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Lloyd, K. J., Oosthuizen, W. C., Fay, R., Bester, M. N. and de Bruyn, P. J. N. 2020. Selective disappearance of frail juveniles: consequences for understanding social dominance in adult male elephant seals. – Oikos doi: 10.1111/oik.07434

Appendix 1

State transitions

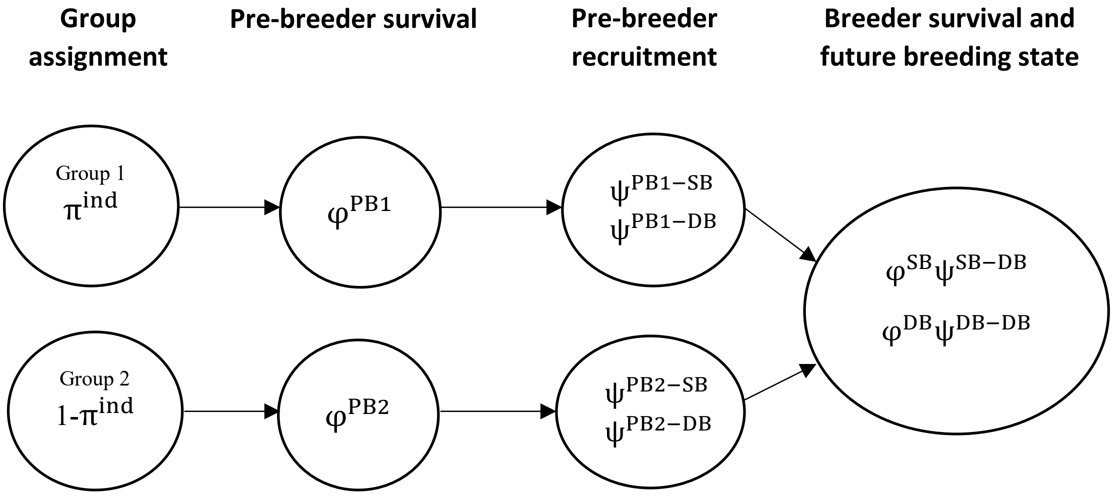

Figure A1. Possible transitions among breeding states when pre-breeding male elephant seals were assigned to hidden states (Group 1 - PB1 and Group 2 - PB2). Group assignment was based on how pre-breeders survived and recruited to the breeding population.

Appendix 2

Specifying elementary matrices

Finite-mixture multievent models were parameterised using initial state, transition and event matrices in the programme E-SURGE ver. 2.1.4 (Choquet et al. 2009). Mark–recapture data were imported in Text format and the overdispersion factor was set to $\hat{c} = 1.7$ (Lloyd et al. 2020). Under

‘Modify’, the number of states along with hidden states (13), events (9) and age classes (14) were set in order to determine the number of rows and columns of each matrix. Pre-breeder states were duplicated to make two hidden states represented as Group 1 (PB1) and Group 2 (PB2; Pledger et al. 2003). Pre-breeders alive elsewhere (PBAE) was also a hidden state constructed to account for individuals not observed in a particular year that may have temporarily migrated from the study population (Schaub et al. 2004). The following thirteen (biological) states were recognised:

PB1-T2 – Group 1 pre-breeder with two tags (had not previously participated in a breeding event)

PB2-T2 – Group 2 pre-breeder with two tags

PB1-T1 – Group 1 pre-breeder with one tag

PB2-T1 – Group 2 pre-breeder with one tag

PBAE1-T2 – Group 1 pre-breeder alive elsewhere with two tags (temporarily migrated and last seen with two tags)

PBAE2-T2 – Group 2 pre-breeder alive elsewhere with two tags

PBAE1-T1 – Group 1 pre-breeder alive elsewhere with one tag

PBAE2-T1 – Group 2 pre-breeder alive elsewhere with one tag

SB2 – Subordinate breeder with two tags (attended breeding season but did not mate)

SB1 – Subordinate breeder with one tag

DB2 – Dominant breeder with two tags (attended breeding season and mated)

DB1 – Dominant breeder with one tag

D – Dead (an absorbing state representing death, loss of all tags, and permanent emigration)

Events related in a probabilistic framework to the nine possible breeding states that an individual could occupy each year. The following nine (observed) events were recognised:

0 – Not seen

1 – Seen as a pre-breeder with two tags

2 – Seen as a pre-breeder with one tag

3 – Seen as a subordinate breeder with two tags

4 – Seen as a subordinate breeder with one tag

5 – Seen as a dominant breeder with two tags

6 – Seen as a dominant breeder with one tag

7 – Seen with an unknown breeding state and two tags

8 – Seen with an unknown breeding state and one tag

GEPAT (for GEnerator of PATtern of elementary matrices) is an interface in E-SURGE used to specify transitions among states and events (Choquet *et al*. 2009). Estimated parameters were assigned with alphabetical letters, "-" indicates that the corresponding parameter was set to 0, and "*" means (1 - Σ (all other parameters on the same row)). There was always only one "*" per row.

