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Causes and consequences of pair-bond disruption in a sex-skewed population of a long-lived monogamous seabird

Author list:
RUIJIAO SUN\textsuperscript{1,2}, CHRISTOPHE BARBRAUD\textsuperscript{3}, HENRI WEIMERSKIRCH\textsuperscript{3}, KARINE DELOLD\textsuperscript{3}, SAMANTHA C. PATRICK\textsuperscript{4}, HAL CASWELL\textsuperscript{1,5}, STEPHANIE JENOUVRIER\textsuperscript{1}
\textsuperscript{1}. Biology Department, Woods Hole Oceanographic Institution, Woods Hole, MA 02543, USA
\textsuperscript{2}. Department of Earth, Atmospheric and Planetary Science, Massachusetts Institute of Technology, Cambridge, MA 02139, USA
\textsuperscript{3}. Centre d’Etudes Biologiques de Chizé, CNRS-La Rochelle University UMR7372, 79360 Villiers en Bois, France
\textsuperscript{4}. School of Environmental Sciences, University of Liverpool, Nicholson Building, Brownlow Street, Liverpool, L69 3GP, UK
\textsuperscript{5}. Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, 1090 GE Amsterdam, The Netherlands

Appendix S1
Section S1 Methods

Section S1.1 MECMR model construction

To construct the structure of our MECMR models, we extended the framework of Culina et al. (2013) by distinguishing divorce from widowhood and including a quasi-biennial breeding strategy. Eight states were defined in the population including a dead state \( (S, ND, ND, Post-S, Post-N, D, W, Dead) \), see Table 2 in the main paper for detailed definitions). Four matrices were defined to describe the transitions between individual states including survival, widowhood, breeding probability and divorce. At each capture occasion, individual states are linked to the capture histories as a series of 13 conditional observed events in Table S1. Three matrices were defined to characterize the observations in order to account for state uncertainties.

Table S1: Description of the events in our MECMR model. The definition of observation events include capture of the focal individual, capture of the current partner of the focal individual and the previous partner from last breeding attempt. Event number appears in bold.

| Events | Definition |
|--------|------------|
| 1      | the focal individual is captured at \( t \) and is breeding during breeding season \( t \) with the same previous partner |
| 2      | the focal individual is captured at \( t \) and is breeding with a different partner while its previous partner is alive at \( t \) |
| 3      | the focal individual is captured at \( t \) and is breeding with a different partner while its previous partner is dead at \( t \) |
| 4      | the focal individual is captured at \( t \), its current partner is not captured, and its previous partner is alive and either not captured in \( t \) or is breeding with an unknown partner |
| 5      | the focal individual is captured at \( t \), its current partner is not captured, and its previous partner is alive and is breeding with another partner (hence the focal individual is divorced) |
| 6      | the focal individual and its partner are both captured at \( t \), but the previous partner is unknown |
| 7      | the focal individual is captured at \( t \), its current partner is not captured, and the previous partner is unknown |
| 8      | the focal individual is captured at \( t \) but does not breed (and hence its current partner is unknown), its previous partner is either known and alive at time \( t \) or unknown |
| 9      | the focal individual is captured at \( t \) but does not breed (and hence its current partner is unknown) but its previous partner is alive at time \( t \) and is breeding with another partner since their last breeding season together (hence the focal individual is divorced at \( t \)) |
| 10     | the focal individual is captured at \( t \) but does not breed, while its previous partner is dead at \( t \) |
| 11     | the focal individual is not captured at \( t \), but its previous partner is captured and breeding with another individual (hence the focal individual is divorced at \( t \)) |
| 12     | the focal individual is not captured at \( t \) while its previous partner is dead at \( t \) |
| 13     | the focal individual is not captured in the current breeding season (i.e., at \( t \)), its partner from the previous season is not captured at \( t \) or \( t - 1 \), or is captured breeding at \( t \) with an unknown partner |
Individual survival from year $t-1$ to year $t$ based on pair bond and breeding status was modeled by including survival rates in matrix $S$ (Eq. 1). Rows of the matrix $S$ (Eq. 1) correspond to the state of an individual at $t-1$. Columns of this matrix define the state an individual is in at $t$. The transitions probabilities included in the matrix describe whether the focal individual survived from year $t-1$ to year $t$ with probability $s$ given its state at $t-1$ (e.g. $s_1$ is the survival probability of individuals of state 1, i.e. state breeding with same partner noted $S$ in year $t-1$). The notation and number of the states are provided for clarity:

$$S = \begin{pmatrix}
  S & ND & NW & Post-S & Post-N & D & W & Dead \\
  1 & 2 & 3 & 4 & 5 & 6 & 7 & \end{pmatrix}
$$

(S1)

Conditional on the survival, we characterized $w$ the probability of becoming a widow for the focal individual at the beginning of the breeding season of year $t$ as the probability that the partner from the previous breeding event is dead from $t-1$ to $t$. The rows of the widowhood matrix $W$ (Eq. 2) specify the state of the focal individual at the previous breeding season $t-1$.

$$W = \begin{pmatrix}
  S & ND & NW & Post-S & Post-N & D & W & Dead \\
  1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\
  S & 1 & 1 - w_1 & 0 & 0 & 0 & 0 & w_4 \\
  ND & 2 & 0 & 1 - w_2 & 0 & 0 & 0 & w_5 \\
  NW & 3 & 0 & 0 & 1 - w_3 & 0 & 0 & w_6 \\
  Post-S & 4 & 0 & 0 & 0 & 1 - w_4 & 0 & w_7 \\
  Post-N & 5 & 0 & 0 & 0 & 0 & 1 - w_5 & w_8 \\
  D & 6 & 0 & 0 & 0 & 0 & 0 & w_9 \\
  W & 7 & 0 & 0 & 0 & 0 & 0 & w_{10} \\
  Dead & 8 & 0 & 0 & 0 & 0 & 0 & 1 \\
\end{pmatrix}
$$

(S2)

