analysis was performed (130). We used the function “cpt.reg” of the *R* package “change point” (131). This function enabled calculation of the optimal positioning of a change-point. This analysis was performed on the predicted values based on the GAM.

To test the validity and robustness of the calculated threshold we estimated potential bias in threshold estimates with respect to the sample size (number of years analyzed). The aim was also to estimate the number of years required to estimate the threshold. From the pooled dataset, we randomly drew “X” consecutive years from the breeding success and prey time-series, where “X” is comprised between 5 and 42 years. From this subset we calculated the threshold and compare it to its value as estimated from the global dataset. We repeated this operation 1000 times to test a wide range of subsets and calculated a confidence interval for the estimated threshold from the subset of “X” consecutive years. The minimum number of years required to estimate the threshold was determined using the significance of the mean value of the threshold, given the confidence intervals for both the subset and global dataset, i.e. the minimum number of consecutive years where the threshold value estimated from the subset dataset was within the confidence interval of the threshold estimated from the global dataset (fig. S1). To evaluate the number of years of observations needed to determine the maximum observed biomass in prey time series, we calculated the number of years between the beginning of the data collection and the year when the maximum biomass was observed (fig. S2).

Estimation of the threshold confidence interval

We used a bootstrap procedure to estimate the confidence interval of the threshold estimate. We sampled the global dataset 1000 times to estimate the value of the threshold. The values of the 2.5% and 97.5% quantiles of the 1000 estimates of the threshold were considered as the 95% confidence interval (CI) for the threshold.

Accounting for “ecosystem” variation using a general additive mixed model

To test the hypothesis that systematic ecosystem by ecosystem variation may have resulted in the apparent asymptotic (saturation) relationship between predators and prey based on the pooled global dataset, we added a random effect to the GAM formulation, i.e. a general additive mixed model (GAMM); this accounted for the potential ‘ecosystem effect’. This approach corresponds to generalized linear mixed model (GLMM), in which the linear predictor depends linearly on unknown smooth functions of some of the covariates. We used the **R** package “*gamm4*” (132).

Using the GAMM, the asymptotic form of the pooled data was validated. Moreover, the threshold value (-0.12) obtained using this method was not different from the result obtained using the simple GAM analysis (-0.092; fig. S3). Uncertainties for the extreme values were larger, but not unreasonably so. We followed the GAMM with the bootstrap analysis to verify the CI. This analysis provided a larger confidence interval than the simple GAM, but CIs were remarkably similar. We think that these minor differences stemmed from the fact that inclusion of “ecosystem” in the model created another source of variability around the main pattern. The similar results in terms of threshold identification and uncertainty illustrate the robustness of our analyses (Fig. 2A).

Accounting for stochasticity in the identified globally-coherent pattern of the predator-prey relationship

The GAM analysis revealed an average asymptotic relationship between seabird breeding success and prey abundance. We investigated whether the form of this relationship was influenced by extreme values (very high/low breeding success) using quantile GAMs. Our aim here was to examine whether the variability driving the “average” asymptotic relationship could be replicated using just extreme values from our data distribution. We used the **R** package “*vgam*” for this test (133, 134), with quantile values at 10% and 90%. The quantile GAM performs as a GAM model which is fitted on the quantiles of the response variable (here the 10% and 90% of the seabird breeding success). This analysis reveals that a very similar pattern is obtained using the extreme values. In other words, for an analysis using only low/high breeding success, there still exists a threshold value (fig. S4). This analysis demonstrated that our results are robust while accounting for the stochasticity over the average relationship. This shows robustness of the threshold to the accuracy of measurement of breeding success. The identified threshold using

these quantiles is very similar to the threshold calculated using all data (~-0.14 for the quantile 10 and 90%, and -0.92 for the simple GAM analysis – Fig. 2A) and is within the CI of the simple GAM analysis.

Calculating the variance in the breeding success relative to prey abundance

The variance in seabird breeding success was calculated for each prey abundance class (every 0.5 from -1.5 to 2; Fig. 2B). Prey biomass values (6 data points) that were either below and above those extreme values were not included in the variance analysis to avoid “edge” effects as they were too few data points for each class to calculate the variance. An F-test was used to test for significant differences in variance from low to high levels of prey abundance. This test showed significant difference in variance ($p < 10^{-5}$) as well as mean breeding success.

b) Testing alternative forms of the global (asymptotic) model (table S2)

Model fitting

We used a series of parametric models to evaluate possible inconsistency in the global asymptotic model. We examined 11 equations that covered a range of log-linear relationships (table S2); we fit these equations to the pooled dataset using the “nls” function in **R** (135). To select the best model, we used the Akaike Information Criterion (AIC). The model 4 in table S2 ($y = c + a \cdot (1 - e^{-b \cdot x})$) was selected as the “best” model. In order to validate the global analysis and to examine the robustness of the fitted functional relationships, we fitted this parametric model to the data for each ecosystem (Fig 2C & Fig 3) and for each seabird species (Fig. 2D). To examine effects at the ecosystem level, data were pooled across the seabird species within each ecosystem.

Hierarchical model fitting

Using the same basic procedure we used for the GAM/GAMM analysis, we added “ecosystem” as a random effect to the model showing the lowest AIC value. We used the “nlme” function of the **R** package (136). We added two random effects for the parameters a and c ($r_{i,1}$ and $r_{i,2}$ where i is the ecosystem) using the procedure described in (136) (table S2). Fitting this hierarchical model to data showed that the results were similar between ecosystems (table S2). Resulting values were, however, slightly different from the fixed-effect model. Autocorrelation in the data was checked with an analysis of the model residuals. Residuals were randomly distributed and an *qqnorm* plot showed that they did not differ from the normality assumption.