References

Choquet, R. et al. R. 2009. Program E-SURGE: a software application for fitting multievent models. – In: Thomson D. L. et al. (eds), Modeling demographic processes in marked populations. Springer, pp. 845–865.

Lloyd, K. J. et al. 2020. Tradeoffs between age-related breeding improvement and survival senescence in highly polygynous elephant seals: dominant males always do better. – J. Anim. Ecol. 89: 897–909.

Pledger, S. et al. 2003. Open capture-recapture models with heterogeneity: I. Cormack-Jolly-Seber model. – Biometrics 59: 786–794.

Schaub, M. et al. 2004. Estimating survival and temporary emigration in the multistate capture–recapture framework. – Ecology 85: 2107–2113.

GEPAT matrices (in order of appearance in the interface)

Group assignment matrix:

Group1	Group2
π^{ind}	*

Initial breeding state and number of tags matrix:

	PB1-T2	PB1-T1	PB2-T2	PB2-T1	PBAE 1-T2	PBAE 2-T2	PBAE 1-T1	PBAE 2-T1	SB2	SB1	DB2	DB1
Group 1	π^{tag}	*	-	-	-	-	-	-	-	-	-	-
Group 2	-	-	π^{tag}	*	-	-	-	-	-	-	-	-

First tag loss matrix:

	PB1-T2	PB1-T1	PB2-T2	PB2-T1	PBAE1-T2	PBAE1-T1	PBAE2-T2	PBAE2-T1	SB2	SB1	DB2	DB1	Dead
PB1-T2	*	τ^{2-1}	-	-	-	-	-	-	-	-	-	-	-
PB1-T1	-	*	-	-	-	-	-	-	-	-	-	-	-
PB2-T2	-	-	*	τ^{2-1}	-	-	-	-	-	-	-	-	-
PB2-T1	-	-	-	*	-	-	-	-	-	-	-	-	-
PBAE1-T2	-	-	-	-	*	τ^{2-1}	-	-	-	-	-	-	-
PBAE1-T1	-	-	-	-	-	*	-	-	-	-	-	-	-
PBAE2-T2	-	-	-	-	-	-	*	τ^{2-1}	-	-	-	-	-
PBAE2-T1	-	-	-	-	-	-	-	*	-	-	-	-	-
SB2	-	-	-	-	-	-	-	-	*	τ^{2-1}	-	-	-
SB1	-	-	-	-	-	-	-	-	-	*	-	-	-
DB2	-	-	-	-	-	-	-	-	-	-	*	τ^{2-1}	-
DB1	-	-	-	-	-	-	-	-	-	-	-	*	-
Dead	-	-	-	-	-	-	-	-	-	-	-	-	*

Second tag loss matrix:

	PB1-T2	PB1-T1	PB2-T2	PB2-T1	PBAE1-T2	PBAE1-T1	PBAE2-T2	PBAE2-T1	SB2	SB1	DB2	DB1	Dead
PB1-T2	*	-	-	-	-	-	-	-	-	-	-	-	-
PB1-T1	-	*	-	-	-	-	-	-	-	-	-	-	τ^{1-0}
PB2-T2	-	-	*	-	-	-	-	-	-	-	-	-	-
PB2-T1	-	-	-	*	-	-	-	-	-	-	-	-	τ^{1-0}
PBAE1-T2	-	-	-	-	*	-	-	-	-	-	-	-	-
PBAE1-T1	-	-	-	-	-	*	-	-	-	-	-	-	τ^{1-0}
PBAE2-T2	-	-	-	-	-	-	*	-	-	-	-	-	-
PBAE2-T1	-	-	-	-	-	-	-	*	-	-	-	-	τ^{1-0}
SB2	-	-	-	-	-	-	-	-	*	-	-	-	-
SB1	-	-	-	-	-	-	-	-	-	*	-	-	τ^{1-0}
DB2	-	-	-	-	-	-	-	-	-	-	*	-	-
DB1	-	-	-	-	-	-	-	-	-	-	-	*	τ^{1-0}
Dead	-	-	-	-	-	-	-	-	-	-	-	-	*

Survival matrix:

	PB1-T2	PB1-T1	PB2-T2	PB2-T1	PBAE1-T2	PBAE1-T1	PBAE2-T2	PBAE2-T1	SB 2	SB 1	DB 2	DB 1	Dead
PB1-T2	φ	-	-	-	-	-	-	-	-	-	-	-	*
PB1-T1	-	φ	-	-	-	-	-	-	-	-	-	-	*
PB2-T2	-	-	φ	-	-	-	-	-	-	-	-	-	*
PB2-T1	-	-	-	φ	-	-	-	-	-	-	-	-	*
PBAE1-T2	-	-	-	-	φ	-	-	-	-	-	-	-	*
PBAE1-T1	-	-	-	-	-	φ	-	-	-	-	-	-	*
PBAE2-T2	-	-	-	-	-	-	φ	-	-	-	-	-	*
PBAE2-T1	-	-	-	-	-	-	-	φ	-	-	-	-	*
SB2	-	-	-	-	-	-	-	-	φ	-	-	-	*
SB1	-	-	-	-	-	-	-	-	-	φ	-	-	*
DB2	-	-	-	-	-	-	-	-	-	-	φ	-	*
DB1	-	-	-	-	-	-	-	-	-	-	-	φ	*
Dead	-	-	-	-	-	-	-	-	-	-	-	-	*