We then characterized $\beta$ the breeding probability in year $t$ for the focal individual conditional on survival and widowhood. In this process, we included four new hidden states indicating whether the focal individual skips breeding in year $t$ ($Post-S, Post-N, D, W$).
The probability of divorce $d$ was included in the matrix $D$ (Eq. S4). The probability of divorce at $t$ for the focal individual present at the breeding site from the beginning of the breeding season $t$ are noted $d_1, \ldots, d_5$. If the focal individual skips breeding at season $t$, i.e. individual in states $\text{Post-S, Post-N}$, the probability that its partner breeds with another individual, hence to divorce, is $d_6$ and $d_7$.

\begin{equation}
B = \begin{bmatrix}
S & ND & NW & Post-S & Post-N & Post-S & Post-N & D & W & \bar{D} & W & \text{Dead} \\
1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 12 \\
S & 1 & \beta_1 & 0 & 0 & 0 & 0 & 1 - \beta_1 & 0 & 0 & 0 & 0 & 0 \\
ND & 2 & 0 & \beta_2 & 0 & 0 & 0 & 0 & 1 - \beta_2 & 0 & 0 & 0 & 0 \\
NW & 3 & 0 & 0 & \beta_3 & 0 & 0 & 0 & 1 - \beta_3 & 0 & 0 & 0 & 0 \\
Post-S & 4 & 0 & 0 & 0 & \beta_4 & 0 & 0 & 0 & 1 - \beta_4 & 0 & 0 & 0 \\
Post-N & 5 & 0 & 0 & 0 & 0 & \beta_5 & 0 & 0 & 1 - \beta_5 & 0 & 0 & 0 \\
D & 6 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \beta_6 & 0 & 1 - \beta_6 & 0 \\
W & 7 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \beta_7 & 0 & 1 - \beta_7 \\
\text{Dead} & 8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 \\
\end{bmatrix}
\end{equation}

\begin{equation}
D = \begin{bmatrix}
S & ND & NW & Post-S & Post-N & D & W & \text{Dead} \\
1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\
S & 1 & 1 - d_1 & d_1 & 0 & 0 & 0 & 0 & 0 \\
ND & 2 & 1 - d_2 & d_2 & 0 & 0 & 0 & 0 & 0 \\
NW & 3 & 1 - d_3 & d_3 & 0 & 0 & 0 & 0 & 0 \\
Post-S & 4 & 1 - d_4 & d_4 & 0 & 0 & 0 & 0 & 0 \\
Post-N & 5 & 1 - d_5 & d_5 & 0 & 0 & 0 & 0 & 0 \\
Post-S & 6 & 0 & 0 & 1 - d_6 & 0 & d_6 & 0 & 0 \\
Post-N & 7 & 0 & 0 & 0 & 1 - d_7 & d_7 & 0 & 0 \\
D & 8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
W & 9 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\
\bar{D} & 10 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\
W & 11 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\
\text{Dead} & 12 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 \\
\end{bmatrix}
\end{equation}

To account for uncertainties in the pairing state, the detection process was decomposed into a model described by three events matrices: $P_1, P_2, P_3$. $P_1$ describes the capture of the focal individual, $P_2$ describes the capture of the current partner of the focal individual and $P_3$ describes the capture of the previous partner from last breeding attempt. $P_1$ (Eq. S5) describes the detection probabilities of the focal individual. Columns of $P_1$ describe whether the focal individual is captured at time $t$ (noted $C_j$) or not ($\bar{C}_j$) given its state at the previous breeding season $t - 1$ (indicated as a subscript).
P₂ (Eq. S6) describes the detection probabilities of the focal individual’s current partner at time \( t \) with their pair-bond states (same as or different to previous partner). Columns of \( P₂ \) describe whether the current partner is captured at time \( t \) (noted \( PC_j \)) or not (\( PC_{̄j} \)) given its previous state (indicated as a subscript), or whether its current partner is captured but the focal individuals’ previous partner is not known (\( PP_{胄j} \); hence it is not known if the current partner is the same or different from the one in the last breeding season). If the focal individual is not captured at time \( t \) then its current partner is unknown (\( U_j \)).

\[
P₂ = \begin{pmatrix}
S & 1 & p₁ & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
ND & 2 & 0 & p₂ & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\
NW & 3 & 0 & 0 & p₃ & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\
Post-S & 4 & 0 & 0 & 0 & p₄ & 0 & 0 & 0 & 1 & 0 & 0 \\
Post-N & 5 & 0 & 0 & 0 & 0 & p₅ & 0 & 0 & 1 & 0 & 0 \\
D & 6 & 0 & 0 & 0 & 0 & 0 & p₆ & 0 & 0 & 1 & p₆ \\
W & 7 & 0 & 0 & 0 & 0 & 0 & 0 & p₇ & 0 & 0 & 1 & p₇ \\
Dead & 8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1
\end{pmatrix}
\] (S5)