Figures S1 to S4

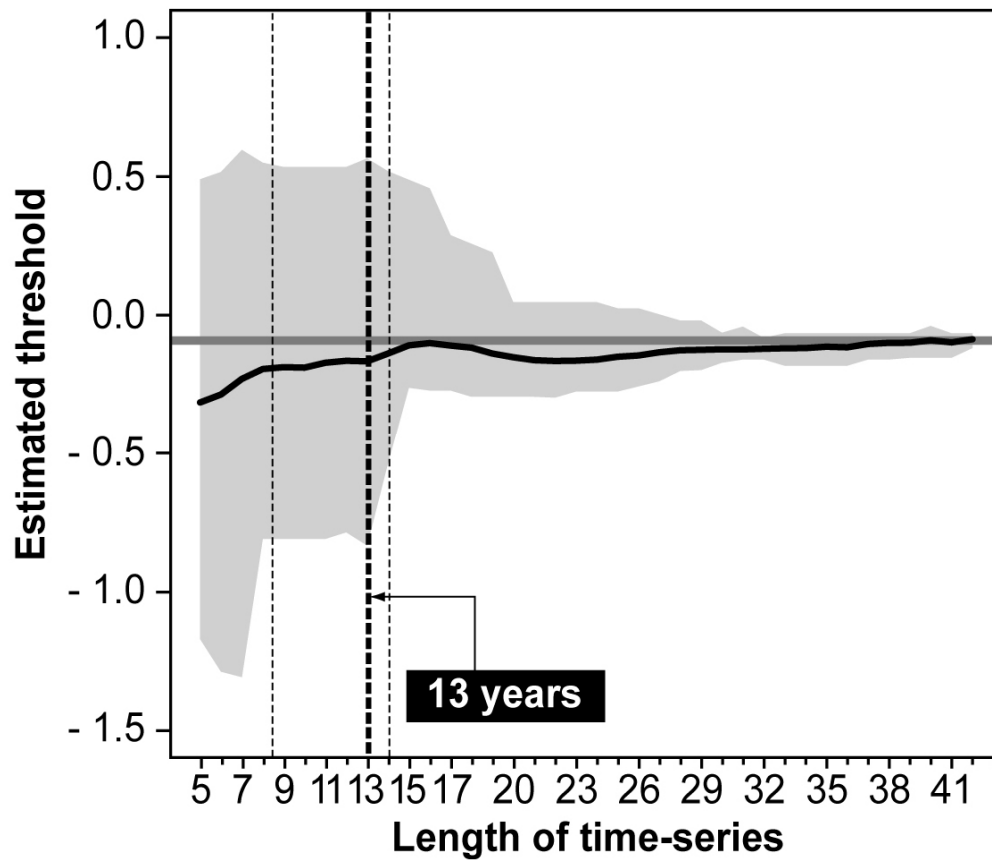


Fig. S1: Minimum number of years required for estimating the threshold. The horizontal grey line represents the threshold estimated from the global dataset while the solid black line is the threshold estimated from a subset of the global dataset. The subset was obtained from the pooled dataset where we randomly drew “X” consecutive years from the breeding success and prey time-series, where “X” is comprised between 5 and 42 years (X-axis). The minimum number of years required for estimating the threshold was determined using the significance of the mean value of the threshold, given the confidence interval for both the subset and global dataset. We repeated this computation 1000 times to obtain a confidence interval over the estimate of the minimum number of years required to calculate the threshold. The vertical dashed line indicates that 13 years of data (the confidence Interval is between 8.5 and 14 years, vertical thin dashed lines) were necessary to detect on average the threshold defined in Fig. 2A (*i.e.*, the value of the estimated threshold is not significantly different from the threshold for the global dataset). All time-series in the global data set of our meta-analysis were between 15 and 47 years long, which makes the detection of the threshold possible in all cases.

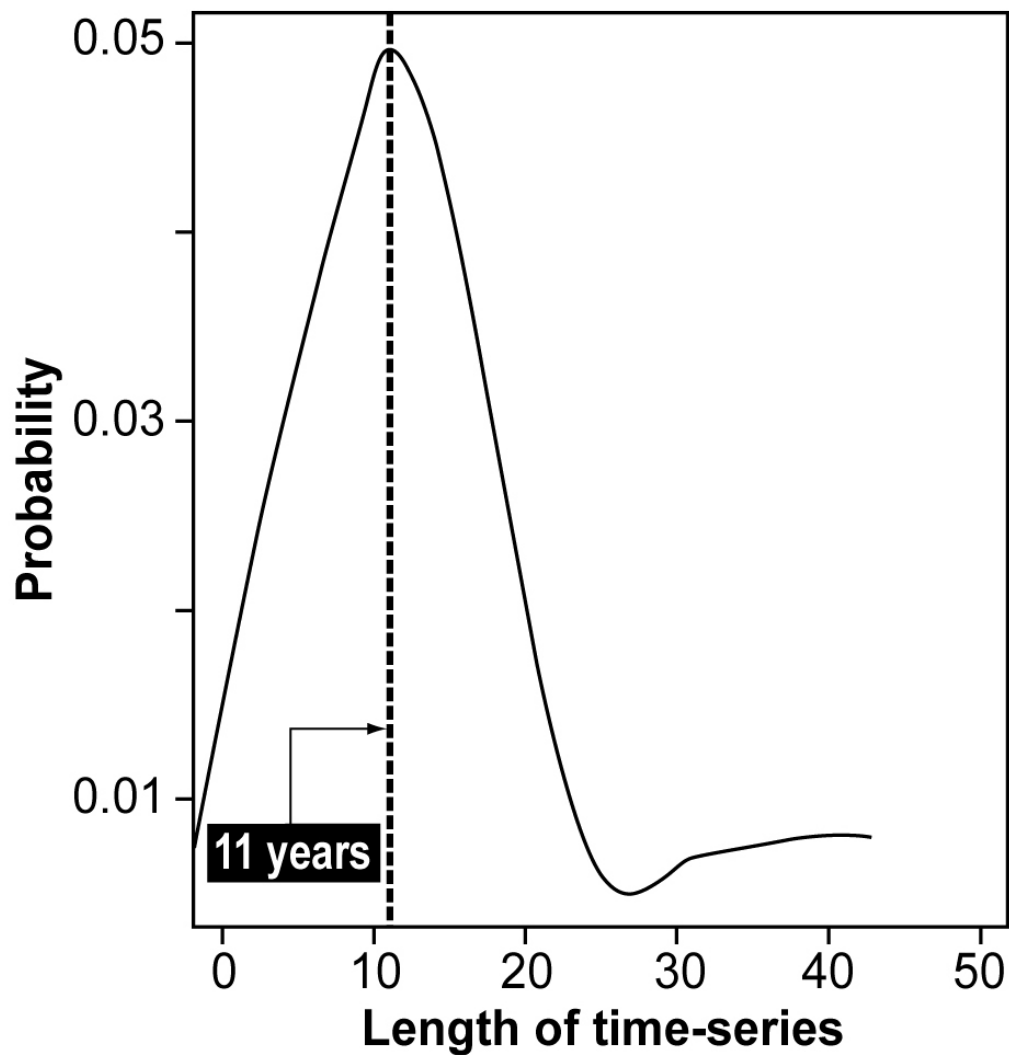


Fig. S2: Probability distribution of the maximum observed biomass detected in the prey abundance time series as a function of the length of the time series. The vertical dashed line indicates that after 11 years of observation most of prey time series revealed the maximum prey biomass. All times series in the global data set of our meta-analysis were between 15 and 47 years long, which makes the detection of the maximum prey biomass possible in all cases.