Breeding matrix (representing recruitment and future breeding state):

	PB1-T2	PB1-T1	PB2-T2	PB2-T1	PBAE1-T2	PBAE1-T1	PBAE2-T2	PBAE2-T1	SB 2	SB 1	DB 2	DB 1	Dead
PB1-T2	*	-	-	-	-	-	-	-	ψ	-	ψ	-	-
PB1-T1	-	*	-	-	-	-	-	-	-	ψ	-	ψ	-
PB2-T2	-	-	*	-	-	-	-	-	ψ	-	ψ	-	-
PB2-T1	-	-	-	*	-	-	-	-	-	ψ	-	ψ	-
PBAE1-T2	-	-	-	-	*	-	-	-	ψ	-	ψ	-	-
PBAE1-T1	-	-	-	-	-	*	-	-	-	ψ	-	ψ	-
PBAE2-T2	-	-	-	-	-	-	*	-	ψ	-	ψ	-	-
PBAE2-T1	-	-	-	-	-	-	-	*	-	ψ	-	ψ	-
SB2	-	-	-	-	-	-	-	-	*	-	ψ	-	-
SB1	-	-	-	-	-	-	-	-	-	*	-	ψ	-
DB2	-	-	-	-	-	-	-	-	*	-	ψ	-	-
DB1	-	-	-	-	-	-	-	-	-	*	-	ψ	-
Dead	-	-	-	-	-	-	-	-	-	-	-	-	*

Temporary migration matrix:

	PB1-T2	PB1-T1	PB2-T2	PB2-T1	PBAE1-T2	PBAE1-T1	PBAE2-T2	PBAE2-T1	SB2	SB1	DB2	DB1	Dead
PB1-T2	*	-	-	-	ψ^E	-	-	-	-	-	-	-	-
PB1-T1	-	*	-	-	-	ψ^E	-	-	-	-	-	-	-
PB2-T2	-	-	*	-	-	-	ψ^E	-	-	-	-	-	-
PB2-T1	-	-	-	*	-	-	-	ψ^E	-	-	-	-	-
PBAE1-T2	ψ^I	-	-	-	*	-	-	-	-	-	-	-	-
PBAE1-T1	-	ψ^I	-	-	-	*	-	-	-	-	-	-	-
PBAE2-T2	-	-	ψ^I	-	-	-	*	-	-	-	-	-	-
PBAE2-T1	-	-	-	ψ^I	-	-	-	*	-	-	-	-	-
SB2	-	-	-	-	-	-	-	-	*	-	-	-	-
SB1	-	-	-	-	-	-	-	-	-	*	-	-	-
DB2	-	-	-	-	-	-	-	-	-	-	*	-	-
DB1	-	-	-	-	-	-	-	-	-	-	-	*	-
Dead	-	-	-	-	-	-	-	-	-	-	-	-	*

Detection matrix:

NS – Not seen

	NS	PB2	PB1	SB2	SB1	DB2	DB1
PB1-T2	*	p	-	-	-	-	-
PB1-T1	*	-	p	-	-	-	-
PB2-T2	*	p	-	-	-	-	-
PB2-T1	*	-	p	-	-	-	-
PBAE1-T2	*	-	-	-	-	-	-
PBAE1-T1	*	-	-	-	-	-	-
PBAE2-T2	*	-	-	-	-	-	-
PBAE2-T1	*	-	-	-	-	-	-
SB2	*	-	-	p	-	-	-
SB1	*	-	-	-	p	-	-
DB2	*	-	-	-	-	p	-
DB1	*	-	-	-	-	-	p
Dead	*	-	-	-	-	-	-

Breeding state assignment matrix:

Column headings represent events.