\( P₃ \) (Eq. S7) describes the detection probabilities of the focal individual’s previous partner at time \( t \) with their pair-bond states (same as or different to previous partner), and the detection probabilities of the focal individual’s previous partner at time \( t \) combined with their living states (alive or dead). Columns of \( P₃ \) correspond to the event code in Table S1. \( l \) is the probability that the previous partner is known to be alive, and \( 1 − l \) is the probability that the previous partner is unknown. \( δ \) is the probability that the previous partner is known to be alive and is captured with another partner (hence divorced), and \( 1 − δ \) is the probability that the previous partner is unknown or the previous partner is known but captured non-breeding or not captured at time \( t \). \( m \) is the probability that the previous partner is known to be dead, and \( 1 − m \) is the probability that the previous partner is unknown. Notation in \( P₃ \) are explained below, \( CPU − PPK \): current partner is not captured (hence unknown) but the focal individual’s previous partner is known and alive; \( CPU − D \): current partner is not captured but the focal individual’s previous partner is captured with another partner (hence divorced); \( CPK − PP \): current partner is captured (hence alive) but the focal individual’s previous partner is not known hence it is not known if the current partner is the same or different to the one in the last breeding season; \( CPU − PP \): current partner is not captured and the focal individual’s previous partner is not known hence it is not known if the current partner is alive and if the current partner is the same or different to the one in the last breeding season.
$$P_2 = \begin{pmatrix}
1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 12 & 13 & 14 \\
C_S & 1 & c_1 & 1 - \sum c & c_{1|2|3} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
C_{ND} & 2 & 0 & 0 & c_{1|2|3} & 1 - \sum c & c_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
C_{NW} & 3 & 0 & 0 & c_{1|2|3} & 0 & 0 & 1 - \sum c & c_3 & 0 & 0 & 0 & 0 & 0 \\
C_{Post-S} & 4 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
C_{Post-N} & 5 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\
C_D & 6 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\
C_W & 7 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\
C_B & 8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\
D & 9 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\
W & 10 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
Dead & 11 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 
\end{pmatrix} \quad (S6)$$
\[
\begin{pmatrix}
\text{Dead} & 14 \\
\text{UW} & 13 \\
\text{UD} & 12 \\
\text{UPost} & 11 \\
\text{UW} & 10 \\
\text{UD} & 9 \\
\text{UPost} & 8 \\
\text{PCNW} & 7 \\
\text{PCND} & 5 \\
\text{PPU} & 3 \\
\text{FC} & 2 \\
\text{PC} & 1
\end{pmatrix}
= \begin{pmatrix}
C_S & C_{ND} & C_{NW} & CPU - PPK & CPU - D & CPK - PPU & CPU - PPU & C_{Post-B} & C_D & C_W & \bar{D} & \bar{W} & \bar{U} - \bar{B} \\
1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
3 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
4 & 0 & 0 & 0 & l & 0 & 0 & 1 - l & 0 & 0 & 0 & 0 & 0 \\
5 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
6 & 0 & 0 & m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
7 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
9 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 - \delta & \delta & 0 & 0 & 0 \\
10 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 - m & 0 & m & 0 & 0 \\
11 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
12 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \delta & 0 & 1 - \delta \\
13 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & m & 1 - m \\
\end{pmatrix}
\]
Figure S1: Structure of the observation process. The Observation process is composed of three steps: Detection of the focal individual $P_1$ (Eq. S5), information on focal individual’s current partner $P_2$ (Eq. S6), and information on focal individual’s previous partner from last breeding attempt $P_3$ (Eq. S7). Event codes are corresponding to the code numbers in Table S1. Arrows indicate the transition probabilities follows the parameters in matrix $P_1$, $P_2$, and $P_3$. 
Section S1.2  Model constraints

Section S1.2.1  Parameter constraints

Survival rates of post-breeding states were estimated at the boundary due to limited field observations. Our aim in this study was to analyse the impacts of changes in pair-bond on survival, we focused on survival differences between pair-bond status rather than between post-breeding and breeding states. Therefore, when estimating survival probabilities, we grouped individuals in state Post-S with S and grouped Post-N with individuals breed with a new partner (ND and NW) in year t − 1.

Section S1.2.2  Temporal constraints

Fully time-varying models had several unidentifiable parameters and rarely converged. Hence, to account for time variations, we included several time period breakpoints in the model. We used two approaches to define the time periods: (1) sub-decadal time breaking points (1967-1975, 1976-1985, 1986-1995, 1996-2005, and 2006-2011) and (2) specific time breaking points based on population time series. For the later we used the time breaking points in Delord et al. 2008, who found 4 periods of contrasted population dynamic trends including: (1) a short stable period at the beginning of the study (1966-1968); (2) a continuous decline period from 1969 to 1986; (3) a slightly increasing trend from 1987 to 2004; (4) a final decreasing period since then. Combined with results in Delord et al. 2008, we defined time breaking points for population dynamics from 1967-1985, 1986-1998, 1999-2011 (See Appendix S1: Fig. S2 for an updated population trend). Breeding states assignments before 1986 was with higher level of uncertainties due to unstandardized protocols (Barbraud & Weimerskirch 2012). Hence, breeding probabilities before 1986 were constrained as constant values to account for the uncertainties before 1986.
Figure S2: Number of annual breeding pairs of wandering albatross in Possession Island, Crozet. Our time breaking points are set as 1967-1985 (decline), 1986-1998 (increase), and 1999-2011 (stable). Two dashed lines indicate year 1967 and 2011. The time period between the dashed lines are used in our analysis.
Section S1.3  Fishery covariates

Figure S3: Foraging grounds of wandering albatrosses (area surrounded by black line) breeding at Possession Island, Crozet, according to sexes and breeding status. The definition of foraging group is based on the utilization distribution estimated by a Kernel analysis from Weimerskirch et al. (2014).
Section S1.4  Model selection and averaging for GLMM analysis

For model selection of GLMM models, we used an information-theoretic approach, using Akaike’s Information Criterion (AIC) and using the MuMIn package in R (Bartoń 2020). From a set of possible models, we selected models within two AIC units of the lowest AIC model and used model averaging to calculate parameter estimates. Complex models can have lower AIC value but not necessarily better predict the response variables (Burnham & Anderson 2002). Therefore, we followed the nesting rule that any model included in the top model set (within $\Delta$ AIC < 2) which was a more complex version of the simpler model within this set was dropped (Arnold 2010, Harrison et al. 2018, Richards et al. 2011). This improves the interpretation of results and increases the accuracy of parameter estimates.

Section S1.5  Correlation between age and breeding experience

In our GLMM framework, we used breeding experience instead of age as a predictor to control for changes of breeding success as senescence occurs because the age of many individuals was unknown and highly correlated with breeding experience which is precisely recorded. The correlation between age and breeding experience are shown in Fig. S5.
Figure S5: Correlation between age and breeding experience. A Generalized linear model (GLM) was used to investigate the correlation between age and breeding experience. We showed that age and breeding experience are highly correlated with a p-value < 0.0001 and $r^2=0.8010$. Blue dots are real data points. The blue line and shaded area are show model fit and 95% confidential interval.