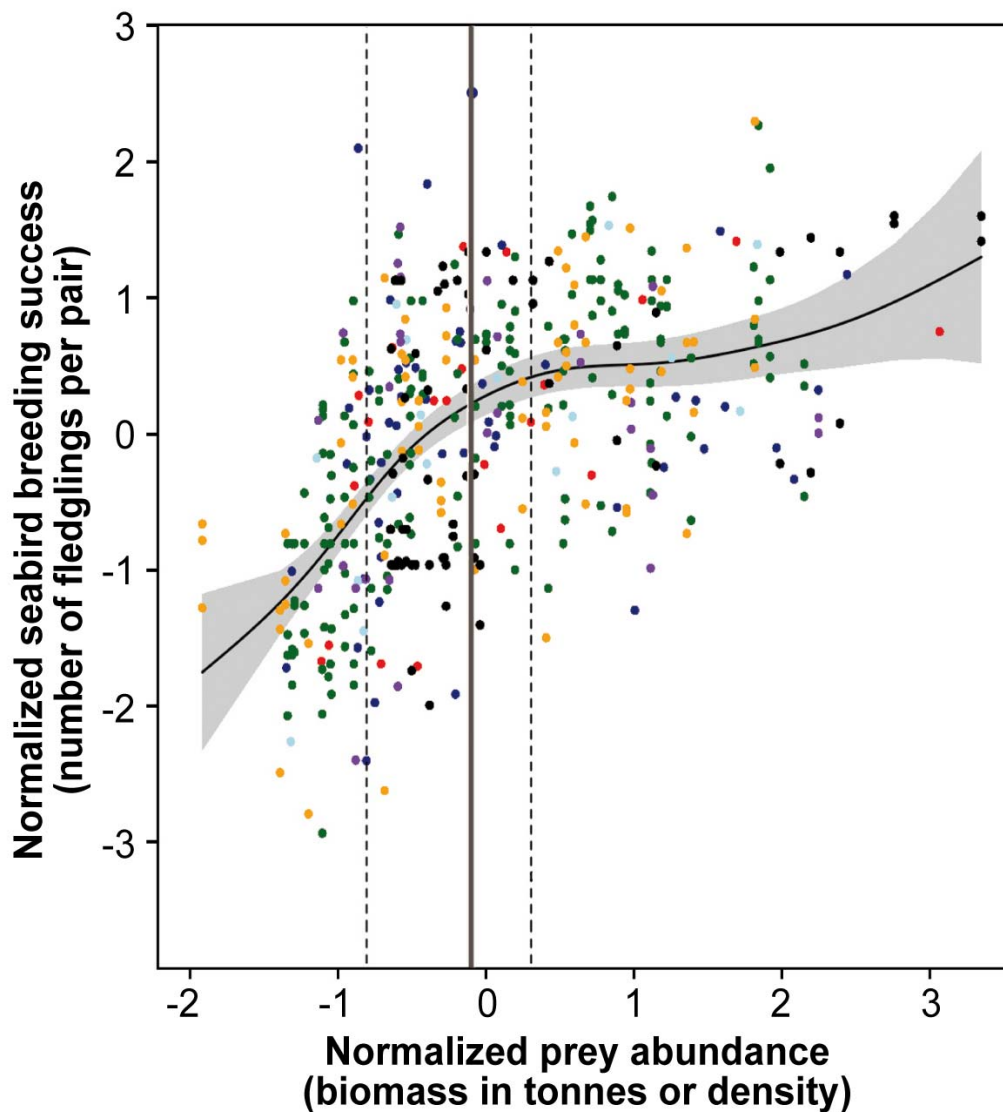


Fig. S3: Relationship between normalized annual breeding success of seabirds and normalized prey abundance. Each data point from all the time series was plotted together with the predictions of a General Additive Mixed Model (GAMM) (solid line) to account for the 'ecosystem effect'. The grey area represents the 95% confidence interval of the fitted GAMM. The threshold in the non-linear relationship (solid vertical line) was detected from a change-point analysis and its confidence interval (black dashed vertical lines) was estimated from a bootstrap analysis. When accounting for the "ecosystem effect" using the GAMM analysis, the results are similar to the GAM analysis (respectively the threshold value is -0.12 here instead of -0.09 in Fig. 2A).

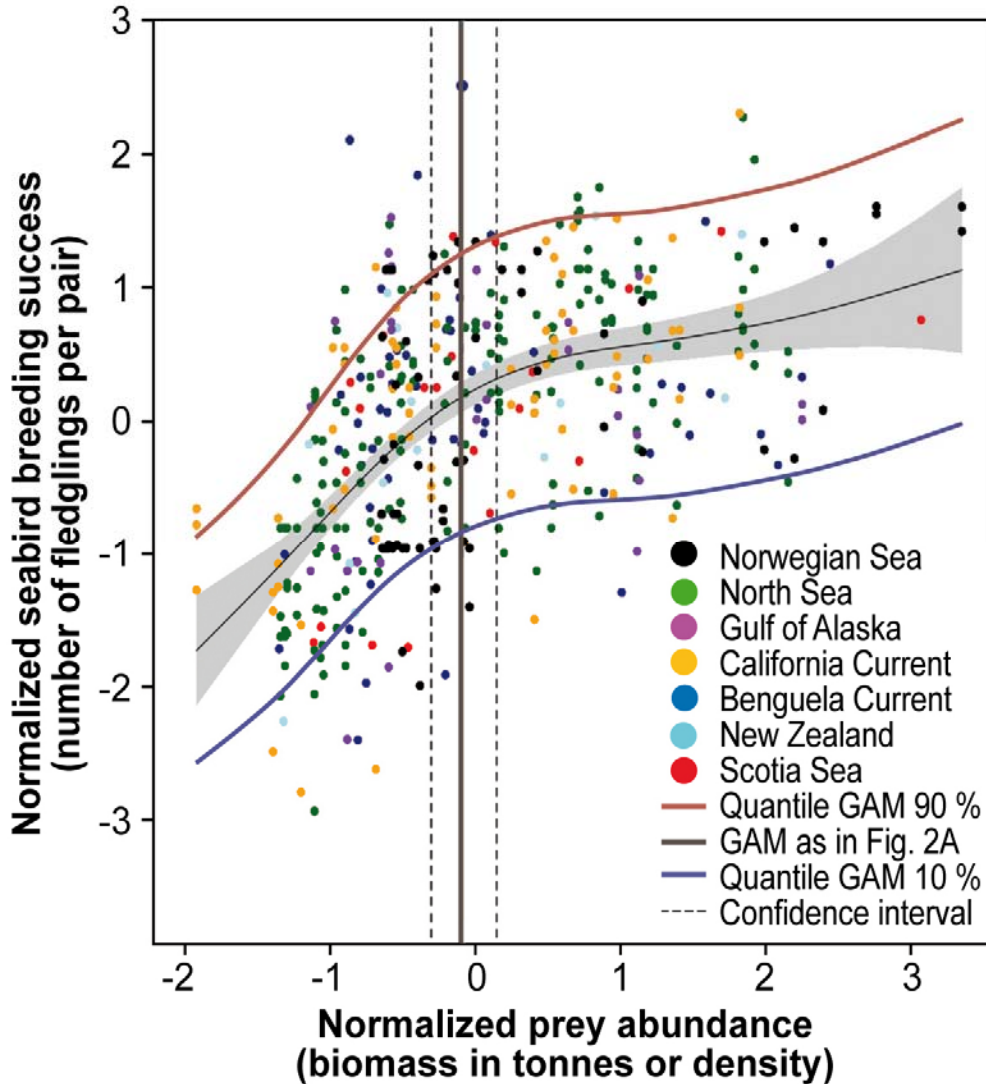


Fig. S4: Relationship between normalized annual breeding success of seabirds and normalized prey abundance. Each data point from all the time series was plotted together with the prediction of a General Additive Model (GAM) (solid black line) and of a quantile GAM (for the 10 and 90% quantile; blue and red solid line respectively). The grey area represents the 95% confidence interval of the fitted GAMM. The threshold in the non-linear relationship (solid vertical line) was detected from a change-point analysis and its confidence interval (black dashed vertical lines) was estimated from a similar bootstrap analysis to Fig. 2A. This analysis showed that a similar pattern can be observed for extreme values. In other words, for a low/high breeding success (10 or 90% quantile resp.), there still exists a threshold below which the breeding success starts to decline. The threshold identified for the two quantile GAM predictions is close to the GAM analysis (respectively the threshold value is -0.14 here instead of -0.09 in Fig. 2A).

Table S1: Time-series used in the global analysis of seabird-forage fish relationships. Each time series is one bird species at one location. Breeding success and prey abundance units are shown. Thresholds for each time series, as computed using Generalized Additive Models, are expressed as a percentage (%) of the maximum prey abundance in the time series considered.

N°	Ecosystem	Location	Bird species (scientific name)	Bird species (common name)	Prey species (scientific name)	Prey species (common name)	Time Series	Seabird breeding success	Prey abundance (unit)	Prey in the diet (% total mass)	Threshold (%)	Notes on data	Reference to data
1	Norwegian Sea	Røst	<i>Fratercula arctica</i>	Atlantic puffin	<i>Clupea harengus</i>	Herring	1964 – 2010	Fledging success (proportion fledged of chicks hatched)	Herring age 0 abundance	23 % to 89%	22%	Categorical data (good, poor, very poor, no fledging success) until 1976	44, 45
	-	Røst	<i>Rissa tridactyla</i>	Kittiwake	<i>Clupea harengus</i>	Herring	1981 – 2010	Number of fledglings/ pair	Herring age 0 abundance	Not available	26%	1984–1987 missing	45
2	North Sea - Shetland	Shetland	<i>Phalacrocorax aristotelis</i>	Shag	<i>Ammodytes marinus</i>	Sandeel	1986 – 2005	Number of fledglings/ pair	Sandeel biomass (t) in the Shetland stock	100%*	39%		75, 79
	-	Foula	<i>Sterna paradisaea</i>	Arctic Tern	<i>Ammodytes marinus</i>	Sandeel	1972 – 2005	Number of fledglings/ pair	Sandeel biomass (t) in the Shetland stock	100%*	No threshold		22, 75
	-	Foula	<i>Stercorarius parasiticus</i>	Arctic skua	<i>Ammodytes marinus</i>	Sandeel	1976 – 2005	Number of fledglings/ pair	Sandeel biomass (t) in the Shetland stock	100%*	36%		22, 75