	0	1	2	3	4	5	6	7	8
NS	*	-	-	-	-	-	-	-	-
PB2	-	*	-	-	-	-	-	-	-
PB1	-	-	*	-	-	-	-	-	-
SB2	-	-	-	δ	-	-	-	*	-
SB1	-	-	-	-	δ	-	-	-	*
DB2	-	-	-	-	-	δ	-	*	-
DB1	-	-	-	-	-	-	δ	-	*

Appendix 3

Specifying model constraints (in order of appearance in Results)

Survival (φ) and Recruitment (ψ)

The analysis of pre-breeder survival and recruitment probabilities considered hidden states, representing robust and frail individuals, and deterministic changes in age. In addition, recruitment probabilities always depended on breeding state (i.e. the transition to subordinate and dominant breeder states) given the results of Lloyd et al. (2020). The majority of pre-breeders that survived from age 7 to 8 recruited to the breeding population, with only 14 pre-breeders recorded at age 8 and 1 pre-breeder at age 9. Age classes were lumped at ages ≥6 for survival and ages ≥8 for recruitment as there was a large enough sample size to estimate recruitment at age 7, but not survival. Robust and frail pre-breeder survival at age 0 was correlated with group assignment and so could not be estimated. Therefore, first-year survival was constrained to be equal between robust and frail pre-breeders in the base model, meaning that only heterogeneity remaining in the population at age 1 was considered (Fay et al. 2018). The first candidate set of models tested if groups differed in survival and recruitment probabilities (i.e. presence of individual heterogeneity), whilst treating age variation as a fixed effect (assuming the parameters to be different and independent of each other at every age). The second candidate set of models investigated at what age observed differences in survival and recruitment probabilities between groups became apparent or disappeared (i.e. onset age of individual heterogeneity detection and disappearance). This was done by constructing models independent of hidden states at various ages. Survival models testing for the onset of individual heterogeneity expression at older ages (4, 5 and ≥6) did not converge. The third candidate set of models tested hypotheses developed by van de Pol and Verhulst (2006) and modified by Hamel et al. (2018) for identifying within- and between-individual changes in heterogeneity (i.e. trends in individual heterogeneity with age). Age variation in survival and recruitment was treated as a continuous logit-linear relationship (1) with different intercepts and slopes between groups (testing for changes in individual heterogeneity between groups); (2) with different intercepts and equal slopes between groups (testing for ontogenetic processes, or selection and ontogenetic processes depending on the population response); and (3) with different intercepts but no slope between groups (testing for selection processes only). To determine the population response, the most parsimonious survival and recruitment models were run without hidden states.

Table A1. Candidate list of survival (φ) models with a description of the tested hypothesis. Southern elephant seals at Marion Island were assigned to hidden states (PB1 and PB2) when entering the marked population at weaning. Superscripts and subscripts indicate variation or equality between pre-breeder groups and among age classes (a).

Model	Parameters	Hypothesis
	Survival (φ) – presence of individual heterogeneity	
1	$\varphi_{\mathrm{a}\ 0}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 1,2,3,4,5,\geq 6}^{\mathrm{PB1\neq PB2}}$	Different survival probabilities between groups (expressed from age 1) with age variation treated as a fixed effect.
2	$\varphi_{\mathrm{a}\ 0,1,2,3,4,5,\geq 6}^{\mathrm{PB1=PB2}}$	Equal survival probabilities between groups with age variation treated as a fixed effect.
3	$\varphi_{\mathrm{cst}}^{\mathrm{PB1\neq PB2}}$	Different survival probabilities between groups with no age variation.
4	$\varphi_{\mathrm{cst}}^{\mathrm{PB1=PB2}}$	Equal survival probabilities between groups with no age variation. Null model
	Survival (φ) – onset age of individual heterogeneity detection and disappearance	
5	$\varphi_{\mathrm{a}\ 0,1}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 2,3,4,5,\geq 6}^{\mathrm{PB1\neq PB2}}$	Differences in survival probabilities between groups expressed from age 2.
6	$\varphi_{\mathrm{a}\ 0,1,2}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 3,4,5,\geq 6}^{\mathrm{PB1\neq PB2}}$	Differences in survival probabilities between groups expressed from age 3.
7	$\varphi_{\mathrm{a}\ 0,1,2,3}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 4,5,\geq 6}^{\mathrm{PB1\neq PB2}}$	Differences in survival probabilities between groups expressed from age 4.
8	$\varphi_{\mathrm{a}\ 0}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 1,2,3,4,5}^{\mathrm{PB1\neq PB2}}$ $+ \varphi_{\mathrm{a}\ \geq 6}^{\mathrm{PB1=PB2}}$	Differences in survival probabilities between groups disappear from age 6.
9	$\varphi_{\mathrm{a}\ 0}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 1,2,3,4}^{\mathrm{PB1\neq PB2}}$ $+ \varphi_{\mathrm{a}\ 5,\geq 6}^{\mathrm{PB1=PB2}}$	Differences in survival probabilities between groups disappear from age 5.
10	$\varphi_{\mathrm{a}\ 0}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 1,2,3}^{\mathrm{PB1\neq PB2}}$ $+ \varphi_{\mathrm{a}\ 4,5,\geq 6}^{\mathrm{PB1=PB2}}$	Differences in survival probabilities between groups disappear from age 4.
	Survival (φ) – trends in individual heterogeneity with age	
11	$\varphi_{\mathrm{a}\ 0,1}^{\mathrm{PB1=PB2}}$ $+ \varphi_{\mathrm{a}\ \mathbf{2,3,4,5},\geq \mathbf{6}(\mathrm{linear}^{\mathrm{PB1\neq PB2}})}^{\mathrm{PB1\neq PB2}}$	Age variation treated as a logit-linear relationship from age 2 with different intercepts and slopes between groups. Variance changes between groups (Fig. 1G, H).
12	$\varphi_{\mathrm{a}\ 0,1}^{\mathrm{PB1=PB2}}$ $+ \varphi_{\mathrm{a}\ \mathbf{2,3,4,5},\geq \mathbf{6}(\mathrm{linear}^{\mathrm{PB1=PB2}})}^{\mathrm{PB1\neq PB2}}$	Age variation treated as a logit-linear relationship from age 2 with different intercepts and equal slopes between groups. Ontogenetic processes (Fig. 1A, B), or selection and ontogenetic processes (Fig. 1E, F).
13	$\varphi_{\mathrm{a}\ 0,1}^{\mathrm{PB1=PB2}} + \varphi_{\mathrm{a}\ 2:\geq 6}^{\mathrm{PB1\neq PB2}}$	Different survival probabilities between groups from age 2 with no age variation. Selection processes only (Fig. 1C, D).