Section S1.6  Life-history outcomes, breeding intervals, divorce probabilities and time to next divorce

Section S1.6.1 Remaining lifetime reproductive success (LRS)

Calculations of remaining LRS depending on the initial pair-bond state of an individual followed the procedure in Caswell (2011) considering reproduction as a reward accumulated by an individual each time it enters a breeding state. An individual moving from state $j$ to a breeding state $i$ from time $t-1$ to $t$ collects a reproductive reward $r_{ij}$, where $r_{ij}$ is a random variable. The first moment of the reproductive reward $r_{ij}$ is denoted by matrix $R$.

$$R = (E[r_{ij}]) \quad (S8)$$

A recursive equation used to calculate the mean reproductive rewards to be collected during each time step is given by

$$\rho(t + 1) = (P \circ R)^T 1 + P^T \rho(t) \quad t = 0, ..., T - 1 \quad (S9)$$

with an initial condition $\rho(0) = 0$ indicating that the focal individual has no offspring at the initial stage.
In our case, individuals in states $j$ were only given a reproductive reward when moving to a breeding states which are S, ND and NW. The values of reproductive reward is the probability to successfully rear a chick depending on the current pair-bond status of an individual. The reproductive rewards were parameterized using a GLMM analysis of breeding success as a function of pair bond status. In the GLMM models, probabilities of breeding success were modeled as a binary response variable using pair-bond status $S$, ND and NW as categorical predictors. Year of reproduction was included as random effects. The GLMM analysis was performed in R (Team 2018) using package lme4 (Bates et al. 2015). Then, the mean remaining LRS is given by iterating Eq. S9 to calculated accumulating reproductive rewards until $\rho(t)$ converges to its equilibria.

Section S1.6.2 Calculation of the weighted average of LRS

In the main paper Fig. 6a and 6b, we present the weighted average of the remaining LRS and expected time to the next breeding attempt. To obtain the weighted average of the of state “Mate with a partner” we used the states S, ND, NW, Post-S, and Post-N. In Fig. 6b, expected time for next breeding attempt of state “Divorced and widowed” is a weighted average of state D and W. The average values were weighted corresponding to relative abundance of states in the population. The relative abundance $\hat{n}$ of the 7 states (S, ND, ND, Post-S, Post-N, D, W) is obtained from a stationary population is given by

$$\hat{n} = (I - U)^{-1}b$$

(S10)

Where $b$ is transition probabilities to these 7 states from the first reproduction of an individual obtained from capture-mark-recapture records.

Section S1.6.3 Breeding intervals, probability of future divorce, and time to next divorce

To calculate breeding intervals, divorce probabilities and time to next divorce, we used the framework developed in Roth & Caswell (2018). In order to do so, we will need to construct a killed Markov Chain and a conditional Markov Chain based on the original population projection matrix $P$.

The first step is to define a target set $B$ composed of $\beta$ transient states (i.e., breeding states or divorce states) and we can re-arrange the order of transient states so that the target sets are the last several elements in the vector $B$. With total number of $\omega$ states, we have target set $B$ with $\beta$ states and complementary set $B^c$ with $\alpha$ states, where $\omega = \alpha + \beta$.

$$B = \{\alpha + 1, \alpha + 2, \ldots, \omega\}$$

(S11)

$$B^c = \{1, 2, \ldots, \alpha\}$$

(S12)

We then defined a killed Markov chain $P_K$, which is a is a variation of the original Markov chain that the transition of a individual stops as soon as it enters in the target set. See Roth & Caswell (2018) section 3.1 for details on how to construct the killed Markov chain using $B$ and $B^c$.

$$P_K = \begin{pmatrix}
U_K & 0_{\alpha \times (\beta+1)} \\
-M_K & I_{\beta+1}
\end{pmatrix}$$

(S13)
The matrix $M_K$ is composed of two blocks:

$$M_K = \left( \begin{array}{c} K \\ m^{-T}_\alpha \end{array} \right)$$  \hspace{1cm} (S14)

The matrix $U_K$ and $K$ are both extracted from the original transition matrix $U$. The fundamental matrix of $P_K$ becomes

$$N_K = (I_\alpha - U_K)^{-1}$$  \hspace{1cm} (S15)

We then defined a conditional Markov chain $P_C$ that describes the transitions of an individual before entering the target set given that the individual eventually enters in the target set $B$. See Roth & Caswell (2018) section 3.2 for details on how to construct the conditional Markov chain using $B$ and $B^c$

$$P_C = \left( \begin{array}{c|c} U_C & 0 \\ \hline M_C & I_\beta \end{array} \right)$$  \hspace{1cm} (S16)

The block matrix $U_C$ and $M_C$ are given by

$$U_C = diag(p_a)U_Kdiag(p_a)^{-1}$$  \hspace{1cm} (S17)

$$M_C = Kdiag(p_a)^{-1}$$  \hspace{1cm} (S18)

The fundamental matrix of $P_C$ becomes

$$N_C = (I_\alpha - U_C)^{-1}$$  \hspace{1cm} (S19)

The probability that an individual eventually reaches the target set is that, for each target state $i$ and non-target state $j$, the probability that an individual starting in $j$ passes through $i$ before eventually reaches death. The probability that an individual eventually reaches the target set depending on its current state is given by

$$p_a = 1^T KN_K$$  \hspace{1cm} (S20)

In this study, we calculated the probabilities for an individual eventually to divorce. Here, we defined divorce as the target set $B$ composed of two transient divorce states, $ND$ and $D$. Then, the complemental set $B^c$ contains $S,NW, \text{Post-S, Post-N}$. Then we constructed the killed Markov Chain $P_K$ and conditional Markov Chain using $B$ and $B^c$. The probability for an individual to divorce depending on its current state is given by Eq. S20.

The expected time for an individual to reach the target state $t_B$ is the occupancy time of the conditional Markov chain in its entire transient set. The mean of $t_B$ is yield by

$$E(t_B) = 1^T_\alpha N_C$$  \hspace{1cm} (S21)

Here, we calculated the expected time for an individual to breed and next divorce depending on its current pair-bond states. For expected time to breed, the target set $B$ composed of three transient reproductive states which are $S$, $ND$ and $NW$. Then, the complemental set $B^c$ contains $D,W, \text{Post-S and Post-N}$. Then we constructed the conditional Markov Chain $P_C$ using $B$ and $B^c$. The expected time for an individual to breed again is yield by Eq. S21.

