

Supplementary Appendix 1

Goodness of Fit Tests

Here, we explain our reasoning in exploring the raw encounter histories for resights of southern elephant seals from Macquarie Island that were captured as part of a long-term demographic study from 1993-1999.

Observations were transformed into single-state format encounter histories, creating a string of ones and zeros for each individual ('1' indicating the animal was encountered at any time during a given year, and '0' indicating the individual was not encountered). The first encounter was removed, as per Pradel, Gimenez, and Lebreton (2005). Males and females were grouped and analysed separately, based on prior research and biological knowledge of shared traits in polygynous and sexually dimorphic species.

Our set of candidate models included time- and age-dependent models as well as a fully saturated model with three interaction terms (sex; age and time varying annually).

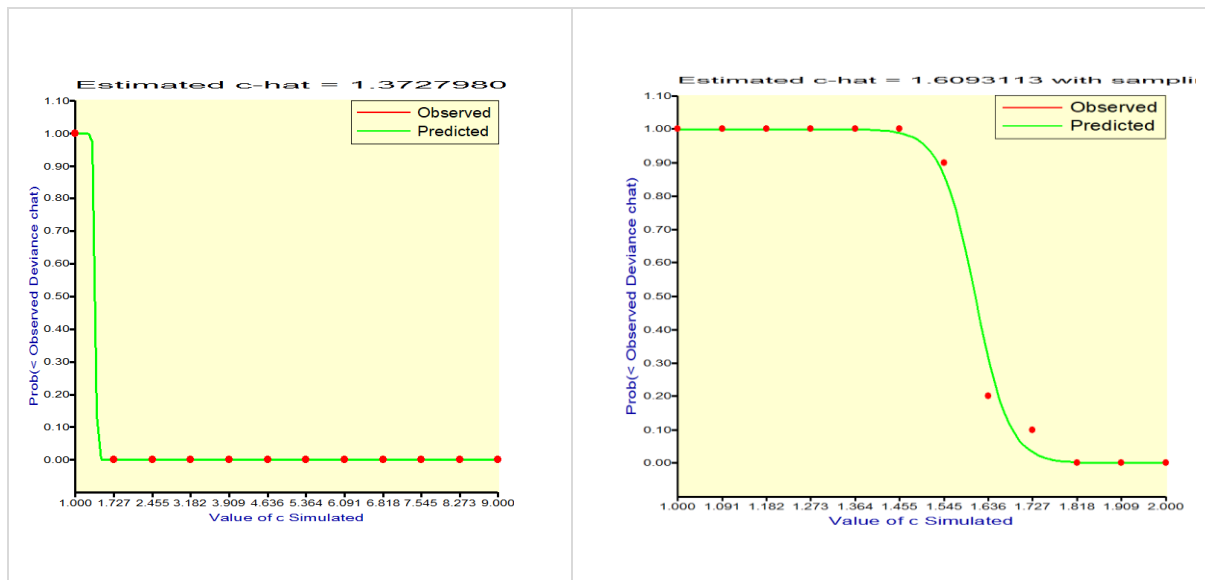
Models were created with RMark package (Laake 2013) in R Version 4.2.1 (R Core Team 2022) with RStudio 2022.07.01 (RStudio Team 2022). The global model results were extracted to MARK ver. 9.0 (White & Burnham 1999) to run goodness of fit tests via c-hat simulation. Results output below:

Median $\hat{c}$

Median $\hat{c}$ is calculated the global (or most parameter saturated) model (Cooch & White 2002), which in our case is the model of the structure $\Phi(\sim \text{time} * \text{SEX} * \text{age})$ $p(\sim \text{time} * \text{SEX})$.

The observed deviance for this model is 8.54.

First simulation run	Second simulation run
Lower bound: 1; Upper bound: 9	Lower bound: 1; Upper bound: 2
10 intermediate steps, 10 repetitions at each step	10 intermediate steps, 10 repetitions at each step
Estimated c-hat = 1.3727980	Estimated c-hat = 1.6093113
Sampling SE = 0.0000000	Sampling SE = 0.0178009
95% Conf. Interval = 1.3192321 to 1.4263639	95% Conf. Interval = 1.4822936 to 1.7363289
One-sided 95% Upper Bound = 1.4158494	One-sided 95% Upper Bound = 1.7113966



References

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