	-	Foula	<i>Stercorarius skua</i>	Great skua	<i>Ammodytes marinus</i>	Sandeel	1972 – 2005	Number of fledglings/ pair	Sandeel biomass (t) in the Shetland stock	38% to 80%	31%		22, 75
	-	Shetland	<i>Fulmarus glacialis</i>	Fulmar	<i>Ammodytes marinus</i>	Sandeel	1986 – 2005	Number of fledglings/ regularly occupied site.	Sandeel biomass (t) in the Shetland stock	50% to 70%	30%		75, 79
	-	Foula	<i>Rissa tridactyla</i>	Black-legged kittiwake	<i>Ammodytes marinus</i>	Sandeel	1974 – 2005	Number of fledglings/ pair	Sandeel biomass (t) in the Shetland stock	100%*	51%		22, 75, 137
	-	Shetland	<i>Uria aalge</i>	Guillemot (Common Murre)	<i>Ammodytes marinus</i>	Sandeel	1989 – 2005	Number of fledglings**/ pair	Sandeel biomass (t) in the Shetland stock	90% to 100%	30%		75, 79
3	Gulf of Alaska	Cook Inlet	<i>Rissa tridactyla</i>	Black-legged kittiwake	<i>Ammodytes hexapterus</i> , <i>Mallotus villosus</i> , <i>Theragra chalcogramma</i> ,	Sand Lance, Capelin, walleye pollock	1995 – 1999	Number of fledglings/ pair	Fish biomass (g.m ⁻³)	83%	36%	Prey biomass measured around 3 colonies in each of 5 years for 15 "colony-years"	16, 36, 41
	-	Cook Inlet	<i>Uria aalge</i>	Guillemot (Common Murre)	<i>Ammodytes hexapterus</i> , <i>Mallotus villosus</i> , <i>Theragra chalcogramma</i> ,	Sand lance, Capelin, walleye pollock	1995 – 1999	Number of fledglings**/ pair	Fish biomass (g.m ⁻³)	91%	50%	Prey biomass measured around 3 colonies in each of 5 years for 15 colony-years per species	16, 36, 41
4	California Current	Southeast Farallon Island	<i>Uria aalge</i>	Guillemot (Common Murre)	<i>Sebastes spp.</i>	Juvenile rockfish	1983 – 2007	Number of fledglings/ pair	Juvenile rockfish abundance (index)	43%	51%		90, 95, 96

	-	Southeast Farallon Island	<i>Cephus columba</i>	Pigeon Guillemot	<i>Sebastes spp.</i>	Juvenile rockfish	1983 – 2007	Number of fledglings/ pair	Juvenile rockfish abundance (index)	20%	31%		90, 95, 96
	-	Southeast Farallon Island	<i>Cerorhinca monocerata</i>	Rhinoceros Auklet	<i>Sebastes spp.</i>	Juvenile rockfish	1986 – 2007	Number of fledglings/ pair	Juvenile rockfish abundance (index)	16%	29%		90, 95, 96
5	Benguela Current	Malgas	<i>Morus capensis</i>	Cape Gannet	<i>Engraulis encrasicolus, Sardinops sagax</i>	Anchovy, Sardine	1988 – 2009	Number of fledglings/ pair	Prey biomass in W Agulhas (Mt)	49%***	44%		138
	-	Lambert's Bay	<i>Morus capensis</i>	Cape Gannet	<i>Engraulis encrasicolus, Sardinops sagax</i>	Anchovy, Sardine	1991 – 2009	Number of fledglings/ pair	Prey biomass in W Agulhas (Mt)	73%***	43%	No data were collected in 2006 in order to minimize disturbance at the colony after all birds abandoned the colony in late 2005	138
	-	Robben Island	<i>Spheniscus demersus</i>	African penguin	<i>Engraulis encrasicolus, Sardinops sagax</i>	Anchovy, Sardine	1989 – 2004	Number of fledglings/ pair	Prey biomass in W Agulhas (Mt)	86%	32%	Year 2000 was excluded because an oil spill in that year resulted in most birds at the colony terminating breeding at an early stage	106

6	New Zealand	Kaikoura Peninsula	<i>Larus novaehollandiae scopulinus</i>	Red-billed gull	<i>Nyctiphanes australis</i>	Krill	1975 – 1993	Number of fledglings/pair	Krill availability index (proportion of adult birds which regurgitated <i>N. australis</i> when captured)	84% (% of adult eating krill)	61%	1977, 1978, 1989 are missing data after 1994 not considered for ecological reasons	23
7	Scotia Sea	Bird Island	<i>Pygoscelis papua</i>	Gentoo penguin	<i>Euphausia superba</i>	Krill	1983 – 2009	Number of fledglings/pair	Krill biomass (g.m ⁻²)	42% to 63%	30%	1984, 1985, 1987, 1988 are missing	19, 125, 121

* the percentage of sandeel in the diet fell after 1985 when the sandeel stock declined, so these values represent the diet in years when food supply was good.

**Fledglings/pair for *Uria aalge* reflect the number of offspring raised to “jumping stage”. Unlike most seabirds, *Uria aalge* male parents take the chick to sea when ~2/3 grown. Thus, for this species, the variable measured is number of chicks/pair raised to the age of colony-departure (typically 20–25 days old).

***For gannets, their dependence on anchovy and sardine is greater during the breeding period.

Table S2: Details of the parametric models tested to fit to the global relationship of normalized breeding success with normalized prey abundance (Fig. 2A). A wide range of linear to non-linear models was tested. Model number 4 was selected as the best model (lowest AIC value). The hierarchical model is a version of model 4 in which the implication of including ecosystems as a random effect is considered.

Model		Parameter estimates			Standard error			AIC	Threshold
		a	b	c	a	b	c		
<i>Linear models</i>									
1	$y = b$	0.005			0.04			1228.6	-
2	$y = ax + b$	0.51	0.005	-	0.04	0.04	-	1091.5	-
<i>Asymptotic models</i>									
3	$y = a * e^{-bx}$	1,2	0,5	-	0,3	0,1	-	1072,3	0,1
4	$y = c + a * (1 - e^{-bx})$	0,7	0,8	0,2	0,2	0,1	0,05	1059,9	-0,3
5	$y = c + a * (1 - b^x)$	1,2	1,6	-	0,3	0,2	-	1072,3	0,1
6	$y = ax / (b+x)$	0,3	1,5	-	0,05	0,04	-	1127,7	-1,5
7	$y = c + (ax / b+x)$	0,3	1,5	0,2	0,05	0,03	0,04	1112,6	-1,5
8	$y = ax / (b+x) + cx$	0,1	1,5	0,4	0,05	0,1	0,05	1066,3	-1,5
9	$y = ax / (1+bx)$	-0,002	1,5	-	0,004	0,01	-	1229,9	-0,7
10	$y = x / (a+bx)$	1,8	0,4	-	0,1	0,1	-	1072,4	-0,2
<i>Sigmoidal model</i>									
11	$y = a / (1 + e^{-(x-c/b)})$	0,6	0,1	0,2	0,1	0,2	0,1	1174,9	0,1
<i>Hierarchical model</i>									
12	$y = (c + r_{i,1}) + (a + r_{i,2}) * (1 - e^{-bx})$	0.48	1.04	0.23	0.13	0.18	0.05	1063.9	-0.3

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Data and codes

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1. Data	35
2. <i>R</i> codes for the analyses	41
2.1 Fig 2 A and B	41
2.2 Fig 2C	43
2.3 Fig 2D	45
2.4 Fig 3	47
2.5 Fig S1	49
2.6 Fig S2	51
2.7 Fig S3	52
2.8 Fig S4	54
2.9 Bootstrapping code	56

1 Data

This is the complete data set that is used throughout the manuscript and in the analyses whose the code is hereinafter. It corresponds to normalized data of the individual data set. See SOM section for further explanations.