For expected time to the next divorce, the target set $B$ composed of two transient divorce states, $ND$ and $D$. Then, the complemental set $B^c$ contained $S,NW, \text{Post-S, Post-N}$. Then we constructed the conditional Markov Chain $P_C$ using $B$ and $B^c$. The expected time for an individual to divorce is yield by Eq. S21.
Section S2  Results

Section S2.1  MECMR models
Section S2.1.1  MECMR model selection
Table S2: MECMR model selection results for females to estimate vital rates in terms of survival and breeding probability and pair-bond disruption rates of divorce and widowhood. Only structures of models within the top 20 model set were presented. “/” indicates group separation and parameters of each states are same within a group. *States* indicates that parameters vary amongst all states. “+” indicates additive effects and “**” indicates interactive effects. “np” indicates number of parameters. Seven temporal covariates were defined as follow: time(1). sub-decadal time breeding points as described in Section Section S1.2.2; time(2). specific time breaking points as described in Section Section S1.2.2; time(3). constant 1967-1985, time(1) since 1986; time(4). constant 1967-1985, time(2) since 1986; time(5). constant 1967-1985, full variation since 1986; time(6). constant 1967-1985, quadratic since 1986; time(7). linear trend since 1967.

| Model rank | Survival | Widowhood | Breed | Divorce | np    | QAIC    |
|------------|----------|-----------|-------|---------|-------|---------|
| 1          | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(1) | States*time(5) | States*time(4) | 312   | 45612.85 |
| 2          | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(1) | States*time(5) | States*time(6) | 315   | 45630.58 |
| 3          | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 302   | 45634.16 |
| 4          | S Post-S/ND NW Post-N/ D W*time(2) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 296   | 45643.03 |
| 5          | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N+time(1) | States*time(5) | States*time(6) | 303   | 45645.76 |
| 6          | S Post-S/ND NW Post-N/ D W*time(2) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 302   | 45647.08 |
| 7          | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(1) | States*time(5) | States*time(3) | 319   | 45645.63 |
| 8          | S Post-S/ND NW Post-N/ D W*time(4) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 292   | 45649.34 |
| 9          | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 294   | 45650.09 |
| 10         | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(4) | States*time(5) | States*time(6) | 307   | 45648.86 |
| 11         | S Post-S/ND NW Post-N/ D W*time(2) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 294   | 45654.05 |
| 12         | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N+time(4) | States*time(5) | States*time(6) | 301   | 45653.45 |
| 13         | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(1) | States*time(5) | States*time(4) | 300   | 45673.21 |
| 14         | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(1) | States*time(5) | States*time(3) | 301   | 45700.71 |
| 15         | S Post-S/ND NW Post-N/ D W*time(4) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 293   | 45703.10 |
| 16         | S Post-S/ND NW Post-N/ D W*time(4) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 291   | 45705.77 |
| 17         | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 293   | 45707.29 |
| 18         | S Post-S/ND NW Post-N/ D W*time(1) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 297   | 45706.61 |
| 19         | S Post-S/ND NW Post-N/ D W*time(2) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 293   | 45710.03 |
| 20         | S Post-S/ND NW Post-N/ D W*time(2) | S/ND/NW/Post-S Post-N*time(7) | States*time(5) | States*time(6) | 297   | 45708.08 |
Table S3: MECMR model selection results for males to estimate vital rates in terms of survival and breeding probability and pair-bond disruption rates of divorce and widowhood. Only structures of models within the top 20 model set were presented. “/” indicates group separation and parameters of each states are same within a group. States indicates that parameters vary amongst all states. “+” indicates additive effects and “*” indicates interactive effects. “np” indicates number of parameters. Seven temporal covariates were defined as follow: time(1). sub-decadal time breeding points as described in Section Section S1.2.2; time(2). specific time breaking points as described in Section Section S1.2.2; time(3). constant 1967-1985, time(1) since 1986; time(4). constant 1967-1985, time(2) since 1986; time(5). constant 1967-1985, full variation since 1986; time(6). constant 1967-1985, linear since 1986; time(7). linear trend since 1967.

| Model rank | Survival | Widowhood | Breed | Divorce | np  | QAIC   |
|------------|----------|-----------|-------|---------|-----|--------|
| 1          | S Post-S/ ND NW Post-N/ D W*time(1) S/ ND/ NW/ Post-S Post-N*time(1) | States*time(5) | States*time(4) | 330 | 56581.40 |
| 2          | S Post-S/ ND NW Post-N/ D W*time(1) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 310 | 56583.46 |
| 3          | S Post-S/ ND NW Post-N/ D W+time(1) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 302 | 56589.76 |
| 4          | S Post-S/ ND NW Post-N/ D W*time(4) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 304 | 56588.27 |
| 5          | S Post-S/ ND NW Post-N/ D W*time(2) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 310 | 56589.39 |
| 6          | S Post-S/ ND NW Post-N/ D W+time(4) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 300 | 56591.64 |
| 7          | S Post-S/ ND NW Post-N/ D W+time(2) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 302 | 56590.49 |
| 8          | S Post-S/ ND NW Post-N/ D W*time(1) S/ND/ NW/ Post-S Post-N*time(1) | States*time(5) | States++time(6) | 324 | 56590.42 |
| 9          | S Post-S/ ND NW Post-N/ D W*time(4) S/ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 299 | 56597.24 |
| 10         | S Post-S/ ND NW Post-N/ D W*time(4) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 301 | 56595.79 |
| 11         | S Post-S/ ND NW Post-N/ D W*time(2) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 301 | 56596.95 |
| 12         | S Post-S/ ND NW Post-N/ D W*time(2) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 301 | 56596.96 |
| 13         | S Post-S/ ND NW Post-N/ D W*time(2) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 305 | 56596.79 |
| 14         | S Post-S/ ND NW Post-N/ D W*time(4) S/ ND/ NW/ Post-S Post-N*time(7) | States*time(5) | States++time(6) | 305 | 56598.686 |
| 15         | S Post-S/ ND NW Post-N/ D W*time(1) S/ND/ NW/ Post-S Post-N*time(4) | States*time(5) | States++time(6) | 316 | 56598.86 |
| 16         | S Post-S/ ND NW Post-N/ D W*time(1) S/ND/ NW/ Post-S Post-N*time(4) | States++time(1) | States++time(6) | 312 | 56602.31 |
| 17         | S Post-S/ ND NW Post-N/ D W*time(1) S/ ND/ NW/ Post-S Post-N*time(4) | States*time(5) | States++time(6) | 310 | 56605.36 |
| 18         | S Post-S/ ND NW Post-N/ D W*time(1) S/ ND/ NW/ Post-S Post-N*time(1) | States*time(5) | States++time(3) | 318 | 56604.85 |
| 19         | S Post-S/ ND NW Post-N/ D W*time(1) S/ ND/ NW/ Post-S Post-N*time(1) | States*time(5) | States++time(4) | 318 | 56606.04 |
| 20         | S Post-S/ ND NW Post-N/ D W*time(1) S/ ND/ NW/ Post-S Post-N*time(1) | States*time(5) | States++time(3) | 319 | 56616.61 |
Section S2.1.2  Results of the best supported MECMR models