Table A2. Candidate list of recruitment (ψ) models with a description of the tested hypothesis. Southern elephant seals at Marion Island were assigned to hidden states (PB1 and PB2) when entering the marked population at weaning. Superscripts and subscripts indicate variation or equality between first-time subordinate breeder groups (PB1-SB and PB2-SB), between first-time dominant breeder groups (PB1-DB and PB2-DB), and among age classes (a).

Model	**Parameters**	**Hypothesis**
	Recruitment (ψ) – presence of individual heterogeneity	
14	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5,6,7,\geq 8} + \psi^{\mathrm{PB1-DB\neq PB2-DB}}_{\mathrm{a}\ 6,7,\geq 8}$	Different recruitment probabilities between groups of first-time subordinate and dominant breeders.
15	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5,6,7,\geq 8} + \psi^{\mathrm{PB1-DB=PB2-DB}}_{\mathrm{a}\ 6,7,\geq 8}$	Different recruitment probabilities between groups of first-time subordinate but not dominant breeders.
16	$\psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ 5,6,7,\geq 8} + \psi^{\mathrm{PB1-DB\neq PB2-DB}}_{\mathrm{a}\ 6,7,\geq 8}$	Different recruitment probabilities between groups of first-time dominant but not subordinate breeders.
17	$\psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ 5,6,7,\geq 8} + \psi^{\mathrm{PB1-DB=PB2-DB}}_{\mathrm{a}\ 6,7,\geq 8}$	Equal recruitment probabilities between groups of first-time subordinate and dominant breeders. Null model.
	Recruitment (ψ) – onset age of individual heterogeneity detection and disappearance	
18	$\psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ 5} + \psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 6,7,\geq 8}$	Differences in recruitment probabilities between groups expressed from age 6.
19	$\psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ 5,6} + \psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 7,\geq 8}$	Differences in recruitment probabilities between groups expressed from age 7.
20	$\psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ 5,6,7} + \psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ \geq 8}$	Differences in recruitment probabilities between groups expressed from age 8.
21	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5,6,7} + \psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ \geq 8}$	Differences in recruitment probabilities between groups disappear from age 8.
22	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5,6} + \psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ 7,\geq 8}$	Differences in recruitment probabilities between groups disappear from age 7.
23	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5} + \psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ 6,7,\geq 8}$	Differences in recruitment probabilities between groups disappear from age 6.
	Recruitment (ψ) – trends in individual heterogeneity with age	
24	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5,6,7(\mathrm{linear}^{\mathrm{PB1-SB\neq PB2-SB}})} + \psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ \geq 8}$	Age variation treated as a logit-linear relationship up to age 7 with different intercepts and slopes between groups. Variance changes between groups (Fig. 1G, H).
25	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5,6,7(\mathrm{linear}^{\mathrm{PB1-SB=PB2-SB}})} + \psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ \geq 8}$	Age variation treated as a logit-linear relationship up to age 7 with different intercepts and equal slopes between groups. Ontogenetic processes (Fig. 1A, B), or selection and ontogenetic processes (Fig. 1E, F).
26	$\psi^{\mathrm{PB1-SB\neq PB2-SB}}_{\mathrm{a}\ 5:7} + \psi^{\mathrm{PB1-SB=PB2-SB}}_{\mathrm{a}\ \geq 8}$	Different recruitment probabilities between groups up to age 7 with no age variation. Selection processes only (Fig. 1C, D).

Group assignment (π^{ind}*)*: Assignment as a robust or frail individual was further explored upon detecting individual heterogeneity in pre-breeder survival, recruitment and detection probabilities. Correlations between group assignment probabilities and various time- and density-related covariates were investigated.