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2 R codes for the analyses

2.1 Fig 2 A and B

```
##### PURPOSE: Relationship between normalized annual breeding success of seabirds and
normalized prey abundance (Fig. 2A) and Change in variance across the range of normalized food
abundance ranging from -1.5 to 2 standard deviations in 8 classes.
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset
##### REQUIREMENTS: you need the script bootstrapping.R and to have the R packages 'gam',
'changepoint', and 'time' installed
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Figs. 2A and B
##### MISCELLANEOUS:
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
#####
### LOAD the required packages
#####
library(gam)
library(changepoint) # package version 0.3
library(time)
#####
### !!! SET the path to the data (download the global_dataset.csv file and paste it in the repository you
want to work in) !!!
#####
setwd('XXX')
#####
### LOAD the data
#####
t_glob <- read.table('./global_dataset.csv', header=F, sep=";")
#####
### Script to bootstrap
bootstrap_size <- 1000
smoother_size <- 3
source('./bootstrapping.R')
#####
### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
#####
##### GLOBAL DATASET FIGURE (Fig 2A) ###
#####
if (png_figure==1){
png('./Fig2A.png', width=1200, height=1200)
}
par(mar=c(5,5,3,1))
plot(min(pre),min(bird), col="transparent", main="", ylab="Breeding success (-)", xlab="Prey
abundance (-)", cex.lab=2.5, cex.axis=2.5, pch=16, cex.main=2, xlim=c(-2,3.5), ylim=c(-3.5, 3))
lines(titu, lwd=2)
xd<-c(fds[fds2,2],rev(fds[fds2,2]))
up.sd<-prediction$fit[fds2]+1.96*prediction$se.fit[fds2]
down.sd<-prediction$fit[fds2]-1.96*prediction$se.fit[fds2]
yd<-c(up.sd,rev(down.sd))
polygon(xd,yd,col="grey81",lty=1,border="transparent")
lines(titu$y~titu$x, lwd=4)
for (i in 1:length(data[,1])){
points(data[i,2]~data[i,3],pch=16, col=paste(data[i,5]), cex=2)
}
}
```

```

### Identify the threshold
data2 <- cbind(titu$y[1:150],1,titu$x[1:150])
change_point <- cpt.reg(data2,penalty="SIC")
threshold <- titu$x[cpts(change_point)[1]]
abline(v=threshold, lwd=4, col="orange")
percentage_threshold <- (threshold+abs(min(pre)))/(max(pre)+abs(min(pre)))
text(threshold,-3.2, paste(signif(threshold,2), "\n i.e.",paste(signif(percentage_threshold*100,2)),"% of
max prey abundance" ), pos=4, cex=2.5)
text(2.5,2.5, paste("AIC=",signif(AIC(gam.object),5),sep=" "), pos=4, cex=2.5)
legend("bottomright", pch=16, col=unique(paste(t_glob[,5])), legend=unique(t_glob[,4]), bty="n",
cex=2)
### plot the confidence interval
IC<-quantile(thresh, c(0.025, 0.975))
abline(v=IC[1], lwd=3, lty=2, col="black")
abline(v=IC[2], lwd=3, lty=2, col="black")
if (png_figure==1){
dev.off()
}
#####
##### VARIANCE FIGURE (Fig 2B) #####
#####
min_pre <- min(pre)
max_pre <- max(pre)
diff_pre <- max_pre-min_pre
variance <- 0
count <- 0
for (i in seq(-2,3, by=0.5)){
  j <- i+0.5
  variance <- c(variance,var(bird[which(pre>i & pre <= j)], na.rm=T))
  count <- c(count,length(bird[which(pre>i & pre <= j)]))
}
variance <- variance[-1]
count <- count[-1]
### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
png('./Fig2B.png', width=1200, height=1200)
}
par(mar=c(6,6,1,1))
plot(smooth(variance[2:9])~seq(-1.5,2,by=0.5), type="l", ylab="Variance of seabird breeding success",
xlab="Prey abundance (-)", cex.axis=3, cex.lab=3, lwd=3)
abline(v=threshold, lwd=3, col="orange")
legend("topright", legend=c("Threshold value as identified\n in the global analysis"), col="orange",
lwd=3, bty="n", cex=3)
if (png_figure==1){
dev.off()
}
#####
##### Test for difference in variance ##
#####
### Bartlett test for variance
first_var <- bird[which(pre < -0.092)]
second_var <- bird[which(pre > -0.092)]
var.test(first_var,second_var)

```

2.2 Fig 2C

```
##### PURPOSE: Script to fit the parametric model (see Table S2) to the global dataset for each
ecosystem
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Fig. 2C
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
#####
### !!! SET the path to the data !!!
#####
setwd('XXX')
#####
### LOAD the data
#####
t_glob <- read.table('./global_dataset.csv', header=F, sep=";")
#####
##### CONTROL PARAMETERS
#####
### for nls to enable larger number of iterations and decrease the minFactor
nls_cont <- nls.control(maxiter = 500, tol = 1e-05, minFactor = 1/(1024*20),
  printEval = FALSE, warnOnly = FALSE)
#####
##### PARAMETER ESTIMATION ###
#####
### Initialization for the first ecosystem
toto <- unique(t_glob[,4])
j <- 1; i <- 1
data <- subset(t_glob, V4==toto[j])
### The global data set contains some holes in the times series. We first select the years we have both a
breeding success and an abundance estimate for the prey
bird<-as.numeric(data[,2])
prey<-as.numeric(data[,3])
req1<-which(is.na(bird)==T)
if (length(req1) > 0){bird<-bird[-req1];prey<-prey[-req1] }
req2<-which(is.na(prey)==T)
if (length(req2) > 0){bird<-bird[-req2];prey<-prey[-req2] }
model3 <- nls(bird~c+a*(1-exp(-b*prey)), start=list(a=1, b=1, c=0),control=nls_cont)
x_prey <- seq(min(prey),max(prey),by=(max(prey)-min(prey))/200)
y_bird <- coef(model3)[3]+coef(model3)[1]*(1-exp(-coef(model3)[2]*x_prey))
### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
png('./Fig2C.png', width=1200, height=1200)
}
par(mar=c(5,5,3,1))
plot(bird~prey, xlim=c(-2,3.5), ylim=c(-2,2), ylab="Breeding success (-)", xlab="Prey abundance (-)",
  cex.lab=2.5, cex.axis=2.5, pch=16, cex.main=2, col="transparent", main="", cex.main=2.5)
lines(smooth(y_bird)~x_prey,col=paste(data[i,5]), lwd=4)
for (j in 2: length(toto) ) {
  data <- subset(t_glob, V4==toto[j])
  bird<-as.numeric(data[,2])
  prey<-as.numeric(data[,3])
  req1<-which(is.na(bird)==T)
  if (length(req1) > 0){bird<-bird[-req1];prey<-prey[-req1] }
  req2<-which(is.na(prey)==T)
  if (length(req2) > 0){bird<-bird[-req2];prey<-prey[-req2] }
  model3 <- nls(bird~c+a*(1-exp(-b*prey)), start=list(a=1, b=1, c=0),control=nls_cont)
  x_prey <- seq(min(prey),max(prey),by=(max(prey)-min(prey))/200)
```

```

      y_bird <- coef(model3)[3]+coef(model3)[1]*(1-exp(-coef(model3)[2]*x_prey))
      lines(smooth(y_bird)~x_prey,col=paste(data[i,5]), lwd=4)
    }
    legend("bottomright", pch=16, col=unique(paste(t_glob[,5])), legend=unique(t_glob[,4]), bty="n",
    cex=2)
    if (png_figure==1){
    dev.off()
    }