Here we present the estimates of the MECMR models with lowest AIC for females and males.

Figure S6: Survival probabilities from year $t - 1$ to year $t$ of females and males depending on pair-bond status in year $t - 1$. In both females and males, survival probabilities present sub-decadal temporal variations and vary between the following periods: 1967-1975, 1976-1985, 1986-1995, 1996-2005, and 2006-2011. Survival probabilities are different between individuals: (a,b) staying with the same partner ($S$ and Post-$S$), (c,d) individuals that changed partner (ND, NW and Post-N), and (e,f) individuals that were not mated with a partner (D and W).
Figure S7: Widowhood rates in year \( t \) of females and males depending on pair-bond status in year \( t-1 \). In both females and males, widowhood rates present sub-decadal temporal variations and vary between periods: 1967-1975, 1976-1985, 1986-1995, 1996-2005, and 2006-2011. Widowhood rates are different between (a,b) breeders staying with the same partner (S), (c,d) breeders that changed partner after a divorce (ND), (e,f) breeders that changed partner after widowhood (NW), (g,h) and individuals in post breeding states (Post-S and Post-N).
Figure S8: Breeding probabilities in year $t$ of females and males depending on pair-bond states in year $t - 1$. In both females and males, breeding probabilities are fixed as constant between 1967-1985 due to large uncertainty in state assignment and present fully annual variations between 1986-2011. Breeding probabilities are different amongst all pair bond status ((a,b) S, (c,d) ND, (e,f) NW, (g,h) Post-S, (i,j) Post-N, (k,l) D, (m,n) W).
Figure S9: Divorce rates in year $t$ of females and males depending on pair-bond status in year $t-1$. In both females and males, divorce rates are different depending on time breaking points of population dynamics which correspond to the following periods 1967-1985, 1986-1998, and 1999-2011. Divorce rates are different amongst all pair bond status ((a,b) S, (c,d) ND, (e,f) NW, (g,h) Post-S, (i,j) Post-N).
Section S2.1.3  Covariance matrix of MECMR model estimates
Table S4: Covariance matrix for survival, widowhood, breeding, and divorce rates estimated in MECMR models of female wandering albatrosses. Variables $X_{1-3}$ correspond to the survival rates depending on pair-bond status shown in Fig. 5a from the main manuscript; $X_4$ corresponds to the widowhood rate shown in Fig. 3a of the main manuscript; $X_{5-11}$ correspond to the breeding probabilities depending on pair-bond status shown in Fig. 5b of the main manuscript; $X_{12-16}$ correspond to the divorce rates depending on pair-bond status shown in Fig. 3b of the main manuscript.

| Variables | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|-----------|-------|-------|-------|-------|-------|-------|-------|-------|-------|----------|----------|----------|----------|----------|----------|----------|
| $X_1$     | 0.004 |       |       |       |       |       |       |       |       |          |          |          |          |          |          |          |
| $X_2$     | 0.000 | 0.005 |       |       |       |       |       |       |       |          |          |          |          |          |          |          |
| $X_3$     | 0.000 | 0.000 | 0.009 |       |       |       |       |       |       |          |          |          |          |          |          |          |
| $X_4$     | 0.000 | 0.000 | 0.000 | 0.002 |       |       |       |       |       |          |          |          |          |          |          |          |
| $X_5$     | -0.001| 0.000 | 0.000 | 0.000 | 0.005 |       |       |       |       |          |          |          |          |          |          |          |
| $X_6$     | 0.000 | 0.000 | 0.000 | 0.000 | 0.001 | -0.003|       |       |       |          |          |          |          |          |          |          |
| $X_7$     | -0.001| 0.000 | 0.000 | 0.000 | 0.000 | -0.011| 0.002 |       |       |          |          |          |          |          |          |          |
| $X_8$     | 0.001 | 0.000 | 0.000 | 0.010 | 0.018 | -0.004| -0.125|       |       |          |          |          |          |          |          |          |
| $X_9$     | 0.000 | 0.000 | 0.000 | 0.000 | 0.001 | 0.000 | -0.001| 0.001 | 0.000 |          |          |          |          |          |          |          |
| $X_{10}$  | -0.001| 0.000 | 0.000 | 0.000 | 0.001 | 0.000 | -0.001| 0.001 | 0.000 | 0.002 | 0.001   |          |          |          |          |          |
| $X_{11}$  | 0.000 | 0.000 | 0.000 | 0.000 | 0.001 | 0.000 | 0.000 | 0.000 | 0.000 | 0.002 | 0.001   | 0.001    |          |          |          |          |
| $X_{12}$  | 0.021 | 0.002 | 0.001 | 0.001 | -0.050| 0.000 | -0.007| -0.011| -0.013| -0.003 | -0.026 | 0.024    |          |          |          |          |
| $X_{13}$  | 0.003 | -0.002| 0.000 | 0.016 | 0.004 | 0.003 | -0.003| 0.009 | 0.004 | 0.081 | -0.268 |          |          |          |          |          |
| $X_{14}$  | 0.000 | 0.002 | -0.001| 0.000 | 0.235 | 0.033 | 0.014 | -0.025| 0.099 | 0.016 | -0.015 | 0.048 | 0.082    |          |          |          |
| $X_{15}$  | 0.005 | 0.001 | 0.000 | 0.000 | -0.013| 0.001 | -0.003| -0.010 | 0.003 | -0.005 | 0.625 | 1.007 | -0.079 | 0.024   |          |          |
| $X_{16}$  | -0.001| 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | -0.001| 0.001 | 0.000 | 0.000 | 0.030 | -0.014 | -0.023 | 0.030    | -0.002 |          |
Table S5: Covariance matrix for survival, widowhood, breeding, and divorce rates estimated in MECMR models of male wandering albatrosses. Variables $X_{1-3}$ correspond to the survival rates depending on pair-bond status shown in Fig. 5a from the main manuscript; $X_4$ corresponds to the widowhood rate shown in Fig. 3a of the main manuscript; $X_{5-11}$ correspond to the breeding probabilities depending on pair-bond status shown in Fig. 5b of the main manuscript; $X_{12-16}$ correspond to the divorce rates depending on pair-bond status shown in Fig. 3b of the main manuscript.