Table A3. Candidate list of group assignment (π^{ind}) models with a description of the tested hypothesis. Southern elephant seals at Marion Island were assigned to hidden states when entering the marked population at weaning. Subscripts indicate time- and density-related covariates.

Model	**Parameters**	**Hypothesis**
27	π_{cst}	Group assignment probability constant. Null model.
28	$\pi_{\mathrm{cohort\ year}}$	Group assignment probabilities vary annually. This serves as a proxy for any annual variation in environmental effects.
29	$\pi_{1983:1997,1998:2009}$	Group assignment probabilities vary between 1983-1997 (population decrease) and 1998-2009 (population increase; Pistorius *et al*. 2011).
30	$\pi_{\mathrm{cohort\ size}}$	Group assignment probabilities depend on cohort size (number of pups produced per breeding season).
31	$\pi_{\mathrm{cohort\ sex\ ratio}}$	Group assignment probabilities depend on cohort sex ratio (proportion of male to female pups; Trivers-Willard hypothesis; Trivers and Willard 1973).

Detection (p): Resight abilities may differ among field researchers, which would result in detection differences among years. Seals grouped according to a particular state may behave more similarly than seals of another state. These behavioural differences may translate into different detection probabilities. However, subordinate and dominant breeders likely have the same detection probabilities given the results of Lloyd *et al*. (2020). Individuals with one tag are less likely to be resighted as a marked animal than individuals with two tags. Therefore, detection models were structured according to year, state (hidden and breeding) and number of tags.

Table A4. Candidate list of detection (p) models with a description of the tested hypothesis. Southern elephant seals at Marion Island were assigned to hidden states (PB1 and PB2) when entering the marked population at weaning. Superscripts and subscripts indicate variation or equality among pre-breeder (PB), subordinate breeder (SB) and dominant breeder (DB) states, pre-breeders with two tags (T2) and one tag (T1), and years (t).

Model	Parameters	Hypothesis
32	$p_{\mathrm{t\ 1984-2016}}^{\mathrm{PB1=PB2=SB=DB}}$	Differences in detection probabilities across years but not among breeding states, hidden states and number of tags.
33	$p_{\mathrm{cst}}^{\mathrm{PB1-T2\neq PB1-T1\neq PB2-T2\neq PB2-T1\neq SB=DB}}$	Differences in detection probabilities among breeding states, hidden states and number of tags but not years.
34	$p_{\mathrm{cst}}^{\mathrm{PB1\neq PB2\neq SB=DB}}$	Differences in detection probabilities among breeding states and hidden states but not number of tags and years.
35	$p_{\mathrm{cst}}^{\mathrm{PB1=PB2\neq SB=DB}}$	Differences in detection probabilities among breeding states but not hidden states, number of tags and years.
36	$p_{\mathrm{cst}}^{\mathrm{PB1=PB2=SB=DB}}$	Equal detection probabilities among breeding states, hidden states, number of tags and years. Null model.

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Appendix 4

Projecting the population model

Age- and stage-structured population matrix $\boldsymbol{A}$ assumed a post-breeding census and annual projection interval for male elephant seals (Appendix 4 Table A1). As this was a single-sex matrix, individuals entered the matrix at weaning (age 0) without replacement (i.e. no fertility estimates). The pre-breeder (PB) component was age structured from age 0 to 7, with recruitment to the subordinate (PB–SB) and dominant (PB–DB) breeder states starting at age 5 and 6, respectively. Pre-breeders that did not recruit by age 8 were removed from the matrix (i.e. 0 survival probability from age 7 to age 8), as only n = 14 pre-breeders were recorded at age 8 in the observed population (Lloyd et al. 2020). The subordinate breeder (SB) component was age structured from age 5 to 11 and the dominant breeder (DB) component from age 6 to 11. Subordinate breeders could become dominant (SB–DB) from age 6, whilst dominant breeders could lose their status and become subordinate (1 – DB–DB) from age 7. Diagonal elements represented the probability of surviving (φ) and remaining in the same breeding state ($1 - \psi$). Sub-diagonal elements represented the probability of surviving (φ) and transitioning (ψ) to a different breeding state. Probabilities were derived from estimates of the most parsimonious survival and recruitment (including future breeding state) models from this study. Two separate population matrices were constructed for robust and frail pre-breeders. A total of 260 pups (average number of male pups produced annually from 1985 to 2016 assuming a 1:1 sex ratio; Pistorius et al. 2011) were divided between matrices according to the group assignment probability (π^{ind}) estimated in model 27 (Appendix 3 Table A3). The population matrix was projected in R ver. 3.5.2 (<www.r-project.org>).