```

2.3 Fig 2D

```
##### PURPOSE: Script to fit the parametric model to the global dataset for each species
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Fig. 2D
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
#####
### !!!! SET the path to the data (download the global_dataset.csv file and paste it in the repository you
want to work in) !!!
#####
setwd('XXX')
#####
### LOAD the data
#####
t_glob <- read.table('./global_dataset.csv', header=F, sep=";")
#####
##### CONTROL PARAMETERS
#####
### for nls to enable larger number of iterations and decrease the minFactor
nls_cont <- nls.control(maxiter = 500, tol = 1e-05, minFactor = 1/(1024*20),
printEval = FALSE, warnOnly = FALSE)
#####
##### Model FITS
#####
colors <- rainbow(18)
data <- t_glob
un_data <- unique(paste(t_glob[,6])) # Get the tag for each data sea

### Initialization for the first species
i <- 1
subset_data <- subset(t_glob, subset=c(t_glob[,6]==paste(un_data[i])))
### The global data set contains some holes in the times series. We first select the years we have both a
breeding success and an abundance estimate for the prey
bird <- as.numeric(subset_data[,2])
prey <- as.numeric(subset_data[,3])
req1 <- which(is.na(bird)==T)
if (length(req1) > 0){bird <- bird[-req1];prey <- prey[-req1] }
req2 <- which(is.na(prey)==T)
if (length(req2) > 0){bird <- bird[-req2];prey <- prey[-req2] }
model3 <- nls(bird~c+a*(1-exp(-b*prey)), start=list(a=1, b=1, c=0), control=nls_cont)
x_prey <- seq(min(prey),max(prey),by=(max(prey)-min(prey))/200)
y_bird <- coef(model3)[3]+coef(model3)[1]*(1-exp(-coef(model3)[2]*x_prey))
### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
png('./Fig2D.png', width=1200, height=1200)
}
par(mar=c(5,5,3,1))
plot(bird~prey, xlim=c(-2,3.5), ylim=c(-2,2), main="", ylab="Breeding success (-)", xlab="Prey
abundance (-)", cex.lab=2.5, cex.axis=2.5, pch=16, cex.main=2, col="transparent")
lines(smooth(y_bird)~x_prey,col=colors[i], lwd=4)
legend_text <- paste(subset_data[1,6])
counter <- 1
for (i in 2:length(un_data)){
if (i<6) {i2 <- i} else {i2 <- i-1}
if (i!=6){
subset_data <- subset(t_glob, subset=c(t_glob[,6]==paste(un_data[i])))
}
```

```

bird<-as.numeric(subset_data[,2])
prey<-as.numeric(subset_data[,3])
req1<-which(is.na(bird)==T)
if (length(req1) >0){bird<-bird[-req1];prey<-prey[-req1] }
req2<-which(is.na(prey)==T)
if (length(req2) >0){bird<-bird[-req2];prey<-prey[-req2] }

model3 <- nls(bird~c+a*(1-exp(-b*prey)), start=list(a=1, b=1, c=0),control=nls_cont)
x_prey <- seq(min(prey),max(prey),by=(max(prey)-min(prey))/200)
y_bird <- coef(model3)[3]+coef(model3)[1]*(1-exp(-coef(model3)[2]*x_prey))
lines(smooth(y_bird)~x_prey,col=colors[i2], lwd=4)
legend_text <- c(legend_text,paste(subset_data[1,6]))
counter<- c(counter,i2)
}

}
legend_text <- paste(seq(1,13), paste(un_data[-6]))
legend("bottomright",cex=2, col=colors[counter], legend=legend_text, bty="n", lwd=2)
if (png_figure==1){
dev.off()
}

```

2.4 Fig 3

```
##### PURPOSE: Script to fit the parametric model to the global dataset for each ecosystem with
the data overplotted
##### INSTRUCTIONS: run this script to
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset, install the
package splines, quantreg and VGAM
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Fig. 3
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
#####
### LOAD the required packages
#####
library(gam)
library(changepoint)
library(time)
#####
### SET the path to the data
#####
setwd('XXX')
#####
### LOAD the data
#####
t_glob <- read.table('./global_dataset.csv', header=F, sep=";")
#####
##### CONTROL PARAMETERS
#####

### for nls to enable larger number of iterations and decrease the minFactor
nls_cont <- nls.control(maxiter = 500, tol = 1e-05, minFactor = 1/(1024*20),
  printEval = FALSE, warnOnly = FALSE)
### Initialization for the first ecosystem
toto <- unique (t_glob[,4])
j=1; i=1
data <- subset(t_glob, V4==toto[j])
### The global data set contains some holes in the times series. We first select the years we have both a
breeding success and an abundance estimate for the prey
bird<-as.numeric(data[,2])
prey<-as.numeric(data[,3])
req1<-which(is.na(bird)==T)
if (length(req1) >0){bird<-bird[-req1];prey<-prey[-req1] }
req2<-which(is.na(prey)==T)
if (length(req2) >0){bird<-bird[-req2];prey<-prey[-req2] }
model3 <- nls(bird~c+a*(1-exp(-b*prey)), start=list(a=1, b=1, c=0),control=nls_cont)
x_prej <- seq(min(prey),max(prey),by=(max(prey)-min(prey))/200)
y_bird <- coef(model3)[3]+coef(model3)[1]*(1-exp(-coef(model3)[2]*x_prej))

### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
png('./Fig3.png', width=1200, height=1200)
}
par(mar=c(5,5,3,1), mfrow=c(3,3))
plot(bird~prey, xlim=c(-2,3.5), ylim=c(-2,2), ylab="Breeding success (-)", xlab="Prey abundance (-)",
cex.lab=2.5, cex.axis=2.5, pch=16, cex.main=2, col="transparent", main=toto[j], cex.main=2.5)
lines(smooth(y_bird)~x_prej,col=paste(data[i,5]), lwd=4)
points(bird~prey, pch=17,col=paste(data[i,5]), lwd=4)
```

```

for (j in 2: length(toto) ) {
  data <- subset(t_glob, V4==toto[j])
  bird<-as.numeric(data[,2])
  prey<-as.numeric(data[,3])
  req1<-which(is.na(bird)==T)
  if (length(req1) >0){bird<-bird[-req1];prey<-prey[-req1] }
  req2<-which(is.na(prey)==T)
  if (length(req2) >0){bird<-bird[-req2];prey<-prey[-req2] }
  model3 <- nls(bird~c+a*(1-exp(-b*prey)), start=list(a=1, b=1, c=0),control=nls_cont)
  x_prey <- seq(min(prey),max(prey),by=(max(prey)-min(prey))/200)
  y_bird <- coef(model3)[3]+coef(model3)[1]*(1-exp(-coef(model3)[2]*x_prey))
  plot(bird~prey, xlim=c(-2,3.5), ylim=c(-2,2),ylab="Breeding success (-)", xlab="Prey
abundance (-)", cex.lab=2.5, cex.axis=2.5, pch=16, cex.main=2, col="transparent", main=toto[j],
cex.main=2.5)
  lines(smooth(y_bird)~x_prey,col=paste(data[i,5]), lwd=4)
  points(bird~prey, pch=17,col=paste(data[i,5]), lwd=4)
}
  legend("bottomright", pch=16, col=unique(paste(t_glob[,5])), legend=unique(t_glob[,4]), bty="n",
cex=2)
if (png_figure==1){
dev.off()
}