| Variables | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|----------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| $X_1$    | 0.022 |       |       |       |       |       |       |       |       |            |            |            |            |            |            |            |
| $X_2$    | -0.011 | 0.107 |       |       |       |       |       |       |       |            |            |            |            |            |            |            |
| $X_3$    | 0.000 | 0.000 | 0.009 |       |       |       |       |       |       |            |            |            |            |            |            |            |
| $X_4$    | 0.000 | -0.001 | 0.000 | 0.021 |       |       |       |       |       |            |            |            |            |            |            |            |
| $X_5$    | -0.001 | 0.001 | 0.000 | 0.000 | 0.501 |       |       |       |       |            |            |            |            |            |            |            |
| $X_6$    | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.377 |       |       |       |            |            |            |            |            |            |            |
| $X_7$    | 0.001 | 0.002 | 0.001 | 0.000 | 0.000 | 0.000 | 0.009 | 0.223 |       |            |            |            |            |            |            |            |
| $X_8$    | 0.000 | 0.000 | 0.000 | 0.000 | -0.002 | 0.000 | 0.000 | 0.000 | 0.016 |            |            |            |            |            |            |            |
| $X_9$    | -0.004 | 0.002 | 0.000 | 0.000 | 0.000 | 0.000 | 0.021 | 0.001 | 0.000 | -0.004 | 0.000 | 0.000 | 0.015 | 0.000 | 0.015 | 0.348 |
| $X_{10}$ | 0.000 | 0.001 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.015 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.115 |
| $X_{11}$ | -0.001 | 0.001 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | -0.008 | 0.000 | -0.008 | 0.000 | -0.003 | 0.000 | 0.000 | 0.000 | 0.182 |
| $X_{12}$ | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.119 |
| $X_{13}$ | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.013 |
| $X_{14}$ | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.139 |
| $X_{15}$ | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.098 |
| $X_{16}$ | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | -0.005 | 0.000 | -0.001 | 0.000 | -0.001 | 0.002 | 0.000 | 0.000 | 0.072 |
Section S2.2  Longevity

Figure S10: Expected remaining lifetime (life expectancy) of an individual depending on their current pair bond status (±90% CI).
Section S2.3  Causes and consequences of divorce

We used a GLMM framework to analysis whether divorce is a result of poor reproductive performance at the previous breeding season (short-term annual breeding success at the previous breeding season), or during the entire duration of the pair-bond with previous partner (long-term breeding success averaged during the entire pair-bond). Table S6 show the list of models we ran with model structures and associated results.

Table S6: Model selection for studying the impact of reproductive performance with a partner on whether a pair-bond disruption happens through divorce or widowhood. “bexp” indicates breeding experience which is the number of breeding attempts ever made by an individual, “nbreed” indicates the breeding attempts made with a partner which is used to describe pair-bond duration, “ltBS” indicates averaged breeding success of a pair across the pair-bond duration (long-term), “stBS” indicates breeding success of the very last breeding attempt made by a pair before pair-bond disruption (short-term). Here we only showed the models weighting more than 0.01.

| Sex  | Model description         | df | AICc  | ΔAICc | AICc weight |
|------|---------------------------|----|-------|-------|-------------|
| Female | bexp+bexp2+ltBS+nbreed  | 6  | 706.0 | 0.00  | 0.183       |
|       | bexp+bexp2+stBS+nbreed  | 6  | 706.6 | 0.64  | 0.133       |
|       | bexp+nbreed              | 5  | 707.0 | 0.96  | 0.113       |
|       | bexp+bexp2+ltBS+stBS+nbreed | 7  | 707.9 | 1.86  | 0.072       |
|       | bexp+ltBS+nbreed        | 5  | 708.6 | 2.64  | 0.049       |
|       | bexp+stBS+nbreed        | 5  | 709.4 | 3.41  | 0.033       |
|       | bexp+nbreed              | 4  | 710.2 | 4.16  | 0.023       |
|       | bexp+ltBS+stBS+nbreed  | 6  | 710.5 | 4.49  | 0.019       |
| Male  | bexp+nbreed              | 4  | 894.8 | 0.00  | 0.282       |
|       | bexp+bexp2+nbreed       | 5  | 896.1 | 1.27  | 0.150       |
|       | bexp+stBS+nbreed        | 5  | 896.8 | 1.97  | 0.105       |
|       | bexp+ltBS+nbreed        | 5  | 896.8 | 2.01  | 0.103       |
|       | bexp+bexp2+stBS+nbreed  | 6  | 898.0 | 3.21  | 0.057       |
|       | bexp+bexp2+ltBS+nbreed  | 6  | 898.1 | 3.29  | 0.055       |
|       | bexp+ltBS+stBS+nbreed  | 6  | 898.7 | 3.88  | 0.041       |
|       | bexp+bexp2+ltBS+stBS+nbreed | 7  | 900.0 | 5.14  | 0.022       |