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Table A1. Single-sex population matrix for male southern elephant seals at Marion Island. Matrix elements comprise survival (φ) and recruitment/breeding (ψ) probability estimates derived from the most parsimonious finite-mixture multievent models (Table 2). Superscripts represent pre-breeder (PB), subordinate breeder (SB) and dominant breeder (DB) states, whilst subscripts represent age classes.

$$\left[\begin{matrix}
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\varphi_0^{PB} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \varphi_1^{PB} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \varphi_2^{PB} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \varphi_3^{PB} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \varphi_4^{PB}(1 - \psi_5^{PB-SB}) & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \varphi_5^{PB}(1 - \psi_6^{PB-SB})(1 - \psi_6^{PB-DB}) & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \varphi_6^{PB}(1 - \psi_7^{PB-SB})(1 - \psi_7^{PB-DB}) & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \varphi_4^{PB}\psi_5^{PB-SB} & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \varphi_5^{PB}\psi_6^{PB-SB} & 0 & 0 & \varphi_5^{SB}(1 - \psi_6^{SB-DB}) & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \varphi_6^{PB}\psi_7^{PB-SB} & 0 & 0 & \varphi_6^{SB}(1 - \psi_7^{SB-DB}) & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \varphi_7^{PB}\psi_8^{PB-SB} & 0 & 0 & \varphi_7^{SB}(1 - \psi_8^{SB-DB}) \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \varphi_5^{PB}\psi_6^{PB-DB} & 0 & 0 & \varphi_5^{SB}\psi_6^{SB-DB} & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \varphi_6^{PB}\psi_7^{PB-DB} & 0 & 0 & \varphi_6^{SB}\psi_7^{SB-DB} & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \varphi_7^{PB}\psi_8^{PB-DB} & 0 & 0 & \varphi_7^{SB}\psi_8^{SB-DB} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{matrix}\right.$$

$$
\left.\begin{matrix}
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \varphi_{6}^{\mathrm{DB}}(1 - \psi_{7}^{\mathrm{DB-DB}}) & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \varphi_{7}^{\mathrm{DB}}(1 - \psi_{8}^{\mathrm{DB-DB}}) & 0 & 0 & 0 & 0 \\
\varphi_{8}^{\mathrm{SB}}(1 - \psi_{9}^{\mathrm{SB-DB}}) & 0 & 0 & 0 & 0 & 0 & \varphi_{8}^{\mathrm{DB}}(1 - \psi_{9}^{\mathrm{DB-DB}}) & 0 & 0 & 0 \\
0 & \varphi_{9}^{\mathrm{SB}}(1 - \psi_{10}^{\mathrm{SB-DB}}) & 0 & 0 & 0 & 0 & 0 & \varphi_{9}^{\mathrm{DB}}(1 - \psi_{10}^{\mathrm{DB-DB}}) & 0 & 0 \\
0 & 0 & \varphi_{10}^{\mathrm{SB}}(1 - \psi_{11}^{\mathrm{SB-DB}}) & 0 & 0 & 0 & 0 & 0 & \varphi_{10}^{\mathrm{DB}}(1 - \psi_{11}^{\mathrm{DB-DB}}) & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \varphi_{6}^{\mathrm{DB}}(\psi_{7}^{\mathrm{DB-DB}}) & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \varphi_{7}^{\mathrm{DB}}(\psi_{8}^{\mathrm{DB-DB}}) & 0 & 0 & 0 & 0 \\
\varphi_{8}^{\mathrm{SB}}\psi_{9}^{\mathrm{SB-DB}} & 0 & 0 & 0 & 0 & 0 & \varphi_{8}^{\mathrm{DB}}(\psi_{9}^{\mathrm{DB-DB}}) & 0 & 0 & 0 \\
0 & \varphi_{9}^{\mathrm{SB}}\psi_{10}^{\mathrm{SB-DB}} & 0 & 0 & 0 & 0 & 0 & \varphi_{9}^{\mathrm{DB}}(\psi_{10}^{\mathrm{DB-DB}}) & 0 & 0 \\
0 & 0 & \varphi_{10}^{\mathrm{SB}}\psi_{11}^{\mathrm{SB-DB}} & 0 & 0 & 0 & 0 & 0 & \varphi_{10}^{\mathrm{DB}}(\psi_{11}^{\mathrm{DB-DB}}) & 0
\end{matrix}\right]
$$

Appendix 5

Additional results

Table A1. Finite-mixture models for detection probabilities (p) of male southern elephant seals at Marion Island. Pre-breeders were assigned to hidden states (PB1 and PB2) when entering the marked population at weaning. Superscripts and subscripts indicate variation or equality among pre-breeder (PB), subordinate breeder (SB) and dominant breeder (DB) states, number of tags (-T2 and -T1) and years (t). Small sample corrected quasi-likelihood Akaike's information criterion (QAIC$_c$; $\hat{c} = 1.7$) was used to select models, with the following measurements: ΔQAIC$_c$ (the difference in QAIC$_c$ between the model with the lowest QAIC$_c$ value and the relevant model), ω_i (Akaike weight), K (number of parameters), Deviance (-2 multiplied by log likelihood). The model in bold font was used to derive estimates.