```


2.5 Fig S1

```
##### PURPOSE: Script to estimate the minimum of number of years required to estimate the
threshold
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Fig. S1
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
##### WARNINGS: this is a bootstrap procedure. It will repeat 100 times this procedure (100
bootstraps...) so get some coffee.
#####
#####
### LOAD the required packages
#####
library(gam)
library(changepoint)
library(time)
#####
### !!!! SET the path to the data (download the global_dataset.csv file and paste it in the repository you
want to work in) !!!
#####
setwd('XXX')
#####
### LOAD the data
#####
t_glob <- read.table('./global_dataset.csv', header=F, sep=";")
### GAM
nb_boot <- 100
year_est <- rep(0,nb_boot)
threshold <- array(0,dim=c(nb_boot,38,nb_boot))
years <- 1964:2010
for (j in 1:nb_boot){
  prev <- progressBar()
  for (year_size in 5:42){
    prev2 <- progressBar()
    for (i in 1:nb_boot){
      prev2 <- progressBar(i/nb_boot, prev2)
      year_start <- sample(years[1:(length(years)-year_size)], size=1)
      data <- subset(t_glob,subset=c(t_glob[,1]>=year_start &
t_glob[,1]<(year_start+year_size)))
      bird <- as.numeric(data[,2])
      prey <- as.numeric(data[,3])
      req1 <- which(is.na(bird)==T)
      if (length(req1) >0) {bird<-bird[-req1];prey<-prey[-req1] }
      req2<-which(is.na(prey)==T)
      if (length(req2) >0) {bird<-bird[-req2];prey<-prey[-req2] }
      gam.object<-gam(bird~s(prey,3), na.action='na.omit')
      prediction<-predict.gam(gam.object, se.fit=T)
      fds<-cbind(prediction$fit,prey,prediction$se.fit,0,0)
      fds2<-order(fds[,2])
      titu <- spline(prediction$fit[fds2]~prey[fds2],n=200)
      data2 <- cbind(titu$y[1:150],1,titu$x[1:150])
      change_point <- cpt.reg(data2,penalty="SIC")
      threshold[i,(year_size-4),j] <- titu$x[cpts(change_point)[1]]
    }
  }
}
year_est <- rep(0,nb_boot)
year_mean <- rep(0,38)
```

```

year_2_5 <-rep(0,38)
year_97_5 <-rep(0,38)
for (j in 1:nb_boot){
  xd<-c(1:38,rev(1:38))
  up.sd<-smooth(apply(threshold[,j],2, quantile, probs=c(0.9)))
  down.sd<-smooth(apply(threshold[,j],2, quantile, probs=c(0.1)))
  yd<-c(up.sd,rev(down.sd))
  year_est[j] <- max(which(up.sd>0.13),which(down.sd<-0.3))
}
for (j in 1:38){
  year_mean[j] <- mean(threshold[,j])
  year_2_5[j] <- quantile(threshold[,j],probs=0.0225)
  year_97_5[j] <- quantile(threshold[,j],probs=0.975)
}
save(threshold,file=paste("./threshold_sim.Rdata", sep=""))
save(threshold,file=paste("./threshold_sim",j,".Rdata", sep=""))
### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
pdf('./FigS1.pdf')
}
plot(year_mean, xaxt="n", xlab="Length of the time series (years)", ylab="Estimated threshold",
ylim=c(-1.5,1), type="l", lwd=3)
axis(side=1, at=1:42, labels=5:46)
xd<-c(1:38,rev(1:38))
yd<-c(year_97_5,rev(year_2_5))
polygon(xd,yd,col="grey81",lty=1,border="transparent")
abline(h=-0.092, lwd=3, col="dark red", lty=1)
lines(year_mean,lwd=2)
abline(v=(mean(year_est)-4), lwd=2, col="orange")
abline(v=(quantile(year_est, probs=c(0.025,0.975))-4), lwd=2, lty=2, col="orange")
legend("bottomright", legend=c("Estimated threshold (global dataset)", "Estimated threshold (subset)",
"Minimum number of years required \n to estimate the threshold","Confidence interval for \n the
minimum number of years required"), cex=1, bty="n", lwd=2, col=c("dark red", "black", "orange",
"orange" ), lty=c(1,1,1,2))
if (png_figure==1){
dev.off()
}

```

2.6 Fig S2

```
##### PURPOSE: Script to estimate when the maximum prey biomass is observed in the global
dataset
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Fig. S2
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
#####
### SET the path to the data (download the global_dataset.csv file and paste it in the repository you
want to work in)
#####
setwd('XXX')
#####
### LOAD the data
#####
data <- read.table('./global_dataset.csv', header=F, sep=";")
year <- rep(0,19)
for (i in 1:19){
  data2 <- subset(data, subset=c(data[,8]==i))
  iwh <- which(data2[,3]==max(data2[,3], na.rm=T))
  year[i] <- data2[iwh,1]-data2[1,1]+1
}
names <- c("Krill_biomass", rep("Sardine_anchovy_w_agulhas",3),
rep("Sandeel",4),rep("Shetland_sandeel_TSB",3),"Euphausiid_availability_index",rep("biom",2),rep("
all_rockfish",3),rep("herring_vpa_0",2))
max_bio <- as.data.frame(cbind(year,names))
index <- max_bio[1:(length(max_bio[,1])-1),2]!=max_bio[2:length(max_bio[,1]),2]
year2 <- year[index][year[index]>0]
### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
png('./FigS2.png')
}
par(mar=c(5,5,1,4))
titi<-lowess(density(year2)$y~density(year2)$x, f=0.56)
plot(titi, type="l", xlab="Years after the beginning of data collection", ylab="Probability",
cex.axis=2.5, cex.lab=1.7, xlim=c(0,50), lwd=2)
abline(v=round(titi$x[which(titi$y==max(titi$y))]), lwd=3)
text(5,.006, paste(round(titi$x[which(titi$y==max(titi$y))])," years", sep=""), pos=1, cex=2)
if (png_figure==1){
dev.off()
}
}
```

2.7 Fig S3

```
##### PURPOSE: Script to run the generalized additive mixed model (GAMM) analysis on the data
set
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset, install the
package gamm4
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Fig. S3
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
#####
### LOAD the required packages
#####
library(gam)
library(changepoint)
library(time)
library(gamm4)
#####
### !!!! SET the path to the data (download the global_dataset.csv file and paste it in the repository you
want to work in) !!!!
#####
setwd('XXX')
#####
### LOAD the data
#####
t_glob <- read.table('./global_dataset.csv', header=F, sep=";")
data <- t_glob
### The global data set contains some holes in the times series. We first select the years we have both a
breeding success and an abundance estimate for the prey
bird <- as.numeric(data[,2])
prey <- as.numeric(data[,3])
Eco <- as.numeric(data[,4])
req1 <- which(is.na(bird)==T)
if (length(req1) >0) {bird<-bird[-req1];prey<-prey[-req1]; Eco<-Eco[-req1] }
req2<-which(is.na(prey)==T)
if (length(req2) >0) {bird<-bird[-req2];prey<-prey[-req2] ; Eco<-Eco[-req2]}
### GAMM
gam.object <- gamm4(bird~s(prey), random = ~ (1|Eco), na.action="na.omit")
prediction <- predict.gam(gam.object$gam, se.fit=T)
fds <- cbind(prediction$fit,prey,prediction$se.fit,0,0)
fds2 <- order(fds[,2])
titu <- spline(prediction$fit[fds2]~prey[fds2],n=200)
### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
png('./FigS3.png', width=1200, height=1200)
}
plot(min(prey),min(bird), col="transparent",main="",ylab="Breeding success (-)", xlab="Prey
abundance (-)", cex.lab=2.5, cex.axis=2.5, pch=16, cex.main=2, xlim=c(-2,3.5), ylim=c(-3.5, 3))
lines(titu, lwd=2)
xd<-c(fds[fds2,2],rev(fds[fds2,2]))
up.sd<-prediction$fit[fds2]+1.96*prediction$se.fit[fds2]
down.sd<-prediction$fit[fds2]-1.96*prediction$se.fit[fds2]
yd<-c(up.sd,rev(down.sd))
polygon(xd,yd,col="grey81",lty=1,border="transparent")
lines(titu$y~titu$x, lwd=4)
for (i in 1:length(data[,1])){
points(data[i,2]~data[i,3],pch=16, col=paste(data[i,5]), cex=2)
}
## Identify the threshold
```

```

data2 <- cbind(titu$y[1:150],1,titu$x[1:150])
change_point <- cpt.reg(data2,penalty="SIC")
threshold <- titu$x[cpts(change_point)[1]]
abline(v=threshold, lwd=4, col="orange")
percentage_threshold <- (threshold+abs(min(pre)))/(max(pre)+abs(min(pre)))
text(threshold,-3.2, paste(signif(threshold,2), "\n i.e.",paste(signif(percentage_threshold*100,2)),"% of
max prey abundance" ), pos=4, cex=2.5)
legend("bottomright", pch=16, col=unique(paste(t_glob[,5])), legend=unique(t_glob[,4]), bty="n",
cex=2)
if (png_figure==1){
dev.off()
}