When controlling the effects of breeding experience and pair-bond duration with a particular partner, females that succeeded at the previous reproduction has a divorce probability of 0.241 (SE=0.570) higher than that of females that failed in their previous breeding attempt (0.172, SE=0.591). The relationship between divorce probability and long-term breeding performance is presented in Fig. S11.
Figure S11: The relationship between divorce probability of females and the long-term averaged reproductive performance with a partner (±90% CI).
Section S2.4 Age structure

Figure S12: Averaged age of individuals available to mate (±90% CI). Only divorced and widowed individuals with known age were included. The demographic field work started in 1960. As field work is still going on annually, more and more individuals ringed as chicks and thus of known age recruit in the population resulting in the increasing trend here.
Section S2.5  Annual breeding success depending on current pair-bond status

Figure S13: Annual breeding success depending on the current pair-bond status of an individual in year $t$ (±90% CI).
Section S2.6  Time series of pair-bond disruptions

Figure S14: The number of divorce events for females and males in wandering albatross breeding in Possession Island generated from raw capture-mark-recapture data between 1967-2011. This time series of divorce events holds no information for the temporal variation of divorce rates, as the raw data set did not account for uncertainty due to imperfect detection nor uncertainties in divorce states. The number of individuals included in the capture-mark-recapture data set had been accumulated gradually because individuals only start breeding at an age of 7-9 (Weimerskirch 1992) resulting in an increasing trend for the number of marked individuals returning to the colony, hence increasing trend for the number of divorce events observed.
Figure S15: The number of widowhood events for females and males in wandering albatross breeding in Possession Island generated from raw capture-mark-recapture data between 1967-2011. This time series of widowhood events holds no information for the temporal variation of widowhood rates, as the raw data set did not account for uncertainty due to imperfect detection nor uncertainties in widowhood states. The number of individuals included in the capture-mark-recapture data set had been accumulated gradually because individuals only start breeding at an age of 7-9 (Weimerskirch 1992) resulting in an increasing trend for the number of marked individuals returning to the colony, hence increasing trend for the number of widowhood events observed.
References

Arnold, T. W. (2010), ‘Uninformative Parameters and Model Selection Using Akaike’s Information Criterion’, *Journal of Wildlife Management* **74**(6), 1175–1178. Publisher: The Wildlife Society.

URL: https://bioone.org/journals/journal-of-wildlife-management/volume-74/issue-6/2009-367/Uninformative-Parameters-and-Model-Selection-Using-Akaikes-Information-Criterion/10.2193/2009-367.full

Barbraud, C. & Weimerskirch, H. (2012), ‘Estimating survival and reproduction in a quasi-biennially breeding seabird with uncertain and unobservable states’, *Journal of Ornithology* **152**(2), 605–615.

URL: https://doi.org/10.1007/s10336-011-0686-1

Bartoń, K. (2020), ‘MuMIn: Multi-Model Inference’.

URL: https://CRAN.R-project.org/package=MuMIn

Bates, D., Mächler, M., Bolker, B. & Walker, S. (2015), ‘Fitting Linear Mixed-Effects Models Using lme4’, *Journal of Statistical Software* **67**(1), 1–48. Number: 1.

URL: https://www.jstatsoft.org/index.php/jss/article/view/v067i01

Burnham, K. P. & Anderson, D. R. (2002), *Model Selection and Multimodel Inference: A Practical Information-Theoretic Approach*, 2 edn, Springer-Verlag, New York.

URL: https://www.springer.com/gp/book/9780387953649

Caswell, H. (2011), ‘Beyond R0: Demographic Models for Variability of Lifetime Reproductive Output’, *PLoS ONE* **6**(6), e20809.

URL: https://dx.plos.org/10.1371/journal.pone.0020809

Culina, A., Lachish, S., Pradel, R., Choquet, R. & Sheldon, B. C. (2013), ‘A multievent approach to estimating pair fidelity and heterogeneity in state transitions’, *Ecol Evol* **3**(13), 4326–38.

URL: https://www.ncbi.nlm.nih.gov/pubmed/24340175

Delord, K., Besson, D., Barbraud, C. & Weimerskirch, H. (2008), ‘Population trends in a community of large Procellariiforms of Indian Ocean: Potential effects of environment and fisheries interactions’, *Biological Conservation* **141**(7), 1840–1856.

URL: http://www.sciencedirect.com/science/article/pii/S0006320708001602

Harrison, X. A., Donaldson, L., Correa-Cano, M. E., Evans, J., Fisher, D. N., Goodwin, C. E. D., Robinson, B. S., Hodgson, D. J. & Inger, R. (2018), ‘A brief introduction to mixed effects modelling and multi-model inference in ecology’, *PeerJ* **6**, e4794. Publisher: PeerJ Inc.

URL: https://peerj.com/articles/4794

Richards, S. A., Whittingham, M. J. & Stephens, P. A. (2011), ‘Model selection and model averaging in behavioural ecology: the utility of the IT-AIC framework’, *Behavioral Ecology and Sociobiology* **65**(1), 77–89.

URL: https://doi.org/10.1007/s00265-010-1035-8
Roth, G. & Caswell, H. (2018), ‘Occupancy time in sets of states for demographic models’, *Theoretical Population Biology* **120**, 62–77.
**URL:** https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5861321/

Team, R. C. (2018), ‘R: A Language and Environment for Statistical Computing’.
**URL:** https://www.R-project.org/

Weimerskirch, H. (1992), ‘Reproductive Effort in Long-Lived Birds: Age-Specific Patterns of Condition, Reproduction and Survival in the Wandering Albatross’, *Oikos* **64**(3), 464–473.
**URL:** https://www.jstor.org/stable/3545162

Weimerskirch, H., Cherel, Y., Delord, K., Jaeger, A., Patrick, S. C. & Riotte-Lambert, L. (2014), ‘Lifetime foraging patterns of the wandering albatross: Life on the move!’. 