Model	Parameters	ΔQAIC$_c$	ω_i	K	Deviance
32	$p^{\mathrm{PB1=PB2=SB=DB}}_{\mathrm{t\ 1984-2016}}$	346.95	0.00	67	290.99
33	$\boldsymbol{p^{\mathrm{PB1-T2\neq PB1-T1\neq PB2-T2\neq PB2-T1\neq SB=DB}}_{\mathrm{cst}}}$	**0.00**	**1.00**	**48**	**398.95**
34	$p^{\mathrm{PB1\neq PB2\neq SB=DB}}_{\mathrm{cst}}$	15.96	0.00	45	425.90
35	$p^{\mathrm{PB1=PB2\neq SB=DB}}_{\mathrm{cst}}$	366.91	0.00	36	542.12
36	$p^{\mathrm{PB1=PB2=SB=DB}}_{\mathrm{cst}}$	368.00	0.00	35	557.64

Detection probabilities were dependent on hidden states and breeding states, as well as number of tags (model 33, Appendix 5 Table A1). Robust pre-breeders with two tags (0.97; CI: 0.96, 0.98) and one tag (0.97; CI: 0.94, 0.98) were more likely to be detected than frail pre-breeders with two tags (0.41; CI: 0.34, 0.48) and one tag (0.17; CI: 0.10, 0.28). Subordinate and dominant breeders had a high detection probability (0.95; CI: 0.90, 0.97) similar to robust pre-breeders.

Table A2. Parameter estimates (maximum likelihood estimate with 95% confidence intervals) on the logit scale of the most parsimonious survival (φ, model 12), recruitment (ψ, model 21), group assignment (π^{ind}, model 30) and detection (p, model 33) models. Superscripts indicate pre-breeder (PB1 – robust, PB2 – frail), subordinate breeder (SB) and dominant breeder (DB) states, and number of tags (T2 – two tags, T1 – one tag). Subscripts indicate specific ages (a) or regression parameters.

Parameters	**Estimate**	**Lower 95% confidence interval**	**Upper 95% confidence interval**
Survival (φ)			
$\varphi_{\mathrm{a\,0}}^{\mathrm{PB1=PB2}}$	0.47	0.33	0.60
$\varphi_{\mathrm{a\,1}}^{\mathrm{PB1=PB2}}$	1.34	1.16	1.52
$\varphi_{\mathrm{intercept}}^{\mathrm{PB1}}$	1.02	0.89	1.14
$\varphi_{\mathrm{intercept}}^{\mathrm{PB2}}$	-0.19	-0.40	0.02
$\varphi_{\mathrm{slope}}^{\mathrm{PB1=PB2}}$	-0.15	-0.24	-0.05
Recruitment (ψ)			
$\psi_{\mathrm{a\,5}}^{\mathrm{PB1-SB}}$	-3.60	-4.26	-2.95
$\psi_{\mathrm{a\,6}}^{\mathrm{PB1-SB}}$	-1.39	-1.72	-1.06
$\psi_{\mathrm{a\,7}}^{\mathrm{PB1-SB}}$	0.44	0.05	0.82
$\psi_{\mathrm{a\,5}}^{\mathrm{PB2-SB}}$	-69.17	-69.17	-69.17
$\psi_{\mathrm{a\,6}}^{\mathrm{PB2-SB}}$	-2.12	-3.65	-0.58
$\psi_{\mathrm{a\,7}}^{\mathrm{PB2-SB}}$	-2.47	-6.49	1.56
$\psi_{\mathrm{a\,\geq 8}}^{\mathrm{PB1-SB=PB2-SB}}$	0.75	-0.02	1.52
$\psi_{\mathrm{a\,6}}^{\mathrm{PB1-DB=PB2-DB}}$	-3.32	-4.04	-2.59
$\psi_{\mathrm{a\,7}}^{\mathrm{PB1-DB=PB2-DB}}$	-1.42	-2.04	-0.81
$\psi_{\mathrm{a\,\geq 8}}^{\mathrm{PB1-DB=PB2-DB}}$	-0.06	-0.96	0.85
Group assignment (π^{ind})			
$\pi_{\mathrm{intercept}}^{\mathrm{ind}}$	0.24	0.07	0.42
$\pi_{\mathrm{slope}}^{\mathrm{ind}}$	-0.20	-0.33	-0.07
Detection (p)			
$p_{\mathrm{cst}}^{\mathrm{PB1-T2}}$	3.52	3.08	3.95
$p_{\mathrm{cst}}^{\mathrm{PB1-T1}}$	3.40	2.67	4.13
$p_{\mathrm{cst}}^{\mathrm{PB2-T2}}$	-0.37	-0.66	-0.08
$p_{\mathrm{cst}}^{\mathrm{PB2-T1}}$	-1.57	-2.19	-0.95
$p_{\mathrm{cst}}^{\mathrm{SB=DB}}$	2.87	2.19	3.54