```

2.8 Fig S4

```
##### PURPOSE: Script to run the quantile regression analyses on the global dataset
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset, install the
package splines, quantreg and VGAM
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Fig. S4
##### REQUIREMENTS: you need the script bootstrapping.R
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
#####
### LOAD the required packages
#####
library(gam)
library(changepoint)
library(time)
library(splines)
library(quantreg)
library(VGAM)
#####
### !!! SET the path to the data (download the global_dataset.csv file and paste it in the repository you
want to work in) !!!
#####
setwd('XXXX')
t_glob <- read.table('./global_dataset.csv', header=F, sep=";")
data <- t_glob
### The global data set contains some holes in the times series. We first select the years we have both a
breeding success and an abundance estimate for the prey
bird <- as.numeric(data[,2])
prey <- as.numeric(data[,3])
req1 <- which(is.na(bird)==T)
if (length(req1) >0) {bird<-bird[-req1];prey<-prey[-req1] }
req2<-which(is.na(prey)==T)
if (length(req2) >0) {bird<-bird[-req2];prey<-prey[-req2] }
#####
### Script to bootstrap to plot as in Fig 2A
bootstrap_size <- 1000
smoother_size <- 3
source('./bootstrapping.R')
### Classic GAM as for the Figure 1A of the manuscript
gam.object<-gam(bird~s(prey,3), na.action='na.omit')
prediction<-predict.gam(gam.object, se.fit=T)
fds<-cbind(prediction$fit,prey,prediction$se.fit,0,0)
fds2<-order(fds[,2])
titu <- spline(prediction$fit[fds2]~prey[fds2],n=200)
### Fit a "quantile" gam on the data (with an offset of 10 since vgam requires that the response variable
is positive (then offset subtracted for the plot)
fit <- vgam(bird+10 ~ s(prey), lms.bcn(zero=c(1,3)),trac=TRUE)
###quantile regression with GAM
qtreg_gam <- qtplot.lmsreg(fit, percentiles=c(10,90), main="Quantiles",pch=16, las=1,
ylab="Breeding success (-)", xlab="Prey abundance (-)", lwd=2, lcol=4, yaxt="n")
quant_matrix <- cbind(prey,qtreg_gam$fitted.values-10)
order_quant_matrix <- order(quant_matrix[,1])
titu95 <- spline(quant_matrix[order_quant_matrix,3]~quant_matrix[order_quant_matrix,1],n=200)
titu5 <- spline(quant_matrix[order_quant_matrix,2]~quant_matrix[order_quant_matrix,1],n=200)

### Figure (set png_figure to 1) or not (any other value)
png_figure <- 0
if (png_figure==1){
png('./FigS4.png', width=1200, height=1200)
```

```

}
par(mar=c(5,5,3,1))
plot(titu95, lwd=2, col="dark red", type="l", main="", ylab="Breeding success (-)", xlab="Prey
abundance (-)", cex.lab=2.5, cex.axis=2.5, pch=16, cex.main=2, xlim=c(-2,3.5), ylim=c(-3.5, 3) )
lines(titu, lwd=2)
lines(titu5, lwd=2, col="dark blue")
xd<-c(fds[fds2,2],rev(fds[fds2,2]))
up.sd<-prediction$fit[fds2]+1.96*prediction$se.fit[fds2]
down.sd<-prediction$fit[fds2]-1.96*prediction$se.fit[fds2]
yd<-c(up.sd,rev(down.sd))
polygon(xd,yd,col="grey81",lty=1,border="transparent")
for (i in 1:length(data[,1])){
  points(data[i,2]~data[i,3],pch=16, col=paste(data[i,5]), cex=2)
}
lines(titu, lwd=2)
lines(titu5, lwd=2, col="dark blue")
lines(titu95, lwd=2, col="dark red")
### Identify the threshold for each GAM
data2 <- cbind(titu$y[1:150],1,titu$x[1:150])
change_point <- cpt.reg(data2,penalty="SIC")
threshold <- titu$x[cpts(change_point)[1]]
abline(v=threshold, lwd=4, col="orange")
data5 <- cbind(titu5$y[1:150],1,titu5$x[1:150])
change_point5 <- cpt.reg(data5,penalty="SIC")
threshold5 <- titu5$x[cpts(change_point5)[1]]
data95 <- cbind(titu95$y[1:150],1,titu95$x[1:150])
change_point95 <- cpt.reg(data95,penalty="SIC")
threshold95 <- titu95$x[cpts(change_point95)[1]]
### plot the confidence interval
IC<-quantile(thresh, c(0.025, 0.975))
abline(v=IC[1], lwd=3, lty=2, col="black")
abline(v=IC[2], lwd=3, lty=2, col="black")
legend("bottomright", pch=16, col=unique(paste(t_glob[,5])), legend=unique(t_glob[,4]), bty="n",
cex=2)
legend("topleft", legend=c("Quantile GAM 90%", "GAM as in Fig 1A","Quantile GAM 10%",
"Confidence interval"), lwd=4, lty=c(1,1,1,2,1),col=c("dark red", "black", "dark blue", "black",
"orange"), bty="n", cex=2)
if (png_figure==1){
dev.off()
}

```

2.9 Bootstrapping code

```
##### PURPOSE: Script to bootstrap on the data set to find the confidence interval for the threshold
estimate (for Fig 2A)
##### INSTRUCTIONS: set the bootstrap sample size you want to do in the Fig2A_B.R script
##### INSTRUCTIONS: set the path where you downloaded and saved the global dataset
##### REQUIREMENTS: you need the script bootstrapping.R and to have the R packages 'gam',
'changepoint', and 'time' installed
##### INPUTS: the global_dataset.csv file
##### OUTPUTS: Figs. 2A and B
##### MISCELLANEOUS:
##### AUTHORS: Sylvain Bonhommeau & Philippe Cury (Last update 23rd of August 2011)
#####
### The global data set contains some holes in the times series. We first select the years we have both a
breeding success and an abundance estimate for the prey
data <- t_glob
bird <- as.numeric(data[,2])
prey <- as.numeric(data[,3])
req1 <- which(is.na(bird)==T)
if (length(req1) >0) {bird<-bird[-req1];prey<-prey[-req1] }
req2<-which(is.na(prey)==T)
if (length(req2) >0) {bird<-bird[-req2];prey<-prey[-req2] }
##### RESAMPLING #####
nb <- bootstrap_size
thresh <- vector(length=nb)      ## create a vector to be filled with the estimated threshold
prev <- progressBar()           ## just to display how long it remains for the bootstrap
for (i in 1:nb) {
  prev <- progressBar(i/nb, prev)
  bootsample <- sample(1:length(bird), replace=T)
  birdi <- bird[bootsample]
  preyi <- prey[bootsample]
  #####Computing threshold on new sample #####
  gam.object <- gam(birdi~s(preyi, smoother_size), na.action='na.omit')
  prediction <- predict.gam(gam.object, se.fit=T)
  fds <- cbind(prediction$fit,preyi,prediction$se.fit,0,0)
  fds2 <- order(fds[,2])
  titu <- spline(prediction$fit[fds2]~preyi[fds2],n=200)
  data <- cbind(titu$y[1:150],1,titu$x[1:150])
  change_point <- cpt.reg(data,penalty="SIC") ## Calculate the position of the threshold (see
changepoint package)
  thresh[i] <- titu$x[cpts(change_point)[1]]
}
### Reset the values to initial values
data <- t_glob
bird<-as.numeric(data[,2])
prey<-as.numeric(data[,3])
req1<-which(is.na(bird)==T)
if (length(req1) >0){bird<-bird[-req1];prey<-prey[-req1] }
req2<-which(is.na(prey)==T)
if (length(req2) >0){bird<-bird[-req2];prey<-prey[-req2] }
gam.object<-gam(bird~s(prey,smoother_size), na.action='na.omit')
prediction<-predict.gam(gam.object, se.fit=T)
fds<-cbind(prediction$fit,prey,prediction$se.fit,0,0)
fds2<-order(fds[,2])
titu <- spline(prediction$fit[fds2]~prey[fds2],n=200)
```